SB³C2021
Summer Biomechanics, Bioengineering and Biotransport Conference
June 14-18, Virtual

A DEEP-LEARNING APPROACH FOR DIRECT WHOLE-HEART MESH RECONSTRUCTION

Fanwei Kong and Shawn C. Shadden

Department of Mechanical Engineering
University of California, Berkeley
Berkeley, California, USA

INTRODUCTION

Computer models of anatomical structures reconstructed from volumetric medical images are increasingly used for a number of clinical applications. In particular, computer models of the heart, if combined with biophysical simulations, can assist understanding, diagnosis and treatment of cardiac diseases [1-2]. Creating accurate patient-specific models of the heart from image data requires significant time and human efforts; this is arguably the #1 factor limiting clinical applications. Deep learning methods can train neural networks from existing data to automatically process medical images and generate whole heart reconstructions. Such methods may accelerate the model generation process to enable high-throughput, large-cohort analyses of patient-specific cardiac function.

Most deep learning methods have focused on segmentation of the cardiac structures by pixel classification [3-4]. This results in an implicit representation of cardiac structures, however simulation and even some visualization methods require explicit representations—typically as unstructured meshes. Besides requiring additional surface processing techniques to generate meshes from the segmentation, these prior approaches suffer from a number of limitations including disconnected regions or incorrect surface topology due to erroneous segmentation and stair-case artifacts from limited image resolution [3].

We propose a novel approach that directly predicts whole heart surface meshes from volumetric images by predicting deformation on mesh vertices from a pre-defined mesh template using a graph convolutional neural network. We demonstrate promising performance of generating high-resolution and high-quality heart reconstructions from both CT and MR data. Furthermore, our method shows improved robustness to limited data, and can more efficiently produce temporally-consistent and feature-corresponding predictions of heart motion from CT or MR cine sequences, and therefore can potentially be applied for efficiently constructing 4D whole heart dynamics.

METHODS

Dataset Information: Contrast-enhanced CT images or MR images that cover the whole heart were obtained from four existing public datasets: multi-modality whole heart segmentation challenge (MMWHS), orCalScore challenge, left atrial wall thickness challenge and left atrial segmentation challenge. From these data, we used a total of 87 CT images and 41 MR images to train our model, and 15 CT images and 6 MR images to validate the model. The final performance of our model was evaluated on the MMWHS held-out test dataset that contains 40 CT images and 40 MR images. Furthermore, additional time-series CT images were collected to evaluate the performance of our approach on time-series image data.

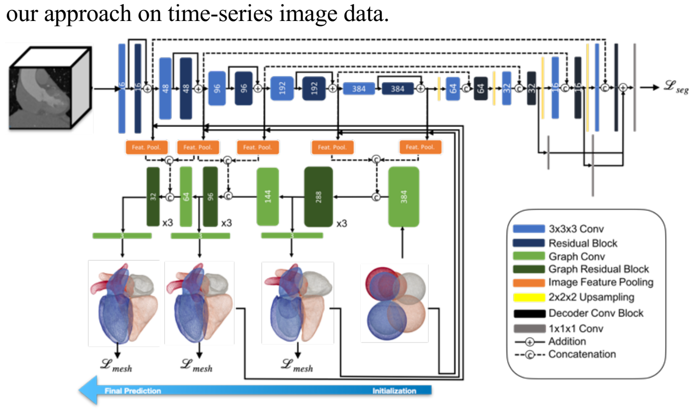

Figure 1: Proposed automatic whole heart reconstruction approach

Neural Network Architecture: As shown in Fig 2, our framework consists of three components to predict the whole heart meshes from a volumetric input image. For an 3D image volume, our framework uses an image encoding module that extracts and encodes image features. From these image features, we use a mesh deformation module that combines features from images and meshes to predict deformation of mesh vertices from sphere mesh templates. The mesh deformation module consists of three deformation blocks with graph convolutional layers that progressively deform mesh templates to match with the corresponding tissue boundaries. Furthermore, our framework uses a segmentation module that predict a binary segmentation map to enable additional supervision using ground truth annotations.

Neural Network Optimization: The training of the neural network model was supervised by 3D ground truth meshes of the whole heart as well as a binary segmentation representing the occupancy of the heart in the input image. The ground truth whole heart meshes were extracted from the segmentation of cardiac structures using a marching cube algorithm. We considered two categories of loss functions for the mesh predictions, geometry consistency losses and regularization losses in the training process. The geometry consistency losses include point and normal consistency losses while the regularization losses include edge length and Laplacian losses. The parameters in the neural network models were optimized by minimizing the loss functions using the Adam stochastic gradient descent algorithm.

RESULTS

Our method is able to automatically generate high-resolution whole-heart reconstructions (10k surface vertices for each cardiac structure) from an input image within half a second on a modern GPU. We compare the performance of whole-heart reconstructions from our method against two baselines: 2D UNet [5] and a modified 3D UNet [6]. Table 1 shows the average Dice score (a similarity index) of the reconstruction results of both the whole heart and individual cardiac structures for the MMWHS test dataset. For both CT and MR data, our method consistently outperformed our baselines in terms of Dice scores for both whole heart and all individual cardiac structures.

		EPI	LA	LV	RA	RV	AO	PA	WH
CT	Ours	**0.899**	**0.932**	**0.940**	**0.892**	**0.910**	**0.950**	**0.852**	**0.918**
	2D UNet	**0.899**	0.931	0.931	0.877	0.905	0.934	0.832	0.911
	3D UNet	0.863	0.902	0.923	0.868	0.876	0.923	0.813	0.888
MR	Ours	**0.797**	**0.881**	**0.922**	**0.888**	**0.892**	**0.890**	**0.816**	**0.882**
	2D UNet	0.795	0.864	0.896	0.852	0.865	0.869	0.772	0.859
	3D UNet	0.761	0.852	0.879	0.866	0.828	0.742	0.764	0.840

Table 1: A comparison of prediction accuracy on MMWHS MR and CT test datasets from different methods.

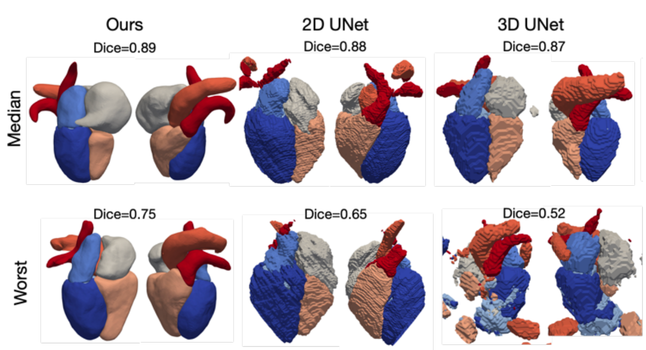

Figure 2: Visualizations of the median and worst reconstruction results among the test dataset in terms of whole-heart Dice scores.

Figure 2 visualize the median and worst results from the different methods for MR images, respectively, from the MMWHS test dataset. As shown, our method is able to construct smooth geometries while segmentation-based methods, such as the 2D UNet or 3D UNet, produced surfaces with staircase artifacts or disconnected regions that would require post-processing to remove or connect.

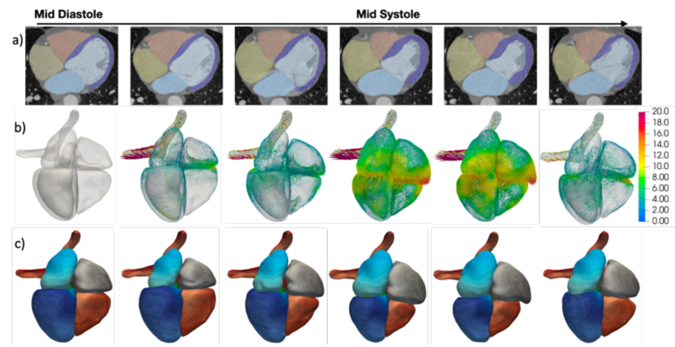

Figure 3: Whole-heart reconstruction results for time-series CT data. A) predicted segmentation b) mesh deformation vectors since late diastole and c) the feature correspondence maps of meshes.

Figure 3 displays example whole-heart reconstructions from our methods on time-series CT data. Although our model predicts mesh reconstructions independently from each time frame, it is able to consistently deform the template meshes so that the same mesh vertices on the template are generally mapped to the same region of the reconstructed geometries across different time frames, as shown by the color maps of vertex IDs in Figure 3. Moreover, as shown, our method is able to capture the minor changes between time frames whereas 2D and 3D UNet results (not shown) often had significant segmentation discrepancies between time frames. Therefore, our method can potentially be applied to efficiently construct 4D dynamic whole-heart models to capture the motion of a beating heart by computing the deformation field on each mesh vertex, as displayed in Figure 3.

DISCUSSION

Automated image-based reconstruction of cardiac anatomy and the concomitant geometric representation using unstructured meshes is important to a number of applications, including visualization of patient-specific heart morphology and computational simulations of cardiac function. We have demonstrated the advantages of this method over prior segmentation-based approaches in terms of both precision and surface quality [4-6]. Namely, the use of a template mesh can introduce topological constraints so that predicted cardiac structure are diffeomorphic to the template. Thus, our template-based approach enables one to eliminated disconnected regions and greatly reduce erroneous topological artifacts often encountered with prior methods. Furthermore, the method produced temporally consistent and feature-corresponding predictions by consistently mapping mesh vertices on the templates to similar structural regions of the heart. While the cardiac structures of interest were diffeomorphic to spheres, the presented method has the potential to be generalized to anatomical structures with a different topology, by using a different template mesh with the required topology.

ACKNOWLEDGEMENTS

This work was supported by the NSF, Award #1663671.

REFERENCES

[1] Prakosa et al., *Nature Biomed Eng*, 2(10), Oct, pp. 732–740, 2018.
[2] Chnafa et al., *Annals of Biomed. Eng.* 44(04), 2016
[3] Kong et al., *J of Biomechanical. Eng.* 142(11), 09. 111011, 2020.
[4] Zhuang et al., *Med Image Analysis*, 58, 101537, 2019.
[5] Ronneberger et al., *MICCAI*, *Springer*, pp 234-241, 2015.
[6] Isensee et al., *MICCAI*, *Springer* pp. 287–297, 2017.