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Tag-Free Myocardial Function Analysis from Cine MRI via Spatiotemporal Motion Estimation

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Introduction/Background

Accurate assessment of regional myocardial function is critical for early detection of subclinical cardiac dysfunction, especially in cancer patients at risk of treatment induced cardiotoxicity. While tagging MRI remains the clinical gold standard for strain analysis, it suffers from prolonged acquisition times and laborious post processing, limiting its routine use.

Methods/Intervention

We developed a deep learning framework to infer myocardial strain directly from standard cine MRI, obviating the need for dedicated tagging sequences. Our architecture combines a modified 3D U Net generator with a ResNet based discriminator to facilitate adversarial training. The generator employs spatiotemporal 3D convolutions to capture volumetric myocardial motion, while gated recurrent units (GRUs) model temporal dependencies across cardiac phases. Training was performed on a cohort of paired cine and tagged MRI scans (n = 150 patients), optimizing a joint loss function of adversarial cross entropy and mean squared error (MSE) between reconstructed and ground truth strain maps. Model performance was evaluated on a held out test set (n = 30) against tagging derived reference, using MSE, peak signal to noise ratio (PSNR), structural similarity index (SSIM), and Pearson correlation.

Results/Outcome

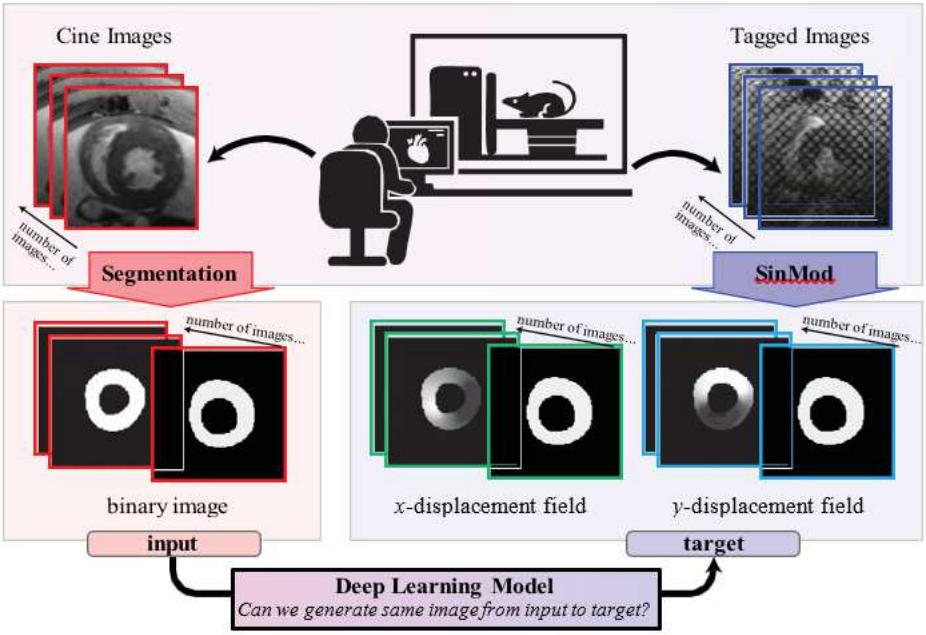
On the test set, our model achieved an MSE of 0.09 ± 0.02, PSNR of 58.5 ± 1.1 dB, and SSIM of 92.1% ± 1.5%, indicating high-fidelity reconstruction of strain patterns. Predicted strain maps demonstrated strong agreement with ground truth, with a Pearson correlation coefficient of 0.93 (p 0.05). Inference time per cine series averaged 1.2 s on a single GPU, representing a >90% reduction compared to conventional tagging workflows.

Conclusion

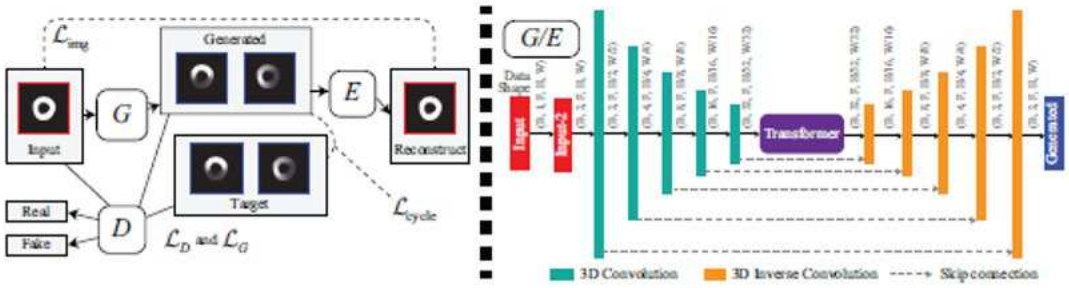
Our approach accurately reproduces tagging quality myocardial strain maps from routine cine MRI, delivering rapid, fully automated analysis without specialized acquisitions. This framework streamlines strain quantification, making advanced myocardial function assessment feasible in standard clinical protocols.

Statement of Impact

By eliminating the need for time consuming tagging MRI, this deep learning solution promises to democratize quantitative myocardial strain analysis, enabling earlier detection of cardiotoxicity, guiding treatment decisions, and ultimately improving cardiac care in vulnerable patient populations.



Overview of the deep learning framework for myocardial function analysis Cine MRI images are segmented into binary images, which are used as input to the model. Tagged MRI images are processed using the SinMod technique to generate x- and y-displacement fields as target outputs. Our model learns to map the segmented cine images to the corresponding displacement fields.



The left part presents an overview of the TFMyoNet framework, while the right part shows the detailed structure of the generator G and encoder E.

Visual comparison of input, target, output, and error images. The figure displays 20 images representing the input segmented cine MRI images, target displacement fields derived from tagged MRI using the SinMod technique, the predicted output displacement fields generated by the deep learning model, and the error maps showing the difference between the predicted and target displacement fields.

Keywords

Gated Recurrent Units (GRUs); Myocardial Strain; Cine MRI; 3D Unet; Adversarial Training; Cardiotoxicity