

A Multiresolution Impedance Method for Bioelectromagnetic Problems

Michael Eberdt⁽¹⁾ and Gianluca Lazzi^{*(2)}

(1) Dept. of Computer Science and (2) Dept. of Electrical and Computer Engr.
North Carolina State University
EGRC Box 7914, Raleigh NC 27695-7914

Abstract

The impedance method is an electromagnetic simulation method for quasistatic problems. It is based on the discretization of object(s) upon which electromagnetic radiation is incident, and it requires solving a system of equations in which the number of equations is determined by the number of grid cells in the discretized model. We investigate the feasibility of employing a grid generation method that does not yield equal-sized cells everywhere, as a means of decreasing the size of the linear system to be solved. We apply the method to a simple test case for which analytical results are available, and examine the accuracy and computational efficiency of our method with respect to the standard uniform grid.

Introduction

The impedance method was introduced by Gandhi, et al [1] as a simulation method suitable for quasistatic electromagnetic radiation problems, particularly biomedical applications such as the study of radiation-induced currents in the human body. It is a conceptually simple technique that easily accommodates anisotropic, inhomogeneous materials in the physical model, as well as spatially-varying electromagnetic sources. The model may be 2-dimensional or 3-dimensional, although we restrict our attention in this paper to the 2-dimensional case.

In the impedance method, after a grid is applied to the physical model, an impedance network is constructed using lumped impedances derived from the material properties of each grid cell. A linear system of equations is solved to obtain the branch currents within the impedance network; the correspondence between branches in the network and cells in the gridded material is then used to obtain current magnitudes and directions in the material itself.

In the original formulation of the impedance method [1-2], the model is discretized into a grid having a uniform cell size. The obvious drawback, in this case, is that the smallest geometric feature that must be accurately discretized will determine the grid cell size to be used throughout the entire region, leading to a

very large number of unknowns when very small features of the geometry need to be accurately represented.

This paper describe a novel multiresolution formulation of the impedance method which discretizes the model into non-uniform cell sizes by utilizing the smallest cells along boundaries between materials, and transitioning to progressively larger cells in large homogeneous regions. Thus, the method leads to a considerable reduction in computational resources and execution times in problems where high resolution is needed only in some regions of the discretized model.

Implementation

In order to show the feasibility of the method and its accuracy, we focused on the two-dimensional implementation of the proposed method. The three-dimensional implementation can be approached in an analogous manner. To limit the number of possible cases that can be encountered by the automatic multigrid meshing algorithm, we adopted the following restrictions:

- Each cell in the mesh may only have an aspect ratio of 1:1, 1:2, or 2:1;
- Adjacent cells may differ in size along a given axis by a 2:1 ratio only;
- When a cell shares an edge with a pair of neighbors, the neighbors must abut at the midpoint of that shared edge.

These restrictions facilitate simpler data structures and algorithms by limiting the number of neighbors a cell can have and the manner in which they can abut.

The proposed discretization algorithm is an iterative one: within an enclosed region comprised of a single material, minimum-sized cells (or "unit cells") are placed everywhere; those cells are then successively recombined, subject to the restrictions outlined above, until no more combining is possible. Unit cells are retained adjacent to material boundaries, where higher resolution is generally needed. As a consequence of the non-uniform meshing, a single expression cannot describe the loop equation for each and every cell, as was possible with a uniform grid. An algorithm has been developed to examine each cell individually to determine the number of neighbors and their locations. This complicates the application of an iterative solution method such as that described in [2]; however, the substantial reduction in the number of equations makes a direct solution method much more feasible.

The current density within the mesh is computed as follows:

- Densities along cell edges correspond directly to branch current densities in the impedance network;
- Densities at the junctions of collinear cell edges are averaged;
- Densities at locations other than cell edges are obtained by linear interpolation.

Results

To test the proposed method we use a concentric cylinder model similar to that used in [1]. This geometry is used because it has a readily-obtainable analytical solution. It is simply a pair of concentric circles surrounded by free space (Figure 1), with material values chosen to approximate muscle tissue ($\epsilon_r = 2000$ and $\sigma = 0.42$ S/m in the inner circle) and fat ($\epsilon_r = 50$ and $\sigma = 0.01$ S/m in the region between the circles). The inner circle is 23 cm in diameter, and the outer circle is 32 cm in diameter; we have added 1.5 cm on all sides to obtain a model measuring 35 cm by 35 cm. One difference in our use of the model here is that we employ only real-valued conductivities, rather than the complex ones employed in [1], an approximation that is valid at low frequencies. The incident radiation has a frequency of 1MHz, with a 10^{-4} T magnetic field oriented along the axis of the cylinder.

In [1], a 0.5cm square cell was employed; we use this as our minimum-sized unit cell. Thus, our model will require 4900 unit cells if discretized in the conventional manner. In contrast, our current filling algorithm can discretize this model, subject to the constraints mentioned above, using only 1727 rectangular cells (35% of the number of unit cells required, shown in Figure 2).

To illustrate our results, we limit ourselves to a visually manageable number of points, choosing locations along the coordinate axes at 0.5 cm intervals. This encompasses points entirely within cells, as well as points on cell edges and corners. Results obtained according to these criteria are shown in Figure 3. Despite the relatively few rectangles used in the grid, the agreement between the proposed method and the analytical solution is good.

Conclusions

We have presented a two-dimensional implementation of a novel multiresolution impedance method that can significantly reduce the computational resources and execution times necessary to solve low frequency bioelectromagnetic problems. The proposed method solved with good accuracy the test case presented in [1], achieving a reduction in cell count of 65%. Novel algorithms for optimal automatic meshing, as well as the use of triangular elements to better conform to the object contours, are currently under investigation.

References

- [1] O.P. Gandhi, J. DeFord, and H. Kanai, "Impedance Method for Calculation of Deposition Patterns in Magnetically Induced Hyperthermia," *IEEE Trans. on Biomed. Eng.*, Vol. 31, No. 10, pp. 644-651, 1984.
- [2] N. Orcutt and O.P. Gandhi, "A 3-D Impedance Method to Calculate Power Deposition in Biological Bodies Subjected to Time Varying Magnetic Fields," *IEEE Trans. on Biomed. Eng.*, Vol. 35, No. 8, pp. 577-583, 1988.

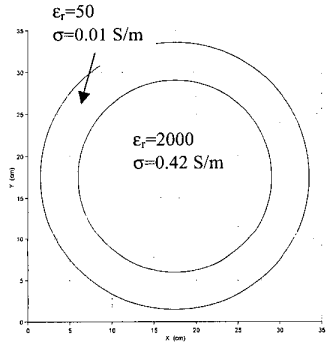


Fig. 1. Geometry of the concentric cylinder model test case. Diameter of the inner cylinder = 23 cm. Diameter of the outer cylinder = 32 cm.

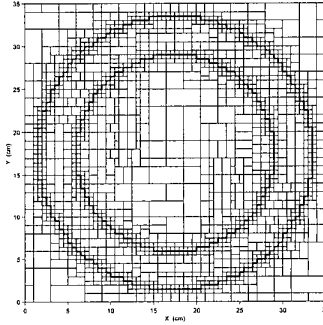


Fig. 2. Discretized version of the geometry of Fig. 1, obtained with the multiresolution discretization algorithm

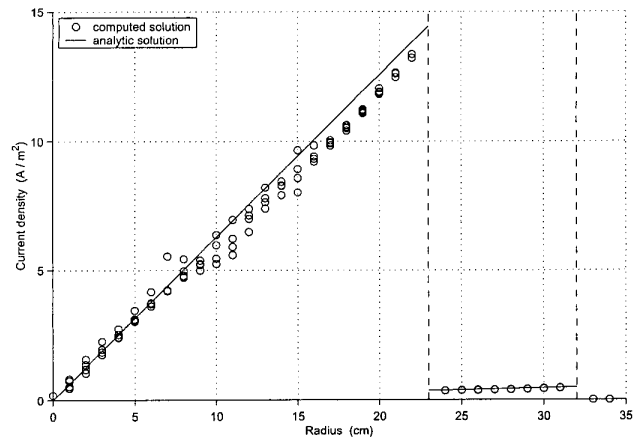


Fig. 3. Comparison between theoretical results and results computed with the multiresolution impedance method for the geometry of Fig. 1.