

SCUOLA DI INGEGNERIA INDUSTRIALE E DELL'INFORMAZIONE

Fast Marching Method for the Eikonal model of the Cardiac Electrophysiology

ARICOLO DI PROGETTO IN

NUMERICAL ANALYSIS FOR PARTIAL DIFFERENTIAL EQUATIONS

MATHEMATICAL ENGINEERING - INGEGNERIA MATEMATICA

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Academic year: 2020-2021

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1. Introduction

One of the most challenging problems nowadays consists in describing biological processes through a formal mathematical framework. Fitting accurate numerical models upon relevant medical phenomena often requires a huge number of experimental data and getting them revealed to be troublesome. As a consequence adjusting complete models to specific medical cases is often hard and reduced ones are of great interest.

In this paper, we consider as physiological process the propagation of the electrical signal through the myocardium. This process is well described by the Bidomain Model whose equations derive from a circuital representation of the heart's muscle cells. For computational reason, two simplification are usually adopted: the Monodomain model and the Eikonal model; in particular, we will focus on the latter whose general formulation, neglegting boundary conditions, reads

 $F\sqrt{\nabla T^t D \nabla T}$

This is a function of T, where $T(\mathbf{x})$ is the arrival time at which the electric signal reaches the position \mathbf{x} , F is the speed term, and D the conductivity stress tensor.

The clinical usage of these results forces to find an accurate and fast way to solve this problem. Our analysis relies on the so called *Fast Marching Method* (FMM), which aims at satisfying both these requirements. The core idea of FMM consists in exploiting the physical properties of the signal spread inside the myocardium, computing the arrival time of the peak value isocontour at each point.

Our work mainly aims at implementing this method in the LIFEX environment, highlighting its advantages and drawbacks with respect to the already implemented solution of the Eikonal Model which relies on FEM.

The report will be organized as follows: a first part will be devoted to a theoretical introduction to heart electrophisiological dynamics together with its reduced mathematical representation, the eikonal model, then we will present the FMM, sketching a complete (condensed) version of the algorithm and its main numerical features; the second part will present the key steps of our implementation, and the results obtained compared to FEM performances.

2. Cardiac Electrophisiology and Eikonal Model

To give a framework to what is discussed here it, is convenient to illustrate the main processes involved in the cardiac electrophisiology in a nutshell.

In a heartbeat, a group of cardiac cells, called pace-maker, produce a periodic signal. There are different clusters of these cells and the one that in normal condition (i.e. non pathological) starts it is the senoatrial node placed in the right atrium. The potential wave is first transmitted through the whole atrium and then it reaches the ventricles through the Purkinje fibers. This electric signal originates from the change of membrane potential due to ions entering and living heart's cells. This event, the action potential, has the same waveform for each cell which let to derive some simplification in the model. This peculiar response is because trans-membrane channels are voltage dependent and have different time responses.

Hodgkin and Huxley had the idea of modeling this behaviour with a circuital representation who take as main element a capacitor to represent the membrane and some voltage depending resistances to represent the channels. This leads to the so called Bidomain Model. Despite of its completeness, this model has some drawbacks in terms of computational complexity. For this reason two reduced models are preferred: the Monodomain and the Eikonal. While the former still describes the entire potential through time with the reducing assumption that membrane external potential is proportional to the internal potential, the latter exploit the property of constant waveform taking into account just the peak isocontour.

It can be said, with a naive approach, that the Monodomain model should be preferred when we need more precision and is actually mandatory in order to have knowledge of the entire potential distribution; the Eikonal one instead shines for its computational timing performance.

This work involves just the Eikonal model and consequently a deeper description of it is required.

Starting from the bidomain model, in addition with some simplifications related to the signal's features underlined above it is possible to derive, negletting the diffusivity term, the following eikonal equation:

$$\begin{cases} F\sqrt{\nabla TD\nabla T} = 1 & \text{in } \Omega\\ (D\nabla T) \cdot \mathbf{n} = 0 & \text{on } \partial\Omega \end{cases}$$
 (1)

Where Ω is the domain, which is in this case study the *myocardium*; T is the arrival time, i.e. the time at which in the position \mathbf{x} the potential reaches is peak; F is the velocity of the depolarization wave along the fiber direction for a planar wavefront; D is the diffusivity tensor, which describes the anisotrophies in the model and \mathbf{n} is the normal to the domain boundary $\partial\Omega$.

Starting from this formulation many resolution methods arise. Here we analyze the FMM.

3. Algorithm FMM main features

The idea behind the Fast Marching Method is to exploit, in its recursive structure, the physical propagation properties of the electric signal. Starting from the source of the impulse (received as datum), it applies a front tracking approximation of the signal and follows the characteristic lines of its propagation.

In particular as we have previously seen T(X) represents the peak value isocontour of the electric signal, and it's exactly the propagation of this wave to be under investigation.

This way, T(x) will not be computed "all at once" but each iteration physically represents an instant, when some points have already be striked by the impulse while other have not.

As a consequence it is necessary, at each stage, to rely on the situation in the previous step and approximate the process evolution for a new time step, expanding in space the front of the wave.

It's straightforward then, that value of T(X) computed at new points are only determined by a subset of its neighboring points since the expansion of the wave over the domain is continuous.

To be coherent to what we just sad, the algorithm will have to obey to one central constraint: points with larger value of T(X) cannot affect points with a smaller one.

Physically speaking this decision can be agreed observing that the direction of the signal cannot be affected by points where it has not arrived yet, while points where signal has already arrived can modify it. This logical imposition, as we'll see, will be of huge importance in the construction of algorithm.

Finally, to conclude this introduction it is important to stress that we are dealing with a specific version of the FMM: the anisotropic FMM; it means that the information spread does not follow the gradient direction, but the characteristic lines of propagation are imposed through a tensor D.

This issue is physically explained by the presence of fibers inside myocardium and its numerical implications will cause some modification to the algorithm, detaching the proposed version from the standard FMM.

Before presenting a detailed description of the algorithm, a broad-term explanation of its main passages is offered. Suppose we are at iteration k. Firstly we have to consider a source node X for which we know the solution. Then we take the set of all its neighbours N(X) and for any element inside N(X) compute T. If any of them have been solved in previous iterations the lower value of T is confirmed, while the bigger is discarded. The reason of this recursive correction relies inside anisotropy, which causes characteristic lines of propagation not to follow the gradient direction. If in isotropy conditions it's enough to follow the characteristic direction of the PDE contained in the immediate neighbourhood, in anisotropic condition this idea is no more true. We must be sure to approximate correctly the wave motion, and to do it we must account for all possible directions of propagation.

Any point can be part of many N(X), i.e. can be reached from different directions, and the right one will be that associated to the smallest T(X). At this step we points can be divided in three categories: some still have not been reached by the signal and have no solution, others have mantained the previous one, and others more have changed their status, or because firstly reached by the impulse in the current iteration or because their T have been now corrected.

In next iterations it is important to consider the corrected nodes as new sources, because the new value of Twill affect the whole dynamic around.

Once selected the new source node X it is possible to repeat the same passages as before. We can keep repeating this loop till all the nodes inside the domain have been solved and FMM provided the desired solution.

Now the formal description of the Recursive Anisotropic FMM follows:

- 1. Define four empty vectors: CHANGED, KNOWN, FAR, TRIAL.
 - FAR will contain points not still handled.
 - TRIAL will contain points whose T have been computed, still never considered as sources.
 - KNOWN will contain points whose T has been computed, still considered as sources.
 - CHANGED will contain points whose T has been computed but then modified, and so must be considered as new sources.

2.

Equations 4.

This section gives some examples of writing mathematical equations in your thesis. Maxwell's equations read:

$$\nabla \cdot \mathbf{D} = \rho, \tag{2a}$$

$$\begin{cases}
\nabla \cdot \mathbf{D} = \rho, & (2a) \\
\nabla \times \mathbf{E} + \frac{\partial \mathbf{B}}{\partial t} = \mathbf{0}, & (2b) \\
\nabla \cdot \mathbf{B} = 0, & (2c) \\
\nabla \times \mathbf{H} - \frac{\partial \mathbf{D}}{\partial t} = \mathbf{J}. & (2d)
\end{cases}$$

$$\nabla \cdot \mathbf{B} = 0, \tag{2c}$$

$$\nabla \times \boldsymbol{H} - \frac{\partial \boldsymbol{D}}{\partial t} = \boldsymbol{J}. \tag{2d}$$

Equation (2) is automatically labeled by cleveref, as well as Equation (2a) and Equation (2c). Thanks to the cleveref package, there is no need to use \eqref. Equations have to be numbered only if they are referenced in the text.

Equations (3), (4), (5), and (6) show again Maxwell's equations without brace:

$$\nabla \cdot \boldsymbol{D} = \rho,\tag{3}$$

$$\nabla \times \mathbf{E} + \frac{\partial \mathbf{B}}{\partial t} = \mathbf{0},$$

$$\nabla \cdot \mathbf{B} = 0,$$
(4)

$$\nabla \cdot \boldsymbol{B} = 0, \tag{5}$$

$$\nabla \times \boldsymbol{H} - \frac{\partial \boldsymbol{D}}{\partial t} = \boldsymbol{J}. \tag{6}$$

Equation (7) is the same as before, but with just one label:

$$\begin{cases}
\nabla \cdot \mathbf{D} = \rho, \\
\nabla \times \mathbf{E} + \frac{\partial \mathbf{B}}{\partial t} = \mathbf{0}, \\
\nabla \cdot \mathbf{B} = 0, \\
\nabla \times \mathbf{H} - \frac{\partial \mathbf{D}}{\partial t} = \mathbf{J}.
\end{cases} (7)$$

5. Figures, Tables and Algorithms

Figures, Tables and Algorithms have to contain a Caption that describes their content, and have to be properly referred in the text.

Figures 5.1.

For including pictures in your text you can use TikZ for high-quality hand-made figures [2], or just include them with the command

\includegraphics[options]{filename.xxx}

Here xxx is the correct format, e.g. .png, .jpg, .eps,



Figure 1: Caption of the Figure.

Thanks to the \subfloat command, a single figure, such as Figure 1, can contain multiple sub-figures with their own caption and label, e.g. Figure 2a and Figure 2b.





(a) One PoliMi logo.

(b) Another one PoliMi logo.

Figure 2: Caption of the Figure.

5.2. Tables

Within the environments table and tabular you can create very fancy tables as the one shown in Table 1.

Example of Table (optional)

	column1	column2	column3
row1	1	2	3
row2	α	β	γ
row3	alpha	beta	gamma

Table 1: Caption of the Table.

You can also consider to highlight selected columns or rows in order to make tables more readable. Moreover, with the use of table* and the option bp it is possible to align them at the bottom of the page. One example is presented in Table 2.

5.3. Algorithms

Pseudo-algorithms can be written in LATEX with the algorithm and algorithmic packages. An example is shown in Algorithm 1.

	column1	column2	column3	column4	column5	column6
row1	1	2	3	4	5	6
row2	a	b	c	d	e	f
row3	α	β	γ	δ	ϕ	ω
row4	alpha	beta	gamma	delta	phi	omega

Table 2: Highlighting the columns

Algorithm 1 Name of the Algorithm

- 1: Initial instructions
- 2: for for condition do
- 3: Some instructions
- 4: **if** if condition **then**
- 5: Some other instructions
- 6: end if
- 7: end for
- 8: while while condition do
- 9: Some further instructions
- 10: end while
- 11: Final instructions

6. Some further useful suggestions

Theorems have to be formatted as follows:

Theorem 6.1. Write here your theorem.

Proof. If useful you can report here the proof.

Propositions have to be formatted as follows:

Proposition 6.1. Write here your proposition.

How to insert itemized lists:

- first item:
- second item.

How to write numbered lists:

- 1. first item;
- 2. second item.

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A final section containing the main conclusions of your research/study and possible future developments of your work have to be inserted in the section "Conclusions".

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Your thesis must contain a suitable Bibliography which lists all the sources consulted on developing the work. The list of references is placed at the end of the manuscript after the chapter containing the conclusions. It is suggested to use the BibTeX package and save the bibliographic references in the file bibliography.bib. This is indeed a database containing all the information about the references. To cite in your manuscript, use the \cite{} command as follows:

Here is how you cite bibliography entries: [3], or multiple ones at once: [4, 5]. The bibliography and list of references are generated automatically by running BibTeX [1].

References

- [1] CTAN. BiBTeX documentation.
- [2] CTAN. pgf create PostScript and PDF graphics in TEX.
- [3] Donald E. Knuth. Computer programming as an art. Commun. ACM, pages 667–673, 1974.
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A. Appendix A

If you need to include an appendix to support the research in your thesis, you can place it at the end of the manuscript. An appendix contains supplementary material (figures, tables, data, codes, mathematical proofs, surveys, ...) which supplement the main results contained in the previous sections.

B. Appendix B

It may be necessary to include another appendix to better organize the presentation of supplementary material.

Abstract in lingua italiana

Qui va l'Abstract in lingua italiana della tesi seguito dalla lista di parole chiave.

Parole chiave: qui, le parole chiave, della tesi, in italiano

Acknowledgements

Here you might want to acknowledge someone. $\,$