Cascaded Framework for Myocardial Infarction Segmentation from Delayed-Enhancement Cardiac MRI

Jun Ma[0000−0002−9739−0855]

Department of Mathematics, Nanjing University of Science and Technology
junma@njust.edu.cn

Abstract. Myocardium and pathology segmentation plays an important role for quantitative analysis of patients suffering from myocardial infarction. In this paper, we present a cascaded convolutional neural network framework for myocardium, infarction, and no-reflow areas segmentation in delayed-enhancement cardiac MRI. Specifically, we first use a 2D U-Net to segment the whole heart, including the left ventricle and the myocardium. Then, we crop the whole heart as a region of interest (ROI). Finally, we train a new 2D U-Net to segment the infraction and no-reflow areas in the whole heart ROI. We evaluate the proposed method on MICCAI 2020 EMIDEC testing set and achieve Dice scores 86.28%, 62.24%, and 77.76% for myocardium, infraction, and no-reflow areas, respectively.

Keywords: Segmentation · Myocardial Pathology · Cascaded Framework.

1 Introduction

Quantitative assessment of myocardial viability is essential in the diagnosis and treatment management for patients suffering from myocardial infarction (MI). Cardiac magnetic resonance (CMR) is particularly used to provide imaging anatomical and functional information of heart, such as the delayed-enhancement (LGE) CMR sequence which visualizes MI.

One of the important tasks is to segment the myocardium into different regions, including normal myocardium, infarction, and no-reflow from multi-sequence CMR dataset. Manual annotation is generally time-consuming, tedious and subjects to inter- and intra-observer variations. Thus, fully automatic segmentation method is highly desired in clinical practice. Figure 1 presents some images from different myocardial infraction cases and the corresponding left ventricle, healthy myocardium, infraction, and no-reflow annotations. It can be observed that the intensity appearances vary significantly among different cases, and the both infraction and no-reflow areas have ambiguous boundaries and low contrast. Thus, it is very challenging to automatically segment them.

To the best of our knowledge, most of CMR segmentation related studies focus on left ventricle, right ventricle, and myocardium segmentation ([1] [11]

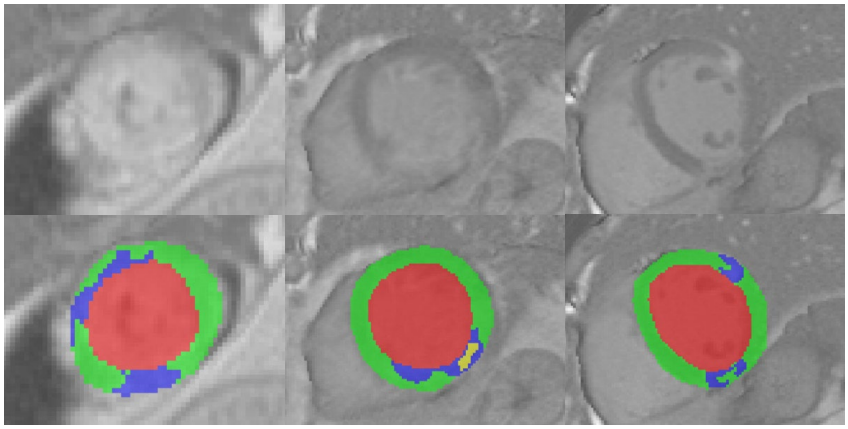

Fig. 1: Visual examples of different myocardial infraction delayed-enhancement cardiac MR images. The 1st row and the 2nd row are the original image and ground truth, respectively. In the 2nd row, the red, green, blue,and yellow color denote left ventricle, healthy myocardium, infraction, and no-reflow, respectively.

[2], [7]), little work has been done in the fully automatic cardiac pathology segmentation ([10], [6], [5]). Zhuang [10] proposed a multivariate mixture model and maximum of log-likelihood framework for simultaneous registration and segmentation of multi-source CMR images, achieving a Dice score of 0.4779 ± 0.1855 for scars segmentation. Recently, Li et al. [6] proposed a new framework of scar quantification based on surface projection and graph-cuts framework, achieving a mean accuracy of 0.856 ± 0.033 and mean Dice score of 0.702 ± 0.071 for LA scar quantification.

2 Method

This paper focuses on both healthy and pathology pathologic myocardium segmentation from the delayed-enhancement cardiac MRI. One of the main challenges is how to exploit rich and reliable information regarding to the pathological as well as morphological information of the myocardium. To this end, we design a cascaded framework that comprises two 2D U-Net to segment the left ventricle and myocardium, and the pathology regions, respectively. Figure 2 presents the whole pipeline of the proposed method. Specifically, the proposed method contains three steps[1]:

– Step 1 (whole LV segmentation). Train a 2D U-Net [9] on the original CMR images to segment the whole LV (including left ventricular blood pool and myocardium);

[1] In step 1 and step 3, the networks are trained end-to-end, while the whole framework is not end-to-end.

– Step 2 (creating ROI). Crop LV region of interest (ROI) from the original CMR images based on the segmentation results in step 1. In this way, the unrelated background can be excluded;
– Step 3 (infraction and no-reflow segmentation). Train a new 2D U-Net to segment the infraction and no-reflow from the ROI images.

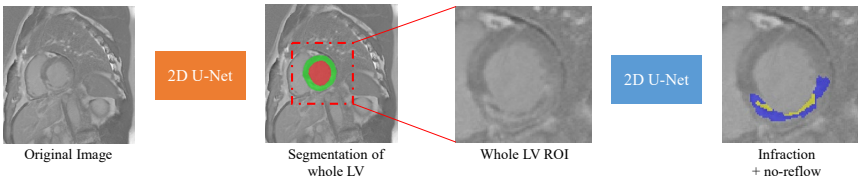

Fig. 2: Pipeline of the proposed method. we first use a 2D U-Net to segment the whole LV (left ventricle), including LV blood pool and myocardium. Then, we crop the LV region of interest (ROI). Finally, a new 2D U-Net is used to segment the infraction and no-reflow areas.

3 Dataset and Training protocols

The official myocardial infarction delayed-enhancement cardiac MRI dataset [4] provides 100 cases for the training and 50 cases for the testing. In particular, Every training and test case represents a DE-MRI exam of the left ventricle. An exam (i.e. a case) consists of a series of 5 to 10 short-axis slices covering the left ventricle from the base to the apex. The ground-truths (contours of the relevant areas) will be provided with the training dataset. The training set with full ground-truth will comprise 100 cases (67 pathological cases, 33 normal cases) randomly selected among the 150 subjects. The testing set is made of data from 50 subjects (33 pathological cases, 17 normal cases), all different from those in the training set.

During preprocessing, we apply z-score to normalize the image intensity, and resample all the images to the same spacing $10.0 \times 1.458 \times 1.458\ mm^3$. We employ nnU-Net [3] as the main network. Due to the fact that the CMR data has large slice thickness, 2D U-Net is more suitable in this task. During training of the first U-Net, the patch size is 256×224 and the batch size is 16. During training of the second U-Net, the patch size is 66×66, and the batch size is 32. The loss function is the sum between Dice loss [8] and cross entropy. We use stochastic gradient descent with momentum to optimize the networks. Each model is trained on a TITAN V100 GPU. During testing, we use five-fold ensemble to predict each testing cases.

4 Results and Discussion

4.1 Cross-validation segmentation results

Table 1 presents the quantitative cross validation results of the first U-Net. The U-Net can achieve very high accuracy for the whole LV, which can insure the cropped ROI can cover most of the LV and also the lesions.

Table 1: Quantitative segmentation results of the left ventricle, myocardium and whole LV on training set.

Metrics	Left Ventricle (LV)	Myocardium (Myo)	Whole LV (LV+Myo)
Dice (%)	93.47 ± 2.06	85.38 ± 3.94	95.51 ± 1.83

Table 2 shows the quantitative segmentation results of the infection and no-reflow. The sensitivity of all lesions are significant worse than the corresponding specificity, indicating that most segmentation results are right but many lesions are missed by the proposed method.

Table 2: Quantitative segmentation results of the infraction and no-reflow on training set.

Metrics	Infraction	No-reflow	Infraction + No-reflow
Dice (%)	57.96 ± 16.64	77.19 ± 31.33	59.23 ± 17.85
Sensitivity (%)	53.61 ± 19.23	74.02 ± 34.88	54.16 ± 20.20
Specificity (%)	99.21 ± 0.62	99.94 ± 0.10	99.26 ± 0.61

4.2 Testing set segmentation results

We evaluate the proposed method on the official testing set with 50 cases. Table 3 presents the quantitative results.

Table 3: Quantitative segmentation results of the testing set. NR stands for no-reflow

Metrics	Myocardium (%)	Infarction (NR included) (mm^3)	NR (%)
Dice	86.28	62.24	77.76
Volume difference	10152.85	4873.98	829.65
Volume difference ratio according to volume of myocardium	-	3.50	0.49%

4.3 Classification

The final segmentation results can be used for classifying the cases in normal or pathological. In particular, if the segmentation of one case does not have lesions (infraction or no-reflow), it will be classified in a normal case. Otherwise, it will be a pathological case. Currently, we do not have a plan to merge with the clinical features. Detailed results will be announced during the conference, the 4th of October, as the organizer will give us a new dataset for the classification task at the day of the symposium.

5 Conclusion

This paper present a simple fully automatic method for myocardium and its pathology segmentation from enhanced cardiac MR images. Experiments on the MICCAI 2020 EMIDEC challenge datasets show that the proposed method can achieve a very high specificity. However, the sensitivity is relative low. In the future work, we would improve the learning ability of the network to be more sensitive to the lesions.

Acknowledgement

The author of this paper declare that the segmentation method they implemented for participation in the EMIDEC challenge has not used any pre-trained models nor additional MRI datasets other than those provided by the organizers. The author also highly appreciates the organizers of automatic Evaluation of Myocardial Infarction from Delayed-Enhancement Cardiac MRI (EMDEC 2020) for their public dataset and organizing the great challenge.

References

1. Bernard, O., Lalande, A., Zotti, C., Cervenansky, F., Yang, X., Heng, P.A., Cetin, I., Lekadir, K., Camara, O., Ballester, M.A.G., et al.: Deep learning techniques for automatic mri cardiac multi-structures segmentation and diagnosis: is the problem solved? IEEE Transactions on Medical Imaging **37**(11), 2514–2525 (2018)
2. Chen, C., Qin, C., Qiu, H., Tarroni, G., Duan, J., Bai, W., Rueckert, D.: Deep learning for cardiac image segmentation: A review. Frontiers in Cardiovascular Medicine **7**, 25 (2020)
3. Isensee, F., Jäger, P.F., Kohl, S.A., Petersen, J., Maier-Hein, K.H.: Automated design of deep learning methods for biomedical image segmentation. arXiv preprint arXiv:1904.08128 (2020)
4. Lalande, A., Chen, Z., Decourselle, T., Qayyum, A., Pommier, T., Lorgis, L., de la Rosa, E., Cochet, A., Cottin, Yves; Ginhac, D., Salomon, M., Couturier, R., Meriaudeau, F.: Emidec: A database usable for the automatic evaluation of myocardial infarction from delayed-enhancement cardiac mri. Data **5**(4), 89 (2020)

5. Li, L., Weng, X., Schnabel, J.A., Zhuang, X.: Joint left atrial segmentation and scar quantification based on a dnn with spatial encoding and shape attention. arXiv preprint arXiv:2006.13011 (2020)
6. Li, L., Wu, F., Yang, G., Xu, L., Wong, T., Mohiaddin, R., Firmin, D., Keegan, J., Zhuang, X.: Atrial scar quantification via multi-scale cnn in the graph-cuts framework. Medical image analysis **60**, 101595 (2020)
7. Ma, J., He, J., Yang, X.: Learning geodesic active contours for embedding object global information in segmentation cnns. IEEE Transactions on Medical Imaging (2020). https://doi.org/10.1109/TMI.2020.3022693
8. Milletari, F., Navab, N., Ahmadi, S.A.: V-net: Fully convolutional neural networks for volumetric medical image segmentation. In: 2016 fourth international conference on 3D vision (3DV). pp. 565–571 (2016)
9. Ronneberger, O., Fischer, P., Brox, T.: U-net: Convolutional networks for biomedical image segmentation. In: Navab, N., Hornegger, J., Wells, W.M., Frangi, A.F. (eds.) Medical Image Computing and Computer-Assisted Intervention. pp. 234–241 (2015)
10. Zhuang, X.: Multivariate mixture model for myocardial segmentation combining multi-source images. IEEE Transactions on Pattern Analysis and Machine Intelligence **41**(12), 2933–2946 (2018)
11. Zhuang, X., Li, L., Payer, C., Štern, D., Urschler, M., Heinrich, M.P., Oster, J., Wang, C., Smedby, Ö., Bian, C., et al.: Evaluation of algorithms for multi-modality whole heart segmentation: an open-access grand challenge. Medical Image Analysis **58**, 101537 (2019)