CRIMSON: Towards a Software Environment for Patient-Specific Blood Flow Simulation for Diagnosis and Treatment

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Abstract. In this paper, we introduce the new software environment CRIMSON: CardiovasculaR Integrated Modelling and SimulatiON. This software provides a number of tools for medical image data analysis, preprocessing, segmentation and blood flow simulation. In this paper we describe the work flow necessary to perform such tasks as well its implementation in CRIMSON based on multiple well-established open-source libraries, such as MITK and OpenCASCADE. We show that the software is easy to use for both experts and non-experts in the field of hemodynamic modelling. The intuitive and responsive interface of CRIMSON facilitates learning and speeds up the model building process by up to a factor of two compared to the existing tool being used for the same purpose. The overall goal of this work is to produce a feature-rich and intuitive open-source blood flow modelling framework that can be used both by engineers and medical personnel.

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1 Introduction

According to the World Health Organization, cardiovascular disease is the leading cause of death worldwide. In recent years, significant resources have been devoted to cardiovascular research. Computer simulation tools in particular have been developed to understand the origin and progression of cardiovascular disease, study normal and pathologic cardiovascular function, and evaluate in-silico the performance of cardiovascular devices. In all cases, information of the patients' vasculature and physiology is required. In particular, the creation of a computer model from imaging data such as computed tomography (CT) or magnetic resonance imaging (MRI) is often the first step in the simulation effort. This task is followed by mesh generation, material and boundary condition specification, and simulation of physics. In this paper, we describe the design of CRIMSON (CardiovasculaR Integrated Modelling and SimulatiON), a software framework for patient-specific blood flow simulation. This framework has two major, albeit contradicting to some extent, goals. First, the framework should be easy-to-use by medical personnel without large amounts of training. Secondly, the framework should be flexible and powerful enough to support further the research in the field of cardiovascular modelling.

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Given that the second goal implies the use of the system in academic institutions, we further add the need to avoid any commercial components that would require these institutions to pay significant license fees. In the same spirit of supporting collaboration within and between the users, we aim to keep the software open-source with a license that does not restrict modification and distribution of the software.

2 System Design

We aim at developing a software system to support the main tasks of the patient-specific modelling process - from image processing to assessment of the simulation results. The following major blocks must to be implemented in such a system: medical image processing, geometric modelling, boundary condition specification, mesh generation, blood flow simulation, and assessment of simulation results.

Medical image processing is relevant to many applications and is therefore implemented in a wide variety of existing tools, both proprietary and open source. However, the remaining tasks need to be structured together specifically for blood flow modelling. In this paper, we focus on the general design of the framework as well as on the geometric modelling task, which is described in detail.

3 Background

Existing Software. There are several software systems for patient-specific blood flow simulation. HemeLB system uses the lattice-Boltzmann method to allow for high-performance distributed flow simulation [4]. However, the lattice-Boltzmann method has several drawbacks when applied to blood flow simulation. For instance, in a lattice-based method the vessel wall boundary is approximated by a Cartesian grid and therefore important metrics obtained from the simulation results, such as wall shear stress, which plays a significant role in estimating the severity of several cardiovascular diseases, are error-prone. Therefore, in this work, we adopt the finite-element method (FEM) which considers a continuous representation of the underlying physics and can easily work with unstructured 3D meshes.

Another academic tool for patient-specific blood flow modelling is the SimVascular system[1], which allows to solve all the tasks necessary to efficiently use blood flow simulation in a variety of scenarios [6]. However, despite the flexibility of the system, the software is hindered by its complex and un-intuitive user interface which entails a steep learning curve for new users as well as difficulties in day-to-day use by experienced users. Furthermore, SimVascular is also limited by several commercial components, notably the solid modeller (Parasolid, Siemens PLM Software) and the mesh generator (Meshsim, Simmetrix, Inc.).

[1] https://simtk.org/home/simvascular.

Given that our goal is to create a software system capable of supporting the use of patient-specific blood flow simulation for diagnosis and treatment, it is mandatory to combine the power of a complex system such as SimVascular with a modern user interface which hides as much of this complexity as possible from the user.

Implementation Basis. We adopted the Medical Imaging Interaction Toolkit (MITK, [9]) as the base framework for our system for several reasons. First, it is based on widely adopted open source toolkits for visualization (VTK), segmentation and registration (ITK) and versatile DICOM format support (GDCM). Therefore, MITK provides a significant amount of functionality necessary for processing and visualizing images stored in multiple image formats. Furthermore, MITK is a free open source project with a non-restrictive BSD-style license. MITK is based on the BlueBerry framework and the Common Toolkit[2] (CTK) which allows building highly customized applications. Finally, MITK provides a familiar interface for medical personnel with readily available multi-planar reconstruction and 3D views of the data.

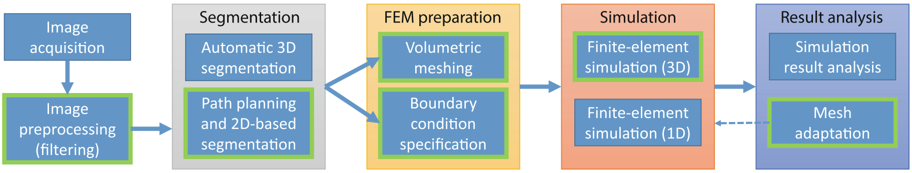


Image acquisition
Image preprocessing (filtering)
Segmentation
Automatic 3D segmentation
Path planning and 2D-based segmentation
FEM preparation
Volumetric meshing
Boundary condition specification
Simulation
Finite-element simulation (3D)
Finite-element simulation (1D)
Result analysis
Simulation result analysis
Mesh adaptation

Fig. 1. The work flow for patient-specific blood flow simulation. The steps currently implemented in CRIMSON have a green outline. The analysis of simulation results is currently performed in ParaView (http://www.paraview.org).

4 Work Flow

The general CRIMSON work flow is outlined in Fig. 1. The major steps of this work flow are:

Image acquisition involves the choice of imaging modalities as well as their setup (e.g. MRI or CT protocols that highlight blood and vessel walls [5]). This step is not in scope of CRIMSON.

Image processing includes various image filtering techniques, such as denoising, which aim to enhance the image quality and target structure visibility. For this step, CRIMSON uses the built-in filters provided by MITK.

Segmentation involves extracting the vessel boundary from the image data in a format suitable for subsequent volumetric meshing. There are several approaches to vessel wall segmentation and that will be discussed it in more detail in Sect. 4.1.

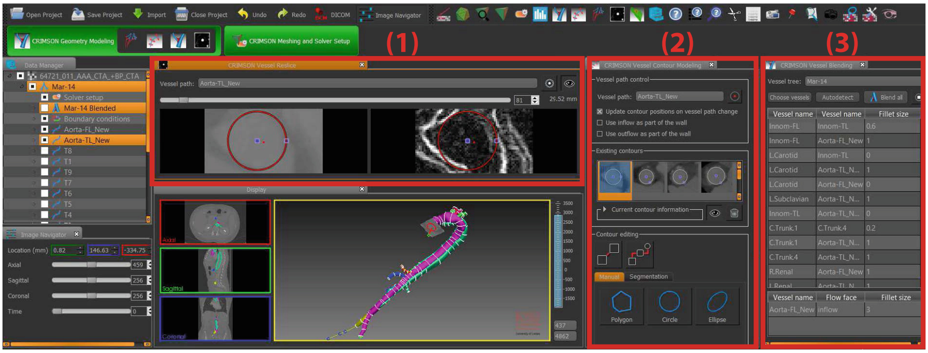
[2] http://www.mitk.org/BlueBerry; http://www.commontk.org.

Volumetric meshing is required to discretize the volume of interest for the blood flow simulation using the finite-element method (FEM).

Boundary condition specification is required to define a well-posed problem for the FEM. This includes a variety of patient-specific properties such as vessel wall stiffness, inflow waveforms, flow splits, pressure measurements, etc.

FEM simulation. In this step, the computation of the solution to the incompressible Navier-Stokes equations is performed. The main quantities (e.g. blood velocity and pressure) as well as derived quantities (e.g., blow, wall shear stress, etc.) can then be extracted and rendered to the medical professional to assist in diagnosis or treatment planning.

Many of these steps have multiple approaches to be completed. In this paper, we discuss a set of particular decisions already implemented in CRIMSON. Note, however, that the overall goal is to allow the user multiple choices of available techniques for each step depending on the task at hand, for example a choice of automatic 3D segmentation for high quality images instead of manual segmentation techniques for lower quality ones.



Location (mm) 0.82 146.63 -334.75
Axial 459
Sagittal 256
Coronal 256
Time 0

Vessel path: Aorta-TL_New
81 29.52 mm

Vessel path: Aorta-TL_New
☒ Update contour positions on vessel path change
☐ Use inflow as part of the wall
☐ Use outflow as part of the wall

Vessel tree: Mar-14

Vessel name	Vessel name	Fillet size
Innom-FL	Innom-TL	0.6
Innom-FL	Aorta-FL_New	1
L.Carotid	Innom-TL	0
L.Carotid	Aorta-TL_N...	1
L.Carotid	Aorta-FL_New	0
L.Subclavian	Aorta-TL_N...	1
Innom-TL	Aorta-TL_N...	0
C.Trunk.1	C.Trunk.4	0.2
C.Trunk.1	Aorta-TL_N...	1
C.Trunk.4	Aorta-TL_N...	1
R.Renal	Aorta-FL_New	1
L.Renal	Aorta-TL_N...	1

Vessel name	Flow face	Fillet size
Aorta-FL_New	inflow	3

Fig. 2. Overview of the customizable user interface of CRIMSON with Vessel Reslice (1), Contour Modelling (2) and Vessel Blending (3) views.

4.1 Segmentation Step

The vessel wall segmentation method currently implemented in CRIMSON relies on a path-planning and 2D segmentation paradigm [3,8]. Here, paths are defined through roughly the centreline of the vessels to be included in the model. Then, a semi-automatic 2D segmentation operation is performed at multiple locations along the paths is performed. Lastly, lofted NURBS surfaces are generated to produce a smooth solid model that must then be meshed. The vessel paths of anatomical features of interest can also be used to set up 1D simulations of blood flow, an approach that offers significantly faster simulation times than those of full-blown 3D Navier-Stokes simulations. 2D segmentation methods, albeit requiring a larger degree of user intervention, are more robust than 3D segmentation approaches in situations of poor image data quality.

Vessel Path Planning. The process of building a geometric model starts with the specification of a vessel path. The MPR views are used to create the control points whose coordinates are reflected in the *Vessel Path Editing* view which shows the control points of the vessel path selected in the standard MITK *Data Manager* view. The interpolation between control points is performed using a Catmull-Rom spline which limits the interaction only to the control points.

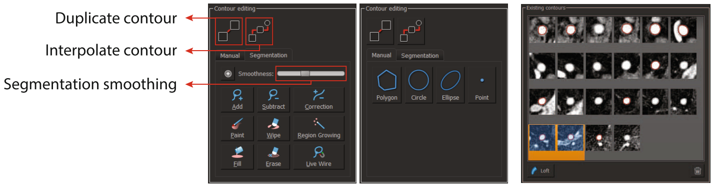


Fig. 3. Contour Modelling View. Segmentation-based and manual contour creation tools (left and centre). Contour thumbnails (right). The interpolation is made using a shape-based interpolation algorithm [2]. Contour type may be changed using either contour rasterization for conversion to 2D image segmentation, or by fitting using the Geometric Tools library [7].

For each vessel path, we calculate the reference frame at each position using the algorithm proposed by Bloomenthal [1] which is well defined along the curve and avoids sudden changes in the reference frame orientation. We then use the vessel path together with the computed reference frame to provide a *Vessel Reslice* view which shows the image data, as well as the image gradient magnitude, resliced perpendicularly to the vessel path. Note, that the Vessel Reslice view can be used to modify the spline itself by moving the control points within the slice, e.g. to position the control point at the vessel centre.

Vessel Contour Modelling. The Vessel Reslice view is used to create the vessel contours. The contour can be created using two techniques – by manually placing the contour represented as an analytical curve (e.g. circle or smoothed polygon), or by performing a binary 2D segmentation of the resliced data. The segmentation is performed using a set of tools provided by MITK, which includes simple painting operations as well as more complex ones, such as region growing and live wire segmentation. The segmentation contour is then smoothed using a windowed sinc filter with user-defined number of iterations.

Model Lofting and Blending. The next step in creating a geometric model is to interpolate the contours to create the surface of the vessel. This operation is performed using the OpenCASCADE[3] open source solid modelling library.

[3] http://www.opencascade.org.

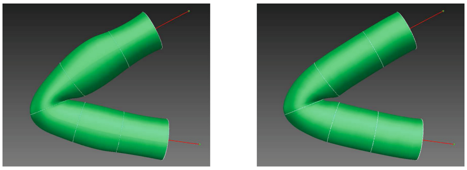


Fig. 4. The lofting algorithm may produce unintended bulges for tortuous vessels (left). In this case, the sweeping approach allows to avoid them at a cost of need for more accurate centre line specification (right).

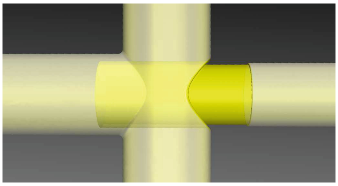


Fig. 5. An example of using various boolean operations for creating a model for simulation with an inserted stent.

If the user is not satisfied with the lofted model, the contours can be easily changed, created or removed. Alternatively, for very tortuous vessels, the lofting algorithm may be changed to a sweeping algorithm which takes the vessel path into account (see Fig. 4) for the lofting operation. Using this iterative process, the vascular geometric model is refined until a satisfactory result is achieved.

Once models of each vessel are created, they are blended into a single model representing the patient-specific vasculature (see Fig. 6). We achieved this via the fusion and filleting operations of the OpenCASCADE library. For each pair of intersecting vessels, the user specifies the desired fillet size in the *Vessel Blending* view. Furthermore, different boolean operations may be specified by the user

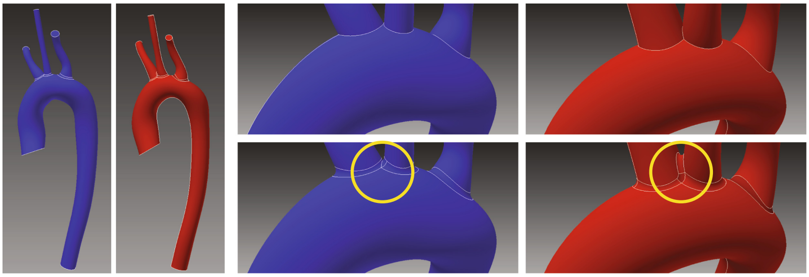


Fig. 6. Comparison of the models created with CRIMSON (red), and SimVascular (blue). Close up views (middle and right) show the vascular models before (top) and after (bottom) the blending process. Note that CRIMSON can create multi-vessel fillets, a feature not available in SimVascular (see circle detail).

to simulate virtual deployment of vascular grafts (see Fig. 5). Note, that all the information regarding the order and type of boolean operations as well as filleting is preserved and persists through any modifications of the model including modification, addition or removal of vessels.

4.2 FEM Preparation Step

In order to prepare the geometric model for finite-element simulation, it is necessary to create a volumetric mesh as well as to prescribe initial and boundary conditions. Currently, volumetric meshing is performed using the MeshSim software[4], which is the only non-open-source library used in CRIMSON. However, in the near future an open source alternative, such as Gmsh[5] will be incorporated to the simulation framework.

To preserve the boundary condition specification and the user-prescribed local mesh properties through the potential modifications of the model, each face is assigned a unique identifier containing the type of face (inflow, outflow or a wall), and the list of vessels that have influenced the creation of the face. For example, for two-way fillets this list contains two vessels and for three-way fillets, the list contains three vessels.

5 Evaluation

We conducted a two-day workshop at the University of Michigan with 15 participants with background in surgery, physiology, biomedical and mechanical engineering. We compared the participants' answers to the post-workshop questionnaire based on their self-reported familiarity with hemodynamic modelling (on a scale from 0 to 4, values 0 to 2 considered non-experts and 3 and 4 considered experts). The two one-way tests (TOST) showed that the non-expert and expert groups were equivalent in assessing the GUI intuitiveness on a scale from 0 to 4 ($\mu_e = 3.43$, $\mu_{ne} = 3.28$, $\delta = 1$, $\alpha = 0.05$, $p = 0.0144$, where μ_e and μ_{ne} are the mean values for expert and non-expert groups respectively, δ is the equivalence margin in points and α is the significance level) as well as ease to follow the work flow ($\mu_e = 3.25$, $\mu_{ne} = 3.07$, $\delta = 1$, $\alpha = 0.05$, $p = 0.0404$). Interestingly, the experts group was more tolerant towards software failures ($\mu_e = 3.12$, $\mu_{ne} = 2.86$, $\delta = 1$, $\alpha = 0.05$, $p = 0.0507$) which shows the importance of building reliable software to be used by non-experts even in a research setting.

In addition, we have asked two expert users of the SimVascular software (a cardiac surgeon and a biomedical engineer) to compare the vascular model building process using CRIMSON and SimVascular. The same vascular model was also created using SimVascular (see Fig. 6). Due to its greatly simplified user interface, it took approximately 25 min to build the aortic model using our software as opposed to 45 min using SimVascular. The overall impression of

[4] http://simmetrix.com.

[5] http://geuz.org/gmsh.

the expert users was highly positive. They estimated that a simpler and more intuitive interface will reduce the time required to build a complex model by 30 % to 50 %. In addition, the learning curve to use our software was much smoother, a very desirable feature in a clinical setting.

6 Conclusions and Future Work

In this paper, we have presented the components of the CRIMSON software framework for patient-specific blood flow modelling. We have described the overall work flow and provided an overview of the geometric model building task. With CRIMSON users are able to perform blood flow simulations for highly complex cases starting from image data in a user-friendly integrated environment. The software will be open-source[6] and is based on multiple well-established open-source software libraries. The response of the prospective users was highly positive and shows that building vascular models was greatly simplified.

Future work will incorporate the integration of automatic 3D segmentation approaches (including MITK and VMTK), integration with 1D blood flow FEM package, a module for specification of tissue properties, and support for simulation result analysis. With these additions, CRIMSON will become a fully integrated end-to-end software for patient-specific blood flow modelling.

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