

Background

CMR cine and tagging sequences are typically used for quantifying global and regional cardiac functions, respectively. Nevertheless, the need for acquiring additional tagged images and using special software packages for tagged images analysis contributes to longer and more expensive CMR exam. The CMR feature tracking technique has been proposed to generate regional cardiac function measures from cine images, although the lack of intramyocardial markers poses a limitation of the technique compared to conventional CMR tagging. In this study, we developed a deep neural network algorithm for extracting regional cardiac function parameters from the cine images after the network is trained on corresponding gold-standard tagged images.

Methods

The developed algorithm (**Figure 1**) is based on image-to-image translation using generative adversarial network (GAN) to generate the myocardial displacement fields from cine images. During the training phase, the inputs of the network are: 1) cine difference images, generated by subtracting consecutive cine images using a fine-tuned segmentation U-net; and 2) corresponding tagged images acquired of the same slice and cardiac phases. The target image of the network is the corresponding gold-standard myocardial displacement field generated by analyzing the tagged image using the SinMod method. We used a dataset of 1134 images acquired from rats scanned on a 9.4T Bruker MRI scanner, where 1114 images were used for training and 20 were used for testing. Bland-Altman plots, student's t-test, and correlation analysis were conducted to compare the generated displacement fields, on a segmental basis, against the gold-standard measurements generated from the tagged images.

	Target	Output
Radial strain	34.92 ± 2.1	33.44 ± 2.8
Circumferential strain	-28.61 ± 3.2	-29.50 ± 1.6

Table 1. Mean \pm standard deviation in radial and circumferential strains are shown from the test datasets. Target values are from tagged images and output values are from cine images by the developed network. Student t-test showed insignificant differences between all paired strain measurements ($p > 0.05$).

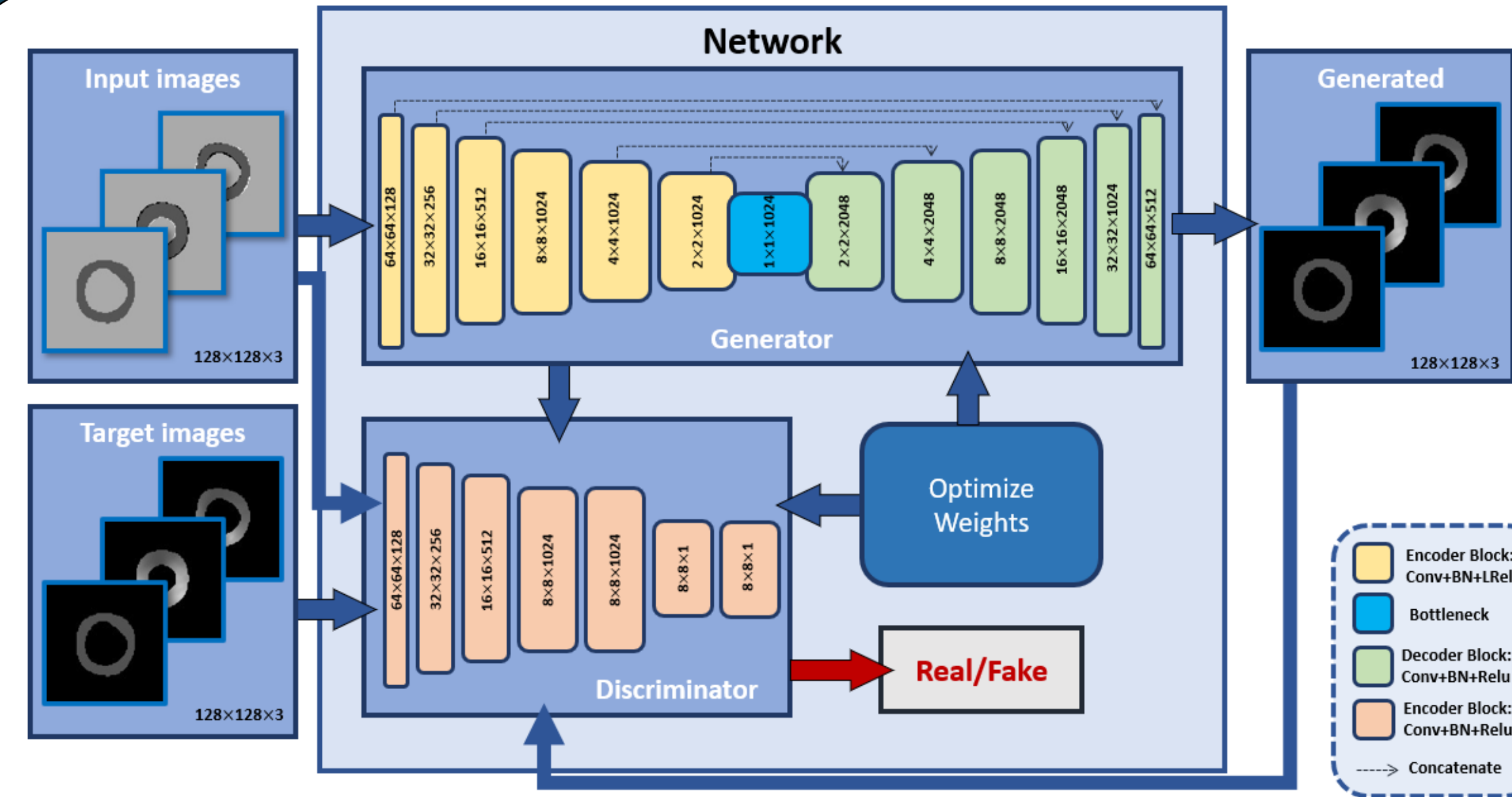


Figure 1. The developed network is a modified version of image-to-image translation network, which is adjusted and tuned to the tagged image analysis task while minimizing noise. The input consists of endo- and epicardium contours generated by subtracting consecutive cine images. The target is corresponding strain map. The generator creates strain images to fool the discriminator until the discriminator decides that the generated strain maps are real.

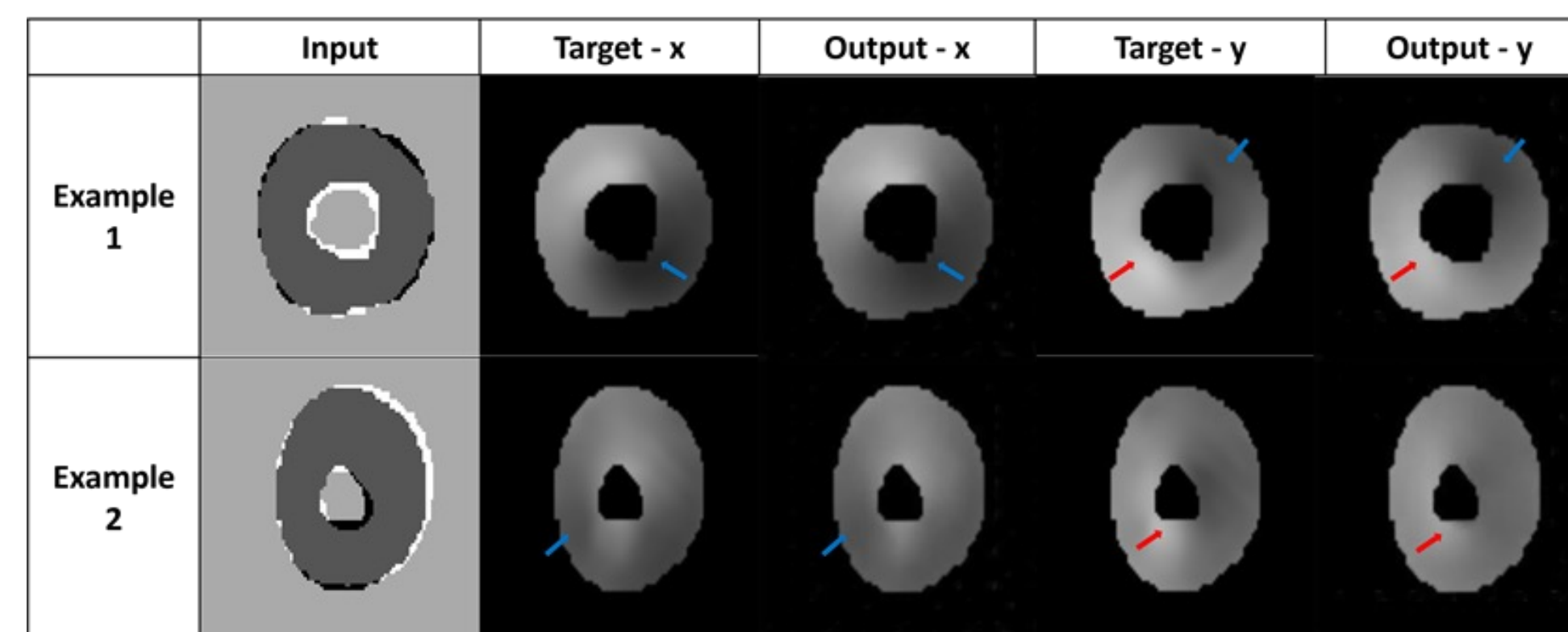


Figure 2. Comparison of x- and y-displacement fields generated from the cine images using the proposed method versus gold-standard displacement fields generated from the corresponding tagged images using the SinMod method. The input images are cine difference images, where the myocardium and background are represented by dark-gray and mid-gray colors, respectively, while the myocardium border movement is represented by white and black in opposite directions. The arrows point to similar features in the output and target images

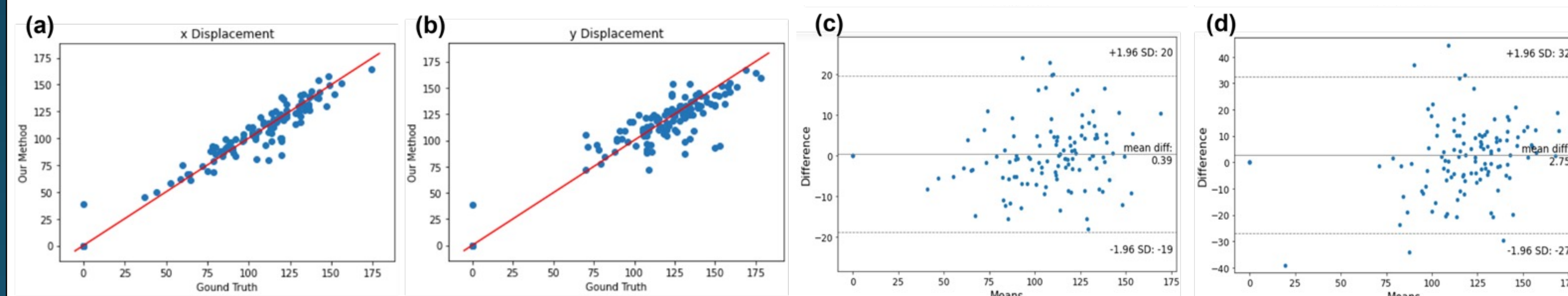


Figure 3. Scatter plots showing the generated vs. gold-standard measurements for (a) x- and (b) y-displacements of all myocardial segments in the test data. (c,d) Bland-Altman plots showing good agreements between the generated and gold-standard displacements in the (c) x- and (d) y-directions, where almost all differences lied within the ± 2 -SD agreement level.

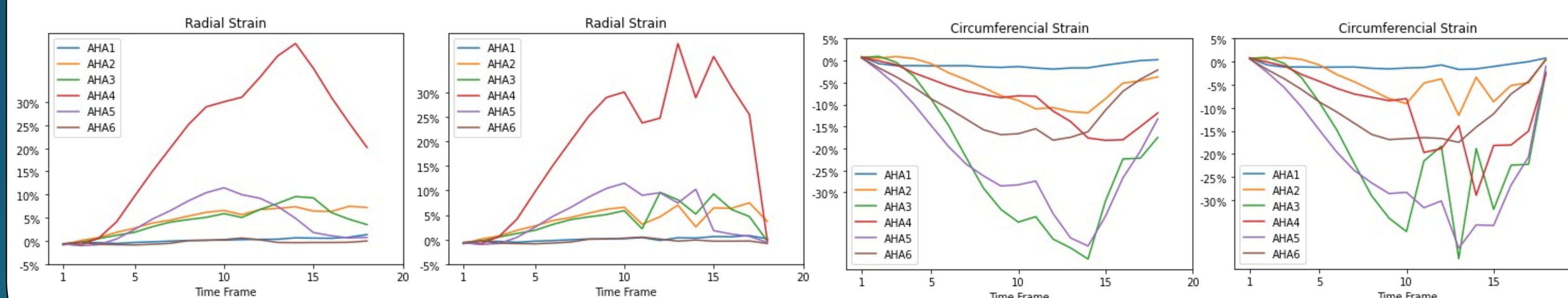


Figure 4. Radial and circumferential strain curves generated using the proposed method and those generated from the tagged images, gold standard. Myocardial strains are quantified based on AHA 6 segments per slice and drawn through the whole cardiac cycle.

Results

- The generated output displacement fields (**Figure 2**) showed myocardium shape similar to that in the input images as well as regional bright and dark areas (representing tissue displacements) at corresponding locations to those in the gold-standard displacement fields generated from the tagged images.
- Bland-Altman analysis (**Figure 3**) showed good agreement between the output measurements and corresponding gold-standard displacement fields, where almost all the measurement differences lied within the ± 2 SD agreement level.
- Student t-test showed insignificant differences between all paired measurements ($p > 0.05$).
- Lin's concordance correlation coefficients (CCC) were 0.96 and 0.89 for x- and y-displacement fields, respectively.
- The calculated radial and circumferential strains by displacement fields are insignificant differences ($p > 0.05$) in **Table 1**.
- Myocardial strain curves (**Figure 4**) have similar patterns between generated and gold-standard measurements.
- The developed method reduced the time required for generating the displacement field by two orders of magnitude to < 1 second.

Conclusions

The developed deep-learning based method allows for ultrafast and accurate generation of myocardial tissue displacement fields from conventional CMR cine images without the need for acquiring additional tagged images or using special tagging analysis software, which would help reduce scan time and data analysis time and improve CMR value imaging.

References

- Isola et al. Proceed IEEE computer vision and pattern recognition. 2017:1125-1134.
- Ronneberger et al. MICCAI 2015:234-241.
- An and Ibrahim. Proceed Soc Cardiovascular Magnetic Resonance 2021.
- Clarysse and Croisille. Proceed *Multi-Modality Cardiac Imaging: Processing and Analysis*. 2015:247-255.
- Ibrahim. Heart Mechanics. Magnetic Resonance Imaging. CRC Press, 2017.