**INTRODUCTION**

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Cardiovascular Segmentation with Convolutional Neural Networks

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In recent years, numerical simulations of cardiovascular biomechanics have been shown to have a range of useful applications, such as aiding in understanding cardiovascular biomechanics and clinical applications such as analysis of atherosclerosis [**samady]** and coronary artery disease [**taylor]**. However, cardiovascular biomechanics simulations require accurate three dimensional digital models of the cardiovascular anatomy of the subject under consideration. The process of digital anatomical model construction for a particular subject is known as patient-specific modeling [**taylor**]. During model construction, typically volumetric medical images, such as magnetic resonance (MR) or computed tomography (CT) scans, are used.

SimVascular is an open-source software package with which users can perform patient-specific blood flow simulations [**sv website] [sv paper]**. SimVascular contains functionality to visualize and segment medical images, construct meshes for numerical simulations and perform cardiovascular fluid dynamics and fluid-structure interaction simulations. At present, to segment medical images with SimVascular, users may perform manual segmentation or use a number of classical image processing methods such as thresholding **[threshold paper?**] or active contours [**sethian**][**ken wang**].

Manual segmentation produces accurate segmentations, however it requires significant time, effort and expertise from the user. Classical image processing methods can also be used to produce high-quality segmentations but typically require significant time investments to tune method specific parameters which are sensitive to individual image quality, anatomical region and vessel size. As such it is difficult to use manual segmentation and classical image processing methods on large numbers of medical images, containing varying anatomical regions. Medical image segmentation is thus a significant bottleneck in performing numerical cardiovascular biomechanics simulations, both for users of SimVascular and for patient-specific modeling in general. It is therefore desirable to find, or develop, cardiovascular medical image segmentation methods that can be used without significant user intervention across a wide range of medical images.

Convolutional Neural Networks (CNNs) are a class of machine learning models tailored towards processing visual data. Recently (CNNs) have been used to develop accurate medical image processing methods. Example applications include, among others, pancreas segmentation [**pancreas**], brain lesion detection [**brain lesion**], brain tumor segmentation [**brain tumor**], kidney segmentation [**unet]** and cardiovascular edge detection [**jameson**]. Segmentation methods developed with CNNs are typically parameter-free making them a promising approach for improving the patient-specific modeling process.

However, it is not evident how to use segmentations produced by CNNs to construct patient-specific models that can be used for cardiovascular biomechanics simulations. Therefore in this work we propose a method with which CNN-based segmentations of medical images can be used to construct accurate 3D cardiovascular models that can then be used for numerical blood flow simulations. The method consists of (1) using CNNs to segment image patches extracted from medical images with user-annotated vessel centerlines (2) extracting vessel boundaries from the produced segmentations and (3) combining the extracted boundaries to form a solid model. We demonstrate that a CNN-based approach outperforms an active contour method when compared to vessel boundaries produced by users with manual segmentation.

**METHODS**

The proposed method for cardiovascular model construction in this work is based on the current model construction process available through SimVascular that is described in [**sv paper**][**ken wang**]. Therefore we briefly describe the current model construction process here.

Explain what was examined, developed or done to answer the research questions. Explain how it was done. Explain how the resulting data/results were analyzed.

Follow directions in the instruction document for equations. Equations should be set apart from the body of the text and centered. Equations should be numbered consecutively, using numerals enclosed in parentheses and positioned flush right along the final baseline of the equation. Here is an example equation:

(1)

**RESULTS**

Present results in decreasing order of importance or chronologically. Refer to figures and tables parenthetically. Do not duplicate data in the text, figures and tables. That the major results in the text, referencing the figures and tables parenthetically as appropriate.

**Figure 1: Follow directions for Figures in the instructions document. Figure captions are centered below the graphic.**

**Table 1: Follow directions for Tables in the instructions document. Table captions are centered above the table.**

**DISCUSSION**

The primary functions of the Discussion are to answer the research question and/or put the results in context and explain their significance. Discuss the results of your study and their significance. Explain how your findings compare with existing knowledge on the subject. Does your answer fit with current thinking? Can you explain conflicts or discrepancies between your results and the results of others? What new information is provided by your study that complements or contradicts previous work? Provide the reader with a balanced presentation of the strengths and limitations. End with a clear statement such as the implications of your findings, or with speculations based on the findings.

**ACKNOWLEDGEMENTS**

Please acknowledge any grant or other funding support or the assistance of others as appropriate.

**REFERENCES**

References should be arranged in numerical order according to the sequence of citations within the text. Each reference should include the last name of at least the first author followed by his/her initials, the journal name, volume, pages and year. You may include more detailed reference information if space in your particular abstract allows.

Sample Reference:

[5] Bergmann, G et al., *J Biomech*, 34:859-871, 2001.