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MedFDTD: A Parallel and Open-Source Cross-Platform Framework for Bioelectromagnetics Field Simulation

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ABSTRACT MedFDTD, a new parallel and open-source cross-platform framework for bioelectromagnetics research, has been developed by solving Maxwell's equations using the finite-difference time-domain method. This framework implements the complex-frequency-shifted perfectly matched layer, supports the import of antenna and bioelectromagnetic models through media with non-dispersive/dispersive properties, and can calculate the antenna output power and specific absorption rate of biological tissues, thereby making it favorable for bioelectromagnetics studies. In addition, MedFDTD can be implemented on multiple CPUs or a variety of chip-based GPUs to accelerate all parallel computing tasks.

INDEX TERMS Bioelectromagnetics, cross-platform parallel, electromagnetic simulation, FDTD, SAR.

I. INTRODUCTION

Recently, as mobile phones and wireless fidelity networks (Wi-Fi) have become widely used, radio frequency (RF) radiation, which is the most significant source of electromagnetic (EM) exposure, significantly affects the daily lives of humans, and there is increasing public concern about its health implications. An increase in the temperature of human brain tissue, caused by RF exposure, is the primary cause of RF-exposure-related adverse physiological effects [1], [2]. According to the International Commission on Non-Ionizing Radiation Protection (ICNIRP) [4], it is recommended that RF-induced temperature increases in human tissue should not exceed 1 řC. In order to assess the doses of human exposure to EM radiation, the Institute of Electrical and Electronics Engineers (IEEE) has proposed the specific absorption rate (SAR) to measure the electric field strength in organisms [3]. In addition, the ICNIRP established safety protection standards to prevent a level of EM radiation that may be hazardous to the human body [4]. Since human experimentation is restricted, it is difficult to directly measure the SAR. To overcome this limitation, researchers have designed numerical simulation studies based on digital human modeling as an alternative method [5], [6]. Many commercial (CST [7], SEMCAD [8], HFSS [9], Lumerical FDTD Solutions [10], XFDTD [11]) and open-source (MEEP [12], Angora FDTD [13]) software programs developed to numerically simulate the effects of EM radiation. Commercial software has comprehensive features; however, the details regarding the computations are not available to the public. Conversely, the vast majority of currently available open-source software is unable to perform EM parallel computing, to determine the SAR, or to implement dispersive media or an effective absorbing boundary that adequately mimics that of the target organism. Therefore, we developed MedFDTD, which is an open-source EM simulation framework specifically designed for medical applications and bioelectromagnetics research. Our program can easily import bioelectromagnetics media and models, create radiation sources, solve EM fields, calculate the SAR including the whole-body averaged SAR and mass-averaged SAR, and can be implemented on multiple CPUs, computer clusters, or any chip-based GPU to accelerate parallel computing [14].

The general method for MedFDTD development is the implementation of the finite-difference time-domain (FDTD) method [15] to simulate EM radiation. There are several algorithms providing numerical solutions to Maxwell's equations, including the FDTD method; finite integration technology (FIT) method [16], in which the computation is executed in the time domain; finite element method (FEM) [17]; and method of moments (MOM) [18], in which the computation is

executed in the frequency domain. Since the FDTD method is accurate and efficient and can directly simulate EM field distributions, it has been widely used [15].

Bioelectromagnetics research has several critical requirements, such as the application of a high spatial resolution model to achieve high accuracy, simulation of the infinite space radiation, implementation of various and diverse models (i.e., models with different media, conditions, or resolutions, and diverse types of radiation sources) to obtain comprehensive results, and calculation of the SAR in the target biological tissue. It is difficult for a conventional computer to meet the requirements of the high spatial resolution model because of its reduced computation speed and memory limitations. However, MedFDTD provides a distributed-memory parallel acceleration module, which is based on the message passing interface (MPI) [20], and a GPU parallel acceleration module, which is based on the C++ accelerated massive parallelism (C++ AMP) [23]. To simulate the infinite space radiation, the complex-frequency-shifted perfectly matched layer (CPML) [19], which is an excellent representation of human tissue, was applied in the absorbing boundary module. Users can export their own media, human tissue model, and antenna into MedFDTD or create geometric and antenna models by using the modeling module. The radiation module supports various radiation patterns, such as a point source, plane-wave source, and antenna patterns, and can calculate the radiation power and radiation resistance of the antenna. The local SAR, whole-body averaged SAR, and mass-averaged SAR in the biological model can be calculated based on the EM field using the bioelectromagnetics dose module.

II. FDTD METHOD

The FDTD method solves the electromagnetic field by discretizing the Maxwell equations in space and time [15]. The spatial discretization method meshes the computational space, and the electric and magnetic fields on each grid are distributed in the Yee cell format (Fig. 1). The time discretization method alternately samples the electric magnetic fields in chronological order in intervals of half time steps; thus, the discretized Maxwell equation yields explicit difference in equations.

In the case of the 3D model, the methods for solving the electric field in the z direction and the magnetic field in the y direction at the coordinates ((i, j, k)i, j, k) are described using the following updated equations [15]:

$$\begin{aligned} &H_y^{n+\frac{1}{2}}\left(i+\frac{1}{2},j,k+\frac{1}{2}\right)\\ &=H_y^{n-\frac{1}{2}}\left(i+\frac{1}{2},j,k+\frac{1}{2}\right)\\ &\quad-\frac{\Delta t}{\mu\Delta z}\left[E_x^n\left(i+\frac{1}{2},j,k+1\right)-E_x^n\left(i+\frac{1}{2},j,k\right)\right]\\ &\quad+\frac{\Delta t}{\mu\Delta x}\left[E_z^n\left(i+1,j,k+\frac{1}{2}\right)-E_z^n\left(i,j,k+\frac{1}{2}\right)\right] \end{aligned} \tag{1}$$

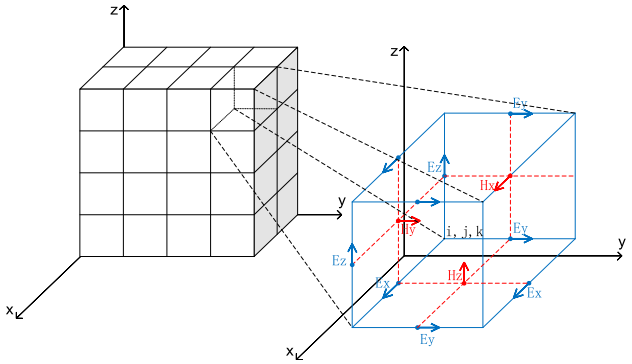

FIGURE 1. Spatial discretization and Yee cells.

$$\begin{aligned} &E_z^{n+1}\left(i,j,k+\frac{1}{2}\right)\\ &=E_z^n\left(i,j,k+\frac{1}{2}\right)+\frac{\Delta t}{\varepsilon\Delta x}\\ &\quad\times\left[H_y^{n+\frac{1}{2}}\left(i+\frac{1}{2},j,k+\frac{1}{2}\right)-H_y^{n+\frac{1}{2}}\left(i-\frac{1}{2},j,k+\frac{1}{2}\right)\right]\\ &\quad-\frac{\Delta t}{\varepsilon\Delta y}\left[H_x^{n+\frac{1}{2}}\left(i,j+\frac{1}{2},k+\frac{1}{2}\right)\right.\\ &\qquad\left.-H_x^{n+\frac{1}{2}}\left(i,j-\frac{1}{2},k+\frac{1}{2}\right)\right] \end{aligned} \tag{2}$$

where Δt is the time interval, Δx, Δy, Δz are the respective spatial intervals, ε is the permittivity, and μ is the permeability.

In order to ensure numerical stability, the spatial intervals Δx, Δy, and Δz and time interval Δt must satisfy the Courant stability condition. In the case of the 3D model, the Courant stability condition is given as [15]

$$c\Delta t\le\frac{1}{\sqrt{\frac{1}{(\Delta x)^2}+\frac{1}{(\Delta y)^2}+\frac{1}{(\Delta z)^2}}}. \tag{3}$$

TABLE 1. Speedup of CPUs in parallel.

Number of cores	Time consumed (s)	Speedup
1	3744	1.00
2	1892	1.98
4	1322	2.83
6	898	4.17
8	652	5.75
10	533	7.02
12	460	8.14
14	411	9.11
16	381	9.83

III. PARALLEL ACCELERATION

A. MPI

MedFDTD implements distributed-memory parallel execution based on MPICH2, which is an implementation of MPI [20]. For the EM simulation, SAR calculations can all be performed in parallel. We evaluated the parallel calculations by using a 257 × 117 × 117 cell computational space over 2000 iterations. The speedup is evident (Table 1) if the iterations are running on a multicore computer.

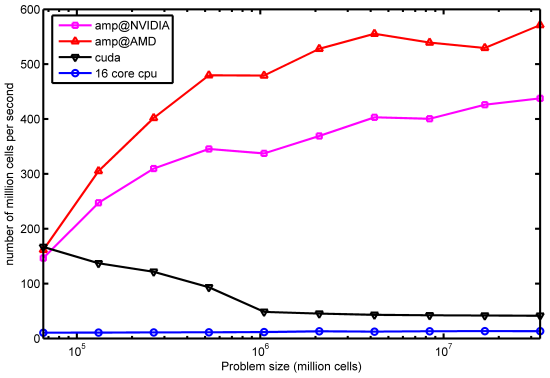

FIGURE 2. Speedup of MedFDTD in parallel.

B. C++ AMP

C++ AMP is a GPU-based parallel computing platform developed by Microsoft [23]. The C++ AMP supports the vast majority of GPU chips, including chips from Intel, AMD, and NVIDIA, which possess a simple logical structure, data implicit copy, and automatic load balancing and are able to run on different hardware platforms without source code modification.

MedFDTD implements the GPU parallel acceleration module according to C++ AMP technology. The calculation speed is 160–600 million Yee cells per second (Mcps) when running on an AMD chip GPU (R9 270X) and 150–450 Mcps when running on an NVIDIA chip GPU (GTX 1050Ti), and the acceleration ratio is significantly higher than that for CUDA without specifically optimize (GTX 1050Ti) and parallel-computing multiple CPUs (Intel Xeon E5-2650 @ 1.80 GHz). The parallel calculation speed by using the AMD chip GPU is higher than that by using the NVIDIA chip GPU in the same product position; thus, the use of an AMD chip GPU to accelerate the FDTD calculation is preferred.

IV. APPLICATION

A. ABSORBING BOUNDARY

As computer memory is limited, the computational space is terminated by the absorbing boundary when simulating infinite space radiation. Moreover, the absorbing boundary should absorb lay waves and reduce the intensity of the reflected wave. A reflected wave on an absorbing boundary cannot be prevented; thus, the reflected wave will flow into the space apportioned for calculations, thereby directly affecting the accuracy of the results. Therefore, the reflectivity of the absorbing boundary is an important factor when evaluating the accuracy of the result. However, to overcome this problem, MedFDTD employs CPML region surround the computational space to terminate it, and use the CPML formula [19] to absorb lay waves in the region.

To study the influence of the absorbing boundary on the reflectivity, two simulations were performed: Example A has a $126 \times 51 \times 26$ cell lattice, while Example B has a $276 \times 201 \times 176$ cell lattice in which 75 cells are extended across all dimensions, and the spatial resolution was $1 \times 1 \times 1$ mm^3 in both examples. The excitation point was located at the center of the computational space. Sampling point P was selected such that it was 15 cells away from the excitation point. The following field values of the sampling point were obtained: $e(t)$ in Example A and $E(t)$ in Example B. Then, the reflectivity was calculated using the following formula:

$$Error_{dB} = 20log_{10}\frac{|e\,(t) - E(t)|}{|max[(E\,(t)]|}. \tag{4}$$

After obtaining the reflectivity of the PML absorbing boundary (Fig. 3), its average reflectivity was found to be −88 dB; therefore, the reflected wave yielded insignificant effects on the accuracy of the results.

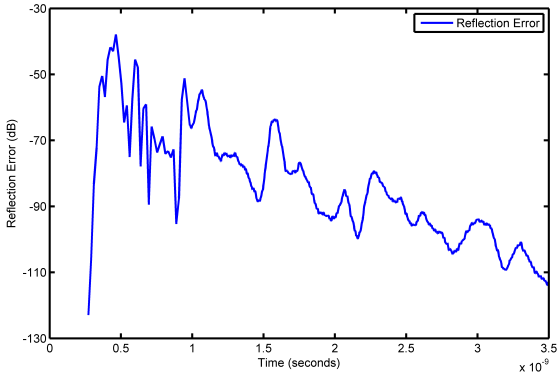

FIGURE 3. Reflectivity of the PML-absorbing boundary.

B. RADIATION SOURCE

The waveform, frequency, amplitude, and source type, such as a point wave, a plane wave, or an antenna, critically affect bioelectromagnetics calculations. In particular, antenna sources have been commonly used in bioelectromagnetics research. Specific knowledge regarding the antenna parameters, such as the radiation resistance, power, and polarization, is necessary to design antenna sources.

MedFDTD implements an antenna module, which can directly create a common dipole antenna, estimate antenna radiation resistance and radiation power before the next iteration, import a user-designed antenna model, and calculate the antenna radiation power by using the Poynting theorem after an iteration.

For example, by using MedFDTD to simulate half-wave dipole antenna radiation in vacuum space, the input to the feed point was a 1.8-GHz 1-V-amplitude sinusoidal voltage source with a 73.1-Ω antenna resistance, and the length of the oscillator was 39 mm. The resulting average radiation power and radiation efficiency of the antenna were 1.5 mW and 87.7%, respectively.

C. SAR CALCULATION

The SAR is an important indicator used to measure the level of EM radiation in the target organism [3]; it is defined as

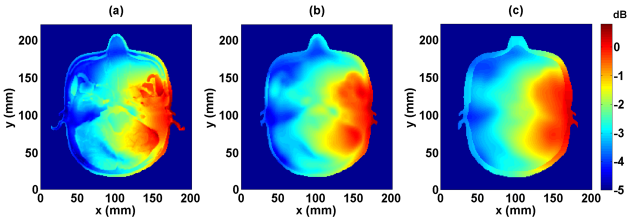

FIGURE 4. Distributions of the SAR across the axial plane for a 900-MHz dipole antenna. (a) Local SAR, (b) 1 g averaged SAR, (c) 10 g averaged SAR.

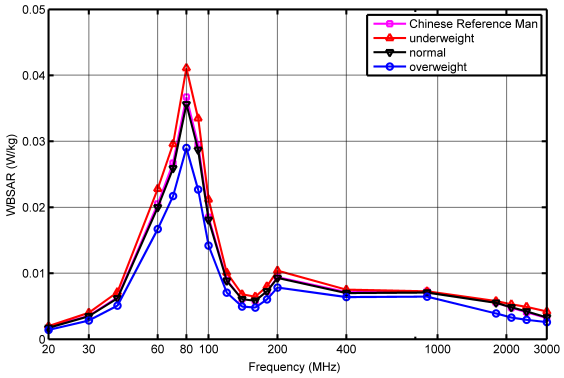

FIGURE 5. WBSAR values for the Chinese reference man. Extrapolations for underweight, normal, and overweight physiques are shown [24].

follows:

$$SAR = \frac{\sigma}{\rho} E_{RMS}^2 (W/kg). \tag{5}$$

In the above equation, σ is the conductivity (S/m), ρ is the density (kg/m^3), and E_{RMS} is the root mean square (RMS) of the electric field (V/m).

To test the MedFDTD bioelectromagnetics module, a high-resolution voxel-based head model was used to assess the SAR. The head model was reconstructed using the visible Chinese human (VCH) dataset [5]. It contains 20 organs and tissues and has a spatial resolution of $1 \times 1 \times 1$ mm^3. The head model has previously been used to evaluate the influence of metallic dentures on mobile phone radiation [6]. In this study, the bioelectromagnetics module was used to simulate the exposure of the head model to EM radiation. The excitation was a 900-MHz-amplitude sinusoid sourced from a dipole antenna. The local SAR distribution across the axial plane is shown in Fig. 4(a).

The method used to calculate the mass-averaged SAR in this study has been described by the IEEE [3]; in addition, the local SAR determined using the method described earlier was used to calculate the mass-averaged SAR. The distributions of the 1 and 10 g mass-averaged SARs across the axial plane are respectively shown in Figs. 4(b) and (c).

In addition, MedFDTD has recently been employed in a bioelectromagnetics study [24] to calculate the whole-body averaged SAR for various body mass index (BMI) models and frequencies.

V. CONCLUSION

Based on the FDTD method, we developed MedFDTD, which is an EM field simulation framework specifically designed for bioelectromagnetics applications. The framework incorporates a distributed-memory CPU parallel module and a cross-platform GPU parallel module to meet the demands of high spatial resolution and large computational space. To simulate infinite space radiation, CPML, which accurately represents human tissue, was implemented. Users can export their own media, model, and antenna into the model file; create their own radiation source by using the radiation source module, which supports various radiation patterns, including a point source, a plane-wave source, and antenna patterns; and calculate the antenna radiation power and radiation resistance. The local SAR, whole-body averaged SAR, and mass-averaged SAR in the biological model can be calculated according to the IEEE standard features and EM field.

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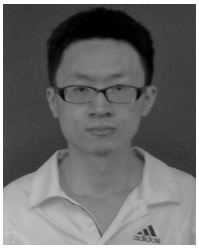

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