Simulation of Fractionated Electrograms at Low Spatial Resolution in Large-Scale Heart Models

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introduction To compute extracellular potentials from transmembrane potentials an elliptic boundary-value problem must be solved [2, 7]. To avoid artefacts, this must be done at a spatial resolution of 0.2 mm or better [1]. For macroscopic heart models this leads to very large linear systems.

purpose We attempted to reduce such artefacts by using a special downsampling method for the source data.

conclusion This method is sufficiently accurate for visualization of electrograms in a human-heart model, even in inhomogeneous tissue.

Methods

Simulations were performed using previously-described software [6]. Uniform finite-difference meshes were used. Simulations were performed on 32–128 processors of an SGI Altix 4700 supercomputer.

Propagating action potentials were simulated with a monodomain reaction-diffusion equation at 0.2-mm resolution in a model of the human ventricles.

Extracellular potentials (electrograms) ϕ_e were computed by solving the bidomain equation

$$\nabla \cdot [\mathbf{G}_i(\mathbf{x}) + \mathbf{G}_e(\mathbf{x})] \nabla \phi_e(\mathbf{x}, t) = I(\mathbf{x}, t) \qquad (1)$$

where $\mathbf{x}$ is position, t is time, $\mathbf{G}_i$, $\mathbf{G}_e$ are the intracellular and extracellular conductivity tensor fields, and I is the transmembrane current given by

$$I(\mathbf{x}, t) = -\nabla \cdot \mathbf{G}_i(\mathbf{x}) \nabla V_m(\mathbf{x}, t), \qquad (2)$$

where V_m is the membrane potential. We evaluated $I(\mathbf{x}, t)$ at the full 0.2-mm resolution of the reaction-diffusion model.

To solve equation (1) at 1-mm resolution, $I(\mathbf{x}, t)$ was taken from the high-resolution propagation model and summed over 1-mm^3 volumes. Each fine-mesh (F) node contributed to 1–8 coarse-mesh (C) nodes. The weight of each contribution was

$$w = \begin{cases} 0, & \text{if } d_x \geq N \vee d_y \geq N \vee d_z \geq N \\ (N - d_x)(N - d_y)(N - d_z)/N^6, & \text{otherwise} \end{cases}$$

where N is the ratio of fine to coarse grid resolution ($N = 5$ here) and d_x, d_y, d_z is the number of fine-mesh edges between the C node and the F node along the x, y, and z axis, respectively.

ϕ_e was computed at 1-mm resolution both for the isolated heart (1 million nodes) and for the in-situ heart (42 million nodes).

To test the validity of the low-resolution results, electrograms were also computed at the full 0.2-mm resolution in the isolated heart (113 million nodes).

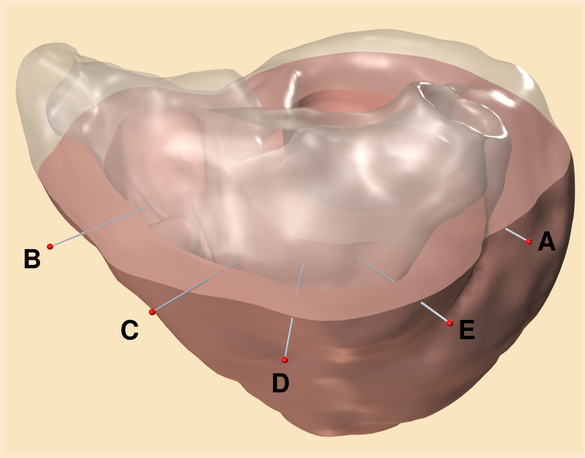
Anatomic model

An anatomic model of a human heart and torso was created from MRI data as described earlier [5]. This model described torso surface, myocardium, intracavitary blood masses, and lungs.

For a severe test of the proposed method, we created a situation where inhomogeneous tissue caused fractionated electrograms. Fibrofatty replacement and Na-channel block were simulated as in previous work [3, 4]. Fibrosis was simulated by introducing barriers with a thickness of 0.2 mm in the outer 50 % of the right ventricular wall. In these barriers, no intercellular coupling was present. In bidomain terms, $\mathbf{G}_i = 0$ but $\mathbf{G}_e$ had the normal value for myocardium. In the barriers, gaps of 0.2×0.2 mm were made. The conductivity of the fast Na current was set to 30 % of its normal value, in the entire heart.

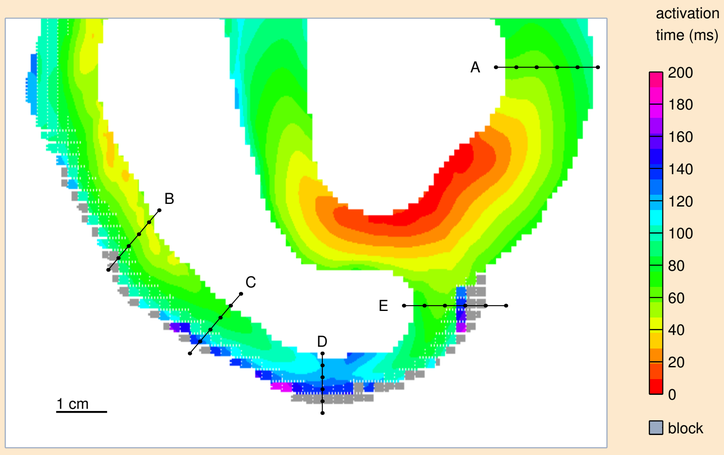
Display of results

Activation times, determined automatically from the activation process of the fast Na current, are shown with colors in a transverse section of the heart model. The plane of section and needle positions (A–E) are shown below.



Unipolar electrograms taken from 6 positions along each of 5 virtual needle electrodes (labeled A–E) are shown.

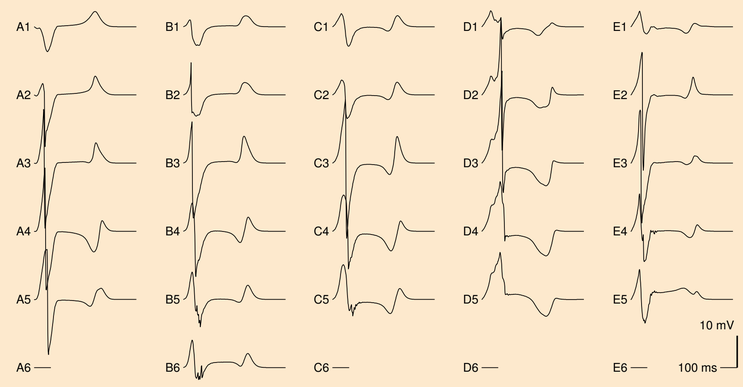
Simulated activation pattern



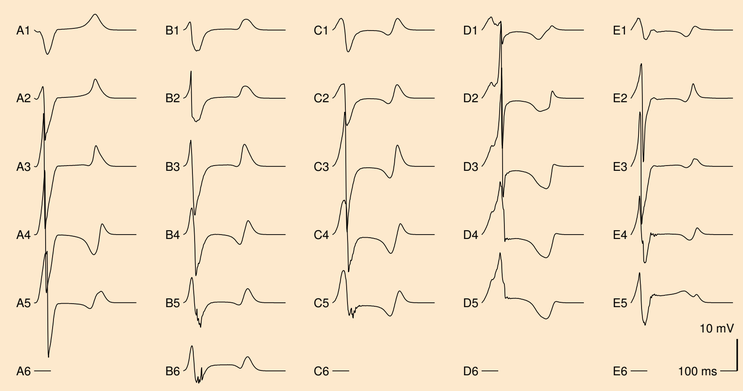
The figure above shows simulated activation times in a single plane of the three-dimensional heart model, with the positions of the virtual needle electrodes.

Simulated electrograms

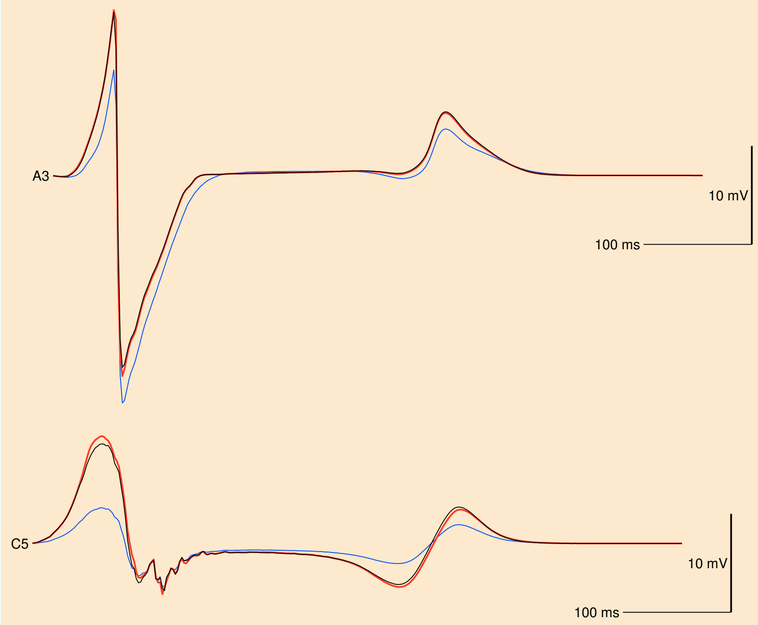
Electrograms computed at 0.2-mm resolution:



Electrograms computed at 1-mm resolution:



Close-up (black, 1-mm resolution isolated heart; red, 0.2-mm resolution isolated heart; blue, 1-mm resolution in-situ heart):



References

[1] P. Colli Franzone et al. *Ann. Biomed. Eng.*, 28:1326–1342, 2000.

[2] C. S. Henriquez. *CRC Crit. Rev. Biomed. Eng.*, 21:1–77, 1993.

[3] M. G. Hoogendijk, M. Potse, et al. *Heart Rhythm*, 7:238–248, 2010.

[4] M. G. Hoogendijk, M. Potse, et al. ST-segment elevation by current-to-load mismatch: An experimental and computational study. *Heart Rhythm*, 7, 2010. (in print).

[5] A. Linnenbank et al. A generic model of overall heart geometry for model based studies of electrical, mechanical, and ion-kinetics aspects of the heart. In *4th European Congress for Medical and Biomedical Engineering*, Antwerp, Nov. 2008. (abstract).

[6] M. Potse et al. *IEEE Trans. Biomed. Eng.*, 53(12):2425–2435, 2006.

[7] E. J. Vigmond et al. *IEEE Trans. Biomed. Eng.*, 49(11):1260–1269, 2002.

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