Simulated Epicardial Potential Maps with a Membrane-Based Bidomain Model of the Human Heart

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Abstract

Computer models of cardiac activation are constantly growing in terms of accuracy and resource usage. The availability of powerful parallel computers has allowed us to create a program that computes intracellular and extracellular potentials in a model of a complete human heart, basing on a model of the ionic currents in the cell membrane and the bidomain model of cardiac tissue. Potentials were computed on a regular finite-difference grid of 50 million nodes, using a forward-Euler approximation for the membrane potential and a BiCGStab linear-system solver with a parallelized incomplete-LU preconditioner to solve for the extracellular potentials. Realistic extracellular signals and epicardial potential distributions were obtained.

In memory of Prof. Ramesh M. Gulrajani (1944–2004).

1 Introduction

We present a computer heart model that simulates intracellular and extracellular potentials in the entire human heart, based on the bidomain equations for cardiac tissue in combination with a realistic membrane model. It differs from our previous model [8] by solving the general bidomain equations rather than a monodomain approximation and thus augments the simulation results with realistic extracellular potentials. The fine spatial discretization that is required and the difficulty of solving notably the extracellular potential on a large grid make that our model needs powerful supercomputers that have only recently become available.

2 Methods

We used a 50-million node model of the human heart embedded in a thin layer of fluid at 0.2-mm resolution (figure 1). The model is anisotropic with rotating fiber direction [4], and incorporates a representation of the specialized conduction system using the early activation times published by Durrer et al. [2].

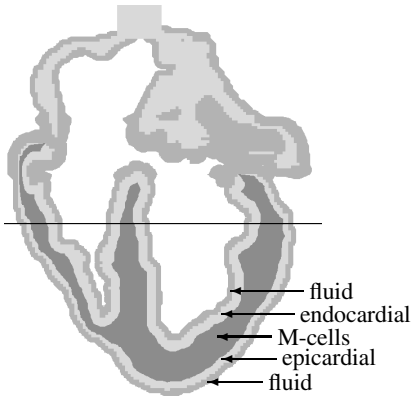

Figure 1: Longitudinal section of the heart model showing the tissue embedded in a thin layer of fluid. The fluid layer and the three cell types are indicated.

The bidomain model [3] describes the cardiac tissue as consisting of two co-located continuous media termed the intracellular and extracellular domain, which are characterized by conductivity tensors G_i and G_e, respectively. Between the two domains a current with density I_m flows. The intracellular and extracellular potentials ϕ_i and ϕ_e are subject to the *bidomain equations*:

$$\nabla \cdot (G_\mathrm{i} \nabla \phi_\mathrm{i}) = I_\mathrm{m} \tag{1}$$

$$\nabla \cdot (G_\mathrm{e} \nabla \phi_\mathrm{e}) = -I_\mathrm{m} \tag{2}$$

The transmembrane current density I_m has a capacitive part as well as an ionic part I_ion generated by the cell membrane and an imposed stimulation current I_s:

$$I_\mathrm{m} = \beta \left(C_\mathrm{m} \partial V_\mathrm{m} / \partial t + I_\mathrm{ion} + I_\mathrm{s} \right) \tag{3}$$

where β is the membrane surface-to-volume ratio and C_m is the membrane capacitance per unit area. The ionic current I_ion is dependent on the membrane potential $V_\mathrm{m} \equiv \phi_\mathrm{i} - \phi_\mathrm{e}$ and on time, and is governed by a membrane model [1].

When the bidomain equations are discretized, they may be written as

$$V_\mathrm{m}^{t+\delta t} = V_\mathrm{m}^t + \frac{\delta t}{\beta C_\mathrm{m}} \left\{ A \cdot (V_\mathrm{m}^t + \phi_\mathrm{e}^t) - \beta (I_\mathrm{ion}^t + I_\mathrm{s}^t) \right\} \tag{4}$$

$$B \cdot \phi_\mathrm{e} = A \cdot V_\mathrm{m} \tag{5}$$

with A and B two $N \times N$ matrices whose coefficients can be computed from $G_\mathrm{e} + G_\mathrm{i}$ and G_i, respectively; N being the number of nodes. We computed these matrices using an algorithm presented by Saleheen and Ng [6]. Propagation of V_m at each time step proceeds by evaluation of (4), after computation of I_ion by the

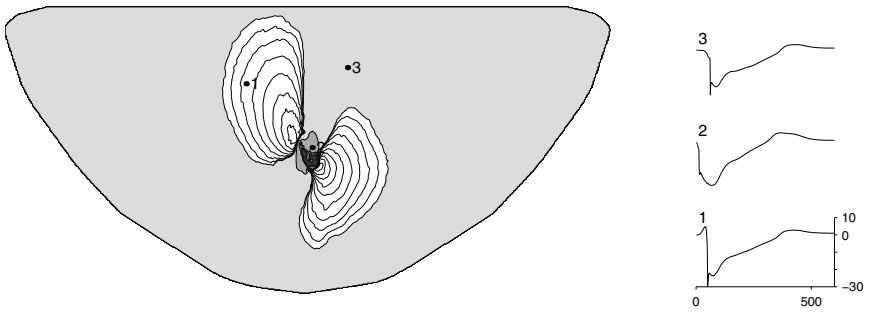

Figure 2: Epicardial potentials 10 ms after sub-epicardial pacing. The epicardium was cut open at the right-ventricular side and folded out to show it entirely. Isopotential lines are drawn at levels of 0.01 mV, 0.02 mV, 0.04 mV etc. Negative potentials are shown in shades of gray, positive in white. The dark grey area thus represents depolarized tissue. The somewhat jagged shape of the isopotential lines is caused by the steps in the discretized shape of the model heart. Selected electrograms are shown.

membrane model. The new V_m is then used to compute ϕ_e using (5). This is a system of N linear equations which can in general be solved with standard software libraries if N is sufficiently small. In our case, where N is typically 50 million, custom routines proved to be necessary. After experiments with other routines, we implemented a biconjugate gradient stabilized (BICGSTAB) solver [9] with a parallelized incomplete-LU preconditioner [5]. Simulations were performed on 32 processors of a 128-processor SGI Altix 3700 computer.

3 Results

A verification of the model was performed by simulating epicardial potential maps obtained after epicardial and intramural pacing in open-chest dogs [7]. Early potentials in our simulations reflected the local fiber direction. Development of the potential pattern reflected the transmural rotation of fibers, showing an expansion and counterclockwise rotation of the positive areas for (sub)epicardial pacing, expansion and clockwise rotation for sub-endocardial pacing, and a more symmetric expansion for mid-wall pacing. Early potentials and epicardial electrograms in case of sub-epicardial pacing are illustrated in figure 2.

4 Discussion

We presented a bidomain model of the entire human heart incorporating anisotropic tissue with rotating fiber direction, which can realistically simulate epicardial, endocardial, intracavitary, and intramuscular signals that can be compared to mea-

sured signals, and can simulate the changes that occur in these signals as a result of e.g. abnormalities in ion channels, ischaemia, hypertrophy and fibrosis. Torso coupling can be employed to obtain highly realistic ECG waveforms as well.

5 Acknowledgments

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References

[1] O. Bernus, R. Wilders, C. W. Zemlin, H. Verschelde, and A. V. Panfilov. A computationally efficient electrophysiological model of human ventricular cells. *Am. J. Physiol. Heart Circ. Physiol.*, 282:H2296–H2308, 2002.

[2] D. Durrer, R. T. van Dam, G. E. Freud, M. J. Janse, F. L. Meijler, and R. C. Arzbaecher. Total excitation of the isolated human heart. *Circulation*, 41:899–912, June 1970.

[3] C. S. Henriquez. Simulating the electrical behavior of cardiac tissue using the bidomain model. *CRC Critical Reviews in Biomedical Engineering*, 21:1–77, 1993.

[4] M. Lorange and R. M. Gulrajani. A computer heart model incorporating anisotropic propagation: I. Model construction and simulation of normal activation. *J. Electrocardiol.*, 26(4):245–61, Oct. 1993.

[5] Y. Saad. *Iterative Methods for Sparse Linear Systems*. PWS publishing, New York, 1996. `ftp://ftp.cs.umn.edu/dept/users/saad/PS/all_pdf.zip`.

[6] H. I. Saleheen and K. T. Ng. A new three-dimensional finite-difference bidomain formulation for inhomogeneous anisotropic cardiac tissues. *IEEE Trans. Biomed. Eng.*, 45:15–25, 1998.

[7] B. Taccardi, E. Macchi, R. L. Lux, P. R. Ershler, S. Spaggiari, S. Baruffi, and Y. Vyhmeister. Effect of myocardial fiber direction on epicardial potentials. *Circulation*, 90:3076–3090, Dec. 1994.

[8] M.-C. Trudel, B. Dubé, M. Potse, R. M. Gulrajani, and L. J. Leon. Simulation of propagation in a membrane-based computer heart model with parallel processing. *IEEE Trans. Biomed. Eng.*, 51(8):1319–1329, 2004.

[9] H. A. van der Vorst. Bi-CGSTAB: A fast and smoothly converging variant of Bi-CG for the solution of nonsymmetric linear systems. *SIAM J. Sci. Stat. Comput.*, 13:631–644, 1992.