2019 IEEE 19th International Conference on Bioinformatics and Bioengineering (BIBE)

Automated Segmentation and 4D Reconstruction of the Heart Left Ventricle from CINE MRI

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***Abstract*—Heart disease is highly prevalent in developed countries, causing 1 in 4 deaths. In this work we propose a method for a fully automated 4D reconstruction of the left ventricle of the heart. This can provide accurate information regarding the heart wall motion and in particular the hemodynamics of the ventricles. Such metrics are crucial for detecting heart function anomalies that can be an indication of heart disease. Our approach is fast, modular and extensible. In our testing, we found that generating the 4D reconstruction from a set of 250 MRI images takes less than a minute. The amount of time saved as a result of our work could greatly benefit physicians and cardiologist as they diagnose and treat patients.**

***Index Terms*—Magnetic Resonance Imaging, segmentation, reconstruction, cardiac, machine learning, ventricle**

I. Introduction

Heart diseases are the leading cause of death for both men and women; just in the United States, approximately 630,000 people die each year of heart disease [1]. Due to the high number of cases and the importance of treatment, cardiologists have limited time to perform the tests and screenings required to diagnose heart disease. One method for diagnosing heart disease consists of measuring the amount of blood that is flowing through the heart. This measurement is called the ejection fraction (EF) and is usually measured in the left ventricle of the heart. A normal person will have an EF between 50 and 70 percent [2].

Currently, physicians can measure the EF through various medical imaging modalities, including ultrasound and MRI. In either modality, this requires prior knowledge of the left ventricle location and area, as well as an expert radiologist that is able to correctly identify the left ventricle. Although there are automatic methods to identify and segment the left ventricle, they may not be as accurate as manual methods. Therefore, in many cases, the radiologist must manually analyze the images, segment the left ventricle, and measure the EF. This process is prone to human error and can take a long time to complete, as seen in [3], where the average time it took per image to manually trace the epicardium and endocardium was 25.4 seconds. When heart disease affects so many people, the time it takes for diagnosis is valuable and shortening it is of the utmost importance. In addition, state-of-art MRI scanners enable interactive control of the MRI scanner during data acquisition (i.e. on-the-fly). These emerging techniques offer unique opportunities in optimizing data acquisition; albeit require fast and reliable data processing.

Within this context, we propose a fast, fully automated method that generates a 4-dimensional (4D) reconstruction of the left ventricle (LV). This reconstruction can be used to quickly and accurately calculate the ventricular motion parameters such as the end-diastolic volume (EDV), end-systolic volume (ESV), and the EF. Our approach takes as input a CINE sequence of MRI images of the heart and outputs an accurate 4D reconstruction of the left ventricle that is able to visualize motion as the heart is beating. Our approach is able to generate a reconstruction from a set of 250 images in under a minute, greatly reducing the amount of time it could take a radiologist to perform the same process manually and in turn reducing the amount of time required for a diagnosis. In the following sections, we explain how our method works, describe the datasets we use, show our experiments and results, and discuss the ramifications of our findings.

II. Methods

One of the complaints we most often hear from physicians is that it takes too long to perform a test and obtain the results. Furthermore, there is great interest in the continuous development of new imaging and data visualization methods. For these reasons, we constrained our system to be fast, modular, and extensible. Each step in our process is independent to any other process and can be exchanged with new or improved methods as our work moves forward. In Fig. 1, we show the complete

end-to-end automated process we designed for 4D ventricle reconstruction. First, we obtain a complete set of CINE images from the MRI machine. We then feed these images to a machine learning module that automatically segments the left ventricle. Afterwards, we pass the segmentation masks to the 3D reconstruction module which generates a 3D model of the ventricle for each frame in the CINE sequence. Finally, we interpolate the frames together to obtain our final 4D reconstruction and interpose it with the original MRI scan for visualization. We go into more details for each main step in the following sub-sections. All experiments and tests were performed on a single desktop computer equipped with a quad-core 3.5 GHz CPU, 16 GB RAM and an NVIDIA GTX 1080 Ti GPU.

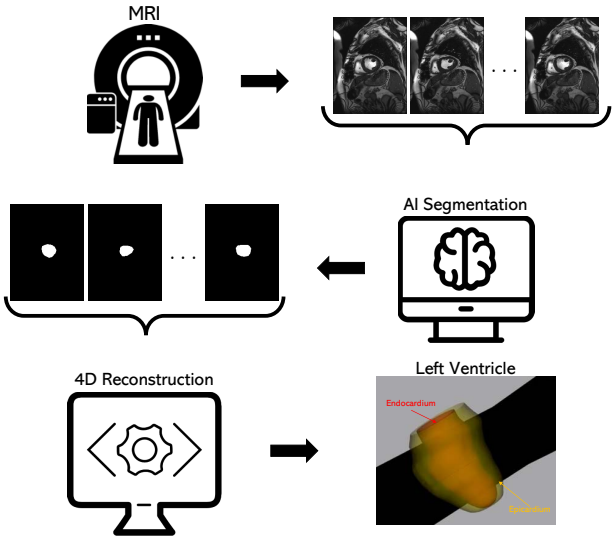

Fig. 1. Diagram showing the design of our fully automated 4D ventricle reconstruction system.

A. Datasets

For this work, we use two different datasets to design, develop, and test our methods. The first dataset is the *Left Ventricle Segmentation Challenge* (LVSC) [4] dataset obtained from The Cardiac Atlas Project [5]. This dataset consists of two partitions of 100 different cases each, one for training and one for validation. For the training partition there is an average of 378 images per case and a total of 37860 images. The training partition also includes ground truth segmentation masks obtained by expert rating consensus. The segmentations cover both the endocardium and epicardium of the left ventricle. We use the training partition to train our segmentation model.

The second dataset was obtained from the Methodist Hospital in Houston. The dataset consists of short-axis cardiac MRI images from a single patient. The dataset has 10 heart slices over 25 frames, a total number of 250 images. Along with the MRI images, we were provided with manual segmentation masks of the left ventricle endocardium for each image. These masks were segmented by a radiologist belonging to the Methodist staff. Since we have the privilege of working with data, we rely on it as the ground truth for our reconstruction efforts. For clarity, we will refer to this dataset as Methodist Left Ventricle Segmentation (MLVS) from now on.

B. Segmentation

There have been various proposed methods for left ventricle segmentation, ranging from thresholding methods that compare signal intensities in the image against a threshold value to obtain the segmentation [6], [7], atlas based methods that use a statistical atlas to compare and adjust the segmentations into accurate ones [8]–[10], to more recent deep learning methods that rely on prior data to form a probabilistic model capable of identifying new instances of input data [11]–[15]. In order to select the best available segmentation method, we had to make sure that it complied with our system constraints. We analyzed and explored our options and opted for a machine learning approach due to the massive segmentation speed advantages over the other methods. There were two different segmentation algorithms that we investigated: U-Net [15] and a Fully Convolutional Neural Network (FCNN) approach [11].

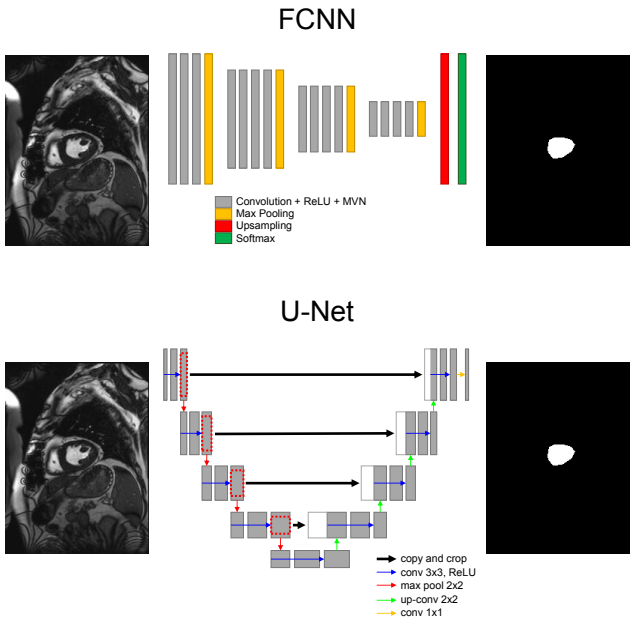

Fig. 2. Diagrams of (a) the U-Net architecture and (b) the FCNN architecture.

U-Net is itself a fully convolutional neural network architecture designed specifically for biomedical image segmentation. The network famously consists of a downsampling or encoding path and an upsampling or decoding path, giving it its namesake U shape. The FCNN proposed by Phi Vu Tran in [11] consists of a simpler feed-forward architecture. We compare both architectures briefly in Fig. 2. In order to reliably compare both algorithms, we first trained them using the same training portion from the LVSC dataset. To

verify the segmentation performance, we used the ground truth segmentation masks from the MLVS dataset to compute the DICE Similarity Coefficient and the Jaccard Index metrics. These metrics can be used to compare the similarity of two sets, and in our case the similarity between two segmentation masks.

The DICE Similarity Coefficient is defined as:

$$D = \frac{2 \times |A \cap B|}{|A| + |B|} \tag{1}$$

where A and B are two different sets. In terms of a binary segmentation mask, A = True Positives and B = True Negatives. Having this in mind, we find that the DICE similarity is an equivalent to the F1-Score, which is often used as machine learning performance metric. On the other hand, the Jaccard Index is defined as:

$$J = \frac{|A \cap B|}{|A \cup B|} \tag{2}$$

where Equation (2) is the intersection of the sets (or binary masks) over the union. These are two of the most commonly used metrics for segmentation.

TABLE I
COMPARISON OF SEGMENTATION PERFORMANCE

Model	DICE Similarity	Jaccard Index
U-Net	0.83	0.76
FCNN	**0.90**	**0.82**

In Table I, we can see that the FCNN model outperformed the U-Net model significantly. Additionally, we noted that the U-Net model requires a larger amount of memory to run when compared to the FCNN model which is another advantage of using the FCNN over the U-Net model. This smaller memory footprint allowed us to run multiple instances of the FCNN in a single GPU which contributed to faster inference of the left ventricle's epicardium and endocardium. Therefore, we decided to move forward with the FCNN model for the automated segmentation aspect of our system since it would enable the most accurate 4D reconstruction.

C. 4D Reconstruction

For a dataset of *M* frames and *N* slices per frame, the 4D reconstruction is obtained by performing a 3D surface reconstruction of each frame in the CINE sequence and then adding them together into a 4D motion visualization. The 3D surfaces are modeled from the segmentation masks and the meta-data found in the MRI DICOM file. To create the 3D surface for one frame, the first step is to extract a set of 3D points from the segmentation mask of each slice. We then interpolate the points of each slice using a closed spline, resulting in *N* different rings. We then choose a point in ring_0 and find the closest point to it in ring_1. This is repeated for each pair of rings until ring_{n-1}. Taking those *N* points and their mirrored points across the rings, we interpolate an open spline. Once we have the splines, we apply Hugues Hoppes surface reconstruction algorithm [16] on the points constituting the splines to generate the 3D mesh. Finally, this entire process is repeated on every frames segmentation to create the 4D motion.

III. EXPERIMENTS AND RESULTS

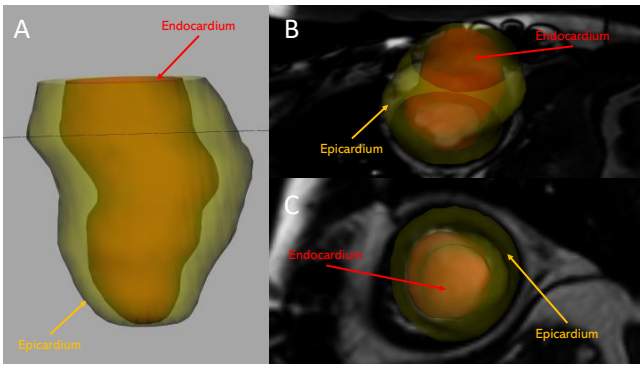

Fig. 3. Final 4D reconstruction. We can see the MRI image interposed with the 3D volume of the left ventricle, with the endocardium in red and the epicardium in yellow.

In Fig. 3 we show the final 4D reconstruction as it is output by our system. The resulting reconstruction seems of great quality from a qualitative viewpoint. In order to provide a more quantitative assessment, we decided to use the 4D reconstruction to do some real-world scenario computations that cardiologists would be interested in. Mainly, we used the reconstruction to compute the EDV, ESV, and the EF for the left ventricle. The EDV and ESV are found by simply measuring the volume in the ventricle during the heart's diastole phase (muscle relaxes) and the systole phase (muscle contracts), respectively. The EF is a function that describes how much blood is ejected from the left ventricle on each heartbeat. It is defined as:

$$EF = \frac{EDV - ESV}{EDV} \tag{3}$$

We performed the 4D reconstruction using the ground truth segmentation masks (GT 4D) and the automated segmentation masks (Auto 4D) and computed the values for each by looking at the 3D volumes exclusively. We also estimated the values from the MRI images directly by using the ground truth segmentations (GT Seg) and the automated segmentations (Auto Seg) to compute the area of the segmentation mask for each slice and then extrapolating the volume with the information in the DICOM meta-data. In Table II, we show the results from our tests.

From these results, we see that although the values for ESV and EDV vary across the different methods, the EF is within a small percentage of error of 7.3% from the ground truth. Based on this observation, we consider that our 4D reconstruction is quantitatively correct and accurate. Finally, in Fig. 4, we present a graph showing how the left ventricle volume changes through time as the heart is beating. The graph compares the

TABLE II
COMPARISON OF HEART FUNCTION BIO-MARKERS.

Method	EDV	ESV	EF
GT 4D	184.59 ml	128.96 ml	30.14%
Auto 4D	158.54 ml	114.25 ml	27.94%
GT Seg	179.2 ml	125.15 ml	30.16%
Auto Seg	170.75 ml	123.01 ml	27.96%

values obtained from the 4D reconstruction against the values obtained from the MRI image estimations.

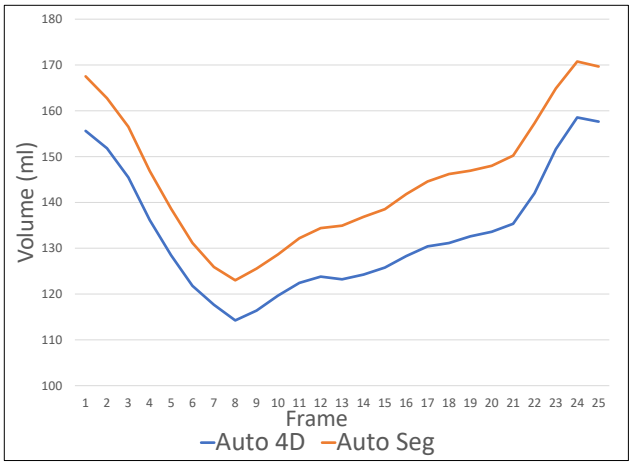

Fig. 4. Plot showing the volume of the left ventricle as it changes though time. We compare the values given by the 4D volume reconstruction against the estimated values computed from the MRI images and meta-data.

IV. CONCLUSION

In this work, we described a computational pipeline for automated segmentation and 4D reconstruction of the LV of the human heart from CINE MRI sets. The automated pipeline was investigated by comparing clinically relevant parameters that characterize the LV motion to the corresponding ground truths for the same datasets. We calculated the end-diastolic volume (EDV), end-systolic volume (ESV) and ejection fraction (EF); these are clinically important in the detection and characterization of heart wall abnormalities secondary to heart disease. We found that the values calculated from the automated pipeline were within 7.3% error compared to those calculated from the ground truth. Furthermore, the proposed pipeline was proved to be fast within the clinical realm. On a personal computer with a quad-core 3.5 GHz CPU, 16 GB RAM and an NVIDIA GTX 1080 Ti GPU, the automatic segmentation and 4D reconstruction of the beating heart from a set of 250 CINE MRI images (10 slices and 25 time frames) took 35 seconds on average. We are further developing the pipeline toward two directions: (a) link it to the MRI scanner for data segmentation and reconstruction on-the-fly, i.e. as the raw MRI data are collected, and (b) to entirely run on a GPU for further acceleration so it can be used with MRI guided cardiac interventions. With its current and future features, the described pipeline will benefit conventional diagnosis by speeding up the workflow, as well as enhance MR guided interventions and enable interactive scanner control.

ACKNOWLEDGMENT

This work was supported by the National Science Foundation award CNS-1646566. All opinions, findings, conclusions or recommendations expressed in this work are those of the authors and do not necessarily reflect the views of our sponsors.

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