PARALLEL FDTD AND PARALLEL GA FOR MICROWAVE TOMOGRAPHY IN BREAST CANCER DETECTION

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Abstract

Asymptomatic screening methods are import to lower the mortality rate of breast cancer patients. Technologies available in clinics have weaknesses in terms of sensitivity and specificity. Microwave imaging technique uses the apparent dielectric property contrasts between different breast tissues at microwave frequencies and is a prospective direction to find small tumor at their early stage. Microwave tomography falls in one category of microwave imaging technique. There are two main components in microwave tomography to detect abnormalities in breasts: Genetic Algorithm (GA) and Finite-Difference Time-Domain (FDTD). Both GA and FDTD are time-consuming, but, they are data-parallel in nature. In this paper, we have designed a parallel framework for microwave tomography: parallel GA combined with parallel FDTD. The algorithms are implemented on distributed memory machines running MPI. It achieves a result of finding a 1.5cm tumor in a breast phantom of 12cm in diameter, with a speedup of 6.25 using 16 processors.

1 Introduction and Motivation

Breast cancer is the second leading cause of cancer deaths in women today and is the most commonly diagnosed cancer in women. In North America, an estimated 202,044 cases were diagnosed and 51,184 patients died from the disease in 2000 [9]. A promising way to lower the mortality rate is to detect the tumor at its early stage, followed by effective treatments.

Currently, the most common methods for breast cancer detection are regular physical examination by women themselves or their doctors, and X-ray mammogram screening [21]. The disadvantage of physical examinations is that it is a subjective-prone process. Human beings are easily negligible on the small lumps, which may be the first sign of asymptomatic tumors. Compared to physical examinations, X-ray screening raises the possibilities to find small lumps by expert radiologists, but it has its own weaknesses. The process is uncomfortable for patients because of the compression on the breast. It also poses the patients to possibly harmful ionizing radiation, which is recognized as a cause of cancer. Besides, the resolution of this technique is limited because the absorption of X-rays is similar for a large number of tissues [12]. Thus, the contrast of different tissue imaging is low, resulting in approximately 20% of missed breast cancer detection and leading to low sensitivity rate. Sensitivity is defined as the rate at which tumors are detected [26].

There are other technologies for breast cancer detection as a second aid to X-ray screening: ultrasound imaging and Magnetic Resonance Imaging (MRI). Ultrasound imaging removes the ionizing radiation in X-ray screening, but it does not solve the problem of low resolution and cannot detect small tumors less than 5mm [21]. For this reason, MRI is a suitable choice because MRI has high sensitivity at detecting tissue abnormalities. But, MRI cannot distinguish malignant tumors from benign tumors, which may increase false positive rate and lead to unnecessary biopsies. This drawback makes MRI a technique with low specificity rate, which is related to false positive error. Also, an MIR system is too expensive and not too many systems can be installed in clinics.

A comparatively more recent technology is microwave imaging (MWI) for breast cancer detection [7, 8, 11, 15]. It reconstructs the material properties of the breast by measuring the scattering of the electromagnetic signals posed on the breast. It is an application of the inverse scattering problem. The inverse scattering problem determines the characteristics of an unknown object (its shape, internal material profile, etc.) from measurement data of radiation from the object [22].

The feasibility of MWI technique relies on the high contrasts between the dielectric properties of tumors and those of normal breast tissues at microwave frequencies [24, 28]. Typically, tumors have a permittivity 10-20% higher than that of normal tissues.

Microwave imaging can be classified into active imaging technique and passive imaging technique [6]. The difference between them is whether low level microwave radiation given off by all objects in the natural environment. There is no transmitter in passive

imaging system. Active imaging technique, on the other hand, transmits electromagnetic pulses in the direction of object of interest and records the origin and strength of the backscatter received from objects. Active imaging technique is more useful in breast cancer detection and two approaches have been developed: the microwave tomography (MT) [18, 19] and the radar microwave imaging [6]. As an example, confocal microwave imaging falls in the radar imaging category and reconstructs the breast by synthetically focusing reflections from the breast [6].

Confocal microwave imaging [6] reconstructs the breast by synthetically focusing reflections from the breast. Although it can find small tumors, it does not attempt to reconstruct the exact permittivity profile of the breast. Its emphasis is more on detecting the strong scattering center that may be tumors. This assumption leads to its limitations on breast imaging because a breast is an object with inhomogeneous materials, consisting of fatty tissues, glandular tissues, fibrous tissues, and possible malignant tumors. On the contrary, MT is a process during which the image reconstruction process involves iteratively matching measured and forward computed data [18, 19]. The process continues until the calculated data converge with the measured data. The output of the forward computing process is the solution to the inverse scattering problem incurred in microwave scattering and represents the dielectric property profile of the breast. Computed data are based on numerical techniques and a model of the object with estimated material properties. In this paper, we consider MT.

A suitable numerical technique is important to MT and should be efficient as to calculation time and be accurate in terms of the restored unknown object. There are two components in MT: Genetic Algorithm (GA) and Finite-Difference Time-Domain (FDTD). FDTD is normally selected in solving inverse electromagnetic scattering problem as in this application because it can efficiently model an inhomogeneous object of arbitrary shape [29]. GA is used to find the globally optimized solution to the inverse scattering problem in reasonable amount of time. The paper develops a parallel framework for MT involving GA and FDTD to breast cancer detection on a network of computers.

The paper is organized as follows. Section 2 focuses on the framework of MT, illustrating how GA and FDTD interact with each other. Section 3 extends GA and parallel GA for the application. Section 4 introduces FDTD in general, a sequential FDTD and a parallel FDTD for our application. In section 5, the implementation environment of our parallel framework is given, including the runtime comparison. Conclusions are presented in section 6.

2 A Parallel Framework for Microwave Tomography

GA and FDTD are the two key components of MT. The efficiency of GA and FDTD is vital to its applicability clinically. FDTD algorithm is essentially computation-intensive, but shows intrinsic characteristic of data parallelism. Thus, a parallel FDTD (PFDTD) is an important approach to improve the efficiency. MT is an application of the inverse

scattering problem, and the profile of the breast characteristics is unknown. Different presumed profiles need to be tried as the input of FDTD. In breast cancer detection, combinations of the different tumor types (also including non-tumor scenario) at different positions must be calculated by FDTD to determine which combination leads to the closest FDTD calculation result with the measurement. Therefore, the detection problem involves a global optimization problem by searching all profiles. The optimization problem can be defined in equation 1. i ranges from 1 to 4, indicating that plane waves are impinged from four directions: east, south, west, and north. θ represents different angles of the observation points. $E_{i\theta}^{measurement}$ is the measurement at angle θ using i plane wave. $E_{i\theta}^{FDTD}$ is the calculated data at angle θ using i plane wave.

$$f = \max[1 - \frac{\sqrt{\frac{\sum_{i\theta}(E_{i\theta}^{measurement} - E_{i\theta}^{FDTD})^2}{\sum_{i\theta}(E_{i\theta}^{measurement})^2}}}{4}] \quad (1)$$

GA is an efficient search algorithm based on principle of natural selection and genetics [13]. It is generally able to find good solutions in reasonable amount of time. The profile combinations in MT increase dramatically in order to improve the image resolution, the sensitivity, and the specificity. Hence, a parallel GA (PGA) is also vital to an efficient MT. In MT, GA is first executed followed by FDTD. The output of the GA is required as an input to compute FDTD. Therefore, the algorithms in MT work in a synchronous manner. However, GA and FDTD by themselves can be parallelized. Therefore, a two-level parallel framework is designed for MT in breast cancer detection.

There are two parts in the framework: one for PGA and another for PFDTD. A master-slave approach is used in the algorithm. One master process (PGA master process) is used to generate the initial population that consists of different combinations. The initial population is divided into subpopulations and dispatched to a number of slave processes (PGA slave process). All PGA slave processes evolve their own subpopulations simultaneously. Each PGA slave process sends the profiles with highest fitness to a number of processes that act as the master process (PFDTD master process). They work in parallel on different profiles. The PFDTD master processes in turn dispatch work of the calculation to other processes that are called PFDTD slave processes. The PFDTD master processes are responsible to collect the final results and communicate with PGA slave processes. It is the PGA slave processes that determine whether the PFDTD calculation result is close enough with the measurement, thus obtaining the profile of the breast and further determining whether a tumor is present.

3 GA and Parallel GA for MT

3.1 Sequential GA

Sequential GA can be categorized into two kinds of algorithms according to how the population is replaced for the next generation [14, 31]. They are steady-state GA (SSGA) and generational replacement GA (GRGA). For SSGA, one individual of the population is changed at a time. The child individual can be generated by applying crossover on two parent individuals selected from the population, or applying mutation on one selected parent individual. The newly-generated child individual replaces an individual of the population using different replacement strategies to form the new generation. Replacement strategies include: replace the worst and replace a randomly chosen individual. On the contrary, GRGA replaces the whole population at each generation. According to their definition, SSGA appears faster than GRGA although the result of SSGA will not be as satisfactory as that of GRGA because SSGA does not explore the whole generation as well as GRGA does.

3.2 Parallel GA

Parallel GA can be classified into three categories [4]:

- Global single-population master-slave GA
- Single-population fine-grained GA
- Multiple-population coarse-grained GA

The three parallel GAs differ in how the initial population is distributed and how the task of GA is distributed. The most important difference between sequential GA and parallel Gas is the migration operator that is used only in parallel GA. For example, in a multiple-population coarse-grained GA, initial population is partitioned into subpopulations and are distributed to different processors. Each subpopulation evolves as a sequential GA, except that some fittest individuals in one subpopulation are exchanged with those in other subpopulation. It is called migration operator. The migration operator has to decide on the following parameters:

- When to migrate between subpopulations;
- Whom to be migrated to other subpopulations;
- How many individuals (migrants) in the subpopulation should be migrated;
- Where to migrate the selected migrants (migration topology).

Based on the manipulation of the migrants between subpopulations, parallel GA can be classified as Island Model and Shared Pool Model [5]. In the Island Model, all subpopulations evolve independently of each other, except that each subpopulation occasionally migrates individuals to other subpopulations based on the migration topology. This model is suitable for distributed memory parallel environment. On the other hand, in Shared Pool Model, all subpopulations store their best individuals to a

shared pool, and replace some of their own subpopulation with individuals stored in the pool that come from other subpopulations. This model is more suitable for shared memory parallel environment. A parallel SSGA using Island model is shown in Algorithm 1.

4 FDTD and Parallel FDTD for MT

4.1 Sequential FDTD

FDTD is a popular numerical simulation method to solve problems in electromagnetics. It was first proposed by Yee in 1966 [32]. The basic idea is to discretize the electromagnetic computational domain into a collection of Yee cells and calculate the electric fields (E-fields) and magnetic fields (H-fields) of all cells in Cartesian system. There are 6 components in 3D domain: Ex, Ey, and Ez; Hx, Hy, and Hz. An illustration of a 3D Yee cell in FDTD is given in Figure 1 [1].

Because FDTD uses central difference, the vector components of E-fields and H-fields of Yee cells are spatially staggering in the Cartesian computational domain, meaning that each E-field vector is located midway between a pair of H-field vector, and vice versa. Furthermore, as H-fields are sampled at a half sampling interval difference than that of E-fields sampling, E-fields and H-fields are updated in a leapfrog scheme for marching forward in time. This implies that E-fields are updated midway during each time-step between successive H-field updates, and vice versa. The relationship can be manifested in the following equations, which are the solutions to our application.

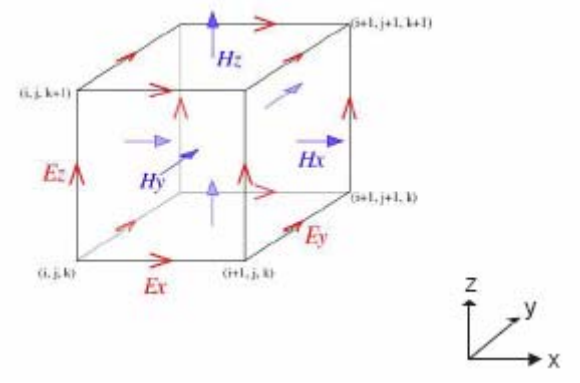

Figure 1: A standard Yee Cell for FDTD

Algorithm 1 Parallel SSGA (Steady-State GA) using Island Model

```
t = 0;
if(processor is master processor)
        initialize P(t);
        partition P(t) into Pi(t) and distribute Pi(t);
else
        receive initial subpopulation Pi(t) from master processor;
evaluated subpopulation Pi(t);
for each generation
        local_search(Xrandom) from Pi(t);
        for each pair in Xrandom
                select (x1, x2) from Xrandom;
                if(r < Pc)
                        Xnew = crossover(x1, x2);
                else
                        Xnew = mutate(x1, x2);
                delete Xworst from Pi(t);
                while(Xnew exists in Pi(t))
                        mutate(Xnew);
                add Xnew to Pi(t) to form Pi(t+1);
        if(migration condition meets)
                find the destination to migrate to;
                select individuals to be migrated according to the parameters;
                send selected individuals;
                receive individuals from other subpopulation Pj(t);
                replace individuals with lower fitness in Pi(t+1) with the received
migrated individuals;
        evaluate Pi(t+1);
        t = t+1;
select the top several number of fittest individuals in Pi(t);
if(processor is master processor)
        receive fittest individuals from other processors; output the results;
else
        send the fittest individuals in Pi(t);
```

$$E_{zx}|_{i,j}^{n+1} = \left[\frac{1-\frac{\sigma\Delta t}{2\varepsilon_0\varepsilon_r}}{1+\frac{\sigma\Delta t}{2\varepsilon_0\varepsilon_r}}\right] E_{zx}\Big|_{i,j}^{n} + \left[\frac{\frac{\Delta t}{\varepsilon_0\varepsilon_r}}{(1+\frac{\sigma\Delta t}{2\varepsilon_0\varepsilon_r})\Delta x}\right] \times \left[H_y\Big|_{i,j}^{n+1/2} - H_y\Big|_{i-1,j}^{n+1/2}\right] \quad (2)$$

$$E_{zy}|_{i,j}^{n+1} = \left[\frac{1-\frac{\sigma\Delta t}{2\varepsilon_0\varepsilon_r}}{1+\frac{\sigma\Delta t}{2\varepsilon_0\varepsilon_r}}\right] E_{zy}\Big|_{i,j}^{n} - \left[\frac{\frac{\Delta t}{\varepsilon_0\varepsilon_r}}{(1+\frac{\sigma\Delta t}{2\varepsilon_0\varepsilon_r})\Delta y}\right] \times \left[H_x\Big|_{i,j}^{n+1/2} - H_x\Big|_{i-1,j}^{n+1/2}\right] \quad (3)$$

$$H_x\Big|_{i,j}^{n+1/2} = H_x\Big|_{i,j}^{n-1/2} - \frac{\Delta t}{\mu\Delta y}\left[E_{zx}\Big|_{i,j+1}^{n} + E_{zy}\Big|_{i,j+1}^{n} - E_{zx}\Big|_{i,j}^{n} - E_{zy}\Big|_{i,j}^{n}\right] \quad (4)$$

$$H_y\Big|_{i,j}^{n+1/2} = H_y\Big|_{i,j}^{n-1/2} + \frac{\Delta t}{\mu\Delta y}\left[E_{zx}\Big|_{i+1,j}^{n} + E_{zy}\Big|_{i+1,j}^{n} - E_{zx}\Big|_{i,j}^{n} - E_{zy}\Big|_{i,j}^{n}\right] \quad (5)$$

Several preconditions must be met before using FDTD method [29]. Firstly, a computational domain must be established on which the Yee cells are based. Normally, the computational domain is the physical region over which the simulation will be conducted, such as the breast in our application. Secondly, the material of each cell within the computational domain must be specified with their permittivity, permeability and conductivity. Since FDTD allows the material at each cell to be specified, an inhomogeneous object of any shape can be easily modeled. This is the reason that FDTD is used in our application since a breast includes fatty tissues, glandular tissues, fibrous tissue, and possible malignant tumor tissues. Thirdly, a source must be specified. As in active microwave imaging, the property of the pulse sent by the transmitters must be considered. Gaussian pulse is used in the application.

The availability of massive computer resources makes FDTD simulation feasible for different applications. But the computational domains must be finite for finite computer memory. Therefore, for open region problems such as our application, absorbing boundary conditions (ABCs) must be considered. Most popular ABCs can either be derived from differential equations (Mur ABC [20], Liao ABC [16]) or by employing a material absorber (Berenger ABC [2], which is also called Perfectly Matched Layer PML) [25].

Another critical issue in FDTD is its stability because FDTD is a time-marching computational simulation. The time step must satisfy certain preconditions to ensure that the simulation result is stable and correct. In our application, the plane waves are propagating across discrete cells. The time step must be less than the time for the waves to travel adjacent grid points. Otherwise, a nonzero field value of a cell is introduced before the wave can reach the cell, violating causality of the simulation system and resulting in an unstable and inaccurate output [33]. This precondition is called Courant condition.

In Figure 2, a 2D computational domain shows the cross section of a dielectric cylinder, which can be simulated as the cross section of a breast. Yee cells are represented by squares. We assume that a transverse magnetic plane wave along Z axis (TMz) is used and the 2D object is placed in X-Y plane [29]. Therefore, there are only 3 components in the application: Ez, Hx, and Hy.

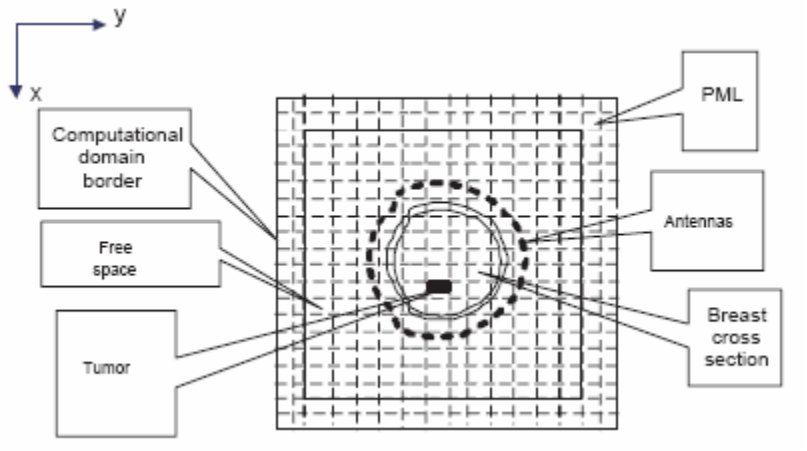

Figure 2: 2D Computational Domain

4.2 Parallel FDTD

FDTD algorithm is computationally intensive due to several reasons. The calculation is complex as shown in equation (2) to equation (5). The size of Yee cells should be small enough such that each cell can be treated as a homogeneous material. The more fine grained the cells are, the more accurate are the results for the inverse scattering problem. This factor is critical for early breast cancer detection to find a tumor at its early stage that is less than several millimeters. However, this granularity implies an increase in the number of cells in the computational domain. The Courant condition posed on a stable FDTD indicates that the largest time-step depends on the number of cells. The complexity of a 2D FDTD algorithm is $O(N^3)$ where N is the number of cells along one axis, assuming that there are same number of cells along two axes. The sequential FDTD algorithm takes about 200 seconds for a 600x600 computational domain. For finer granularity, this timing will increase together with memory.

FDTD is data-parallel in nature [23] and exhibits apparent nearest-neighbor communication pattern [30]. A number of parallel FDTD have been reported using different parallel schemes on different platforms for different applications. The earliest work is done by Mittra et al. [30] in 1994 on an HP-735 workstation cluster via PVM. Liu et al. [17] parallelize the core FDTD, different ABCs and the near-to-far transformation on a CM-5 (32 processors) parallel computer, gaining as high performance as 100 times faster for a parallel core FDTD than that for the sequential version. Guiffaut et al. [10] implement a parallel FDTD on a omputational domain of 150x150x50 cells (with 10 PML layers surrouned) on PC and the Cray T3E. They use

Message Passing Interface (MPI) and adopt vector communication scheme and matrix communication scheme, obtaining higher efficiency by the latter scheme. Su et al. [27] combine OpenMP and MPI to parallelize FDTD: OpenMP used for the one time initialization and each time-step updating of the E-fields and H-fields; MPI is used for the communication between neighboring processors. Brock et al. [3] apply the parallel FDTD to model the light scattering by deformed red blood cells. Ye et al. [33] introduce three communication schemes in parallel FDTD. The three schemes differ in which components of E-fields and H-fields should be exchanged and which process should update the E-fields on the interface. The division of the computational domain is on the E-field along the Cartesian axis.

The communication scheme with one cell overlapping region is adopted to get a robust implementation. The scheme is shown in Figure 3. The division interface is along E-fields. The computational domain is divided along x axis. Each processor attaches one more row of cells to the interface. The extra row of cells are the exact copy of the same row transferred from the neighboring processor. Therefore, for processor with rank 0 and ($size$ – 1) ($size$ is the total number of processors), only one row of cells are added since they only have one neighbor. For other processors, two rows of cells are added as shown in Figure 3. The E-fields on the interface of adjacent processors are calculated on both processors. The purpose of the scheme is to reduce the necessary communication of E-fields, trying to improve the computation/communication efficiency. The parallel FDTD is given in Algorithm 2.

5 Implementations and Results

Both GA and FDTD are parallelized on a network of computers. They are implemented in C++ on Fedora Core 5. The parallel version uses C bindings of LAM/MPI 7.1.2. The hardware configuration is as follows: AMD Athlon™ 64 X2 Dual Core Processor 3800+, with 512KB cache, and 2GHz clock; 1GB of main memory, and 2GB of swap space, for a total of 3GB of virtual memory; 120GB Seagate ST3120813AS SATA (Serial ATA) disk drive; 1Gb/s Ethernet network interface. The machines are connected to the network via a 100Mb/s Ethernet switch.

Figure 4 shows the total execution time of the algorithms involved in MT: parallel GA and parallel FDTD. The algorithms are run on five generations with ten individuals in each generation. As the number of processors increase, the execution time decreases. The speedup on 8 processors is little above 4 while on 16 processors it is close to 6. Though there is an increase in speedup from 8 processors to 16 processors, the speedup increase is gradual. This is due to the synchronization between the genetic algorithm and FDTD. Also, the FDTD algorithm by itself must synchronize the parallel parts on each processor for each time-step. Every i^{th} iteration depends on the $(i-1)^{th}$ iteration.

Figure 5 shows the execution time of parallel FDTD. These figures show clearly that the FDTD algorithm dominates the total execution time of MT. The execution time of the sequential algorithm (GA and FDTD combined) is 10,131 seconds. The total execution

time obtained on 16 processors that is approximately 2000 seconds surpasses the sequential algorithm.

Algorithm 2 Parallel FDTD using TMz mode for breast cancer detection

```
initialize E-fields Ez, H-fields Hx and Hy on each processor to zero;
if(processor is master processor)
        initialize the material of the computational domain, including the cross section of the breast, the free space, and PML layers using the coefficients in equation (2) through equation (5);
        decide the sub-domain for each processor;
        send material parameters of sub-domain to the corresponding processor;
else
        receive the material parameters for the cells residing on the processor;
for n = 1 to MAX_TIMESTEP //for all processors
        compute Ez of all cells residing on the processor based on their previous values and neighboring Hx, Hy at the previous time-step, using equation 2 and equation 3;
        compute Hx of all cells residing on the processor based on their previous values the neighboring Ez at the previous time-step, using equation 4;
        compute Hy of all cells based on their previous values and neighboring Ez at the previous time-step, using equation 5;
        apply Fourier transform;
        exchange Hx and Hy fields with the neighboring processors;
        synchronize among all processors;
if(processor is not master processor)
        send the final results to master processor;
else
        receive results from all other processors;
        apply post processing;
        output the results at the observation points;
```

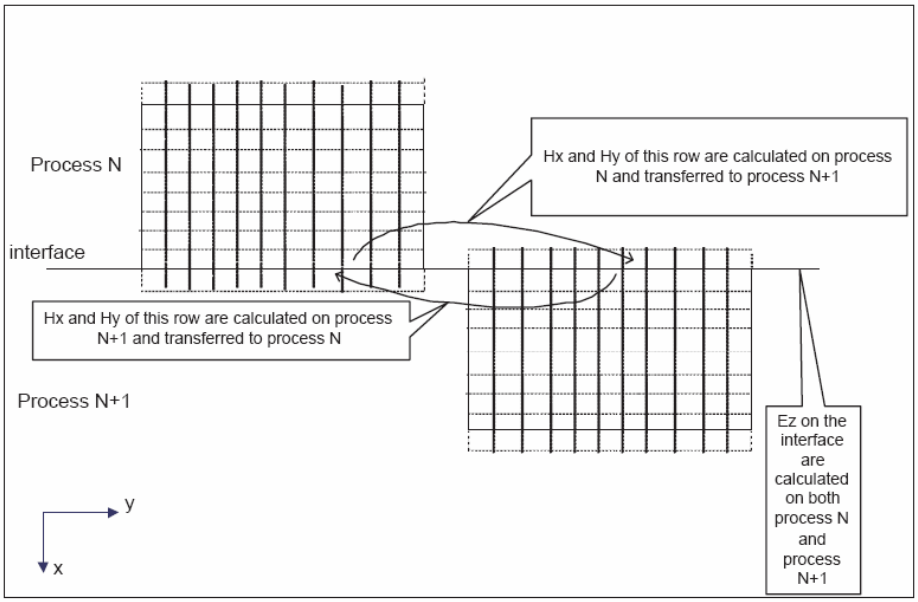

Figure 3: Communication scheme in parallel FDTD

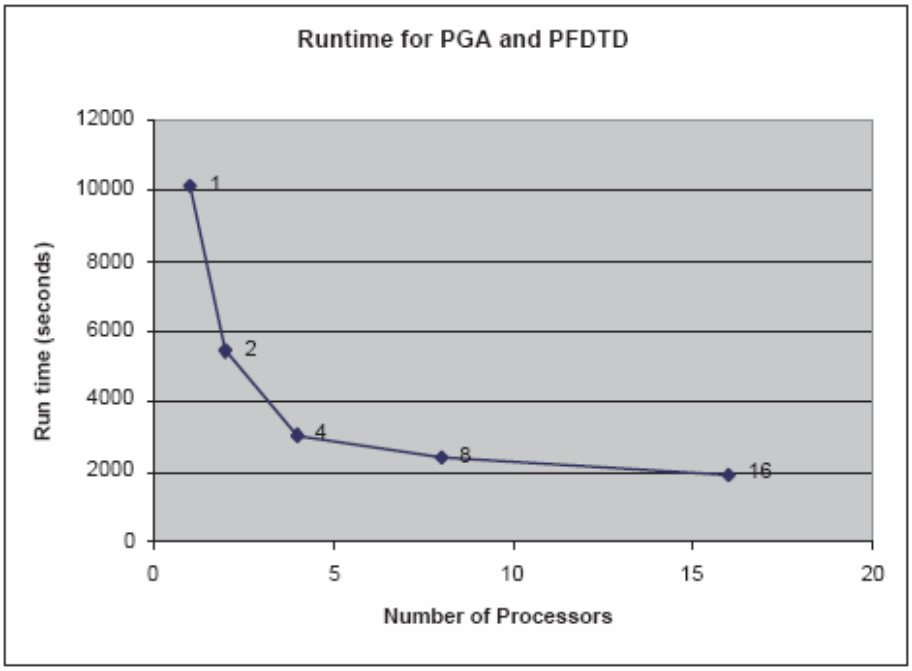

Figure 4: Runtime for PGA and PFDTD

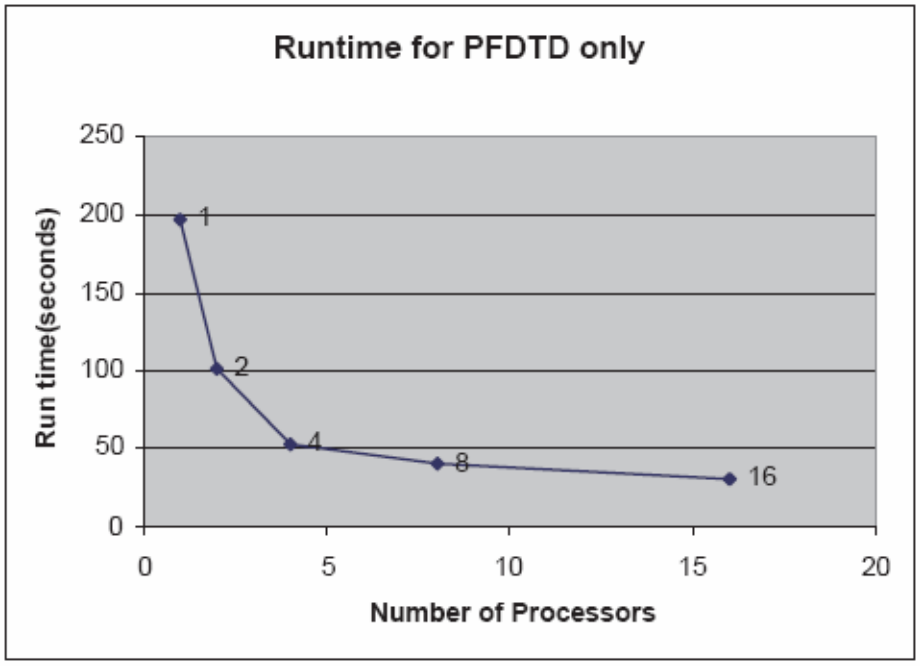

Figure 5: Runtime for PFDTD only

6 Conclusions

The paper focuses on microwave tomography technique to detect abnormalities in breasts. There are two main algorithms in the technique: GA and FDTD. Both of the algorithms are parallelized and implemented on distributed memory machines. The execution time of the sequential algorithm (GA and FDTD combined) is 10,131 seconds. The total execution time obtained on 16 processors that is approximately 2000 seconds surpasses the sequential algorithm. The results are encouraging and have illustrated the need for parallel computers for applications in medical fields.

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