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AN UNCONDITIONALLY STABLE SECOND ORDER METHOD FOR THE LUO-RUDY 1 MODEL USED IN SIMULATIONS OF DEFIBRILLATION

MONICA HANSLIEN, ROBERT ARTEBRANT, JOAKIM SUNDNES AND ASLAK TVEITO

Abstract. Simulations of cardiac defibrillation are associated with considerable numerical challenges. The cell models have traditionally been discretized by first order explicit schemes, which are associated with severe stability issues. The sharp transition layers in the solution call for stable and efficient solvers. We propose a second order accurate numerical method for the Luo-Rudy phase 1 model of electrical activity in a cardiac cell, which provides sequential update of each governing ODE. An *a priori* estimate for the scheme is given, showing that the bounds of the variables typically observed during electric shocks constitute an invariant region for the system, regardless of the time step chosen. Thus the choice of time step is left as a matter of accuracy. Conclusively, we demonstrate the theoretical result by some numerical examples, illustrating second order convergence for the Luo-Rudy 1 model.

Key Words. unconditionally stable, second order method, maximum principle, defibrillation, ODE system

1. Introduction

Computer simulations of cardiac electrophysiology have been established as a helpful tool, particularly in the study of defibrillation where it is hard to observe what is going on through *in vitro* experiments. The simulations are typically based on a system of two PDEs, named the bidomain model of electrical activity in the heart. Normally these equations are coupled to a set of ODEs, which serve to describe the electrochemistry of a single cardiac cell. There is an ever increasing need for efficient numerical methods as the mathematical models tend to expand in size and complexity along with a higher level of realism. However, older cell models such as the Beeler-Reuter model [1] and the Luo-Rudy phase 1 (LR1) model [8] are also commonly used in simulations that involve electric shocks, and serve to describe the electrophysiological membrane dynamics in a fairly realistic way.

Traditional numerical methods used in simulations of cardiac defibrillation are based on forward Euler integrators with poor stability properties. These stability issues are a consequence of the high values that the transmembrane potential undertakes when the electric shock is on, as addressed in [4]. In that study, a numerical method for the LR1 model of order $O(\Delta t)$ was presented. This scheme was proved to be unconditionally stable, leaving the choice of time step as a matter of accuracy. However, the extremely sharp transition layers in the solution present during strong electric shocks put particularly high demands on the accuracy and stability of the solvers. Also, in the strive for realistic simulations of defibrillation one would

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need to solve the equations on 3D geometries with relatively high resolution. Due to these challenges, a numerical method that admits second order accuracy would save considerable computation time. When we are to solve the coupled system of ODEs and PDEs, it is possible to use an operator splitting technique in time which is of order $O(\Delta t^2)$, see [10] and [13]. Therefore, it would be desirable for the ODE solver to preserve the level of accuracy. In the present paper, we propose a second order accurate method for the LR1 model. The numerical scheme is based on a quasi-implicit method, which makes it possible to solve each ODE in separate, where a method of Rush-Larsen type [11] is used for integration of the resulting linear equation, together with a Lobatto IIIC method for the governing equation of the scaled calcium concentration. A maximum principle for this scheme reveals that the numerical solutions yield no numerical instabilities, regardless of the time-step chosen. Thus we have a stable numerical method for the ODE system with the same level of accuracy as can be obtained at the PDE level.

The rest of the paper is organised as follows. In Section 2 we present the mathematical model under consideration, and in Section 3 we derive the numerical method. *A priori* bounds of this scheme are given in Section 4, before we show some simulation results in Section 5.

2. Model equations

Propagation of an electrical pulse in the heart can be formulated mathematically by the bidomain model, and is thoroughly described in [5, 14]. The cardiac tissue is divided into extracellular (e) and intracellular (i) domains, on which the electrical potential is represented by u_e and u_i, respectively. We may then write the transmembrane potential in terms of these two quantities as $v = u_i - u_e$, measured in mV. Moreover, M_i and M_e are conductivity tensors for the intra- and extracellular space, and s is a model dependent state vector. The complete system reads

$$\frac{\partial s}{\partial t} = P(s, v), \tag{1}$$

$$\frac{\partial v}{\partial t} + I_{ion}(v, s) = \nabla \cdot (M_i \nabla v) + \nabla \cdot (M_i \nabla u_e), \qquad x \in H, \tag{2}$$

$$0 = \nabla \cdot (M_i \nabla v) + \nabla \cdot ((M_i + M_e) \nabla u_e), \qquad x \in H, \tag{3}$$

where we have denoted by H our computational domain.

In the simulations we use the boundary conditions presented in [3] wherever the heart is under normal electrophysiological conditions, whereas we incorporate the electric shock as Dirichlet conditions during some time interval $t \in [t_1, t_2]$. The shock is placed on the heart surface, but one could easily extend the model to include torso simulations with the shock delivered through external electrode pads on the surface of the body. For an outer normal vector n_H we set

$$n_H \cdot M_i \nabla (u_e + v) = 0, \ x \in \partial H_1, \tag{4}$$

$$n_H \cdot M_i \nabla (u_e + v) = 0, \ x \in \partial H_2 \cup \partial H_3, \ t < t_1 \text{ or } t > t_2, \tag{5}$$

$$u_e = u_1, \ x \in \partial H_2, \ t_1 \le t \le t_2, \tag{6}$$

$$u_e = u_2, \ x \in \partial H_3, \ t_1 \le t \le t_2, \tag{7}$$

where the values of the shock are given by u_1 (cathode) and u_2 (anode).

Equation (1) is a system of ODEs which describes electrical kinetics of a single cell, and in the present study we let this represent the Luo-Rudy phase 1 model [8]. This cell model comprises eight variables, including the transmembrane potential v,