# G-Heart: A GPU-based System for Electrophysiological Simulation and Multi-modality Cardiac Visualization

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Abstract-Cardiac electrophysiological simulation and multi-modality visualization are computationally intensive and valuable in studying the structure, mechanism, and dynamics of heart. The existing multi-CPU based approaches can reduce the calculation time, but suffer from the hardware and communication cost problems and are inefficient for 3D data visualization. Compared with multi-CPU, the highly parallel and multi-core properties of GPU make it a suitable alternative for accelerating cardiac simulation and visualization. In this paper, we develop a G-Heart system where GPU-based acceleration technologies are adopted for both the simulation of cardiac electrophysiological activities and the online illustration 3D multi-modality (anatomical and electrophysiological) data. In the simulation stage, a phase-field method is employed to cope with the no-flux boundary condition. For heart geometrical structure illustration, a GPU-based ray-casting volume rendering algorithm is implemented and an improved context-preserving model with user interaction is integrated into the proposed framework. Finally, a fusion visualization method is proposed, which can provide 3D visualization results for both the simulation data and the anatomical data simultaneously.

*Index Terms*—visualization, heart modelling, electrophysiological simulation, CUDA, GPGPU

### I. INTRODUCTION

C Ardiac electrical activities are valuable for the investigation of complex heart diseases, e.g., arrhythmias, ischemia, and ventricular fibrillation, and can be invasively measured by medical devices like electrocardiogram (ECG). With the progress in programmed electrical modeling and stimulation, electrophysiological simulation has gradually been a promising direction for cardiac electrophysiology study. By simulating the cardiac electrical activities over a wide variety of scales from single ion channel proteins to whole organs, cardiac electrophysiological simulation can help in revealing the mechanisms of normal and abnormal cardiac electrical activities, interpreting of clinical data, and even designing drugs and therapeutic plans [1], [2].

Over the last decades, cardiac electrophysiological simulation has received considerable research interests, and numerous models have been developed for simulating the functions of protein, single cell, tissue, and whole heart [3]. Recently, benefited by the progress in electrophysiological modeling and medical imaging, anatomically realistic and biophysically detailed multi-scale computer models of the heart are playing an increasingly important role in advancing our understanding of integrated cardiac function in health and disease [4]. For example, action potential propagation simulation of ischemia in 3D anatomically detailed ventricle is valuable in studying the mechanisms and dynamics of ischemia-induced re-entry and arrhythmia [5].

Cardiac electrophysiological model generally is a coupled system of partial differential equations for modeling the electrical wave propagation across tissue and ordinary differential equations for modeling cell dynamics. The solution to typical electrophysiological model, e.g., bidomain and monodomain model, usually involves millions of nodes, and suffers from the complex boundary and computational inefficiency problems. Moreover, the multi-CPU-based high-performance computing is also inefficient for 3D data visualization. To address the complex boundary problem, a phase-field method was proposed in [6], and Lu et al. adopted it for studying the influence of ischemia on 3D human ventricle [7]. To alleviate the computational inefficiency, high-performance computing was developed to speedup electrophysiological simulation. However, the scalability of most bidomain based simulation is limited to hundreds of cores, and only few work circumvented this limitation by using appropriate grid partitioning and asynchronous IO parallel mechanism [8], [9].

With the advent of GPU, general-purpose computing on GPUs (GPGPU) becomes an emerging technology to enhance computational efficiency [10]–[12]. Instead of CPUs, GPU has massively parallel single instruction multiple data processing units with hundreds of stream processors, and these architectural advantages can be utilized to speedup cardiac electrical activity simulation [13], [14]. Most recently, Nimmagadda et al. proposed a bidomain model with multi-GPU implementation for electrophysiological simulation on clinical time-scales [15].

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Another promising advantage of GPU is that it makes the visualization of multi-modality volume cardiac data, i.e., the detailed 3D anatomical data and the electrophysiological simulation results, more convenient. By far, several systems have been developed for the visualization of electrophysiological data. Hurmusiadis developed a simulation system called Virtual Heart [16] for electrophysiological behavior demonstration. Lu et al. proposed an electrophysiology simulation method and assessed the simulation result by a ray-casting method [7].

However, these systems did not unify spatial information of tissues with electrophysiological behavior. Without the context information from anatomical model, one can not understand the visualization results easily. Thus, electrophysiological behavior visualization must deal with multi-volume data, i.e., one anatomical reference and one or more electrophysiological measurements. In this sense, Wang et al. [17] designed multi-dimensional transfer function to visualize cardiac electrophysiology simulation. In their work, an improved LH histogram method was proposed and multi-dimensional transfer function design was discussed. With this method, boundary information was enhanced and cardiac electrophysiology behaviour was accurately presented. Unfortunately, their implementation could not provide real-time rendering results, and results in poor user interaction performance. Moreover, their works could not provide the correspondence of the wave propagation and the time elapsing. To address this problem, Kharche et al. proposed a high-performance computing (HPC)+high-performance visualization (HPV) framework to study the 3D anatomically detailed model of clinical human atria electrophysiology [18]. Unfortunately, the bottleneck of the communication of their method would drastically affect the visualization efficiency when the data transfer increases.

In this paper, we extend our previous work [19], [20] and present a framework named G-Heart to take advantage of GPU computation capability for both cardiac electrophysiology simulation and visualization. The G-Heart takes the parameters of the cardiac electrophysiological model as input, and generates the multi-volume rendering results with spatial and temporal information as output. The workflow of the G-Heart consists of two stages: the simulation stage and the visualization stage.

The remainder of the paper is organized as follows: Section II introduces the main ingredient of the G-heart framework. Section III evaluates the performance of our implementation. Finally, the paper is concluded in Section IV.

### **II. G-HEART FRAMEWORK**

Researches have been focused on GPU-based electrophysiological simulation, but few attention was paid to analysis for the simulation results. Workflow of the proposed G-heart framework can be described as follows. First, the electrophysiological simulation was performed by our GPU-based simulation method. Then the electrophysiological data sets were visualized on-line by multimodality visualization method. Meanwhile, simulation data sets were stored onto the disk and could be visualized by our simulation data sequence visualization method which could provide the animation of the electrophysiological simulation.

### A. GPU-based electrophysiological simulation method

The Compute Unified Device Architecture (CUDA), a heterogeneous CPU+GPU architecture introduced by NVIDIA, has greatly improved the programmability of GPUs for general purpose applications [21], [22]. For cardiac electrophysiological simulation, the state of each cell in cardiac is independent of each other. So the simulation of the cells can be executed in parallel by the Single Instruction Multiple Thread (SIMT) model supported by CUDA. In this study, we use the TNNP model [23] of human ventricle to represent the excitable dynamics of cardiac tissue. The following equation defines the transmembrane voltage V:

$$V_m = \frac{I_{ion} + I_{stim}}{C_m} + \bigtriangledown \cdot (D \bigtriangledown V_m)$$
(1)  

$$I_{ion} = I_{Na} + I_{Kl} + I_{to} + I_{Kr} + I_{Ks} + I_{CaL} + I_{NaCa} + I_{NaK}$$

 $+I_{pCa} + I_{pK} + I_{bCa} + I_{bNa} \tag{2}$ 

where  $\bigtriangledown$  denotes the gradient operator,  $C_m$  is the cellular capacitance, and D is the diffusion tensor.  $I_{ion}$  and  $I_{stim}$  are sum of all transmembrane ionic currents and externally stimulus current, respectively. Eq. (1) subject to the zero flux boundary conditions:

$$\nabla \cdot (D \nabla V_m) = 0 \tag{3}$$

To automatically handle the boundary conditions of anatomical heart geometries, a phase-field method is employed [24]. An auxiliary field  $\phi$  is introduced, which has a value of 1 inside the ventricle and 0 outside the ventricle but within the bounding box [25].

$$\phi(\xi) = \begin{cases} 1, & \text{if } \xi \in \Omega_{ven} \\ 0, & \text{if } \xi \in \Omega_{box} - \Omega_{ven} \end{cases}$$
(4)

The value of  $\phi$  is calculated by the following equation:

$$\frac{\partial \phi}{\partial t} = \xi^2 - \frac{\partial G(\phi)}{\partial \phi} \tag{5}$$

where  $\xi$  is used to control the width of the interface between the ventricle and the bounding box, and  $G(\phi)$ is a double-well function with minima at  $\xi \in \Omega_{ven}$  and  $\xi \in (\Omega_{box} - \Omega_{ven})$ . We choose the function as follows:

. .

$$G(\phi) = -\frac{(2\phi - 1)^2}{4} + \frac{(2\phi - 1)}{8}$$
(6)

and Eq. (6) is modified as:

$$\phi \frac{\partial V}{\partial t} = -\phi \frac{I_{ion} + I_{sim}}{C_m} + \phi \bigtriangledown (D \bigtriangledown V) \tag{7}$$

We denote *phase-field profile* as phase-field information of the tissue.

Finally, we can present the flow of the GPU-based simulation method:

Algorithm 1: GPU-based cardiac electrophysiological
simulation method
Input: Anatomical information.
Output: Cardiac electrophysiological simulation
results.
1 generate phase-field profile, initialize the voltage
volume and the states variables;
2 set up spatial and temporal step size;
3 transfer the phase-field profile, the voltage volume
and the states variables into device memory;
4 while not go through all the temporal steps do
5 <b>if</b> predefined condition satisfied <b>then</b>
6 transfer the voltage volume back into the
host memory and write the voltage volume
into the disk ;
7 end
8 update the voltage of each voxel in the voltage
volume via Eq. (7);
9 go to next temporal step;
o end

During the execution, all state variables associated with the equations of the TNNP model reside on the GPU memory in order to maximize performance. The solution of Eq. (7) is transferred back to the host memory only when the voltage data have to be saved into the disk.

In this study, Eq. (7) is integrated with the spatial step of 0.15mm and the temporal step of 0.02ms. The interface  $\xi$  between the ventricle and the bounding box is 0.33mm, and the forward Euler scheme is adopted.

## B. GPU-based Visualization for 3D Electrophysiological Data

After the simulation of wave propagation on 3D cardiac tissue is completed, we study visualization methods that not only provide the visualization of the simulation results, but also provide the anatomical context and the temporal information of the electrophysiological behaviour.

Volume rendering is an effective method to generate 2D images from volume data, which has been applied in electrophysiological simulation data sets [7]. However, visualizing the tissue with electrophysiological behaviour without spatial supporting information is not a good idea. Inspired by work presented in [26], we need to provide a anatomical context for the given tissue.

1) Visualization of electrophysiological data with anatomical context: Visualizing the whole heart as the anatomical context is a challenging problem. On the one hand, from Fig. 1a we can see if we enhance surface information interior objects will be occluded by other in the front. On the other hand, Fig. 1b shows that if we try to uncover the objects inside the rendering volume the silhouette of the whole will be lost.

To remedy this problem, Wang et al. proposed an improved Context-Preserving model for the heart anatomical structure visualization [19]. The rendering results are shown in Fig. 2. Fig. 2a, and Fig. 2b are rendering results from different viewing positions.

*Context-Preserving* volume rendering model was introduced by Bruckner et al. [27]. It is a function of shading intensity, gradient magnitude, distance to the eye and opacity of voxel. This model provides user another way to view the interior structure while keeping the context information other than conventional clipping technique. So one can visualize the interior structures of interest and the exterior structures simultaneously using the Context-Preserving model.

For the heart anatomical structure visualization, the interior structures and the boundary of different structures are shown simultaneously in Fig. 2. We further discuss the improved Context-Preserving model for the heart anatomical structure in details. Conventional volume rendering [28] method uses discrete approximation of integral along a viewing ray by the front to back formulation to compute opacity  $\alpha_i$  and color  $c_i$ :

$$\alpha_i = \alpha_{i-1} + \alpha(P_i)(1 - \alpha_{i-1}) \tag{8}$$

$$c_{i} = c_{i-1} + c(P_{i})\alpha(P_{i})(1 - \alpha_{i-1})$$
(9)

where  $\alpha(P_i)$  and  $c(P_i)$  are opacity and color contributions at position  $P_i$ ,  $\alpha_{i-1}$  and  $c_{i-1}$  are previous sum of opacity and color. Lighting is another key ingredient of volume illustration [29]. In particular, lighting can enhance the material boundaries for classification and highlight the surface and silhouette of certain object. For the Context-Preserving model, lighting intensity serves as an input to a function for opacity variation. Opacity variation is then used for visual feature selection. In general, direct volume rendering with shading,  $\alpha(P_i)$  and  $c(P_i)$  are defined as follows:

$$\alpha(P_i) = \alpha_{tf}(f_{P_i}) \tag{10}$$

$$c(P_i) = c_{tf}(f_{P_i})s(P_i) \tag{11}$$

where  $\alpha_{tf}$  and  $c_{tf}$  are the opacity and color transfer functions. They map each scalar value to opacity and color in volume illustration literature.  $s(P_i)$ , which is the value of shading intensity at point  $P_i$ , is computed as follows:

$$s(P_i) = c_d(n \cdot l) + c_s(n \cdot h)^{c_e} + c_a \tag{12}$$

where  $c_d$ ,  $c_s$  and  $c_a$  are the diffusion, specular and ambient lighting coefficients, respectively.  $c_e$  is the specular exponent, n is the normal, l is the normalized light vector, and h is the normalized half-way vector. For conventional direct volume rendering, the opacity at point  $P_i$  is only determined by the scalar value  $f_{P_i}$  and the opacity transfer function. For layered heart structure, boundaries information is of great importance to highlight the transformation from one tissue to another. So gradient information should be taken into account for opacity-modulation [30]. The opacity-modulation additionally scales the opacity by the gradient magnitude, causing an enhancement of boundaries information.

For the Context-Preserving model,  $s(P_i)$  also does contribution to the opacity-modulation. To perform the



(a) Visualization of the silhouette information

(b) Visualization of the interior structures

Figure 1: Rendering results of ray-casting method to show the contour information and the interior structures with different opacity set-ups. (a) is used to show the contour of the human heart but the interior information is nearly missing. (b) is used to reveal the interior tissues, while the exterior tissues becomes semitransparent and hard to exhibit the surface curvature.



(a) Contex-Preserving 1

(b) Contex-Preserving 2

Figure 2: Rendering results from two different view points.

effect of clipping-plane, the opacity  $\alpha(P_i)$  is revised as Eq. 13.

$$\alpha(P_i) = \alpha_{tf}(f_{P_i}) \cdot m(P_i) \tag{13}$$

where  $m_{P_i}$  is described as follows:

$$m_{P_i} = |g|^{(\kappa_t \cdot s(P_i) \cdot (1 - |p - e|) \cdot (1 - \alpha_{i-1}))^{\kappa_s}}$$
(14)

where |g| is the gradient magnitude normalized to the range [0, 1] (zero corresponds to the lowest and one to the highest gradient magnitude in the data set),  $s(P_i)$  is the shading intensity at the current sample position p, |p-e|is the distance of the current sample position p to the eye point e.  $\kappa_t$  controls the basic slope, and the parameter  $\kappa_s$ is used to interactively tune the transfer function to view the curvature. For our implementation,  $\kappa_t$  is in the range of [0,2]. The larger of the  $\kappa_t$ , the more tissues near the view point would be deemphasized.  $\kappa_s$  is in the range of [0,3]. The silhouette information of the heart can be enhanced by increasing the  $\kappa_s$  value.

Due to the layered and complex structure, the detailed information will be of great importance. In order to enhance the silhouette and boundary between different tissues we use the Blinn-Phong model [31] to rewrite the color formulation.

$$c_w = c(p) + weight \cdot (LBPShading)$$
(15)

where weight is in the range of [0,1] and *LBPShading* is the Blinn-Phong model. The modified formulation is described as follows:

$$c_i = c_{i-1} + c_w(p) \cdot \alpha(p) \cdot (1 - \alpha_{i-1})$$
 (16)

The boundary information is highlighted via the local shading.

After the improved Context-Preserving model for cardiac anatomical structure is proposed, we adopt the multivolume visualization method [32] to visualize the multimodality volume data which include both the synthetic data from aforementioned simulation and the anatomy data from Visible Human Project [33]. The two different modalities can enhance the in-depth analysis. The electrophysiological simulation data sets which are necessary might be visible in simulation data but not in the other one and vice versa. Therefore, it is possible to see the necessary part for a heart diagnosis in the combination of two different data sets. The rendering results of traditional ray-casting method and the fusion method were shown and discussed in [20], [32].

2) Visualization of the time-varying feature of electrophysiological data sets: After the multi-volume visualization method was adopted to generate anatomical context for the electrophysiological data visualization, the tissue with the electrophysiological behavior was better illustrated. However, the time-varying feature is not explored yet. The ideal method is to visualize the electrophysiological data on-line, i.e., the simulation results are directly visualized via Graphics Interoperability without data transfer between host and device [20]. However, this would be not suitable for the 3D electrophysiological simulation, because the simulation is more time-consuming and the difference of the voltage distribution between two temporal steps is minor. To remedy this problem, we provided an off-line visualization method for 3D electrophysiological data sequence with user interaction.

The proposed method can provide not only the spatial information but also the temporal information. The detail of the proposed method is presented as follows:

Algorithm 2: Visualization method for 3D cardiac		
electrophysiology simulation data sequence		
<b>Input</b> : $Data_A$ , $Data_{Si}$ , $i = 0, 1,, N, T$ .		
Output: Rendering results of simulation data		
sequence to reveal the time varying feature		
1 Initialization: $i = 0$ ;		
2 $V_A = Load(Data_A);$		
3 while $i < N$ do		
4   $V_S = Load(Data_{Si});$		
5 $MultiVolumeVis(V_A, V_S);$		
<b>6</b>    i = i + T;		
7 end		

The method takes the anatomical data  $Data_A$ , the electrophysiological simulation data sequence  $Data_{Si}$ , i = 0, 1, ..., N as inputs first. The *T* is used to control the interval of two data sets. Function *Load* is used for loading volume data into host memory then transferring the volume data into 3D texture on GPU. *MultiVolumeVis* denotes the multi-volume visualization method for both electrophysiological simulation data sets and the anatomical context [32]. During the visualization procedure, user

TABLE I.: Parameters of Multi-Volume visualization method [32]

Parameters	Values
$\kappa_t$	0.1
$\kappa_s$	2
weight	0.06
$\beta$	0.4

interaction is provided for obtaining satisfied visualization results.

### **III. RESULTS AND DISCUSSION**

In order to evaluate the performance of the proposed simulation method, the female heart data of Visible Human Project [33] are used for providing the anatomically detailed information for generating the *phase-field profile*. Our framework is ran on an Intel(R) Core (TM) 2 Duo CPU E7500 with NVidia Tesla C1060 GPU for the simulation of the wave propagation and NVidia GeForce 9600 GPU for visualization methods.

The wave propagation simulation of ischemia kernel code is written in CUDA 4.0. The C1060 GPU is used for evaluating the cardiac electrophysiology model of size  $200 \times 200 \times 300$ . The cells were gathered into a volume stored in GPU global memory and then divided into a 2D memory stack. Each 2D memory stack is consisted of (19,13) grid with each block of size (16,16) and the x-axis iteration was performed [34] in the kernel. In order to perform efficient memory access, the constant parameters of TNNP model during simulation were stored in GPU constant memory and the phase-field profile was stored in a 3D texture, respectively. The experimental results show that the speed-up of our simulation method is more than 20 times faster compared to CPU simulation method.

The proposed multi-modality visualization method for electrophysiological simulation data has been coded in C++ with OpenGL and Cg 3.0. The rendering performance for the multi-modality rendering method is about 25 frames per second and meets the requirement of a real time system. When rendering the simulation sequence, since the I/O of a single simulation data is minor, the multi-modality method for simulation data sequence can also provide real-time rendering results.

The electrophysiological data sequence visualization with GPU-based ray-casting method is shown in Fig.3.

The electrophysiological data sequence visualization with Alg. 2 is shown in Fig.4. The parameters of Fig. 4 used in Alg. 2 are presented in Table I. The values  $\kappa_t$ and  $\kappa_s$  insure that the layered structure of the anatomical context is properly illustrated. The value of *weight* makes the anatomical context an assistant volume by shading the anatomical structure with few effort. And  $\beta$  is used to control the fusion of the anatomical data and the simulation data [32]. The value of  $\beta$  is used to show that the electrophysiological simulation data are predominant in the rendering results.

Compared with Fig.3, the results shown in Fig.4 can convey more spatial information. With the help of anatom-



Figure 3: Electrophysiological simulation set sequence visualization results via ray-casting method.



(a) time 1

(b) time 2

(c) time 3

Figure 4: Data sequence visualization results. From left to right the pictures can provide the time-varying feature of the 3D electrophysiological simulation.

ical context, the tissue with electrophysiological behavior is more easily to recognize in the complex layered structure.

Fig. 5 shows the detailed information of Fig. 4a. The boundary information of the whole heart is clearly rendered, which is surrounded by the blue oval. The boundary between the tissue with electrophysiological simulation and the anatomical context is also clearly conveyed, which is surrounded by the green oval.

### IV. CONCLUSIONS

In this paper, we introduced the G-Heart system, a framework which exploited advanced GPU computing for both simulation 3D electrical wave propagation on human heart tissue and visualization of the simulation results. Other than the studies that were either focused on electrophysiological simulation or the electrophysiological simulation, we presented a unified process for the electrophysiological simulation and the simulation results evaluation by visualization. The advent of the G-Heart has bridged the gap between the electrophysiological simulation and its visualization,



Figure 5: Detailed information of the rendering result.

and made it easy to understand the cardiac electrophysiological simulation. A GPU-based electrophysiological simulation with anatomically detailed information was provided in this paper. And in order to show the precise location of the tissue, we provided an improved Context-Preserving model for generating the anatomical context of the simulation data sets. Furthermore, we presented visualization method for exploring the time-varying feature of the cardiac electrophysiology. Results show that the G-Heart framework, can greatly reduce the electrophysiological simulation time and provide high quality rendering results of the electrophysiological simulation data. The proposed methods in this paper, such as multimodality electrophysiological data sequence visualization, can be easily adopted to other medical applications. In future work, we plan to refine our visualization method for improving both rendering quality and performance.

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