Near Real-Time Interactive Simulations of Complex Cardiac Dynamics in Tissue

A WebGL Approach

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Abstract

Over the past decades, a large number of cardiac cell models have been developed. However, their complexity and many variables have restricted simulation studies in tissue to supercomputers and a handful of research labs.

In this work, the simulation of complex cell models in cardiac tissue for study or demonstrations are accessible for the first time by anyone, from clinicians, researchers, and students to patients, at speeds comparable to those of supercomputers, but on a personal device such as a laptop or even a cell-phone.

Complexity of Cardiac Models
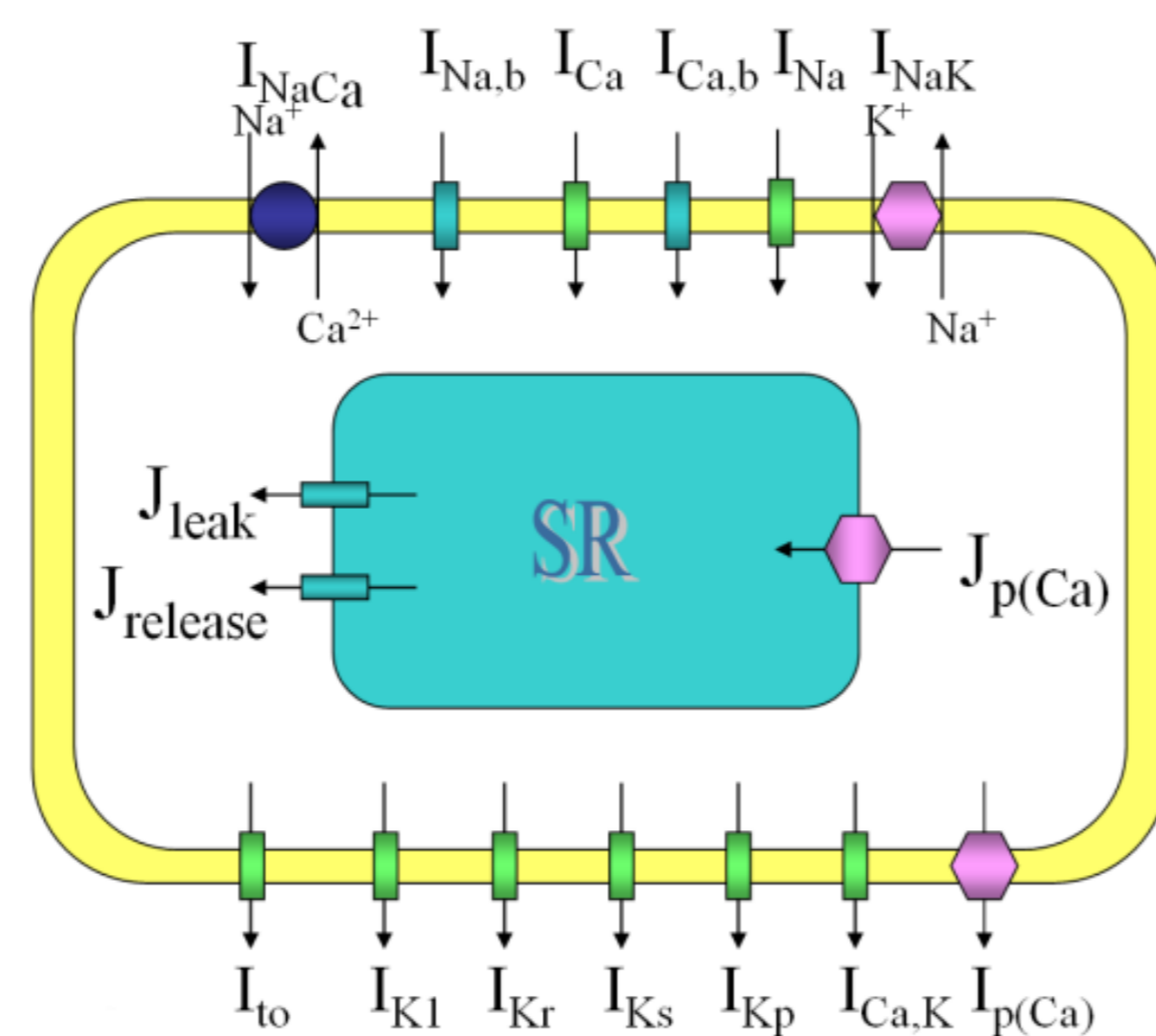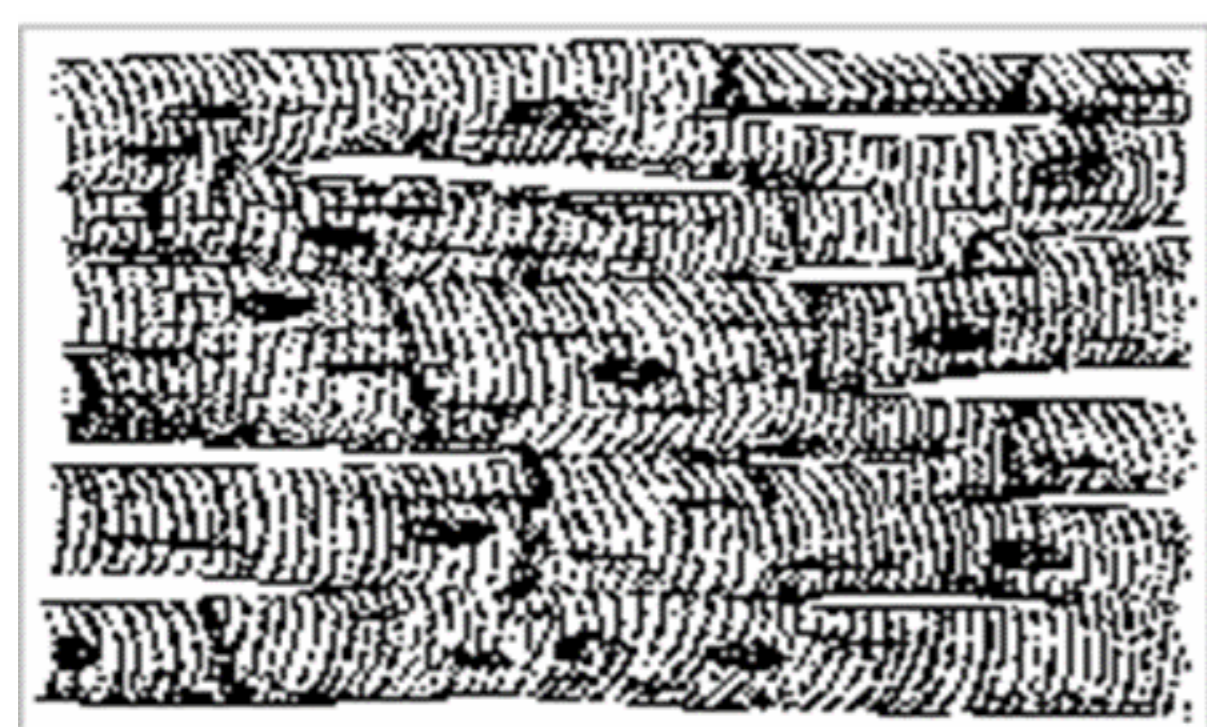
$$C_m \frac{\partial V}{\partial t} = \nabla \cdot (D \nabla V) - I_{ion}$$

- Stiff ODEs ($dt \sim 0.01ms$)
- Spatial resolution ($\sim 200 \mu m$)
- Number of ODE's per computational cell (2-100)

$$I_{ion} = \Sigma I_i$$
$$I_i = g_i(V - E_i)$$
$$g_i = f_i(V, t)$$

So, for a real-time simulation on a $4 \times 4cm$ 2D slab, we will need to solve

$$(200 \times 200) \times 10^5 \times \begin{matrix} 2 \\ 100 \end{matrix} = \begin{matrix} 8 \times 10^9 \\ 4 \times 10^{11} \end{matrix} \text{ ODE's per second!}$$

Power of GPUs

Recently, the advantages of GPU over CPU processing have been established for many areas of science, including biological systems. Graphics processing units (GPUs), now standard in most devices, contain hundreds if not thousands of processor cores which allow massive parallelization. This, effectively, turn GPU enabled devices into personal supercomputers. Using the WebGL, we have been able to exploit the highly parallel and multi-core capabilities of GPUs to achieve extremely fast simulations of complex models in 2D and 3D.
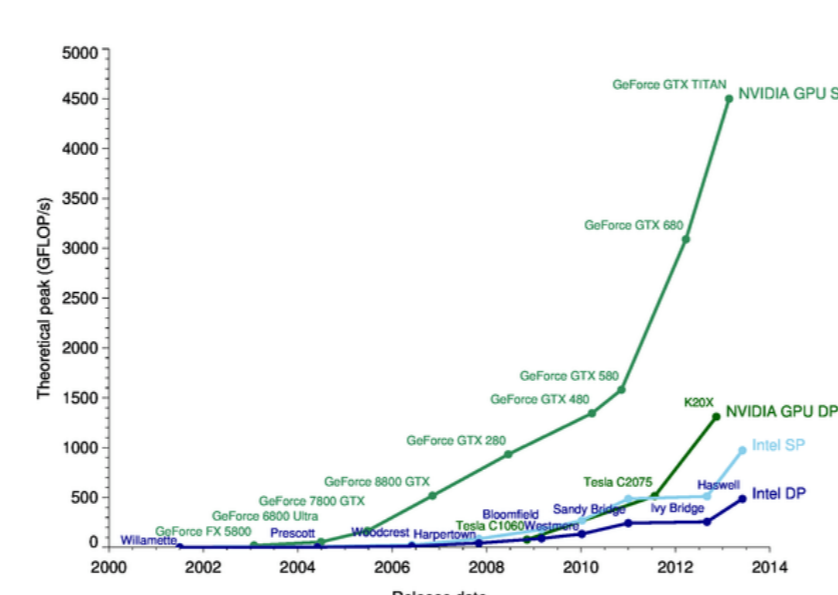

Figure 1: Computational power of CPUs vs GPUs by Michael Galloy.

WebGL

WebGL stands for Web Graphics Library which is a JavaScript API for rendering interactive 2D and 3D computer graphics within any compatible web browser without the use of plug-ins.

WebGL enables us to carry out high-performance parallel simulations over the Web on a local personal computer or a laptop with the following advantages:

- the code will be independent of the operating system;
- there will be no need to install any additional plug-in as long as the user has a modern browser, such as Google Chrome or FireFox;
- users do not need to compile the code;
- the code is instantly available over the Web and the user can run the code by just accessing a URL;
- updates and fixes can be easily sent to all users as the program is over the web;
- JavaScript and HTML enable us to easily interact with the simulation, change parameters, and see the results in real-time;

Real-Time 2D Simulations

Using an NVIDIA GeForce GTX 980M graphics card, we could achieve 12,500 time steps of solution on a 512x512 grid for the 3-variable model [1]. This means we could solve

$$512 \times 512 \times 3 \times 12,500 \approx 10^{10}$$

ODEs per second! As mentioned earlier, this is the order of computational power required to do real-time simulations in 2D, and near real-time simulations in 3D.
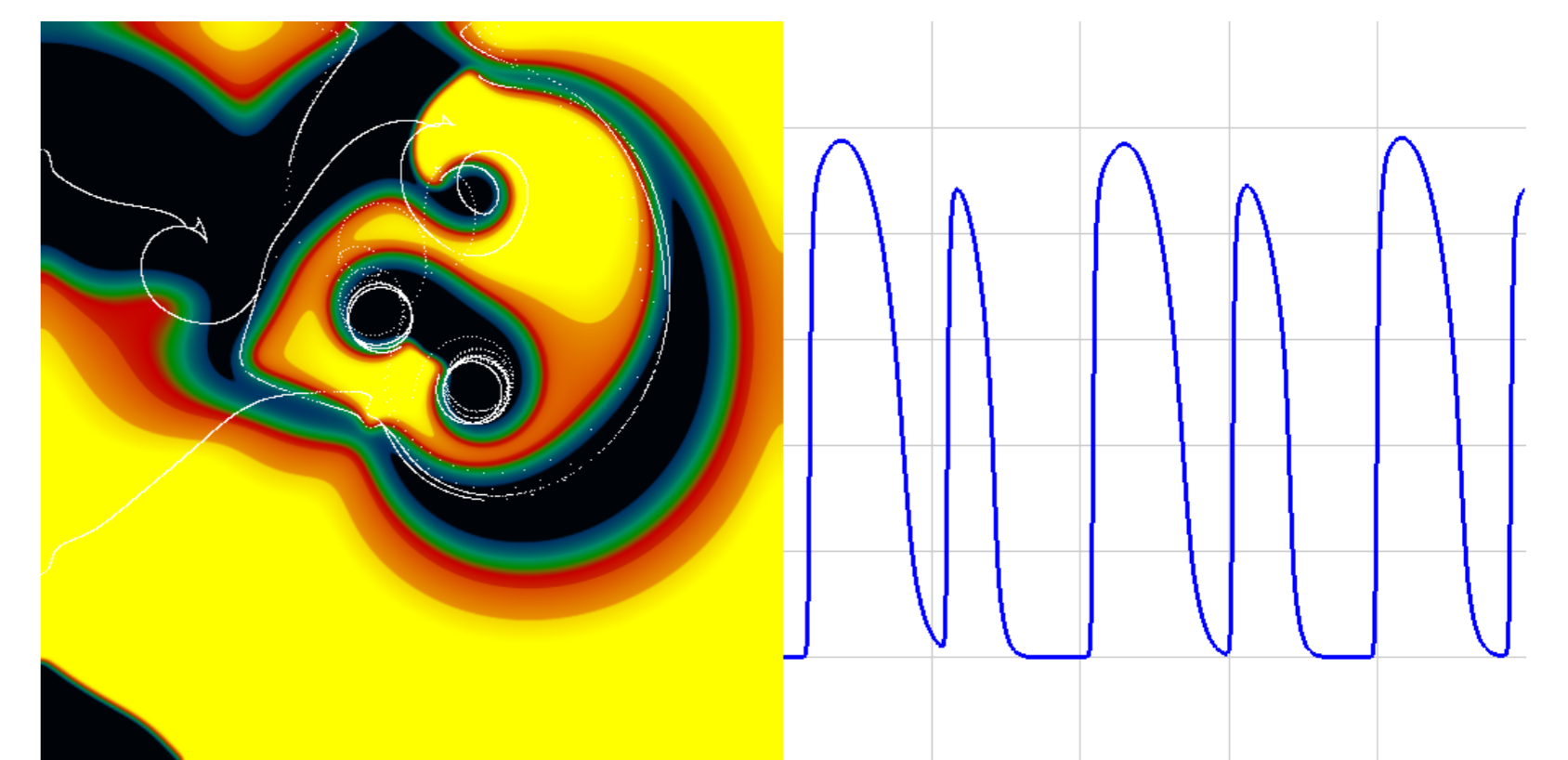

Figure 2: Three-variable model [1] interactive real-time simulations, with tip-trajectories.
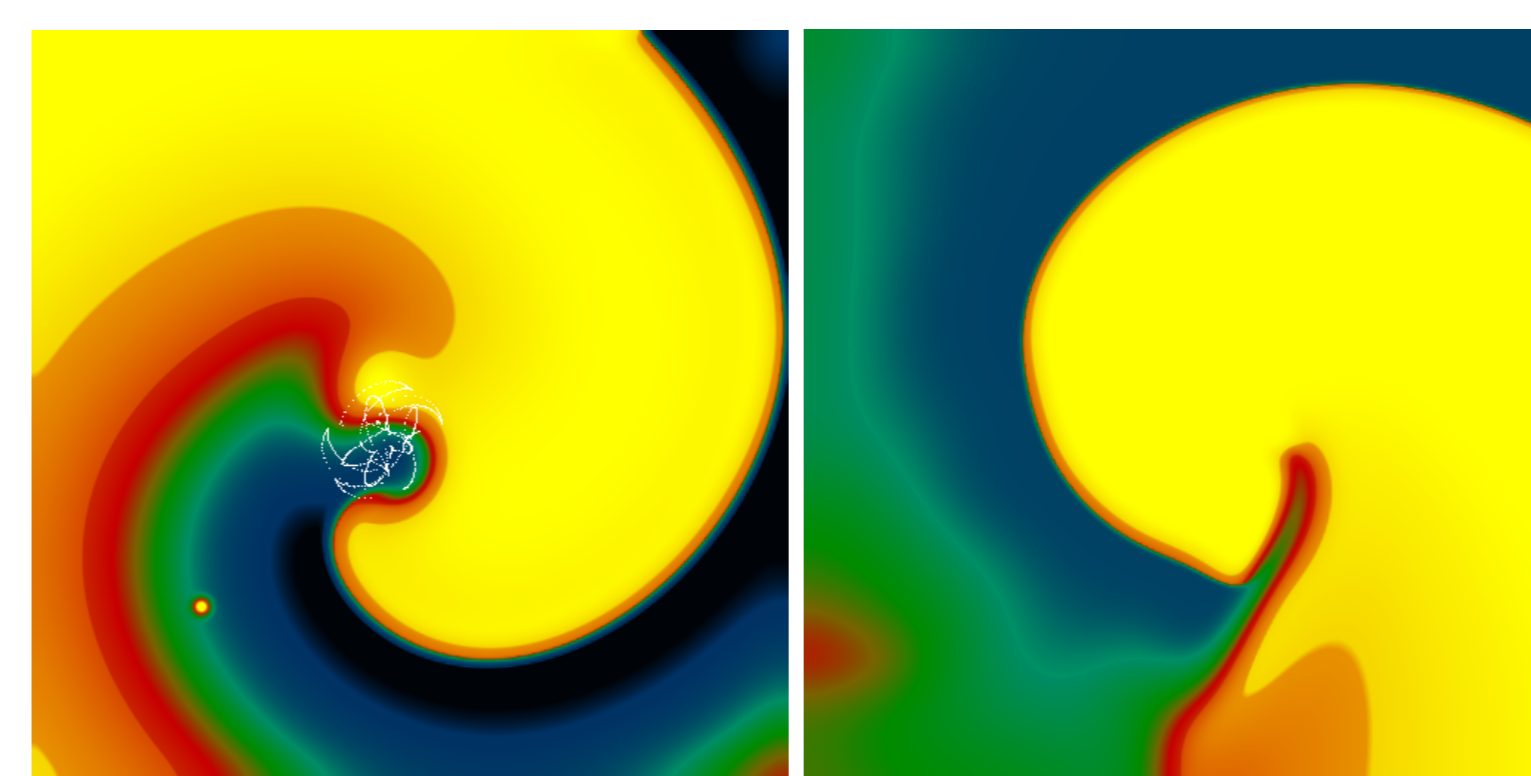
TNNP and ORDP Models

Figure 3: TNNP (left) and ORDP (right) simulated on a laptop.

The 22-variable TNNP Model [2] and 41-variable ORDP [3] were originally solved using a supercomputer. For the first-time, using WebGL, we are able to solve these elaborate models, on a personal computer or laptop or even a cell-phone, and interact with them!

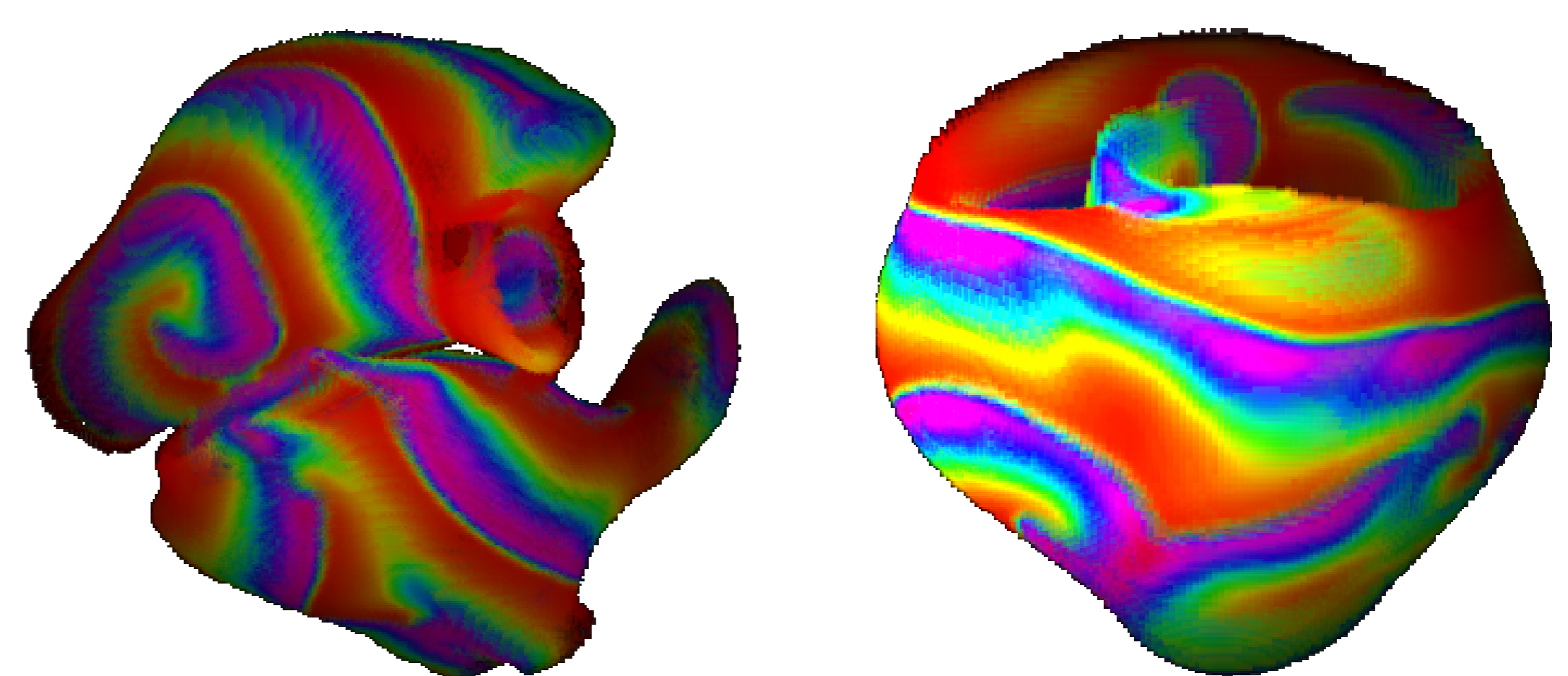## 3D Interactive Simulations on a Realistic Geometry

Figure 4: Interactive 3D simulation of fibrillation in Human Atria (left) and Dog Ventricles (right).

Now, using WebGL, it is possible to model realistic 3D geometries on a personal computer. This can help the clinicians in diagnosing cardiac problems, researches in advancing the frontiers in global system studies, or simply teaching students how re-entry and breakup can lead to fibrillation.

Acknowledgments

References

[1] Flavio H Fenton, Elizabeth M Cherry, Harold M Hastings, and Steven J Evans. Multiple mechanisms of spiral wave breakup in a model of cardiac electrical activity. *Chaos: An Interdisciplinary Journal of Nonlinear Science*, 12(3):852–892, 2002.

[2] Kirsten HWJ ten Tusscher and Alexander V Panfilov. Alternans and spiral breakup in a human ventricular tissue model. *American Journal of Physiology-Heart and Circulatory Physiology*, 291(3):H1088–H1100, 2006.

[3] Thomas O'Hara, László Virág, András Varró, and Yoram Rudy. Simulation of the undiseased human cardiac ventricular action potential: model formulation and experimental validation. *PLoS Comput Biol*, 7(5):e1002061, 2011.

For sample codes, visit *http://chaos.gatech.edu/samplewebgl/*