MonoWeb: cardiac electrophysiology web simulator

Lucas Marins Ramalho de Lima[1][0009−0009−6061−338X], Rafael Rocha Ribeiro[1][0009−0008−6678−019X], Lucas Arantes Berg[2][0000−0002−8777−0125], Bernardo Martins Rocha[1][0000−0002−0508−8959], Rafael Sachetto Oliveira[3][0000−0003−0800−5984], Rodrigo Weber dos Santos[1][0000−0002−0633−1391], and Joventino de Oliveira Campos[1][0000−0003−1899−9441]

[1] Federal University of Juiz de Fora, Juiz de Fora MG, Brazil
[2] University of Oxford, Oxford, United Kingdom
[3] Federal University of São João del-Rei, São João del-Rei MG, Brazil

Abstract. Computational modeling emerged to address scientific problems by developing mathematical models for their description and creating computational codes to obtain solutions. Employing this technique in studying cardiac electrophysiology enables a better understanding of heart function, which requires considerable time and technological expertise. *MonoWeb* is a structured platform for simulating electrophysiological activity in cardiac tissues, using the monodomain model in a browser-based manner. This tool provides not only an accessible platform to simulate cardiac electrical activity but also integrates visualization and flexible configuration with an intuitive interface. Through communication with the *MonoAlg3D* simulator, it allows the input of advanced parameters, and different cellular models, including selecting arrhythmia examples, and stimuli, with the goal of making this experience easier and practical for electrophysiology professionals.

Keywords: Computational Electrophysiology · Web Simulator · Educational simulator for cardiologists.

1 Introduction

Computational modeling of cardiac electrophysiology has advanced significantly in recent decades by studying the electrical activity of the heart under healthy and pathological conditions [2, 10]. Several studies were conducted to investigate the generation of arrhythmias, providing an in-depth view of the influence of various physiological conditions, such as fibrosis, ischemia, hypoxia, and myocarditis [10]. This approach allows for a more comprehensive understanding of the underlying mechanisms of these conditions, providing valuable information for the diagnosis and treatment of patients with heart disease.

The usage of high-performance computing and efficient numerical methods allow simulations to become suitable for clinical applications and several works have presented results in the context of patient-specific simulations [2, 8, 10].

The process involves the acquisition of anatomical data, image segmentation, geometric model reconstruction, discretization and simulations to study cardiac behavior under different conditions.

However, performing these simulations is computationally expensive and requires powerful machines to run the analysis. Furthermore, the simulator usually is developed for researcher use, and it does not present an easy interface for physicians' understanding, which is a barrier to clinical translation.

In this context, the work presented in [3] proposed a simulator based on the *WebGL* library that runs in the web browser, which solves the mathematical model using the graphical process unit (GPU). The *OpenCARP* software [6] has also a tool named *carputilsGUI*, which is a web-based interface to run and visualize simulations, such as single cell action potential and tissue reentry induction. By developing such an interface, the aim is not only to facilitate access to advances in computational modeling of the cardiac system but also to empower healthcare professionals to apply these tools in their daily practice.

Therefore, this work presents *MonoWeb*, a user interface designed to simplify the execution and visualization of electrophysiology simulations, eliminating the need for advanced programming knowledge on the part of users. This tool aims to bridge the gap between the complexity of computational models and the accessibility for physicians and educators, allowing a broader and more effective application of these technologies.

2   Methods

2.1   Monodomain model

To model the electrophysiological activity of the cardiac tissue, the monodomain model was used, which represents the propagation of the transmembrane potential through the tissue using a partial differential equation. It is described by a reaction-diffusion equation coupled with a system of ordinary differential equations (ODEs) that describes the cellular-level excitation [7].

The solution of the monodomain equation in a wide range of cellular models was addressed using *MonoAlg3D* [7]. This is an adaptive simulator that employs the finite volume method for solving the monodomain model. Its implementation is accelerated through parallel programming techniques on GPUs.

The *MonoAlg3D* configuration is done through files in the INI format, in which the user specifies the details of the desired simulation. These files require comprehensive information, including aspects such as domain, discretizations, linear systems, GPU optimization, stimuli, and any other pertinent data to the simulation process. This level of detail can pose challenges for individuals lacking expertise in scientific computing.

2.2   Trame

Trame is a visual analytics application developed by *Kitware* [4]. The framework has integration with various data analysis tools, including *VTK/ParaView*,

PyVista, and *Plotly*. The API gets the data from *Paraview* and allows the user to interact with the loaded model without the need to install anything. The processing functions and the state that must be shared with the user are built in plain Python using Model-View-ViewModel (MVVM). This software architecture separates the user interface from the business logic, facilitating maintenance, testing, and application development, promoting an organized and reusable structure.

2.3   Paraview

ParaView is an open-source data visualization and analysis application designed to handle extremely large datasets [1]. Users import data in several formats and then apply filters and visualization techniques to explore and analyze the data interactively. Paraview also provides *pvpython* (Paraview Python), a way for users to access *ParaView's* extensive library of filters, algorithms, and visualization techniques directly from their Python scripts. This tool was used to interpret the VTU files generated by *MonoAlg3D* and displayed in the *MonoWeb* interface.

3   MonoWeb

MonoWeb is structured into three key areas: a toolbar located at the top of the interface, a parameter input section to the left of the program, and a visualization area, as shown in Figure 1.
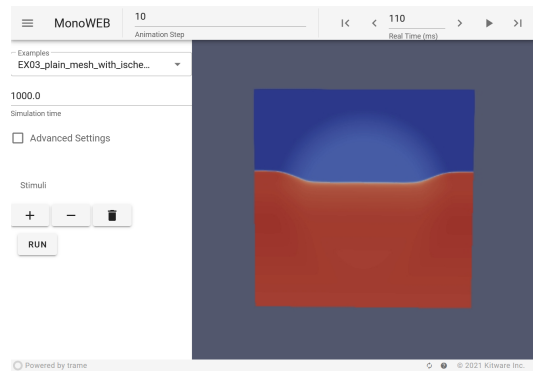

Fig. 1: *MonoWeb* interface with an example experiment being visualized, with the advanced options disabled. There is a toolbar to control the simulation time step, a menu with examples to run, and a section of stimuli configurations.

The visualization area leverages *ParaView* libraries to read *MonoAlg3D's* output files in PVD and VTU formats. This allows the user to interact with the simulation, for example, by adjusting the camera position using the mouse, which facilitates a more dynamic experience during result analysis.

The toolbar in the visualization area enables control over the displayed simulation frame. Additionally, users can select a specific moment in the simulation and adjust the time step size for the animation function.

The simulation parameters can be adjusted on the left side of the window, as depicted in Figure 1. In the first dropdown menu, it is possible to select from four simulation examples with different arrhythmia cases. The following input field represents the total simulation time in milliseconds.

Below, there is a checkbox to display advanced settings, where there are three fields indicating the electrical conductivity of the tissue (σ) in the three Cartesian directions x, y, and z, respectively. There is also a dropdown menu to create the simulation domain. Domain functions define the shape of the tissue for the simulation based on certain parameters. All functions require spatial discretization of the domain, therefore, there are three fields for the values of dx, dy, and dz, respectively.

There are ten domain definition functions available, allowing users to build meshes in spherical, cubic, prismatic, as well as square and rectangular planar shapes. Moreover, within the domain functions, it is possible to configure fibrosis zones of various shapes.

3.1   Configuring the cellular model

Understanding the case studies requires some concepts of action potential generation in cardiac cells, as described by cellular models. Action potentials are initiated by the opening and closing of ion channels within the cell, typically sensitive to the transmembrane potential or the concentration of specific ions inside the cell. Computational modeling aims to represent the transport of these ionic currents through channels, capturing the general behavior of an excitable cell and its action potential. A key characteristic of action potentials is the refractory period, occurring during repolarization and extending slightly after the cell returns to its resting state, preventing the initiation of a new action potential in that cell.
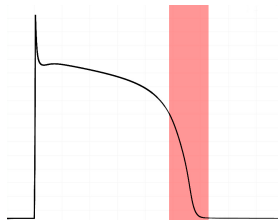

Fig. 2: Example of action potential of the Ten-Tusscher 3 cellular model for endocardial cells [9] showing the refractory period highlighted in red.

The behavior of an action potential is described according to the cellular model. Some models focus only on a general phenomenological description with

few ODEs, while others provide detailed descriptions of ion transport across the membrane and specialized organelles. The first three examples available in *MonoWeb* use the Ten-Tusscher 3 cellular model [9] for endocardial cells while the last example uses Mitchell-Shaeffer [5], but it can be changed to other available cellular models.

3.2   Configuring the stimuli

There is a section for applying stimuli in the computational cardiac tissue, where there are three buttons: one to add a new stimulus, another to remove the last added stimulus, and the third to remove all the included stimuli. *MonoWeb* allows the user to add up to 10 stimuli in a customizable way.

For each stimulus, it is possible to configure the start time, duration and applied current. Additionally, for each stimulus, the user can choose a function to facilitate its placement. Several functions are available to stimulate specific regions of the cardiac tissue, such as those enabling the delineation of boundaries along cartesian directions, facilitating the stimulation of areas within these bounds. Additionally, there are functions that enable the stimulation of spherical regions around a point, with the option to adjust the radius.

4   Case studies

MonoWeb presents four different examples with distinct scenarios, in order to provide preliminary simulations that may be customized and to serve as educational material on computational electrophysiology.

The initial example, named *EX01 3d wedge healthy*, consists of a simulation of a prism-shaped healthy tissue with a rectangular base. This simulation aims to illustrate the propagation of a single stimulus through healthy tissue, highlighting the generation of a planar wave, as presented in Figure 3. For this purpose, a stimulus is applied at time $t = 0.0$ ms with a duration of $t_{stim} = 2.0$ ms at one edge of the domain, as presented in Figure 3(a). As time progresses in the simulation, it is observed that the shape of the wavefront is preserved due to the uniformity of the tissue in the domain, as shown in Figure 3(b).

The second example, *EX02 plain mesh S1S2 protocol*, depicts the application of the S1-S2 protocol of electrical stimulation in a healthy square tissue. The S1-S2 protocol is a commonly performed study to induce arrhythmias in virtual environments and medical examinations.

In this scenario, an initial stimulus is applied at the domain's edge to trigger a planar wave as observed in Figure 4(a). After 360 ms from the application of this first stimulus, a second stimulus is applied in one-quarter of the domain, as shown in Figure 4(b). This second intervention results in unidirectional blockage in the horizontal direction due to the refractory period of cells in that region, which were stimulated more recently than the cells in the vertical direction where propagation occurs.
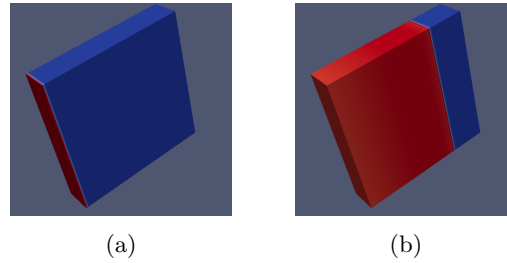
(a)   (b)

Fig. 3: Example 1 visualized in *MonoWeb*, demonstrating the application of a single stimulus in a three-dimensional parallelepiped-shaped tissue.

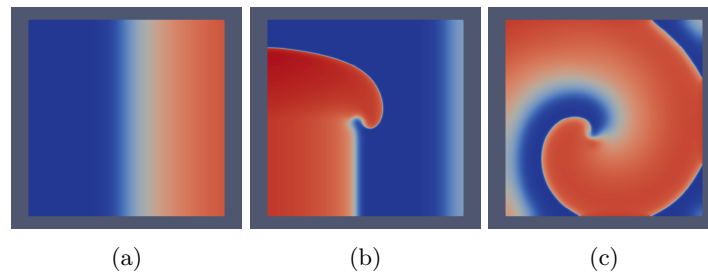(a)   (b)   (c)

Fig. 4: Example 2 visualized in *MonoWeb*, demonstrating the induction of an arrhythmia in a plain healthy tissue by applying the S1-S2 protocol.

As the stimulus propagates vertically, the adjacent tissue segment exits the refractory period, becoming susceptible to stimulation once more. Consequently, the stimulus spreads horizontally and, subsequently, into the region previously subjected to unidirectional blockage. This sequence gives rise to a self-sustaining spiral wave, representing a case of arrhythmia where tissue deviates from its expected behavior, assuming a disordered pattern, as presented in Figure 4(c).

The third example, named *EX03 plain mesh with ischemia*, demonstrates the application of the S1-S2 protocol in ischemic tissue. The domain of this example is a flat mesh with a circular region of ischemia in the center. To model ischemia, certain conditions are applied to the ionic channels in the cellular model, within the circular region, causing a delay in stimulus propagation in that region. The first stimulus propagates through the tissue, stimulating the ischemic region slightly slower than normal, as illustrated in Figure 5(a).

When applying a new stimulus identical to the first one, initially, it propagates around the ischemic region without depolarizing it, indicating unidirectional blockage (Figure 5(b)-(c)). When the stimulus reaches the upper part of the tissue, as shown in Figure 5(d), it stimulates the upper region of the central circle of ischemia, inducing reentry.

The last example, *EX04 plain mesh spiral breakup*, aims to illustrate, using the Mitchell-Shaeffer cellular model [5], the transition from arrhythmia to a

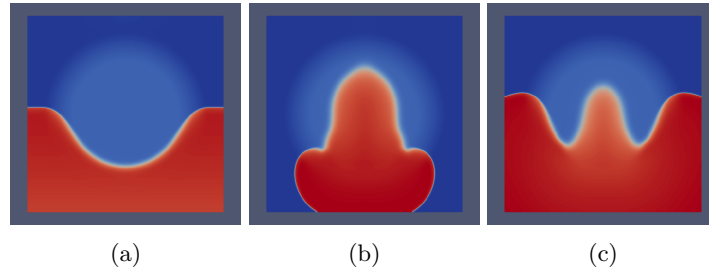(a)   (b)   (c)

Fig. 5: Simulation result of example 3 visualized in *MonoWeb*, demonstrating the induction of an arrhythmia caused by the application of the S1-S2 protocol from the electrophysiological study in flat tissue with circular ischemia.

fibrillation case. To achieve this, stimuli from the S1-S2 protocol are applied to a square tissue, following precisely what was demonstrated in example 2, with the purpose of inducing the formation of a spiral wave, as shown in Figure 6(a). After a period of time, the manifestation of the phenomenon known as Alternans becomes evident. This phenomenon is characterized by variations in the action potential duration (APD), oscillating between long and short periods.

As time progresses, Alternans results in the breakup of the spiral into multiple others, as shown in Figure 6(b)-(c), outlining a fibrillation scenario, which is a more severe form of arrhythmia.

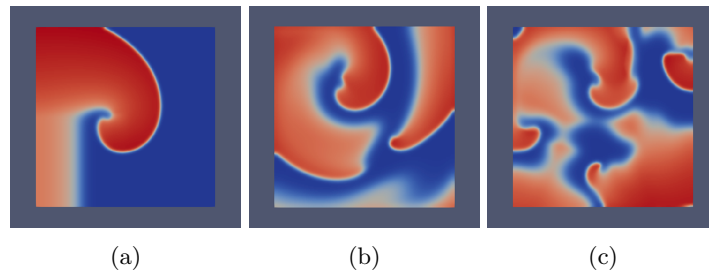

(a)   (b)   (c)

Fig. 6: Simulation result of example 4 visualized in *MonoWeb*, demonstrating the induction of fibrillation caused by the application of the S1-S2 protocol from the electrophysiological study in flat tissue.

5   Conclusion

In summary, this work highlights the value of computational simulations of heart electrical function for educational and clinical purposes. With the development of *MonoWeb*, we aim to overcome the challenges of complexity and resource

demands associated with computational electrophysiology simulations, making its execution and interpretation more accessible.

We intend to improve *MonoWeb* in future work, overcoming limitations related to predefined computational domains and web access, besides providing new case studies in the software in order to present a more robust web-based simulator.

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