An Explicit Space-time Adaptive Method for Simulating Complex Cardiac Dynamics

Elizabeth M. Cherry*, Henry S. Greenside†, and Craig S. Henriquez‡
*Department of Computer Science, Duke U., P. O. Box 90129, Durham, NC 27708-0129
†Department of Physics, Duke U., Durham, NC 27708-0305
‡Department of Biomedical Engineering, Duke U., Durham, NC 27708-0281
(February 2, 2008)

For plane-wave and many-spiral states of the experimentally based Luo-Rudy 1 model of heart tissue in large (8 cm square) domains, we show that an explicit space-time-adaptive time-integration algorithm can achieve an order of magnitude reduction in computational effort and memory—but without a reduction in accuracy—when compared to an algorithm using a uniform space-time mesh at the finest resolution. Our results indicate that such an explicit algorithm can be extended straightforwardly to simulate quantitatively large-scale three-dimensional electrical dynamics over the whole human heart.

05.45.Pq, 87.15.Aa, 87.19.Hh, 87.19.Nn

Understanding the dynamics of excitable media such as heart tissue is a problem of substantial interest to physicists, physiologists, biomedical engineers, and doctors. For reasons not yet understood experimentally, the healthy time-periodic spatially-coherent beating of a human heart will sometimes change to a nonperiodic spatially-incoherent fibrillating state in which the heart cannot pump blood effectively (leading to death if suitable treatment is not administered quickly). It would be valuable to understand how the onset of arrhythmias that lead to fibrillation depends on details such as the heart's size [1], geometry, electrical state, anisotropic fiber structure [2], and inhomogeneities. A deeper understanding of the heart's dynamics may also make possible the invention of protocols by which electrical feedback could be used to prevent fibrillation [3].

Because of many experimental difficulties in studying the three-dimensional dynamics of a heart [4], simulations of cardiac tissue (and more generally of excitable media) play an extremely important role in identifying and testing specific mechanisms of arrhythmia. However, quantitatively accurate simulations of an entire three-dimensional human heart are not yet feasible. The essential difficulty is that human heart muscle is a strongly excitable medium whose electrical dynamics involve rapidly varying, highly localized fronts (see Figs. 1 and 2). The width of such a front is about 0.05 cm and a simulation that approximates well the dynamics of such a front requires a spatial resolution at least 5 times smaller, $\Delta x \approx 0.01\,\mathrm{cm}$. The muscle in an adult human heart has a volume of about $250\,\mathrm{cm}^3$ and so a uniform spatial resolution of 0.01 cm would require a computational grid with $\approx 3 \times 10^8$ nodes. Depending on the assumed material properties of the heart and on the quantities of interest to analyze, up to 50 floating point numbers might be associated with each node, requiring the storage and processing of about 10^{10} numbers per time step. The fastest time scale in heart dynamics is associated with the rapid depolarization of the cell membrane, about 0.1 msec in duration, and a reasonable resolution of this depolarization requires a time step about a fifth of this, $\Delta t \approx 0.02\,\mathrm{msec}$. Since arrhythmias such as fibrillation may require several seconds to become established, the 10^{10} numbers associated with the spatial mesh would have to be evolved over about 10^6 time steps. Such a uniform mesh calculation currently exceeds existing computational resources and has not yet been carried out.

A clue about how to improve heart simulations comes from experiments [4] and simulations [5,2] which suggest that the electrical membrane potential $V(t, \mathbf{x})$ in the fibrillating state consists of many spirals (for approximately two-dimensional tissue such as the atrium, see Fig. 2) or of many scroll waves (for thicker cardiac tissue such as the left ventricle [2]). A striking feature of these spatiotemporal disordered states is that the dynamics is *sparse*: at any given time, only a small volume fraction of the excitable medium is occupied by the fronts, and away from the fronts the dynamics is slowly varying in space and time. It may then be the case that the computational effort and storage can be greatly reduced, from being proportional to the volume of the excitable medium (the case for a spatially uniform mesh) to being proportional to the arclength (in 2d) or surface area (in 3d) of the fronts.

In this Letter, we show for representative solutions of the quantitatively accurate Luo-Rudy 1 (LR1) membrane model of cardiac tissue [6]) that an explicit space-time adaptive-mesh-refinement algorithm (AMRA) [7] can indeed take advantage of the sparse excitable dynamics to reduce by an order of magnitude the computational effort and memory needed to simulate arrhythmias in large domains. Further, we show that there is no significant reduction in accuracy when using an AMRA compared to an algorithm that uses a spatially uniform mesh at the finest resolution of the AMRA. Since the AMRA is explicit in time and has a fairly simple data structure consisting of nested patches of uniform Cartesian meshes, the AMRA can be parallelized straightforwardly [8], leading to a further reduction in computational effort by the number of processors. The AMRA is also general and

does not require the use of reduced models [5,2], which increase efficiency but sacrifice experimental accuracy by using fewer variables and perhaps explicitly eliminating rapid variables. The results presented below suggest that a quantitatively accurate AMRA simulation of fibrillation in an entire human left ventricle for several seconds with an effective 0.01 cm resolution should already be practical with existing computers. This is highly encouraging since further improvements to such algorithms are possible as discussed below.

In the following, we discuss some details of the AMRA and then its accuracy and efficiency for simulations of the LR1 model in large one- and two-dimensional domains. Our particular algorithm was a straightforward modification of an AMRA that has been used by other researchers to integrate hyperbolic sets of partial differential equations such as the Euler equations of fluid dynamics [7]. Since key mathematical and algorithmic details are available elsewhere [7], only some essential ingredients and our modifications of them are briefly described here; a more detailed discussion will be given elsewhere [9].

The AMRA approximates a given continuous field such as the cardiac membrane potential $V(t, \mathbf{x})$ on a set of nested locally-uniform patches of d-dimensional Cartesian meshes in a d-dimensional Cartesian box [7]. On each patch, spatial derivatives in the dynamical equations are approximated by second-order-accurate finite differences and an explicit method (we use forward-Euler [10]) is used to advance in time. The power of the algorithm arises from its ability to automatically and efficiently refine or coarsen the representations of fields by varying the number of grid points locally to achieve a specified truncation error. A further reduction in computational effort is achieved by allowing the the time step to change locally with the spatial mesh [7]. In related prior work, Quan et. al. [11] have studied cardiac models using spatially adaptive time steps but with a uniform spatial mesh and alternation of implicit and explicit time steps, while Moore [12] has studied reaction-diffusion equations using a spatially-adaptive fully-implicit method but with a spatially-uniform adaptive time step. To our knowledge, ours is the first study of an algorithm for excitable media for which the spatial and temporal resolutions change locally.

An important subtlety is that our AMRA was designed for hyperbolic equations but is here applied to an excitable medium which is described by *parabolic* equations. For explicit time integrations of hyperbolic equations, the Courant-Friedrichs-Lewy (CFL) condition for the onset of numerical instability [7] bounds the largest possible local time step Δt by the first power of the local spatial resolution Δx. For parabolic equations, the stability condition for an explicit algorithm bounds the time step by Δx^2 for Δx sufficiently small. In the LR1 model, this dependence is evident only for spatial resolutions an order of magnitude finer ($\Delta x < .0025\ cm$) than those used in our calculations. For resolutions in our range of interest, the fast reaction kinetics, not the diffusion operator, sets the stability limit on the time step [9]. A standard way to avoid the stability restriction on Δt is to use a semi- or fully-implicit time-integration algorithm [2,11,12]. We have estimated that by using an explicit integration scheme, our time steps on the finest meshes are about an order of magnitude smaller than those needed to achieve a 10% relative error in the speed of the front (AMRA uses 0.003 ms as opposed to the value 0.04 ms for the semi-implicit case) [9]. However, one cannot conclude that a semi-implicit algorithm is automatically better than our explicit one since, for a fixed spatial resolution, the larger time step allowed by a semi-implicit method may give less accuracy during the upstroke [13] and require more computation (some of these issues will be discussed quantitatively elsewhere for the 1d case [9]). Since the spatiotemporal dynamics of even the most detailed cardiac membrane models are not yet understood and the relation between specified local truncation error and correct dynamics is also not understood, the present calculations should be considered as an early but significant step in finding a good balance between efficiency and accuracy for simulating arrhythmias in large domains and over long times.

Our results for the AMRA were obtained for the quantitatively accurate LR1 model [6], which in 2d can be written in the form:

$$C_m \partial_t V(t,x,y) = \frac{1}{\beta}\left(g_x \partial_x^2 V + g_y \partial_y^2 V\right) - I_{\rm ion}(\mathbf{m}) - I_{\rm stim}(t,x,y),$$
$$\frac{d\mathbf{m}}{dt} = \mathbf{f}(\mathbf{m}, V), \qquad (1)$$

where $V(t, \mathbf{x})$ is the membrane potential at time t and at position $\mathbf{x} = (x, y)$, C_m is the membrane capacitance per unit area, β is a surface-to-volume ratio of a heart cell, g_x and g_y are membrane conductivities (generally not equal since the heart is anisotropic), $I_{\rm ion}$ is the total ionic current flowing across the membrane, and $I_{\rm stim}$ is a specified current injected to initiate a propagating wave. (For all calculations reported below, the boundary condition $(\hat{n} \cdot \nabla)V = 0$ was used, where $\hat{n}$ is the unit vector normal to a given boundary point.) The seven voltage-sensitive membrane variables $m_i(t, \mathbf{x})$ for the LR1 model determine the flow of various ions across the membrane and satisfy *ordinary* differential equations, which are also integrated by a forward-Euler method. The same membrane parameter values as those of Ref. [6] were used except for the calcium conductivity $g_{\rm Ca}$ in the $I_{\rm ion}$ term, whose value was changed from 0.09 to 0.045 (in units of $\mathrm{m}\Omega^{-1} \cdot \mathrm{cm}^{-2}$). The medium was isotropic with g_x and g_y set to 1 $\mathrm{k}\Omega^{-1} \cdot \mathrm{cm}^{-1}$ and β set to 3000 cm^{-1}. These values shortened the action potential duration and led to dynamical states with many spirals, providing a more challenging test of the AMRA.

In addition to the physical parameters in Eq. (1), many

numerical and algorithmic parameters need to be specified [7,9]. Several of the more important choices are an initial resolution for a uniform coarse mesh covering the domain (we used $\Delta x = 0.05\,\mathrm{cm}$), the temporal resolution for the coarse mesh (we used $\Delta t = 0.012\,\mathrm{ms}$), the maximum number of grid levels allowed for refinement (we used the value 3), the factor by which the spatial mesh is refined locally (we chose the factor 2), the error tolerance used in the Richardson extrapolation estimate of the local truncation error (we chose $\epsilon = 2 \times 10^{-3}$); and the number of time steps to elapse before estimating a local error and regridding (we chose 2).

As a first demonstration of the effectiveness of the AMRA, Fig. 1 summarizes a 3-level calculation of the LR1 model in a 1d domain of length $L = 9\,\mathrm{cm}$. The system was stimulated at $t = 0$ with a $0.2\,\mathrm{cm}$ square pulse along the left edge of the domain, which evolved into a front propagating to the right (the spatial profile is independent of the initial condition and of the system size for $L \geq 9\,\mathrm{cm}$). One can see from the spatial profile in Fig. 1a at time $t = 240\,\mathrm{ms}$ how narrow is the front (region of depolarization) compared to the profile's extent and this specifically is what makes numerical simulation of highly excitable media so difficult. In the vicinity of the front, Fig. 1b shows the grid structure which was automatically calculated by the ARMA; the colors black, green, and red indicate the coarse, fine, and finest mesh regions respectively. Taking into account the reduction of spatial mesh points and the asynchronous updating of grid points using spatially varying time steps [7], the AMRA overall used a factor of 3.6 fewer grid points and did less computational work by a factor of 9 for the LR1 model than a constant-time-step uniform-spatial-mesh forward-Euler code using the finest space-time resolutions of the AMRA. The spatial adaptivity of the time step accounts for a factor of 2 in this factor of 10 and so is an important part of the algorithm. The temporal profiles at a fixed point in space, the front speeds, and the times between peak and recovery at a fixed point in space (action potential duration) for the AMRA and for a high-resolution uniform-mesh code (discussed in Ref. [9]) agree within 0.1% relative errors except at the peaks of the temporal profiles, where the relative error is about 4%. We conclude that there is no significant loss of accuracy when using the more efficient AMRA.

Fig. 2 shows how the AMRA performs for the LR1 model in a large square domain of size $L = 8\,\mathrm{cm}$, using the same parameter values as the 1d case, for which spirals are unstable and break up into other spirals. This complex many-spiral dynamical state is a much stronger test of the efficiency and utility of an AMRA than Fig. 1 since the geometry of the fronts fluctuates strongly in time. A multi-spiral state was initiated by a standard S1-S2 stimulation protocol [5] in which a right-going planar pulse is created by stimulating the left edge of the domain (the S1 stimulus), and the lower left quadrant of the domain is excited (the S2 stimulus) 334 ms later, when the left half of the domain has returned to rest but the right half is still repolarizing. A comparison of the field V with the instantaneous grid structure approximating V is given in Fig. 2 1346 ms after S2 and demonstrates how the AMRA is able to increase automatically the space-time resolution only in the vicinity of the fronts, greatly decreasing the overall computational effort since, at any given time, the sharp fronts indeed occupy only a small fraction of the domain. The total number of mesh points used by the AMR varies substantially with time, from 3×10^4 to 7×10^4 mesh points with an average of 5×10^4. A comparison of these results with those required by a uniform-spatial-mesh constant-time-step code using the finest AMRA resolution [9] shows that the AMRA uses about 8 times fewer mesh points, requires less integration work by a factor of 12, and achieves a speedup of about a factor of 11 [9].

The above results can be used to estimate the computer time needed by the ARMA to integrate for one second the LR1 model for a 3d section of left ventricular wall of dimensions $8\,\mathrm{cm} \times 8\,\mathrm{cm} \times 1\,\mathrm{cm}$, with an effective fine uniform mesh resolution of $\Delta x = 0.0125\,\mathrm{cm}$ in space and $\Delta t = 0.003\,\mathrm{msec}$ in time. On a Pentium III 500 MHz computer, we found that a 3-level 2d AMRA calculation at this resolution takes about 3 days. The time for the 3d calculation then can be estimated by assuming that each of the spirals in Fig. 2 becomes a continuous stack of spirals (a scroll wave), with the stack transverse to the square sides of the domain [2], and correspondingly that the mesh refinements extend uniformly from the 2d case through the transverse direction. A 3d AMRA calculation should then take roughly 15 days, which is a factor of 17 speedup over the 9 months required to complete a similar calculation using a uniform space-time mesh with the above resolution. Without substantial change to the AMRA, an additional speedup of at least 10 can be gained by using a distributed parallel computer with 100 Pentium III processors, and another speedup of 5 by using table-lookups to avoid the many exponentiations associated with the integration of the membrane variables $m_i(t)$. These further gains would reduce the total simulation time for one second of the LR1 model in this 3d domain to 7 hours or less. (With a substantial modification to make the AMRA semi-implicit, another reduction by a factor of 2-3 might be possible.) Simulation of an entire heart (a factor of 4 greater in volume) for one second with a LR 1 model should then be possible on the time scale of one day, which is acceptably fast for exploring many interesting questions about the dependence of arrhythmias on parameters.

In summary, we have shown that an explicit space-time adaptive algorithm [7] using one of the simplest possible data structures (a hierarchy of Cartesian meshes) can already attain an order of magnitude reduction in computational effort and memory when applied to the

experimentally based LR1 cardiac membrane model [6], and that this reduction is achieved without incurring a corresponding reduction in accuracy when compared to an explicit code using a uniform space-time mesh. Important next steps include determining whether the algorithm can be improved by using implicit time integration, generalizing the method to curved boundaries, and making specific applications to the initiation and control of human arrhythmias.

We thank M. Berger, Z. Qu, and A. Garfinkel for useful discussions and especially M. Berger for making available to us one of her AMRA codes. This work was supported by a NSF Graduate Research Fellowship, by NSF grant DMS-9722814, and by NIH grant R29-HL-57478.

FIG. 1. **(a)** Spatial profile $V(t,x)$ at time $t = 240\,\mathrm{ms}$ for a 1d front propagating to the right in a domain of length $L = 9\,\mathrm{cm}$, as calculated by a 3-level adaptive mesh refinement algorithm (AMRA) for the Luo-Rudy 1 (LR1) cardiac model [6]. The three regions of coarse, fine, and finest mesh resolution (from $\Delta x = 0.05\,\mathrm{cm}$, $\Delta t = 0.012\,\mathrm{ms}$ to $\Delta x = 0.0125\,\mathrm{cm}$, $\Delta t = 0.003\,\mathrm{ms}$) are indicated by the black, green, and red portions of the curve. **(b)** Blowup of the small interval indicated near $x = 8.4\,\mathrm{cm}$ in **(a)**, showing how the 3-level mesh structure (vertical lines) has automatically resolved the sharp front.

FIG. 2. **(a)**: Three-level AMRA calculation of the 2d LR1 model at time $t = 1346\,\mathrm{ms}$ after stimulus S2, in a square domain of length $L = 8\,\mathrm{cm}$. Field value ranges for $V(t,x,y)$ are color coded with blue for $V \geq -5\,\mathrm{mV}$, red for $-5 \leq V \leq -65\,\mathrm{mV}$, and yellow for $V \leq -65\,\mathrm{mV}$. Parameter values are the same as in Fig. 1. **(b)**: The hierarchical Cartesian meshes of the AMR algorithm corresponding to the snapshot of V in **(a)**. The yellow and green regions correspond to the fine (level 2) and finest (level 3) grids and track closely the fronts.

* E-mail: emc@cs.duke.edu.

[1] A. T. Winfree, Science **266**, 1003 (1994).
[2] F. Fenton and A. Karma, Chaos **8**, 20 (1998).
[3] A. Garfinkel, M. L. Spano, W. L. Ditto, and J. N. Weiss, Science **257**, 1230 (1992); I. Aranson, H. Levine, and L. Tsimring, Phys. Rev. Lett. **72**, 2561 (1994); G. V. Osipov, B. V. Shulgin, and J. J. Collins, Phys. Rev. E **58**, 6955 (1998).
[4] A. T. Winfree *et al.*, Chaos **6**, 617 (1996); F. X. Witkowski *et al.*, Chaos **8**, 94 (1998).
[5] M. Courtemanche, Chaos **6**, 579 (1996).
[6] S. Luo and Y. Rudy, Circulation Research **68**, 1501 (1991).
[7] M. J. Berger and J. Oliger, J. Comp. Phys. **53**, 484 (1984); M. J. Berger and P. Colella, J. Comp. Phys. **82**, 64 (1989); J. Bell et al, SIAM J. Sci. Comput. **15**, 127 (1994).
[8] M. J. Berger, in *Adaptive Methods for Partial Differential Equations*, edited by J. E. Flaherty *et al.* (SIAM, Philadelphia, 1989), pp. 150-159. See also information on the package DAGH (Distributed Adaptive Grid Hierarchy), written by S. Mitra, M. Parashar, and J. C. Browne, available at http://www.cs.utexas.edu/users/dagh.
[9] E. Cherry, H. Greenside, and C. Henriquez, unpublished (2000).
[10] For strongly excitable media with fast time scales, the simple first-order-accurate forward-Euler method is acceptable since the fronts evolve so quickly that a time step small enough to resolve these fronts also leads to good accuracy.
[11] W. Quan, S. J. Evans, and H. M. Hastings, IEEE Transactions on Biomedical Engineering **45**, 372 (1998).
[12] P. K. Moore, preprint available at http://www.math.tulane.edu/~pkm/papers.html.
[13] A. E. Pollard, N. Hooke, and C. S. Henriquez, Critical Reviews in Biomedical Engineering **20**, 171 (1992).
[14] A. V. Panfilov, Phys. Rev. E **59**, R6251 (1999).

This figure "fig1ab.gif" is available in "gif" format from:

http://arXiv.org/ps/physics/9908008v3


This figure "fig2a.gif" is available in "gif" format from:
http://arXiv.org/ps/physics/9908008v3

This figure "fig2b.gif" is available in "gif" format from:

http://arXiv.org/ps/physics/9908008v3