The Mortar Finite Element Method for Cardiac Reaction-Diffusion Models

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Abstract

We deal with the problem modeling the electrical activity of the heart and a non–conforming non–overlapping domain decomposition method, based on the Mortar FEM, is proposed. The aim is to devise a numerical technique that allows real time solution introducing adaptivity, but maintaining the easiness of implementation and the properties of conforming methods in each subdomain. The numerical tests show how the method works and its efficiency.

1. Introduction

The papers deals with the efficient numerical solution of the problem modeling the electrical activity of the heart. A macroscopic model that can account for the most important features of the myocardium is the so called cardiac "bidomain" model consisting of a Reaction-Diffusion (R-D) system of equations for the intra- and extracellular potential u_i and u, coupled through the transmembrane potential $v = u_i - u$ (see [1]). This system is still computationally prohibitive because of the cardiac excitation wavefront which requires high temporal and spatial resolution [2, 3]. In order to make large scale simulations feasible, some form of spatial and/or time adaptivity need to be considered. However, the use of adaptive methods is not straightforward and moreover fully adaptive methods may be heavy to implement [4, 5].

To get some degree of adaptivity, which is necessary to tackle this problem, we propose in this paper to resort to a non–conforming non–overlapping domain decomposition based on the Mortar Finite Element Method. More specifically, we try to combine the advantages of the adaptive and non–adaptive methods generally used. Indeed, the method we propose is adaptive because we decompose the computational domain and we concentrate the computational work only in regions of high electrical activity, but, in each subdomain a uniform grid is used.

The numerical technique was first applied to the elliptic bidomain equation for the extracellular potential [6] and in [7] a detailed analysis of the discretization errors is developed. Now the method is extended to the R-D system starting with the case of "equal anisotropy ratio". Thus the system of equations reduces to a single parabolic equation and it is easier to test the efficiency of the numerical method proposed.

A comparison is carried out with the standard conforming FEM which was, so far, the method primarily used. The numerical results show the better computational performance of this non–conforming domain decomposition technique. Thus, we may conclude that these promising results can be considered as a first important step towards realistic simulations of the whole myocardial excitation process.

2. Mathematical model

A well known macroscopic representation of the cardiac tissue is given by the *anisotropic bidomain*: the myocardium is seen as two interpenetrating anisotropic continua, intracellular (i) and extracellular (e), connected everywhere by the distributed cellular membrane [1]. Let $\Omega \subset \mathbb{R}^2$ be the domain representing the cardiac tissue, then the typical anisotropic myocardial fiber structure is modeled introducing the intra- and extracellular anisotropic conductivity tensors M_i, M_e and by $M = M_i + M_e$.

The bidomain model describes both the intracellular and extracellular fields, linking them through the membrane behavior and yields the following Reaction–Diffusion (R–D) system of equations:

$$\begin{aligned} c_m \partial_t v - \text{div } M_i \nabla v + I_{ion}(v) &= \text{div } M_i \nabla u + I_a \quad \text{in } \Omega_t \\ -\text{div } M \nabla u &= \text{div } M_i \nabla v \quad \text{in } \Omega_t \end{aligned}$$

where $\Omega_t = \Omega \times]0, T[$, I_a models an applied current used to initiate the process and c_m represents the surface capacitance of the membrane. In this work we focus on the FitzHugh-Nagumo model, then the transmembrane ionic current $I(v)$ is assumed for simplicity to depend only on v and to be a cubic polynomial: $I_{ion}(v) = \chi I(v)$ with $I(v) = Gv(1 - v/v_{th})(1 - v/v_p)$, where χ is the ratio of the membrane area per unit tissue, G is the maximum membrane conductance per unit area and v_{th}, v_p are the threshold and plateau values of v.

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In order to test and validate our adaptive procedure, we concentrate firstly on a simplified model, known as monodomain that can be obtained by considering the case of equal anisotropy ratio. Then the anisotropic conductivity tensors are such that $M_i = \lambda M_e$, with λ constant; hence, defining $\widehat{M} = \lambda/(1+\lambda)\, M_i$ we obtain the following reaction–diffusion equation in v:

$$\begin{array}{ll} c_m \partial_t v - \mathrm{div}\widehat{M}\nabla v + I_{ion}(v) = I_{app} & \text{in } \Omega_t \\ \mathbf{n}^T \widehat{M}\nabla v = 0 & \text{in } \partial\Omega_t \\ v(x,0) = 0 & \text{in } \Omega. \end{array} \quad (1)$$

3. Numerical methods

The method proposed in this paper tries to combine the advantages of the adaptive and non adaptive methods previously used. Indeed

1. some spatial adaptivity is introduced:
the computational domain is decomposed into subdomains and the computational work is concentrated only in subdomains of high electrical activity, i.e. crossed by the cardiac wavefront;
2. in each subdomain a uniform grid can be considered;
3. using the Mortar FEM the matching of different discretizations on adjacent subdomains is weakly enforced.

3.1. Mortar method

The computational domain Ω is decomposed into $N \times N$ subdomains. We consider a geometrically conforming domain decomposition, i.e. the intersection of the closure of two subdomains is either empty, a vertex, or an entire common edge of the two subdomains. Let $\gamma_l^{(i)}$ be the i-th side of the l-domain, i.e. $\partial\Omega_l = \cup_{i=1}^4 \gamma_l^{(i)}$ and setting $\Gamma_{lk} = \partial\Omega_k \cap \partial\Omega_l$ then the so–called skeleton of the decomposition is $S = \cup\Gamma_{lk}$. In order to apply the Mortar Method we start by choosing a splitting of the skeleton S as the disjoint union of a certain number of subdomain sides, called *slave* sides and *master* sides; see ([8, 9]).

By using the above splitting of the domain, we introduce the functional spaces $X = \prod_{l=1}^L H^1(\Omega_l)$ and we define the composite bilinear form $a_X : X \times X \to \mathbb{R}$, $a_X(\psi,\phi) := \sum_{l=1}^L \int_{\Omega_l} (\nabla\phi_l)^T \widehat{M}\nabla\psi_l \, dx$. This bilinear form is clearly not coercive on X hence, to obtain a well posed problem, proper subspaces of X have to be considered consisting of functions satisfying a suitable weak continuity constraint. More precisely, for any subspace $M \subset L^2(S)$, we can consider the *constrained* space $\mathcal{X}(M)$: $\mathcal{X}(M) = \left\{\phi \in X | \int_S [\phi]\, \lambda = 0, \quad \forall \lambda \in M\right\}$ where $[\phi]$ denotes the jump of ϕ across the skeleton S. Under minimal conditions on M (M must contains the constants on each subdomain edge) the bilinear form a_X is coercive on $\mathcal{X}(M)$. In other words, we impose the weak continuity by requiring that the jump of the discrete solution on each side is orthogonal to a multiplier space. We remark that the strong continuity of the solution at the cross points is not required.

The space approximation is performed by introducing, for each subdomain Ω_l, a family $\mathcal{V}_l$ of finite dimensional subspaces of $H^1(\Omega_l) \cap C^0(\bar{\Omega}_l)$ and defining $X_\delta = \prod_{l=1}^L \mathcal{V}_l$, $X_\delta \subset X$. Given a finite dimensional multiplier space $M_\delta \subset L^2(S)$, we introduce the constrained approximation space $\mathcal{X}_\delta \subset \mathcal{X}(M_\delta)$ such that $\mathcal{X}_\delta = \left\{\phi_\delta \in \prod_{l=1}^L \mathcal{V}_l,\ \int_S [\phi_\delta]\lambda = 0,\ \forall \lambda \in M_\delta\right\}$ and finally we can write the discrete **Problem** ($\mathbf{P}_\delta$):

for each $t > 0$, find $v_\delta = v_\delta(t) \in \mathcal{X}_\delta$ such that

$$c_m \frac{\mathrm{d}}{\mathrm{dt}}(v_\delta(t),\phi_\delta) + a_X(v_\delta(t),\phi_\delta) + (I_{ion}(v_\delta(t)),\phi_\delta) = \\ = (I_{app}(t),\phi_\delta) \qquad \forall \phi_\delta \in \mathcal{X}_\delta$$

$$v_\delta(0) = 0.$$

3.2. Time discretization and algebraic formulation

For the time discretization we consider a semi–implicit method where the diffusion term is discretized by the implicit Euler method, while the non linear reaction term I_{ion} is treated explicity. For each subdomain Ω_l we will denote by A^l and M^l the stiffness and mass matrices relative to the discretization in $\mathcal{V}_l$ whereas A will denote the block diagonal stiffness matrix with blocks A^l and M the diagonal mass matrix with diagonal entries M^l. Let τ be the time step, $t^n = n\tau$ and $\mathbf{v}^n = v_\delta(t^n)$, then the fully discretized problem reads as follows: $\forall n = 0, \ldots, N_t - 1$ find $\mathbf{v}^n$ such that:

$$c_m M \frac{\mathbf{v}^{n+1} - \mathbf{v}^n}{\tau} + A\,\mathbf{v}^{n+1} + M\,\mathbf{i}_{ion}(\mathbf{v}^n) = M\,\mathbf{i}_{app}$$

with $\mathbf{i}_{ion}(\mathbf{v}^k)$ and $\mathbf{i}_{app}$ the finite element interpolants of I_{ion} and I_{app} respectively.

Now, we recall [9] that an element u_δ of $\mathcal{X}_\delta$ has the form $u_\delta = \left(u_\delta^l\right)_{l=1,N^2}$ with $u_\delta^l = \sum_k u_k^l \Phi_k^l$ and Φ_k^l nodal basis functions. The coefficients (u_k^l) must satisfy the discrete equivalent of the jump constraint on the interface S. The actual degrees of freedom, denoted by $\mathbf{u}_M$, are all the coefficients corresponding to nodes interior to each subdomain Ω_l or lying on a master side. The value of those coefficients corresponding to basis functions "living" on slave sides is uniquely determined by the remaining coefficients through the jump condition and can be eliminated from the global vector $\mathbf{u}$. Indeed each u_δ can now be represented by the shorter vector $\mathbf{u}_M$, and the corresponding global vector can be obtained thanks to a global "switching" matrix Q that represents also the constraint, i.e. we have $\mathbf{u} = Q\mathbf{u}_M$. Then, for each time step, we get the following algebraic system:

$$\mathcal{A}\mathbf{v}_M^{k+1} = \mathbf{b}_M \qquad \text{with} \qquad \mathcal{A} = Q^T(M_t + A)Q \quad (2)$$

where $M_t = c_m/\tau\, M$ and $\mathbf{b}_M = Q^T\left[-\mathbf{i}_{ion}(\mathbf{v}^k) + \mathbf{i}_{app}\right]$. The final system can be solved by an iterative method such as a suitably preconditioned Conjugate Gradient Method.

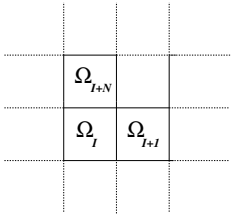
3.3. Remarks on the implementation

The main problem to face is that the mesh can change with the time step and we have to re-assemble the matrices. We remark that during the cardiac excitation phase a moving internal layer of 1 mm thick, associated to a fast variation of the transmembrane potential v, spreads through the myocardium. Thus, each time step, the variation of $v(\mathbf{x}, \mathbf{t})$ over the pair of nodes defining the edges of the subdomains is estimated and if this variation is above a given threshold or not we refine or de-refine the subdomain. In order to limit the computational time required to re-assemble the stiffness and switching matrices A and Q, we choose that each subdomain can have only a coarse mesh or a refined mesh with a fixed level of refinement. The level of refinement is chosen at the beginning of the process to allow an accurate computation of the solution and cannot be modified.

Consequently, the mesh parameters can take only two values (coarse or refined) and we note that

- A is block–diagonal hence only the block corresponding to a subdomain that is refined or de-refined has to be changed. Therefore, we can compute two blocks, the coarse and the refined block, at the beginning of the computation, store them and use the right block when necessary.
- The same can be done also for the switching matrix Q since it can be written as $Q = \left(Q^1 \dots Q^I \dots Q^L\right)$ where each Q^I is associated to the subdomain Ω_I and is defined as:

$$Q^I = \begin{pmatrix} 0 \\ \vdots \\ Q_I \\ Q_{I1} \\ \vdots \\ Q_{IN} \\ \vdots \\ 0 \end{pmatrix}$$



Furthermore, each Q^I is made up of three blocks: Q_I, Q_{I1}, Q_{IN} related to the subdomains Ω_I and to the two adjacent subdomains Ω_{I+1} and Ω_{I+N} respectively (see the above figure). Again, we can compute the blocks Q_I, Q_{I1}, Q_{IN} at the beginning of the computation, store them and use the right one when necessary. Note that now we have to compute 8 blocks to obtain Q^I since 8 is the number of possible combinations of the 3 subdomains $\Omega_I, \Omega_{I+1}, \Omega_{I+N}$ to be refined or not.

4. Results

To show the benefits of this approach we compare it with the standard conforming FEM. For simplicity we consider a domain $\Omega = [0,1] \times [0,1]$ cm modeling the myocardium with cardiac fibers parallel to a diagonal of the square. The domain Ω is decomposed into $N \times N$ subdomains of size $H \times H$ with $H = 1/N$ and $N = 10$. We start with an initial mesh $\mathcal{T}^0$ where each subdomain is decomposed into 3×3 equal square elements. Then, we build iteratively new families of refined mesh $\mathcal{T}^k$ by decomposing each element of the mesh related to a subdomain Ω_l that need a refinement, into 2×2 equal square elements. Hence, we get a mesh with a space step decreasing by a factor of 2 close to the wavefront. Finally, in each subdomain Ω_l, let $\mathcal{V}_l$ be the space of Q_1 finite elements on the mesh $\mathcal{T}_l^k$ and let the multiplier space be based on a dual basis, see [9]; the time step τ was chosen equal to 4×10^{-2} ms. In Fig. 1 we display $v(\mathbf{x}, \mathbf{t})$ and the mesh $\mathcal{T}^k$ with level $k = 2$ of refinement at 20 and 50 msec after stimulation.

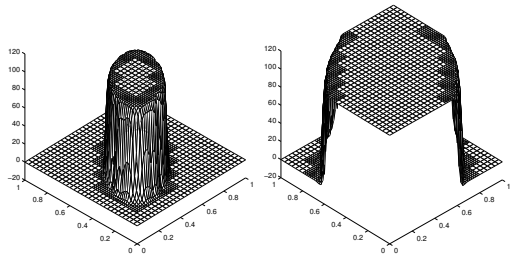


Figure 1. Mesh of $v(\mathbf{x}, \mathbf{t})$ with level 2 of refinement at 20 and 50 msec after stimulation.

The comparison with the conforming FEM is carried out by considering different levels of refinement in the subdomains crossed by the cardiac wavefront. The solution of the conforming FEM was computed by using a uniform space step equal to the one used in the refined subdomains. In Tables 1,2 we present, for each level of refinement, the number of elements considered (min-max for the Mortar FEM) and the cpu–time required to simulate a small wavefront (10 msec after stimulation) and a large wavefront (30 msec), that is 250 and 750 time steps respectively. In order to study the efficiency of the method we also report the cpu–time reduction of the Mortar FEM. Since we simply want to compare the two approaches, conforming and non–conforming, we consider the same preconditioner: the Incomplete Cholesky factorization with no fill-in and dropping tolerance equal to 10^{-5} (Matlab function `cholinc`); the problem of finding the best preconditioner is beyond the scope of this work. The comparison is carried out by measuring the cpu–time (Matlab function `cputime`).

At level 1 of refinement, we have the same number of elements but different cpu–time to solve the problem. This

Table 1. "Small" Wavefront: 16 refined subdomains / 250 time steps

Level		# elem	cpu–time (sec.)	cpu–time reduction
	mortar	900	11.3	NO
1	c. FEM	900	5.9	
	mortar	927/1332	17	23 %
2	c. FEM	3600	22	
	mortar	1035/3060	26	73 %
3	c. FEM	14440	98	
	mortar	1467/9972	62	89 %
4	c. FEM	57600	584	
	mortar	3195/37620	220	92 %
5	c. FEM	240000	2887	

Table 2. "Large" Wavefront: 45 refined subdomains / 750 time steps

Level		# elem	cpu–time (sec.)	cpu–time reduction
	mortar	900	34.2	NO
1	c. FEM	900	17.9	
	mortar	927/2115	66	1 %
2	c. FEM	3600	67	
	mortar	1035/6975	150	48 %
3	c. FEM	14440	290	
	mortar	1467/26415	613	59 %
4	c.FEM	57600	1510	
	mortar	3195/104175	2679	69 %
5	c. FEM	240000	8558	

is due to the fact that the conforming FEM matrix is more sparse than the mortar FEM matrix. The mortar FEM becomes more efficient than the conforming FEM starting from level 2 of refinement. At level 5 we have a space step of $2.08\,10^{-3}$ cm close to the wavefront and we observe a cpu–time reduction of 92% and 69% for 250 and 750 time steps respectively. Thus the method remains efficient also for large wavefronts and big time intervals.

5. Conclusion

This paper provides an efficient solution for the problem modeling the electrical activity of the heart. The essential concept here is to allow some spatial adaptivity but maintaining the easiness of implementation and the properties of conforming methods in each subdomain. The numerical tests show the efficiency of the method when compared to the classical conforming FEM. Moreover, these tests were done without facing the problem of finding the best preconditioner and without using any parallelization. Assuming that more than one processor is at hand, this numerical approach may allow to get real time solutions when the fine discretization on the whole computational domain fails to do so. Although the numerical tests relate to a square domain modeling the cardiac tissue, they are very promising and may be considered as a first step towards large scale simulations, that is for large portions of myocardium.

Acknowledgments

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