An nnU-Net model to Enhance Segmentation of Cardiac Cine DENSE-MRI using Phase Information

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***Abstract*—This study explores the application of deep learning to the segmentation of DENSE cardiovascular magnetic resonance (CMR) images, which is an important step in the analysis of cardiac deformation and may help in the diagnosis of heart conditions. A self-adapting method based on the nnU-Net framework is introduced to enhance the accuracy of DENSE-MR image segmentation, with a particular focus on the left ventricle myocardium (LVM) and left ventricle cavity (LVC), by leveraging the phase information in the cine DENSE-MR images. Two models are built and compared: 1) Model_{M}, which uses only the magnitude of the DENSE-MR images; and 2) Model_{MP}, which incorporates magnitude and phase images. DENSE-MR images from 10 human volunteers processed using the DENSE-Analysis MATLAB toolbox were included in this study. The two models were trained using a 2D UNet-based architecture with a loss function combining the Dice similarity coefficient (DSC) and cross-entropy. The findings show the effectiveness of leveraging the phase information with Model_{MP} resulting in a higher DSC and improved image segmentation, especially in challenging cases, e.g., at early systole and with basal and apical slices.**

***Index Terms*—Image segmentation; nnU-Net; Magnetic resonance imaging; DENSE MRI; Phase and magnitude data.**

I. Introduction

The introduction of deep learning has revolutionized the field of medical image segmentation [1]. One area that has been significantly affected is cardiovascular magnetic resonance (CMR) image segmentation, where deep learning's potential has been particularly evident [2]. In this paper, we compare two models for segmenting cine Displacement Encoding with Stimulated Echoes (DENSE) [3] MR images. Our approach is based on the nnU-Net framework proposed by Isensee et al. [4]. The nnU-Net is a framework for deep learning-driven biomedical image segmentation that automatically adapts and adjusts its settings, covering aspects like data preprocessing (e.g., data augmentation and rescaling of signal intensity), network topology (e.g., pooling behavior and depth of the network architecture), and training (e.g., learning rate and batch size).

The literature on deep learning for medical image segmentation is extensive. In the pursuit of enhancing cardiac image segmentation, researchers have explored a range of strategies, from utilizing innovative architectures to incorporating additional information alongside magnitude images.

In the domain of architectural innovations, Von Zuben et al. [5] utilized a multi-layered machine learning strategy, employing an ensemble-like method of UNet and UNet++ models, and a heart locator for improved accuracy. This approach has improved short-axis cine MR image segmentation. Barbaroux et al. [6] crafted an automated segmentation technique for both long- and short-axis DENSE CMR to compute myocardial strains with spatiotemporal convolutional neural networks, stressing the need for spatial and temporal

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analysis in CMR segmentation. The findings from their study highlighted the improved segmentation performance of spatio-temporal models across the DENSE images, in contrast to 2D architectures, which often struggled to accurately segment end-diastolic frames due to poor blood-to-myocardium contrast. Their spatio-temporal models achieved notable segmentation accuracy, with a Dice similarity coefficient (DSC) of 0.83 $\pm$ 0.05 and a Hausdorff distance of 4.0 $\pm$ 1.1 mm for short-axis segmentations. Similarly, for long-axis segmentations, the models reached a DSC of 0.82 $\pm$ 0.03 and a Hausdorff distance of 7.9 $\pm$ 3.9 mm, demonstrating consistent and reliable performance in capturing cardiac structures throughout the cardiac cycle.

A different set of studies emphasized the integration of additional information besides magnitude. Shen et al. [7] have automated the segmentation of biventricular contours using deep learning and leveraging velocity data in the context of tissue phase mapping MRI to enhance the segmentation process. Similarly, Wu et al. [8] developed a rapid automated segmentation method for cine myocardial velocity mapping, further demonstrating the utility of incorporating velocity data alongside magnitude. This emphasis on velocity information, whether through tissue phase mapping MRI or cine myocardial velocity mapping, highlights a growing trend towards enriching cardiac image segmentation with diverse data sources. Further contributions include Ghadimi et al.'s [9] fully automated method for both global and segmental strain analysis in DENSE CMR, employing deep learning for segmentation and phase unwrapping. These innovative approaches demonstrate the value of incorporating diverse data sources in addition to magnitude but also highlight the potential of novel architectures in pushing the boundaries of cardiac image segmentation.

Although previous studies have made significant progress using various architectures and information sources, there is still a research gap in utilizing phase information for cardiac DENSE-MR segmentation. The utilization of phase information for cardiac DENSE-MR segmentation can result in more accurate segmentations, ultimately improving the downstream task of computing myocardial strains from the segmented images. The present study explores a strategy to start addressing this gap and builds a model that leverages the magnitude and phase data in the nnU-Net framework. Our study introduces two models: the first model – Model_{M} – uses only magnitude DENSE images; while the second model – Model_{MP} – incorporates X, Y, and Z phase data in addition to magnitude data.

II. Methodology

A. Image Acquisition and Preprocessing

The dataset included DENSE MR images acquired in 10 healthy volunteers (IRB consented). Eighty-seven slices corresponding to a total of 3338 frames were used for training and validation. The original image resolutions were 80x80 and 100x100 pixels, while the final resolution prior to introducing the images to the nnU-Net model was 400x400 pixels as a result of resampling. The resampling was introduced to more accurately represent the curved endocardial and epicardial contours. The ground truth for the training and validation images were manually segmented using the DENSE-Analysis MATLAB toolbox [3], [10], specifically designed to segment and analyze DENSE images. This step resulted in a set of processed images (for each image, the epicardial and endocardial contours through time were computed) alongside the corresponding masks that delineated three classes: background, left ventricle myocardium (LVM), and left ventricle cavity (LVC). This study focuses on the segmentation of LVM and LVC.

B. Model Training

Prior to initiating the training process, the preprocessed images and their associated masks were organized to match the particular dataset structure demanded by nnU-Net, which consists of the input images and their respective segmentation maps. The architecture chosen in this work is the 2D UNet-based model, paired with a loss function that combines the Dice similarity coefficient (DSC) and cross-entropy. The input images and masks are then used to train two separate models using the nnU-Net pipeline: Model_{M} (trained solely on the magnitude data) and Model_{MP} (trained on magnitude and phase data). The phase data in Model_{MP} is introduced as additional channels.

In the training process of the proposed models, we adopted a 10-fold cross-validation method where an entire subject is fully excluded in each fold. The training process was extended over 300 epochs to ensure thorough learning. To optimize the training phase, we employed an automatic learning rate adjustment mechanism, which dynamically adapts the learning rate based on training progress and, in doing so, improves convergence and performance. The proposed models were trained on a single NVIDIA A30 GPU with a memory capacity of 24GB. Each fold training duration for both Model_{M} and Model_{MP} was approximately 5 hours. The model with the best weights based on the validation set was employed for inference rather than the model with the final epoch's weights.

III. Results and Discussion

The segmentation models predictive capabilities were evaluated using cross-validation, and it has to be noted that the validation slices belong to hearts that were excluded in the training fold. In the following figure captions we report the slice and frame numbers to locate the image along the LV longitudinal axis and across the cardiac cycle: the slice numbering starts from the most apical slice (slice 1) and advances toward the most basal one (last slice), while the frame numbering starts from 1 at the beginning of systole.

Table I compares the overall segmentation performance of Model_{M} and Model_{MP} based on DSC. Model_{MP} performs better than Model_{M} across all metrics, although the DSC values are close.

In Fig. 1, the Model_{MP}'s predictions for a basal validation slice are displayed throughout the cardiac cycle. Model_{MP} performs well in all phases, even those that may prove challenging for human segmentation, such as in early systole (first

TABLE I
DICE SIMILARITY COEFFICIENT (DSC) FOR MODEL_{M} AND MODEL_{MP}.

Metric	Model_{M}	Model_{MP}
LVM DSC	0.789	0.824
LVC DSC	0.888	0.903
Mean DSC	0.838	0.864

images in the top left corner). Nevertheless, it is noted that the model segmentation of the myocardium in the septal wall toward the right ventricle is slightly underpredicted. In this current stage, Model_{MP} results in a proper initial segmentation that can be further improved manually for downstream tasks, such as motion and strain analysis in the DENSE-Analysis Toolbox. This initial segmentation can significantly reduce the processing time of DENSE images, enabling more efficient and effective data analysis.

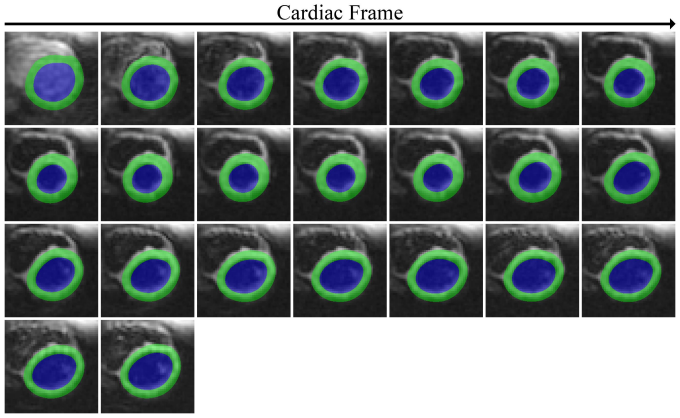

Fig. 1. Model_{MP}'s predicted segmentations for a basal slice (slice 11 out of 14) throughout the cardiac cycle (23 frames).

In Fig. 2, the magnitude and phase images for a basal slice (12 out 14) at the beginning of systole (frame 1) are displayed, and the segmentation resulting from both models is compared. This early systolic phase is often characterized by a low LVC/LVM signal contrast, which makes the segmentation task more challenging. Model_{M}, which utilizes only the magnitude image for prediction, shows an inaccurate segmentation with defects highlighted by the yellow arrows. On the other hand, the prediction of Model_{MP} overcomes the problems encountered by Model_{M}. At the bottom of Fig. 2, the input images and the models' predictions for the next time frame are displayed. These next-frame images confirm that the predicted heart location is correct in the previous time frame. By this time frame, the magnitude image presents a more defined myocardium, and both models lead to similar predictions. This exemplifies that the phase information can be useful for improving the segmentation accuracy in early systole.

Figure 3 compares the predictions of the two models for mid-ventricular and apical slices during systole and diastole. In presence of low contrast or artifacts in the magnitude images,

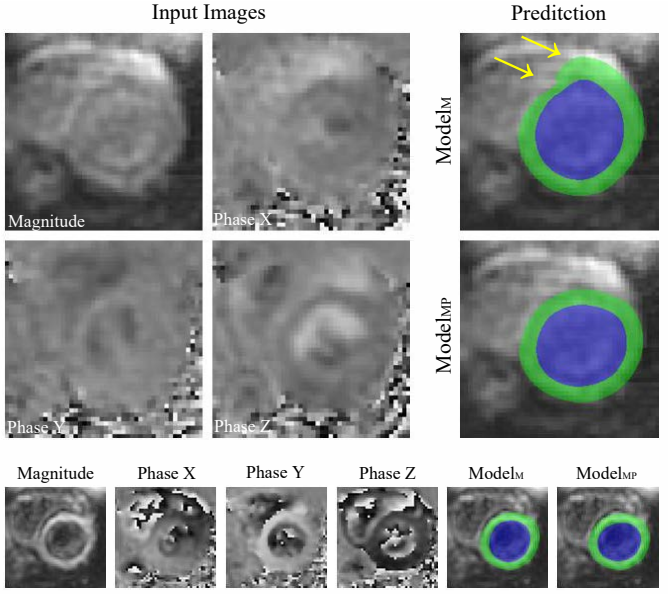

Fig. 2. Top: input images for a basal slice (slice 12 out of 14), including magnitude and phase data, at the beginning of systole (frame 1) and the corresponding predictions for Model_{M} and Model_{MP}. The yellow arrows highlight the anatomically inaccurate regions in Model_{M} predictions. Bottom: input images and predictions corresponding to the subsequent time frame (frame 2) for the same slice.

Model_{M} is more prone to generate an inaccurate mask that either under-predicts (top two rows in Fig. 3) or over-predicts (third row in Fig. 3) the LVM. Despite Model_{MP} performing better than model Model_{M} overall, both models may still fail to accurately predict the LVM in challenging cases as the one shown in the bottom row of Fig. 3.

Mid-ventricular slices are typically easier to segment due to a higher image contrast and a smoother ring shape. For a very basal slice, both models struggled to provide a closed region in the prediction. As the valve structure starts to emerge at the base of the LV, it is expected that the models' predictions will be inaccurate in this region.

Fig. 4 compares the DSC for the LVC and LVM predictions of Model_{M} and Model_{MP} averaged over all slices for one validation subject. The DSC values are reported throughout the cardiac cycle for both models. Model_{MP} results in more accurate segmentations (based on DSC) for both LVM and LVC. In particular, Model_{MP} leads to improved LVM segmentations, which constitute the first step in computing myocardial displacements from DENSE data. We also observe that, overall, the LVM DSC improves after the first few time frames, often characterized by low image contrast.

IV. CONCLUSION

In this study, we have compared two models, Model_{M} and Model_{MP}, for the segmentation of DENSE MR images, focusing on the LVM and LVC. Our preliminary findings show that including phase data alongside magnitude data in Model_{MP} yields more accurate segmentations, especially in cases with lower contrast, for example, at early systole and

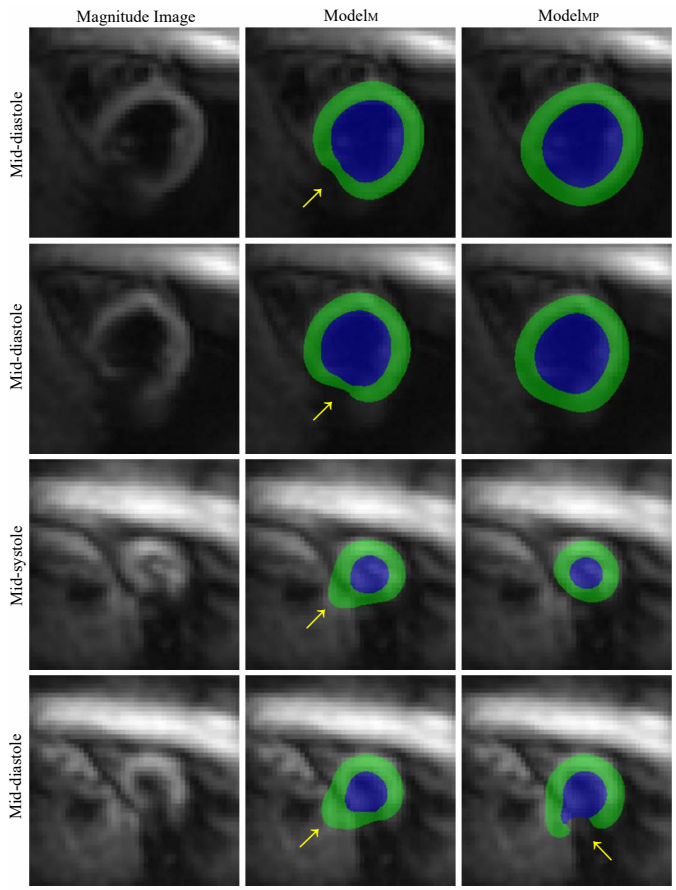

Fig. 3. Model$_{\mathrm{M}}$ and Model$_{\mathrm{MP}}$ predictions for midventricular slices (top two rows, slices 8 out of 14 and 7 out of 14) and an apical slice (slice 3 out of 14) at mid diastole and mid systole.

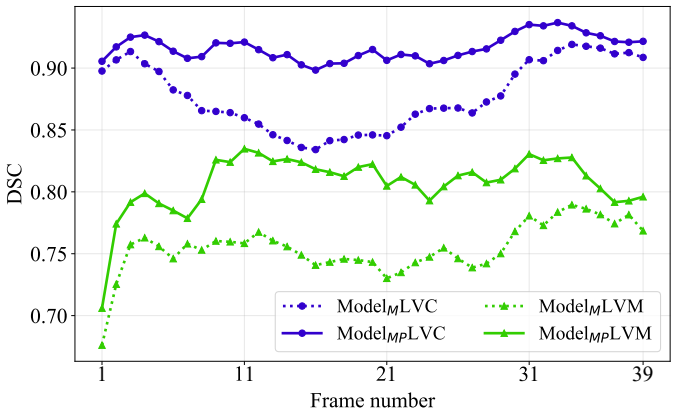

Fig. 4. Left ventricular cavity (LVC) and left ventricular myocardium (LVM) DSC averaged over all slices for one validation subject and obtained with either Model$_{\mathrm{M}}$ or Model$_{\mathrm{MP}}$ throughout the cardiac cycle (39 frames).

in apical and basal slices where even manual segmentation is often challenging. The improved performance of Model$_{\mathrm{MP}}$ is indicated by a higher DSC for both LVM and LVC and fewer anatomically inaccurate features (such as discontinuities and over/under predictions) compared to Model$_{\mathrm{M}}$. Although Model$_{\mathrm{MP}}$ leads, overall, to improved LMV and LVC segmentations, it does not always perform better than Model$_{\mathrm{M}}$. This points to the need of further improving Model$_{\mathrm{MP}}$. Future work will involve exploring a broader range of model architectures and the potential of ensemble methods, together with utilizing a significantly larger dataset for training. Additionally, we aim to integrate the obtained segmentations in the DENSE-Analysis toolbox [3], [10] to facilitate the initial segmentation process and improve accuracy and robustness. This integrated approach is expected to streamline the segmentation workflow, reducing processing time and enabling researchers to analyze DENSE images more efficiently to quantify cardiac motion and deformation.

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