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A Computational Model of Cardiac Electromechanics

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***Abstract*— Driven by the need for a more anatomically realistic ventricular model and with access to greater computational power the Auckland porcine ventricular model has been re-engineered based on the original anatomical recordings. The model retains an accurate representation of the ventricular geometry including the apex and valve rings and also the underlying tissue microstructure. A computational modeling and simulation framework is used to embed biophysically detailed models of cellular electromechanics in the large scale anatomical model. This enables the integrative investigation of feedback mechanisms between the structure and function at the cellular and tissue scales with the macroscopic factors that govern the beating of the heart.**

I. Introduction

The integration of cardiac electrical and mechanical experimental data with hypotheses across multiple spatio-temporal scales and functions via mathematical modeling is arguably the most advanced example of organ system modeling [1]–[3]. A goal of the IUPS (International Union of Physiological Sciences, `www.iups.org`) Physiome Project (`www.physiomeproject.org`) is to develop the technology and methods required to simulate the behavior of biological organisms via numerical simulations using computational mathematical models. Such simulations require the integration of multiple types of physics over a wide variety of spatial and temporal ranges: spatial scales of 10^{-9} m for subcellular structures up to approximately 1 m for the human body; and molecular events occurring on the 10^{-6} s time scale with the human life time on the order of 10^{9} s (Fig. 1).

In this work we describe the application of multiscale and multiphysics simulation and modeling frameworks developed in the IUPS Physiome Project to a new geometric model of the porcine cardiac ventricles. Section II presents the new porcine cardiac ventricular anatomical model we have developed providing the basis for addition of finer anatomical detail than previous models. In Section III an overview of the computational modeling and simulation framework is given and we discuss application of the framework using the new porcine geometric model.

II. Cardiac Ventricular Anatomical Models

Previous computational modeling studies of cardiac ventricular mechanical and electrical behavior at the Auckland Bioengineering Institute have used a canine [4] or, more recently, porcine [5] geometric model (Fig. 2). These models include detailed representation of the underlying tissue microstructure and the porcine model includes an accurate representation of the geometry at the apex and the valve rings (Fig. 3).

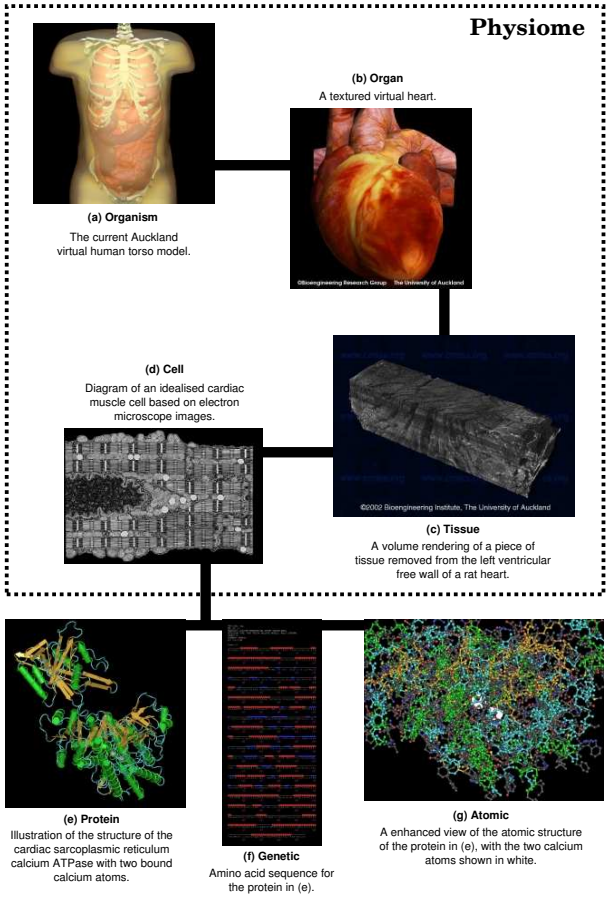
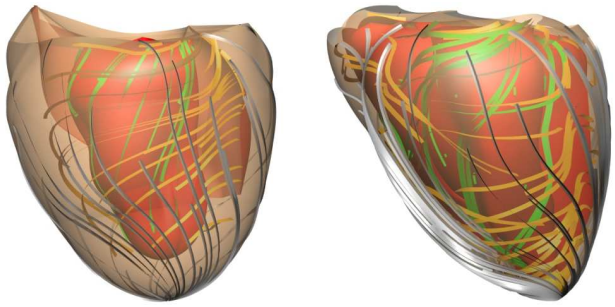


Fig. 1. The hierarchy of spatial scales used in the IUPS Physiome Project (dashed box). Below the dashed box shows the link downwards in scale to the protein and molecular levels.

The development of both the canine and porcine geometric models was performed under tight computational limits to ensure simulations using these models were feasible. Due to these limits, some key anatomical features of the ventricles were not included in the geometric models. Most notably, the papillary muscles are absent – acknowledged as the main



(a) Canine. (b) Porcine.

Fig. 2. Anatomically based finite element models of canine and porcine ventricles. Three sets of streamlines are used to visualise the epicardial (silver), mid-wall (gold), and endocardial (green) fibre directions which vary continuously through the wall. The red surfaces are the endocardial left and right ventricular surfaces in both models.

shortcoming of the porcine model [6].

With more recent access to significantly greater computational power, we are able to push beyond some of these restrictions. Thus, we have re-engineered the porcine ventricular geometric model (Figs 2(b) and 3) based on the original anatomical recordings.

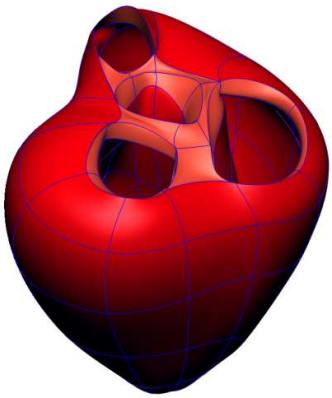
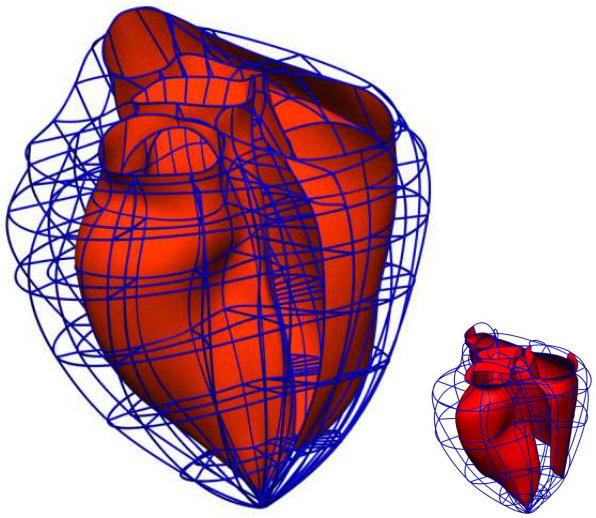


Fig. 3. The previous Auckland porcine ventricular geometry finite element model [5], illustrating the four valve rings at the ventricular base.

The new finite element model consists of 200 elements compared to the 88 elements of the previous model. With this increased finite element mesh resolution we are now able to investigate the addition of the papillary muscles and more accurately represent the four ventricular valve rings. The new model retains an accurate representation of the ventricular geometry and the underlying tissue microstructure.

III. Modeling Cardiac Electromechanics

Various approaches have been used in the development of cardiac electromechanics models providing varying levels of physiological detail and interactions between electrical and mechanical processes. Such tissue models range from tight interaction between mechanics and electrophysiology using



(a) (b)

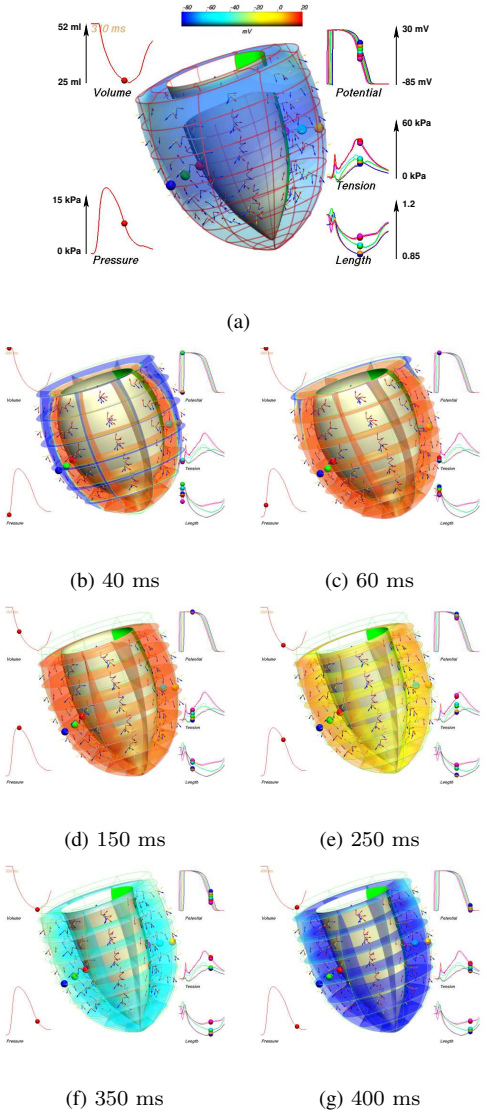
Fig. 4. The new finite element porcine ventricular mesh (a) and the same view of the previous model (b). The red surfaces illustrate the endocardial surfaces of both ventricles and the blue lines represent the finite element mesh.

low-dimensional cellular models [7]–[9], through to models with less interaction between the mechanics and electrophysiology during a simulation (*e.g.,* either excitation-contraction coupling or mechano-electric feedback), but based on more biophysically detailed cellular models (*e.g.,* [10]–[12]). In the latter case, models have typically predicted electrical activation times and used these times to trigger local active contraction of the cardiac tissue. The activation times can be computed either from a simulation of electrical activation or through the use of an eikonal model to directly determine activation times [13]. In these loosely coupled frameworks, the spread of electrical activation is calculated independently of both mechanical deformation and mechano-electric feedback mechanisms, such as stretch-activated channels and calcium buffering by contractile proteins.

Here, we have taken a large scale high order interpolation finite element based method for modeling mechanics and coupled it to a small scale low order interpolation method for modeling electrical activation in order to produce a technique for the numerical solution of biophysically detailed cardiac electromechanics models [14], [15]. Our tightly coupled framework uses cellular models of electromechanics to drive the dynamic material properties of the model, while the properties of the cellular models modulate both the electrical excitation and the deforming mechanical model.

Fig. 5 presents the results of a simulation of the systolic contraction portion of the cardiac cycle in a simple left ventricular geometry. At the cellular level this model consists of the Fenton and Karma electrical activation model [16] coupled to the Hunter-McCulloch-ter Keurs active mechanics model [17] via the calcium dynamics described by Beeler

and Reuter [18]. The pole-zero material constitutive law [19] is used to describe the passive mechanical behavior of the tissue microstructure, and a simple constant volume cavity model provides the pressure boundary condition applied to the endocardial surface of the LV model during the isovolumic contraction and ejection phases of the cycle.



(a)

(b) 40 ms (c) 60 ms

(d) 150 ms (e) 250 ms

(f) 350 ms (g) 400 ms

Fig. 5. Results of the active contraction and ejection of blood using a simple left ventricular geometry. (a) provides the key to describe the simulation results. The color bar above (a) provides the spectrum used for the transmembrane potential values drawn as colored surfaces within the LV model and the arrows within the wall indicate the microstructural fiber (red), sheet (yellow), and sheet-normal (blue) axes. (b)–(g) provide the simulation results at the indicated times.

The next goal in the development of this model is to apply the same methods used for the simulation summarised in Fig. 5 to the new porcine ventricular model (Fig. 4(a)). Current impediments to achieving this goal are the stability of the numerical simulations and the computational time taken to perform such a simulation. The computational time is partially dependent on the numerical stability, as previous simulations like that shown in Fig. 5 have shown that a rather small time stepping is required to prevent the numerical simulation going unstable. The numerical stability of these models will be improved through the use of recent developments in the underlying cellular mechanical model [20] and further refinement of the solution algorithm (as presented in [15]).

By improving the numerical stability of simulations using this model the computational time will be drastically reduced – recent tests have shown a simulation similar to that in Fig. 5 took on the order of ten hours, compared to the hundreds of hours previously taken. In addition, there are also many areas of algorithmic and software design being investigated that will provide improvements in computational cost. Some examples are: compilation of the cellular models into optimized descriptions using look-up tables and partial evaluation; the use of multigrid techniques and adaptive local mesh refinement; and altering code design to make use of distributed massively parallel processing environments.

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