Virtual Heart: Simulation-Based Cardiac Physiology for Education

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Abstract

An investigation into the technical feasibility of computer based interactive simulation of the heart was conducted. The project is currently at prototype development phase, which is focused on the development of a virtual heart organ. The prototype will be customized for clinical skills training for interventional cardiology and electrophysiology, as well as for general cardiology education. Further development will incorporate an interface for handling catheter insertion for cardiac ablation and pacing.

1. Modeling the cardiac anatomy

A combination of automatic and manual segmentation techniques were used to extract a detailed 3D model of cardiac anatomy using the Visible Male image dataset [1]. The technique was based on a recursive 3D region-growing algorithm and the marching cubes algorithm.

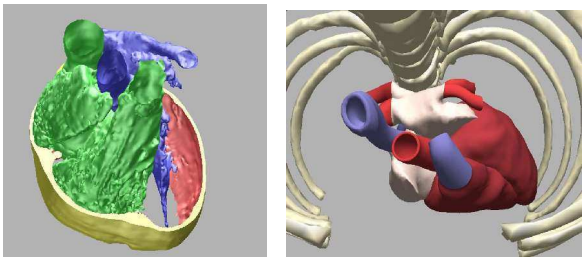

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Figure 1. a) High-res and b) simplified 3D heart model.

2. Myocardium fiber orientations

Fiber orientations of the myocytes are an important physical property for the following reasons [2]:

- For the electrical action potential propagation, the fibers represent the preferential propagation direction.
- For the contractile element of the muscle simulation model, the fibers provide the direction of the contraction.
- For the passive elastic element of the muscle simulation model, the fibers provide the transverse direction.

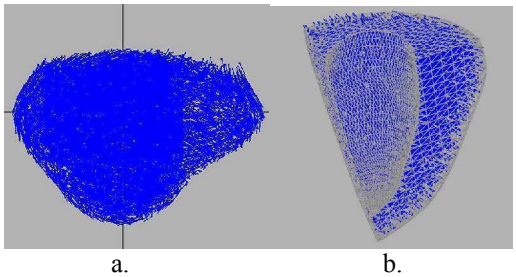

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Figure 2. a) Myocardium fiber orientations in left and right ventricles. b) Fibers fitted in corresponding section of the left ventricle.

A dataset of muscle fiber orientations in the myocardium was downloaded by permission from the Bioengineering Lab of the University of California, UCSD FTP site. This dataset was originally extracted from a canine heart using the method of Diffusion Tensor Magnetic Resonance (DT-MRI) – an imaging process that registers the orientations of water molecules in the tissue. The dataset covers the region of the two ventricles and consists of approximately 1 million fiber nodes (see figure 2a). A section of the left ventricle was specially constructed to accommodate a volumetric sample of the cell-nodes and their respective fiber orientations (see figure 2b). A number of versions of the sample with varying resolutions were created, ranging from 200K nodes down to 10K nodes. The sample versions were used to test near real-time performance of the simulation models.

3. Specialized conduction system

The action potential in the heart is generated by specialized cells in the SA (Sino-Atrial) node and spread throughout the atria primarily by cell-to-cell conduction (see figure 3a).

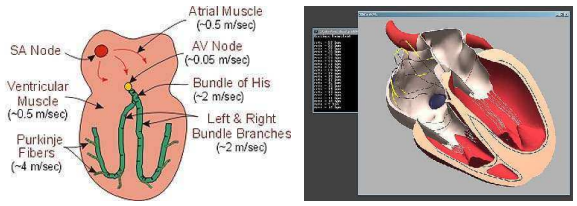

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Figure 3. a) Action potential velocities in the conduction tree (image from [3]). b) A simplified conduction tree with action potential (yellow lines).

A 3D model of the conduction tree was constructed to fit the heart model (see figure 3b). There are no recorded methods for extracting the tree from medical imaging data, so the modeling process was based on anatomical descriptions and illustrations available in medical publications. An action potential velocity simulation model was developed. The velocity model was adapted to the 3D conduction tree. The model is capable of generating the average velocity values in the various parts of the conduction tree. The rate of the SA node can be interactively modified with immediate visual feedback.

4. Electrical excitation model

4.1. Single cell

A number of simulation models of cardiac cellular electrophysiology exist in research literature. The Cell Electrophysiology Simulation Environment is a comprehensive open-source framework, specifically designed to perform computational electrophysiological simulations. CESE is useful for simulations of action potentials, individual ionic currents and changes in ionic concentrations.

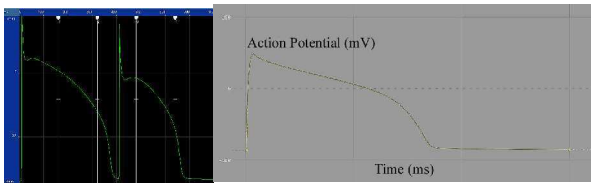

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Figure 4. a) The Luo-Rudy cell activation model [4], and b) action potential (mV)/time (ms) obtained from the CESE application.

A single cell activation sequence was constructed using the CESE application and the Luo-Rudy [4] cardiac action potential model (see figure 4a). In this model the action potential ranges from -86mV at rest state to 50mV at fully depolarized state. The total duration for one complete cell depolarization/re-polarization cycle is 300ms. The cell action potential/time profile was output from the CESE application and imported into the simulation application see figure 4b). This single cell activation profile formed the basis for the construction of an inter-cell (cell-to-cell) activation propagation wave.

4.2. Cellular automaton

The simulation of the inter-cell activation propagation is based on a cellular automaton. The excitation of cells propagates according to simple rules generated from cardiac electrophysiology. No differential equations are solved, so the computational requirement for one cardiac cycle is much lower and interactive near real-time performance is possible. A typical cellular automaton can be divided in two components [5]:

- A regular, discrete, finite network representing the universe.
- At each node of the network there is a working finite automaton.

Each cell-node corresponds with a finite set of other cells, which determines the neighborhood of the cellular automaton. In the case of 3D cellular automata, classical neighborhoods are the nearest 6 or 26 neighbors [6]. The way two cells communicate is local, deterministic, uniform and synchronous. Therefore, a global evolution of the system is pre-determined, running the cellular automaton along discrete time steps.

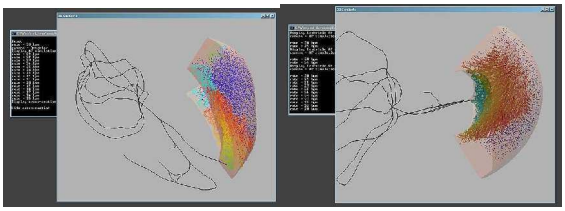

Figure 5. An action potential propagation wave is generated by the cellular automaton. Color coding: blue: re-polarized cells, red: fully de-polarized cells, cyan: Purkinje fiber network.

The 3D cellular automaton is used to simulate the propagation of electrical excitation of each cardiac cell to its neighbors. The model consists of the anatomical tissue sample, the muscle fiber orientation dataset and the specialized cardiac conduction system tree (see figure 5). At anyone time during the simulation each cell-node is defined by its state, which is constantly updated at each millisecond of the simulated cycle. The value of the action potential for each cell is looked up from the pre-calculated profile (see figure 4b).

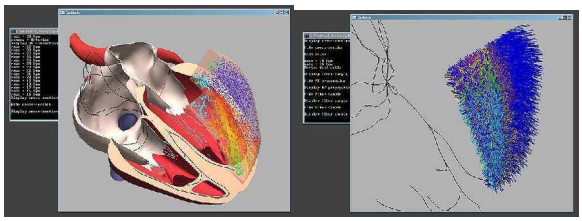

Figure 6. Action potential propagation in relation to heart anatomy (left) and fiber orientations (right).

The action potential is conducted from a cell to one of its neighbors if the cell has reached an action potential threshold (~30mV) and if the neighbor is in a fully re-polarized state (see figures 5, 6). The velocity of the conduction is normally 0.5m/s in the direction of the fiber and approximately 0.025m/s (50% less) in the transverse direction. The model is capable of generating action potential propagation waves through the myocardium tissue sample (with ~100K nodes) in near real-time on a CPU of 1.6GHz.

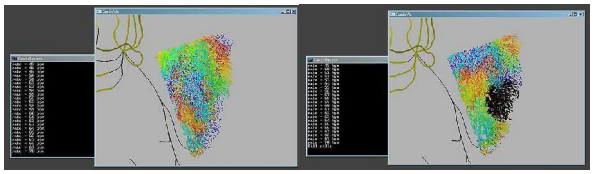

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Figure 7. a) Arrhythmic propagation wave. b) A region of dead cells seen in black.

The model is also capable of generating arrhythmic propagation waves (see figure 7a). Arrhythmic waves can be generated by interactively modifying the heartbeat rate and the refraction period of the cell cycle (the duration of the plateau in the action potential profile). Dead cells can be simulated by adding the "dead cell" state in the simulation of the cellular automaton. In figure 8b, a region of dead cells is being by-passed by the propagation wave. As a result the propagation evolves into an arrhythmia.

5. Mechanical tissue deformation model

A cellular mechanical deformation model was developed. The model is based on the Hill-Maxwell muscle simulation model (see figure 8a) [7]. A simplified version of the model consists of an active contractile element and a passive elastic element connected in parallel (see figure 8b). The non-linear and anisotropic nature of cardiac tissue is addressed by incorporating the fiber orientation in each cell-node.

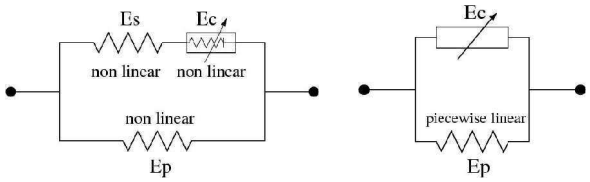

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Figure 8. a) The Hill-Maxwell muscle model [7] and b) a simplified version of the model.

The contractile element of each cell is activated when the respective action potential reaches the activation threshold. The passive element represents the mechanical elasticity of the muscle tissue and is modeled using the elasticity constitutive law. To perform the mechanical simulation the following dynamics equation is solved:

$$[1] \qquad M(d^2D/dt^2) + C(dD/dt) + KU = F$$

where D is the displacement vector, M is the mass matrix, C is the damping matrix, K is the linear elastic stiffness matrix and F is the total external stress, including the stress tensor from the contraction. Equation [1] is integrated in time and space within the sample of the tissue cell-nodes domain. The mechanical contraction can be directly compared with measures from medical images making a validation possible. This model was developed taking into account interactivity and real-time considerations as priorities. The model was based on an earlier version published by the author [8].

6. Electro-mechanical coupling model

The coupling model relates the action potential to an actively developed contractile tension (see figure 9a). The contractile mechanical behavior of each cell-node is coupled to electrical activation by the action potential profile of the same cell.

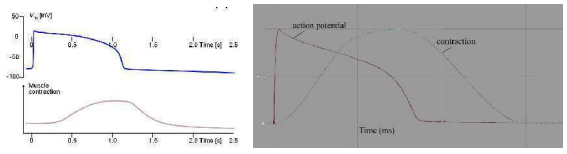

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Figure 9. a) Electrical (blue) and mechanical (grey) activity in a cardiac muscle cell [9]. b) Superimposed normalized action potential (red) and contraction (green) over time.

In the developed model, the contractile element of a cell is activated when the action potential of the cell exceeds an activation threshold (~40mV). The development of the cell contraction takes place over time, following a pre-calculated profile. As a result, cell contraction peaks approximately 200ms after the action potential peak (see figure 9b).

7. Patient data input

Cardiac MRI data (see figure 10a) have been superimposed onto the 3D model of the beating heart, in order to visualize the spatial and temporal correlation (see figure 10b). Other cardiac imaging data that may be imported in the application in the future are echocardiography image sequences and electrophysiology maps.

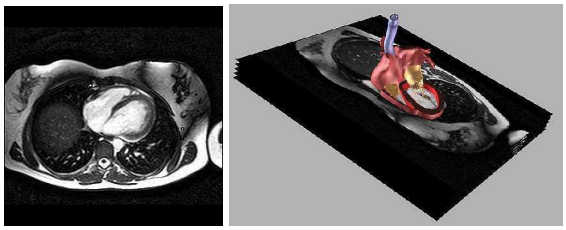

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Figure 10. a) Timed cardiac MRI sequence [10]. b) Cardiac MRI superimposed to the 3D heart model.

8. Results and future work

An experimental research application was developed. This application has served as a proof of concept for the real-time and interaction issues and as a test-bed for the simulation models. The application consists of two main modules: visualization and simulation. The purpose of the visualization module is to import and visualize existing and pre-calculated data, such as the simplified 3D heartbeat model, the CESE action potential/time and the contraction/time profiles. This module can show the beating heart in full views, pre-defined internal close-up views, cross-sections and a camera-on-path pre-recorded sequence (see figure 11). The simulation module accommodates the electro-mechanical simulation models. The electro-mechanical function is demonstrated with the conduction tree, the ventricle tissue sample and the fiber orientation set.

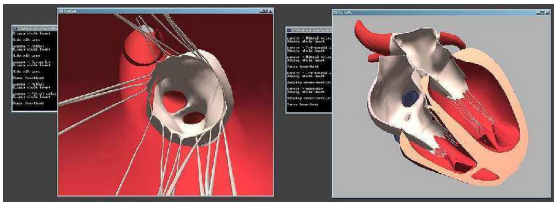

Figure 11. External, internal and cross-section views of the beating heart.

The application provides interactive control of a standard free camera in 3D space (i.e. camera tumble, track, drag, tilt and zoom) and control over certain cardiac parameters, such as the heartbeat rate and the length of the refraction period in cells. The application was developed using the OpenGL and GLUT open source computer graphics libraries. The visualization modules were written in C and the simulation modules in C++ programming languages.

The simulation of the insertion of flexible tools and the simulation of the ablation procedure will be addressed during the development phase which is currently under way. This project is partly funded by a Research & Development grant from the London Development Agency - UK.

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