SB³C2024
Summer Biomechanics, Bioengineering and Biotransport Conference
June 11-14, Lake Geneva, WI, USA

COMPARATIVE STUDY OF IMAGE-BASED MODELING USING A NOVEL MEDICAL-IMAGE-TO-REDUCED-ORDER-SIMULATION FRAMEWORK

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INTRODUCTION

Cardiovascular disease (CVD) remains the global leading cause of death. Recent developments in image-based modeling and patient-specific hemodynamic simulation have proven effective in enabling virtual personalized diagnosis, preventive care, and treatment planning without the risks of invasive measures. Despite the growth of such technologies, creating an image-based simulation from medical image (CT or MRI) scans is labor-intensive [1], and performing accurate computational fluid dynamics (CFD) simulations generally requires extensive technical knowledge of numerical methods and supercomputing resources [2].

Developing automated and efficient capabilities to go directly from medical images to simulation results, even if those results are approximate, can be highly informative in several scenarios including timely decision support, screening, boundary condition tuning, uncertainty quantification, treatment design, etc. With this in mind, we have been developing a streamlined process to produce reduced-order model (ROM) simulations of patient-specific hemodynamics from volumetric angiography. This framework leverages lumped-parameter and 1D Navier-Stokes solvers built into our SimVascular software [3, 4] coupled with recent machine learning (ML) model construction we have developed to automate the segmentation of vascular models from medical images. Work towards a medical-image-to-reduced-order-simulation (MIROS) framework we are developing is presented here and used to conduct a comparative study that examines the impact of machine learning models versus traditionally constructed models on ROM simulation results.

METHODS

The MIROS framework relies on automation of the vascular model construction and setting up and running a ROM flow solver to compute flow rate and pressure through each vessel. To verify our implementation, we compared the output of MIROS (i.e. flow and pressure calculations) to ROM flow and pressure calculations using traditional model construction for a series of cases in the Vascular Model Repository (VMR) (http://vascularmodel.org) – herein referred to as the VMR model/results. The main difference between MIROS and VMR is that we employ ML automated vascular segmentation, whereas the VMR models were manually constructed. We also automate the simulation process, but the flow solvers are the same. Also, to ensure consistent comparison of flow and pressure results, we use the same boundary conditions and solver parameters in MIROS as was used to generate the VMR results.

Segmentation. MIROS relies on a novel method called Sequential Segmentation (SegSeg) for automated segmentation of the vasculature. SeqSeg requires a seed point for initialization (chosen at the inlet) and automatically traces the vasculature based on local vessel segments. The method captures bifurcations automatically and traces down branches as long as image resolution and segmentation quality allow. The local vessel segments are averaged together into a global segmentation that is returned as a binary segmentation map, where pixels labeled 1 represent blood vessel and 0 represent background. These segmentation maps are converted to surface meshes using marching cubes and smoothed using Laplacian smoothing to remove pixel artifacts.

Outlet Definition. SeqSeg can capture more vasculature than contained in the manually segmented VMR models. To apply boundary conditions consistently, we generally needed to truncate the MIROS models to terminate at the same approximate location as in the VMR models. We automatically compute the coordinates, radius, and unit tangent vector of each endpoint in each VMR model and then orient and scale clipping boxes to trim the corresponding MIROS model. We also keep the largest contiguous volume, which is then remeshed to produce our desired surface. This workflow is shown in Figure 1 for two representative models (an aortic arch model and an abdominal aorta model).

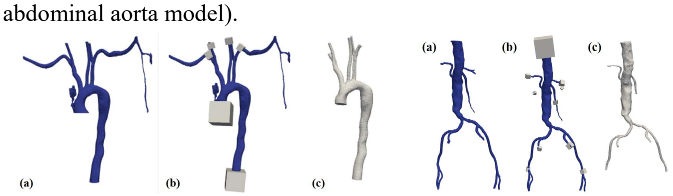


Figure 1: Creating consistent boundaries. (a) ML generated discrete surface (b) clipping boxes on ML surface (c) trimmed and filtered surface

Branch-matching. Because the ML method might capture a different number of branches than existing manually segmented surfaces in the VMR, we must match the branches and apply consistent boundary conditions to only outlets that are in common. Thus, the number of matching branches was determined, and any additional branches were merged into the vessel wall, which then become ignored during centerline extraction.

Centerline extraction. The MIROS and VMR 3D image-based models were used to generate a discrete centerline representation. The centerline extraction was performed using Vascular Modelling Toolkit (VMTK) functions that generated centerlines paths as well as vessel radius information along each vessel path. Both the discrete centerlines paths and associated areas along the paths were required for the ROM flow solver.

Boundary condition file preparation. We applied RCR boundary conditions at all outlets with RCR values tuned to clinical measurements and provided in the VMR [4]. In cases where the VMR contained a branch not included in the MIROS model, we ignore that boundary. Although this does not preserve the global consistency of the boundary conditions, we do this to keep the simulation consistent between MIROS and VMR models.

Solver. ROM simulation of flow and pressure was performed by solving the 1D Navier-Stokes equations using the SimVascular's 1D solver. Blood flow is assumed to be a Newtonian, incompressible fluid in a deforming and elastic domain. The governing equations consist of the continuity equation, a single axial momentum balance equation, a constitutive equation, and suitable initial and boundary conditions [5]. The overall workflow that MIROS models undergo is shown in Figure 2 for a representative model.

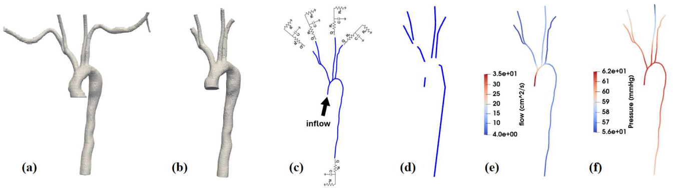


Figure 2: Pipeline workflow. (a) ML based surface (b) trimmed surface (c) centerline extraction (d) 1D model generation with boundary conditions (e)&(f) simulated flow and pressure mapped to centerline

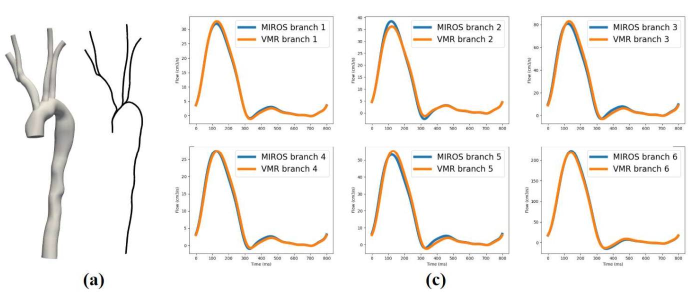
RESULTS

Averaged relative error over time. Each simulation was run for more than 7 cardiac cycles to reach a periodic solution. We compared relative error in mean flow and pressure of the last simulated cardiac cycle. We took the average of relative errors of each branch to get the relative error of the entire model. The results are shown in Table 1.

Table 1: Relative error averaged over the last cardiac cycle.

Surface Name	Relative Error: mean flow	Relative Error: mean pressure
0063_1001	3.575%	7.658%
0090_0001	0.6245%	0.2769%
0131_0000	0.2834%	0.2820%
0146_1001	1.002%	0.7106%
0174_0000	0.3172%	0.1566%
0176_0000	0.3306%	0.1925%
Average	1.022%	1.850%

Qualitative plots of flow and pressure over time. For qualitative comparison, we plotted the average flow and pressure of the same branches between the MIROS and VMR simulations over time to visualize the differences in simulation outcomes between the two modeling methods. As an example, Figure 3 below shows the plots of 0176_0000, whose overall mean relative error in flow was 0.3306% and overall mean relative error in pressure was 0.1925%.



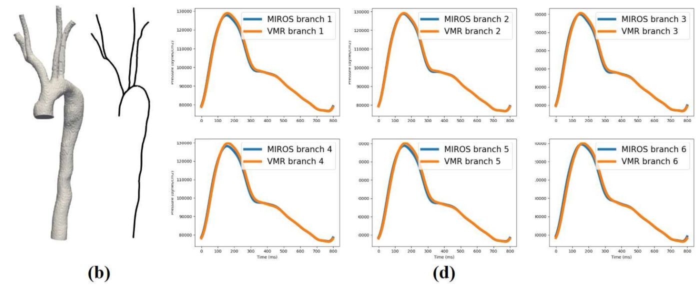


Figure 3. Qualitative comparison of flow and pressure result for each branch. (a) VMR model and its centerline (b) MIROS model and its centerline (c) flow comparison of each branch (d) pressure comparison of each branch.

DISCUSSION

We developed and automated a process for generating patient-specific, reduced-order model simulations of hemodynamics from volumetric angiography, culminating in a Medical-Image-to-Reduced-Order-Simulation (MIROS) framework. This framework significantly accelerates the traditionally hours-long tasks of vascular segmentation and the subsequent setup and execution of flow solvers, reducing overall time to a matter of minutes. Utilizing MIROS, we conducted a comparative analysis to evaluate the impact of different modeling approaches—manual segmentation versus machine learning segmentation—on simulation outcomes. Results indicate relatively modest errors of 1.022% for mean flow and 1.850% for mean pressure when averaged across all models and vessels. Given that consistent boundary conditions were used, these differences reflect errors in geometric reconstruction and are expected to be far less than errors typically associated with uncertainty of boundary conditions. This study demonstrates the efficiency and advantages of employing ML for automated vascular segmentation and highlights MIROS's capability to facilitate rapid hemodynamic simulations.

Limitations and Future Work. There are two noteworthy limitations that arise largely based on the nature of performing a comparative study. First, for some images, there were vessels captured by MIROS not captured by the VMR and vice-a-versa. Our analysis here focused only on models that contained vessels both methods captured. We plan to study this trade-off in future studies. Second, the boundary conditions for the MIROS model were the same as used for the VMR model. While this was necessary for consistent comparison, typical applications of modeling would require generation of de novo boundary conditions. We plan to study the application of MIROS to de novo analysis requiring generation of boundary conditions. Lastly, SimVascular has the ability to perform so-called 0D (also known as lumped-parameter) simulation based on a 3D model. We plan to connect such 0D ROM with MIROS, and to potentially consider more complex boundary conditions, such as used for coronary flow.

ACKNOWLEDGEMENTS

We acknowledge support from the NIH, Award No. 5R01LM013120 the NSF, Award No. 2310910 and 1663747.

REFERENCES

[1] Maher, G et al., *Cardiovasc Eng* Technol, 11(6):621-635, 2020.
[2] Randles, A et al., *Journal of Computational Science,* 9:70-75, 2015
[3] Updegrove, A et al., *Ann Biomed Eng*, 45, 525-541, 2017.
[4] Pfaller, M et al., *Int J Numer Method Biomed Eng*, 38(10):e3639, 2022.
[5] Hughes, T et al., *Mathematical Bioscience,* 18(1-2): 161-170, 1973.