# CHAPTER 3

# LEARNING-BASED IMAGE PROCESSING FOR CARDIAC DIAGNOSIS

***Highlights of the Chapter***

- *Components of Image segmentation*
- *Classical image segmentation approaches*
- *Deep learning image segmentation approaches*
- *Exploration of related literatures*

This chapter encompasses the approaches developed and utilized for the purpose of image segmentation for improved feature extraction and most importantly their role in the field of medical image analysis. Conventionally, manual segmentation of medical images is carried out. Problems with this approach are: requires expert and is time consuming and tedious process. Also, this process still holds the possibilities of error in segmentation due to inter and intra-observer variability. Thus, accurate and fully automated process is required for improving clinical application of imaging modalities. Deep learning based provides the way to segment images in fully automated mode. Deep learning based automatic segmentation of images are, in general, categorized as: (a) Supervised learning (b) Semi-supervised or weakly-supervised learning (c) Unsupervised learning

(a) Supervised learning

(b) Semi-supervised learning

(c) Unsupervised learning

## 3.1 Classical image segmentation approaches

Application of supervised and unsupervised techniques in medical image analysis increased considerably during the period of late 1990s to early 2020s. Some of the main techniques used include but are not limited to image-based techniques (threshold, dynamic programming); pixel classification (clustering, gaussian mixture model); deformable models; graph-based models; and atlas-based methods.

### 3.1.1 K-Means Clustering approach

Clustering is an unsupervised method to split up a set of data into a specific number of groups. One of the popular clustering methods is the K-means technique, which is used in this proposed work to generate a primary segmentation of the region of interest from the cardiac MR images. A collection of data points is partitioned into k number of groups in this technique; the idea is simple and the method has relatively medium computational complexity (based on the number of elements, clusters, and iterations).[1] Since biomedical image segmentation using unsupervised techniques is pretty challenging due to the presence of organs and tissues of similar intensities, minimizing the number of data points will be a smart choice. Hence a manually cropped portion of the images inclusive of the region of interest is provided for clustering which produces the initial (rough) segmentation [1], [2].

The algorithm is executed in several phases. First random cluster centers are initialized for the dataset; based on that, the dataset is divided into K clusters randomly, while assigning each cluster almost the same number of nearest data points. Once the first stage of grouping is completed, the new centroids for each cluster are recalculated. Then, Euclidean distance is computed from each of the data points to each cluster centroid, and based on that, the data point is assigned to the nearest cluster with the minimum Euclidean distance to its centroid[2]. The process continues until the shifting of the centroids becomes less than a predefined threshold or the iteration limit has been reached. The Euclidean distance is defined by $d = ||p(x,y) - c_k||$, where $c_k$ is the centroid of the $k^{th}$ cluster and $p(x,y)$ is any random pixel of the image. The new centroid position is recalculated using $c_k = \frac{1}{k}\sum_{y\in c_k} \sum_{x\in c_k}(p(x,y)$ So, in this unsupervised iterative clustering algorithm, the sum of the distances from each element to its cluster center is minimized over all the clusters. Although random, the initial cluster centroids should be chosen carefully, as the final clustering quality depends on it.

### 3.1.2 Random walker approach

The Random Walker is a well-known algorithm for performing multilabel interactive segmentation. With a small number of predefined pixel labels, the random walking probability to reach a pre-labeled pixel starting from the unlabeled ones can be quickly calculated. Hence the segmentation can be performed by assigning each pixel with the greatest probability. Basically, in this algorithm, the image is represented by an undirected weighted graph, where the pixels of the image constitute the vertices and the intensities are mapped to edge weights. As the algorithm works based on pre-defined labels or seed points, a manual seed point selection work (a few pixels for both foreground and background) have been performed [3].

So at first, a small number of pixels are interactively pointed as “object” seed points (inclusive of the region of interest) and a few “background” seed points are selected from the other portion of the image. Now the unlabeled pixels should release the random walker. The random walker leaving any particular unlabeled pixel will be arriving at a seed point. The probability of the seed point being an “object” rather than a “background” is computed [4]. By using the graph Laplacian matrix, a system of linear equations can be solved which may analytically determine the value of these probabilities. Once all the probabilities for each of the pixels are calculated, they are assigned to the label (object/background) corresponding to the most probable random walker generation (i.e., ‘1’ for the object and ‘0’ for the background) and finally, it produces an image with the primary segmentation of the region of interest.

### 3.1.3 Region growing approach

Seed region growing is one of the popular segmentation approaches which is used in the proposed methodology for extracting the region of interest (ROI) from the cardiac MR images. This method works on the seed indication, or in other words, to choose a point or pixel within the particular region that is going to be extracted. Primarily the idea is to constitute a region by accumulating similar pixels together [5]. Hence the seed point selection should be done very carefully as the segmentation results are directly influenced by this. In this procedure, first, the seed point or the starting point of growth in the image is precisely chosen. Researchers have reported a lot of approaches regarding the initiation of the seed value [6]. A manual seed initiation process has been executed in the proposed methodology based on the required region of interest which in this case is the left ventricle in cardiac cine MR images. Once the first seed point has been selected, the neighbor pixels are automatically compared by the algorithm in search of similar characteristics while satisfying the predefined growth criteria (threshold value). Once the criteria are matched, the seed will grow by adopting the neighbor pixel into the region squad and the grouped pixels become the new seed as a whole. The process is repeated till all the pixels of the same threshold level are grouped and no more pixel is left to add with the region. It is very important to choose the threshold minutely as it is the only growing criteria for the region. In general cases, the value of the threshold is calculated based on the gray level information of the images. Improper threshold selection leads to inappropriate merging of the pixels, while some pixels are not added to the region, resulting in holes in the constructed area of interest.

Now, suppose if pixel similarity is defined by F, then at a certain level, the function $F(R)$ will be defining the regional characteristic for the region R. $p(x, y)$ is the next pixel with eigenvector $F(p)$ on which the threshold criteria is going to be tested. Now, if $|F(R) - F(p)| < T$, where $T$ specify the predefined threshold level, then the pixel is merged, otherwise, the search is carried on for the next neighboring pixel. The process continues till all the similar pixels are grouped and then generates a binary image of the region of interest for further analysis.

### 3.2 Deep learning approaches

The Sunnybrook Cardiac MR Left ventricle division challenge by MICCAI in 2009 is the first publicly available dataset of CMRI after which many cardiac MRI segmentation methods have been proposed varying from semi-automatic to fully automatic methods. Recently, more advanced deep learning methods were developed which eased the automatic segmentation process of medical images. Alongside, advancement in resources and accelerated hardware further increased the efficiency of the system. This led to availability of more and more data in public domain which augmented the development of fast and accurate segmentation model pipelines. Few of the recently developed methods are discussed in the following paragraphs.

Zhang et al [7] reviewed Generative Adversarial Network based fast MRI segmentation methods and shown that the model has good generalizability and robustness. Wu et al [8] proposed use of multi-channel data for mapping by fusion with attention module and shape information-based post-processing to achieve accurate delineation of both epicardial and endocardial contours. Another author proposed bicubic interpolation for MRI pre-processing and trained an improved 3D V-net for segmentation task and shown that the proposed method effectively improved accuracy of the segmentation of prostate [9].

In recent years, the application of deep learning methods in medical image processing such as lesion classification and segmentation, organ segmentation increased considerably. The application of deep learning methods in Cardiac MRI segmentation was very much limited until 2013. Asma et. al. [10] showed that all the existing methods to segment the RV is inaccurate and not enough to remove the challenges which come in RV segmentation.

In 2015, Kaggle organized the Second Annual Data Science Bowl in which a lot of applications of deep learning methods were presented to the community. Since then, a huge number of deep learning methods were applied for CMRI analysis. Deep learning methods used until 2018 were summarized by Bernard et. al. [11]. Several variants of U-Net [12], DenseNets [13], novel localization, and semantic segmentation network, motion estimation and segmentation networks, and different novel variants of fully connected networks had been proposed by different authors [14]. In the MICCAI 2017 Automatic Cardiac Division challenge, 9 out of 10 proposed method is a deep learning-based method and out of 9, 8 were variants of U-Net. A combined deformable model and deep learning method have been proposed by Avendi et. al. [15] for segmentation of the Left ventricle of the heart. Isensee et. al. [16] used an ensemble of modified 2D U-Net and 3D U-Net for segmentation of CMRI. Baumgartner et. al. [17] varied hyperparameters and convolutional neural networks to optimize the CMRI segmentation. U-Net proposed by Ronneberger et. al. [12] with the gated recurrent unit (GRU) on a higher feature level to propagate slice features from one to another. Zotti et. al.. [18] also proposed an extension to U-Net for CMRI segmentation and analysis. Khaned et. al. [19] used multiscale residual DenseNets for segmentation while Oktay et. al.. [20] used residual convolutional neural networks to achieve super-resolution for 3D volumes from 2D image stacks. Recently, machine learning methods were used to predict high-level LV/RV information like volume and ejection fraction without segmenting the images. Although from the above literature it is clear that one can have quantifying parameters for LV/RV without the need for segmentation, cardiac diagnosis is based on physiological parameters and so the need for segmentation maps is required to evaluate the cardiac quantification parameters. Problems associated with the segmentation of CMR images are unique and require customized processing to resolve them [21]. Poor contrast between myocardium and cavity, heterogeneities in the cavity due to blood flow, noise due to motion artifacts and heart dynamics, shape and intensity variability are major causes of inaccurate and clinical insufficient segmentation of CMR images. Apart from these, free-breathing CMR imaging has lower quality compared to breath-hold CMR images and thus there remains a challenge in accurate segmentation of free-breathing CMR images. A cascaded model has been proposed by Luo et. al. [22] using FC-DenseNet and Level set method to automatically segment the RV and reported that the method is able to efficiently and satisfactorily segment the RV.

Also, Zhou et al. [23] proposed a study to segment Ventricle images and reported excellent results. Chen et. al. [24] proposed inter-cascade GAN for segmentation task of unbalanced atrial targets and investigates an adaptive attention cascade to automatically correlate segmentation of unbalanced tasks and then applies adversarial regularization to segment the scars. Li et al. [32] utilized a unified framework for segmentation and classification of echocardiographic sequences segmentation. A modified 2 stage U-net proposed by Mo et. al. [26]simultaneously learned to detect ROI in the full volume and classified voxels without compromising the original resolution. This approach achieved better segmentation performance as compared to state-of-the-art methods. Shi et. al. [27] proposed a probabilistic deep voxel-wise dilated residual network for segmentation of whole heart in 3D MR images.

This chapter outlined the details and importance of image registration, more specifically deformable image registration in the field of medical image analysis. Critical review of existing algorithms helped to understand how previously proposed algorithms encounter the major challenges of this field. Further, the concepts have been utilized to meet the goals of the thesis.

## References

[1] N. Dhanachandra, K. Manglem, and Y. J. Chanu, "Image Segmentation Using K -means Clustering Algorithm and Subtractive Clustering Algorithm," *Procedia Computer Science*, vol. 54, pp. 764–771, 2015, doi: 10.1016/j.procs.2015.06.090.

[2] H. P. Ng, S. H. Ong, K. W. C. Foong, P. S. Goh, and W. L. Nowinski, "Medical Image Segmentation Using K-Means Clustering and Improved Watershed Algorithm," in *2006 IEEE Southwest Symposium on Image Analysis and Interpretation*, Denver, CO, 2006, pp. 61–65. doi: 10.1109/SSIAI.2006.1633722.

[3] C. Dong *et al.*, "An Improved Random Walker with Bayes Model for Volumetric Medical Image Segmentation," *Journal of Healthcare Engineering*, vol. 2017, pp. 1–11, 2017, doi: 10.1155/2017/6506049.

[4] V. G. Kanas, E. I. Zacharaki, E. Dermatas, A. Bezerianos, K. Sgarbas, and C. Davatzikos, "Combining Outlier Detection with Random Walker for Automatic Brain Tumor Segmentation," in *Artificial Intelligence Applications and Innovations*, vol. 382, L. Iliadis, I. Maglogiannis, H. Papadopoulos, K. Karatzas, and S. Sioutas, Eds. Berlin, Heidelberg: Springer Berlin Heidelberg, 2012, pp. 26–35. doi: 10.1007/978-3-642-33412-2_3.

[5] W. Deng, W. Xiao, H. Deng, and J. Liu, "MRI brain tumor segmentation with region growing method based on the gradients and variances along and inside of the boundary curve," in

*2010 3rd International Conference on Biomedical Engineering and Informatics*, Yantai, China, Oct. 2010, pp. 393–396. doi: 10.1109/BMEI.2010.5639536.

[6] N. S. M. Raja, S. L. Fernandes, N. Dey, S. C. Satapathy, and V. Rajinikanth, “Contrast enhanced medical MRI evaluation using Tsallis entropy and region growing segmentation,” *J Ambient Intell Human Comput*, May 2018, doi: 10.1007/s12652-018-0854-8.

[7] G. Yang, J. Lv, Y. Chen, J. Huang, and J. Zhu, “Generative Adversarial Networks (GAN) Powered Fast Magnetic Resonance Imaging -- Mini Review, Comparison and Perspectives,” *arXiv:2105.01800 [cs, eess]*, May 2021, Accessed: Jul. 07, 2021. [Online]. Available: http://arxiv.org/abs/2105.01800

[8] Y. Wu *et al.*, “Fast and Automated Segmentation for the Three-Directional Multi-Slice Cine Myocardial Velocity Mapping,” *Diagnostics*, vol. 11, no. 2, p. 346, Feb. 2021, doi: 10.3390/diagnostics11020346.

[9] Y. Jin *et al.*, “3D PBV-Net: An automated prostate MRI data segmentation method,” *Computers in Biology and Medicine*, vol. 128, p. 104160, Jan. 2021, doi: 10.1016/j.compbiomed.2020.104160.

[10] A. Ammari, R. Mahmoudi, B. Hmida, R. Saouli, and M. H. Bedoui, “A review of approaches investigated for right ventricular segmentation using short-axis cardiac MRI,” *IET image process*, vol. 15, no. 9, pp. 1845–1868, Jul. 2021, doi: 10.1049/ipr2.12165.

[11] O. Bernard *et al.*, “Deep Learning Techniques for Automatic MRI Cardiac Multi-Structures Segmentation and Diagnosis: Is the Problem Solved?,” *IEEE TRANSACTIONS ON MEDICAL IMAGING*, vol. 37, no. 11, p. 12, 2018.

[12] O. Ronneberger, P. Fischer, and T. Brox, “U-Net: Convolutional Networks for Biomedical Image Segmentation,” *arXiv:1505.04597 [cs]*, May 2015, Accessed: Nov. 17, 2019. [Online]. Available: http://arxiv.org/abs/1505.04597

[13] G. Huang, Z. Liu, L. van der Maaten, and K. Q. Weinberger, “Densely Connected Convolutional Networks,” *arXiv:1608.06993 [cs]*, Jan. 2018, Accessed: Nov. 21, 2020. [Online]. Available: http://arxiv.org/abs/1608.06993

[14] C. Luo, C. Shi, X. Li, and D. Gao, “Cardiac MR segmentation based on sequence propagation by deep learning,” *PLOS ONE*, p. 13.

[15] M. R. Avendi, A. Kheradvar, and H. Jafarkhani, “A Combined Deep-Learning and Deformable-Model Approach to Fully Automatic Segmentation of the Left Ventricle in Cardiac MRI,” *arXiv:1512.07951 [cs]*, Dec. 2015, Accessed: Nov. 17, 2019. [Online]. Available: http://arxiv.org/abs/1512.07951

[16] F. Isensee, P. Jaeger, P. M. Full, I. Wolf, S. Engelhardt, and K. H. Maier-Hein, “Automatic Cardiac Disease Assessment on cine-MRI via Time-Series Segmentation and Domain Specific Features,” *arXiv:1707.00587 [cs]*, vol. 10663, 2018, doi: 10.1007/978-3-319-75541-0.

[17] C. F. Baumgartner, L. M. Koch, M. Pollefeys, and E. Konukoglu, “An Exploration of 2D and 3D Deep Learning Techniques for Cardiac MR Image Segmentation,” *arXiv:1709.04496 [cs]*, Oct. 2017, Accessed: Mar. 04, 2021. [Online]. Available: http://arxiv.org/abs/1709.04496

[18] C. Zotti, Z. Luo, A. Lalande, O. Humbert, and P.-M. Jodoin, “GridNet with automatic shape prior registration for automatic MRI cardiac segmentation,” *arXiv:1705.08943 [cs]*, Sep. 2017, Accessed: Mar. 04, 2021. [Online]. Available: http://arxiv.org/abs/1705.08943

[19] M. Khened, V. A. Kollerathu, and G. Krishnamurthi, “Fully convolutional multi-scale residual DenseNets for cardiac segmentation and automated cardiac diagnosis using ensemble of

classifiers," *Medical Image Analysis*, vol. 51, pp. 21–45, Jan. 2019, doi: 10.1016/j.media.2018.10.004.

[20] O. Oktay *et al.*, "Anatomically Constrained Neural Networks (ACNNs): Application to Cardiac Image Enhancement and Segmentation," *IEEE Trans. Med. Imaging*, vol. 37, no. 2, pp. 384–395, Feb. 2018, doi: 10.1109/TMI.2017.2743464.

[21] M. M. A. Hadhoud, M. I. Eladawy, A. Farag, F. M. Montevecchi, and U. Morbiducci, "Left Ventricle Segmentation in Cardiac MRI Images," p. 6.

[22] Y. Luo, L. Xu, and L. Qi, "A cascaded FC-DenseNet and level set method (FCDL) for fully automatic segmentation of the right ventricle in cardiac MRI," *Med Biol Eng Comput*, vol. 59, no. 3, pp. 561–574, Mar. 2021, doi: 10.1007/s11517-020-02305-7.

[23] X. Zhou *et al.*, "Systematic and Comprehensive Automated Ventricle Segmentation on Ventricle Images of the Elderly Patients: A Retrospective Study," *Front. Aging Neurosci.*, vol. 12, p. 618538, Dec. 2020, doi: 10.3389/fnagi.2020.618538.

[24] J. Chen *et al.*, "JAS-GAN: Generative Adversarial Network Based Joint Atrium and Scar Segmentation on Unbalanced Atrial Targets," *IEEE J. Biomed. Health Inform.*, pp. 1–1, 2021, doi: 10.1109/JBHI.2021.3077469.

[25] M. Li, C. Wang, H. Zhang, and G. Yang, "MV-RAN: Multiview recurrent aggregation network for echocardiographic sequences segmentation and full cardiac cycle analysis," *Computers in Biology and Medicine*, vol. 120, p. 103728, May 2020, doi: 10.1016/j.compbiomed.2020.103728.

[26] Y. Mo *et al.*, "The Deep Poincar\'e Map: A Novel Approach for Left Ventricle Segmentation," *arXiv:1703.09200 [cs]*, Oct. 2018, Accessed: May 24, 2021. [Online]. Available: http://arxiv.org/abs/1703.09200

[27] Z. Shi *et al.*, “Bayesian VoxDRN: A Probabilistic Deep Voxelwise Dilated Residual Network for Whole Heart Segmentation from 3D MR Images,” in *Medical Image Computing and Computer Assisted Intervention – MICCAI 2018*, vol. 11073, A. F. Frangi, J. A. Schnabel, C. Davatzikos, C. Alberola-López, and G. Fichtinger, Eds. Cham: Springer International Publishing, 2018, pp. 569–577. doi: 10.1007/978-3-030-00937-3_65.

## Part - II

# Spectroscopy in cardiac diagnosis