International Journal of Engineering & Technology, 7 (4) (2018) 2856-2861

International Journal of Engineering & Technology

Website: www.sciencepubco.com/index.php/IJET
doi: 10.14419/ijet.v7i4.15155
Research paper

Big data simulation software for breast cancer growth repository system

Norma Alias [1] *, Asnida Che. Abd. Ghani [2], Hafizah Farhah Saipan Saipo [1], Waleed Mugahed Al-Rahmi [3], Norafandy Yahaya [3]

[1] Ibnu Sina Institute for Scientific and Industrial Research (ISI-SIR), Faculty of Science, Universiti Teknologi Malaysia, 81310, UTM Skudai, Johor , Malaysia
[2] Department of Mathematics, Faculty of Science, Universiti Teknologi Malaysia, 81310, UTM Skudai, Johor, Malaysia
[3] Faculty of Education, Universiti Teknologi Malaysia, 81310, UTM Skudai, Johor, Malaysia
**Corresponding author E-mail: norm@ibnusina.utm.m*

Abstract

The development of the simulation software aims at anticipating the growth of breast cancer. Based on certain numerical iterative methods, this simulation works with discretization and Partial Differential Equation (PDE). As a class of Helmholtz equations, PDE approach are known to govern the growth of this type of cancer. Considering both time and place, the Helmholtz equation's accuracy visualizes breast cancer and its growth. This growth is of breast cancer is captured and the convergence results in sequential and parallel computing environ-ment is expressed through the numerical libraries available in the repository system. Currently, both the parallel performance measurement and Numerical analysis that involve execution time, speedup, efficiency, effectiveness and temporal performance are being investigated. The process of breast cancer visualization requires a huge memory and expensive calculations. It is observed that both the distributed memory and distributed processors of the parallel computer systems development were required in most of the studies conducted on the growth of this cancer. It is considered as an important computation platform needed to the development of parallel repository system leading to an increase in the speed and a decrease in the cost. The simulation software has several beneficial characteristics such as high performance estimation, multidimensional visualization of breast cancer and being friendly. It also provides a real time solution and strength. This soft-ware is expected to increase the level of confidence in terms of computer-aided decision making which can be reflected positively on com-prehensive breast cancer screening; breast cancer diagnosis; and clinical assessments and treatment.

Keywords: Breast Cancer Growth; Simulation Software Development; Repository Library; Numerical Methods; Helmholtz Equation

1. Introduction

It has been reported the breast cancer is the second deadliest type of cancer among women. It is also reported that around a million women are diagnosed from which tenth is for new cases of cancer and roughly 23% are of women cases [1]. Currently, partial differential equation (PDE) through mathematical modelling and Helmholtz equation type are used to anticipate cancer cases. It is proposed that the process of breast cancer prediction can be facilitated by the use of Helmholtz equation. Figure 1 1illustarted the main system of the breast cancer prediction.

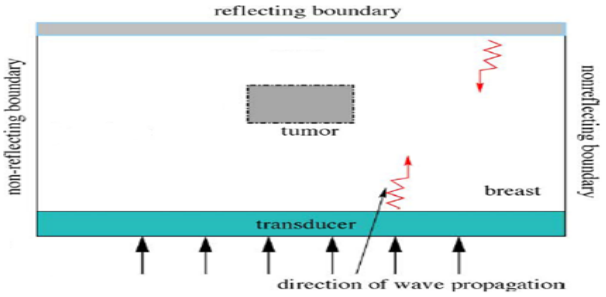


Fig. 1: The Two Dimensional Model Simulation.

Later, a three-point finite difference approximation technique is used in the PDE equation. Jacobi (JB), Red Black Gauss Seidel (RBGS) and Alternating Group Explicit (AGE) methods are considered some of the methods used to solve the PDE under consideration. As for the sequential and parallel algorithms of numerical methods, they are implemented on MATLAB through the use of Distributed Computing (MDC) software assisted by distributed parallel computer platform (DPCS). The huge memory allocation and high speed processor performance are the two main factors that determine the choice of these hardware and software in solving the large sparse matrices. Numerical analysis such as the execution time, number of iteration, computational complexity, maximum error and root means square error (RMSE) are used to graphically analyse Helmholtz equation's visualization. Based on execution time, speedup, efficiency, effectiveness and temporal performance, the analysis of parallel performance evaluations is conducted. After that, it would be the time to develop the repository system. The breast cancer growth repository, which contains distributed parallel simulation, is considered an innovative simulation [2]. The simulation of up to 10-10 computational skill is required for the development of simulation and mathematical modelling. Breast cancer growth characteristics are exploited by the parallel algorithm implementation of large sparse matrix [3].

2. Identification and classification cancer growth

This part presents the steps of MRI cancer growth detection and classification. First, the growth is detected and then followed by the second step called Pre-processing. There are two processes used to identify the kind of cancer growth. These processes are feature extraction and feature selection

2.1. Revealing

Previous research used different kinds of resources such as instance, EEG, proton MR spectroscopy (MRS), long echo proton MRS signals in order to detect cancer growth. One of these attempts developed a precision of cancer growth using both MRI and MRS [4]. The major rules of image processing technique were followed by a strategy of classification which is comprised of segmentation, feature extraction, feature selection, and classification model construction. [5] aimed at detecting tumour through the use of both Fuzzy possibilistic c-means (FPCM) and parametric deformable methods. Brain mass boundaries were detected using automated segmentation according to the Fuzzy technique. This method proved to be efficient based on the results of the research. Moreover, rough detection has been conducted through the use of the improved kernel fuzzy C-mean (IKFCM) [6].

2.2. Pre-processing

In the processes of segmentation and classification, pre-processing steps such as noise removing are considered essential. This step is known as the backbone of image classification. Thus, removing noise and the immunization to data are challenging tasks in random and non-random processes. Gaussian noise [7] and speckle noise [8] which are used in used in ANFIS are examples of these challenges. Examples [9] and [10] illustrate the use of ANFIS in the field of cancer growth segmentation. Other de-noising methods are also reported in [11]. Examples of these methods are Linear, non-linear filters, Markov random field (MRF) models, linear diffusion methods, wavelet models, non-local means models, and analytically correction schemes. The gab is represented by the fact that these mentioned methods are equal in terms of computational costs which means that the door is open for improvements in this regards. [12] and [13] provided some modifications and improvements in relation to linear diffusion methods. Regarding to the issues of improving accuracy and removing noise, Conditional Random Fields (CRF) is deemed as an essential effective factor [14]. In an attempt to solve noise sensitivity of FCM, [6] enhanced the kernel fuzzy C-mean (IKFCM). Another attempt was done by [15] through the use of Kernel-Sobel-Low pass (KSL) to reduce the noise. Fast Discrete Curvelet Transform (FDCT) also proved to be an effective tool for removing noise from MR images by [16].

2.3. Cancer growth, feature extraction, and feature selection

A number of characters were proposed by researchers for the classification of cancer growth in MRI. Examples of these characters are symmetry, statistical, texture features, genetic expression, etc. In the process of cancer growth classification, both processes of feature extraction and feature selection are considered the most important methods in this regard. The former method involves the processes of combining the variables, measuring data and dimensionality reduction. A method for face recognition has been proposed by [17] which utilized dominant frequency features and multi-resolution metric. [18] also utilized several reference images in order to extract features immediately. Similarly, and based on Fisher discriminant analysis, feature extraction method was proposed by [19] as mentioned by [20]. In addition, a successful method for feature extractions was developed by [21] using enhanced stochastic learning. Also, another effective method of selection and extraction was presented by [22] and [23] and it identifies cancer into five features namely: white matter, Gary matter, CSF, abnormal and normal area using Linear Discriminant Analysis (LDA). It has been argued that wavelet transform is the best method that can be used for image feature extraction [24]. As for the latter, feature selection, it refers to the process of selecting a subsection of relevant features and enhancing the learning process in terms of speed by removing redundant features [22].

3. Mathematical modeling

The current study highlights the concept of breast cancer early detection through the use of Helmholtz equation on high performance computing (HPC). Biological aspects of magnetic waves are used to detect the growth of tumour cells. The model is proposed to be more precise in conditions at infinity for Helmholtz equation than Laplace's equation in infinite physical domain as it presents wave motion. the wave equation with elliptic type is described by scalar Helmholtz equation in relation to time harmonic electrical field [25]. Vertically polarized and the object properties are two commonly referred-to characteristic waves. It is observed that there is homogeneity between behaviours of both characteristics along the vertical z-axis. Equation (3) presents the two dimensional problem [2].

$$\left(\nabla^2 + k^2(r)\right)e(r) = 0 \tag{1}$$

Where

$e(r)$ Total electric field (NC-1)

k Wavenumber of electromagnetic wave containing the dielectric properties of the medium of propagation (m-1)

3.1. Finite difference method (FDM)

Helmholtz equation as a mathematical model is discretised by FDM which is a basic alterations and approximate to the PDE. Through the use of FDM approximation, equation (1) can be transformed into linear system of equations and becoming as equation (2).

$$\left[\frac{\partial^2(r)}{\partial x^2} + \frac{\partial^2(r)}{\partial y^2} + k^2(r)\right]e(r) = 0 \tag{2}$$

Symbols x and y represent space variables in x and y direction. Through magnetic waves aspects, this equation illustrates the growth detection of cancer cells. It is noticed that more precise conditions are required at the infinity boundary of Helmholtz equation as this model describes wave motion. Equation (2) can be discretised into Equation (3) through the use of finite difference approximation with second order central difference. This approximation is known as a classical and straightforward method whereby PDE is numerically solved [25, 2].

$$\left(\frac{r_{i+1,j} - 2r_{i,j} + r_{i-1,j}}{(\Delta x)^2} + \frac{r_{i,j+1} - 2r_{i,j} + r_{i,j-1}}{(\Delta y)^2} + k^2 r_{i,j}\right)e(r_{i,j}) = 0. \tag{3}$$

Similarly, MATLAB distributed computing software was used to solve equation (3) with appropriate boundary and initial conditions. the computational molecules or grid system of FDM for two dimensional problems are illustrated in Figure 2.

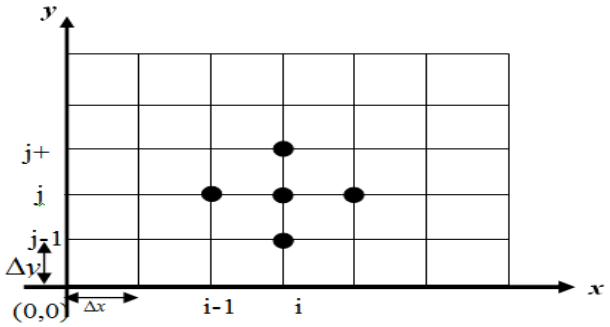


Fig. 2: Grid System for Finite Difference Method on a Two Dimensional.

4. Numerical methods

This section presents the methods used to handle Helmholtz equation. The method related to the growth of breast cancer are Jacobi (JB), Gauss Seidel (GS), Red Black Gauss Seidel (RBGS) and Alternating Group Explicit (AGE) method.

4.1. Jacobi (JB) method

JB is known as a classical iterative method which computes the r value for every single component in respect to space.

$$r_{i,j+1} = \frac{(b_i - \sum a_{i,j} r_{i,j})}{a_{i,i}}, i = 1,2,3,\cdots,m. \tag{4}$$

4.2. Gauss seidel (GS) iterative method

GS is developed and further enhanced based on the Jacobi method. The calculation of this method is illustrated in details below.

$$r_i^{(n+1)} = \frac{1}{\theta}\left[(2+2\theta)r_i^{(n)} - r_{i+1}^{(n)} - r_{i-1}^{(n+1)}\right] - b_i \tag{5}$$

This method is known as the Gauss-Seidel iterative due to the fact that it needs several iterative and its scheme's convergence rate is as double as Jacobi iterative scheme.

4.3. Red black gauss seidel (RBGS) iterative method

RBGS is a combination of both Jacobi and Gauss-Seidel methods. It is characterized by its accuracy and fast convergence.
Red nodes, Ω^{R}

$$r_i^{(n+1)} = \frac{1}{\theta}\left[(2+2\theta)r_i^{(n)} - r_{i+1}^{(n)} - r_{i-1}^{(n)}\right] - b_i \tag{6}$$

i=1,3,5,…

Black nodes, Ω^{B}

$$r_i^{(n+1)} = \frac{1}{\theta}\left[(2+2\theta)r_i^{(n)} - r_{i+1}^{(n)} - r_{i-1}^{(n)}\right] - b_i \tag{7}$$

i=2, 4, 6,$b_i = r_i^{(n-1)}$

There is a similarity between Red Black Gauss Seidel and Gauss-Seidel methods regarding the main step of arriving at the solution. The difference is that this method contains two odd grids of calculation as illustrated in Figure 3. Circling the odd points, it starts from the bottom left and then going up to the next row and so on. The black ones are started as all the odd points are done. Then, the calculation starts at the bottom left node. This method is said to provide more accurate and precise solutions regardless the fact that is divided by two processes of calculation.

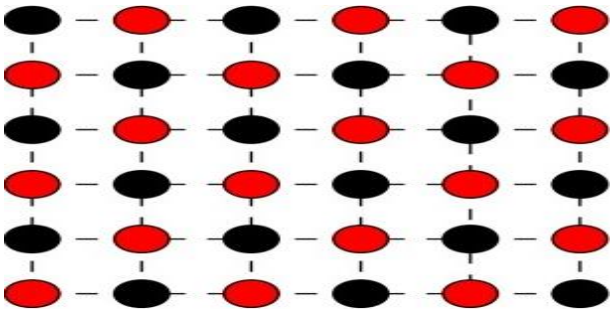


Fig. 3: Red Black Ordering of Nodes on Cartesian Grid.

4.4. Alternating group explicit method

This method that is known as AGE is the most advanced method in comparison with the previous mentioned ones. The solution in this method is computed through two main steps: half time step and one-time step. Due to the existence of the acceleration parameter in this method, the computation process is highly accelerated. This method is commonly used in solving large system of equation where these is a high-level expression of parallelism [3].

$$u_i^{(k+\frac{1}{2})} = (G_1 + rI)^{-1}\left[(rI - G_1 - 2G_2)u_i^{(k)} + 2f\right] \tag{8}$$

The Equation (8) can be simplified into formulae as follows.

For the first node,

$$u_1^{(k+\frac{1}{2})} = \frac{r_3 u_1^{(k)} - 2bu_2^{(k)}}{r_2} \tag{9}$$

For even nodes,

$$u_i^{(k+\frac{1}{2})} = \frac{Au_{i-1}^{(k)} + Bu_i^{(k)} + Cu_{i+1}^{(k)} + Du_{i+2}^{(k)}}{\Delta}, i = 2,4,6,\cdots,m-1. \tag{10}$$

Where

$$A = -cr_2,\ B = bc + r_2 r_3,\ C = -br_2 - br_3,\ D = \begin{cases} 0 & i = m-1 \\ 2b^2 & i \neq m-1 \end{cases}$$

For odd nodes,

$$u_i^{(k+\frac{1}{2})} = \frac{\tilde{A}u_i^{(k)} + \tilde{B}u_{i+1}^{(k)} + \tilde{C}u_{i+2}^{(k)} + \tilde{D}u_{i+3}^{(k)}}{\Delta}, i = 3,5,7,\cdots,m. \tag{11}$$

Where

$$\tilde{A} = 2c^2,\ \tilde{B} = -cr_2 - cr_3,\ \tilde{C} = B = bc + r_2 r_3,\ \tilde{D} = \begin{cases} 0 & i = m \\ -2br_2 & i \neq m \end{cases}$$

This method has a simple computational formula in which the node of one-time step which used the values of nodes in half time step is only computed after all of the nodes in half time step are computed. The general formula atone time step is as in Equation (12).

$$u_i^{(k+1)} = (G_2 + rI)^{-1} r u_i^{(k+\frac{1}{2})} + (G_2 + rI)^{-1} G_2 u_i^{(k)} \tag{12}$$

For even nodes,

$$u_i^{(k+1)} = \frac{Pu_i^{(k+\frac{1}{2})} + Qu_{i+1}^{(k+\frac{1}{2})} + Ru_i^{(k)} + Su_{i+1}^{(k)}}{\Delta}, i = 2,4,6,\cdots,m-1. \tag{13}$$

Where

$$P = -cr,\ Q = rr_2,\ R = -\frac{ac}{2} + cr_2,\ S = \frac{ar_2}{2} - bc.$$

For odd nodes,

$$u_i^{(k+1)} = \frac{\tilde{P}u_{i-1}^{(k+\frac{1}{2})} + \tilde{Q}u_i^{(k+\frac{1}{2})} + \tilde{R}u_{i-1}^{(k)} + \tilde{S}u_i^{(k)}}{\Delta}, \quad i = 3,5,7,\cdots,m-2. \tag{14}$$

Where

$$\tilde{P} = Q = rr_2, \quad \tilde{Q} = -br, \quad \tilde{R} = \frac{ar_2}{2} - bc, \quad S = br_2 - \frac{ba}{2}.$$

For the last node,

$$u_m^{(k+1)} = \frac{ru_m^{(k+\frac{1}{2})} + \frac{a}{2}u_m^{(k)}}{r_2} \tag{15}$$

5. Sequential algorithm

This sequential algorithm is illustrated in Figure 4 where the calculations flow to simulate the growth of breast cancer [26-27]. This takes place in three main steps. First, initial and boundary conditions are defined and initiated. Second, numerical solution is validated using stopping criterion. The last stage is where stopping criterion is fulfilled through the iterating process.

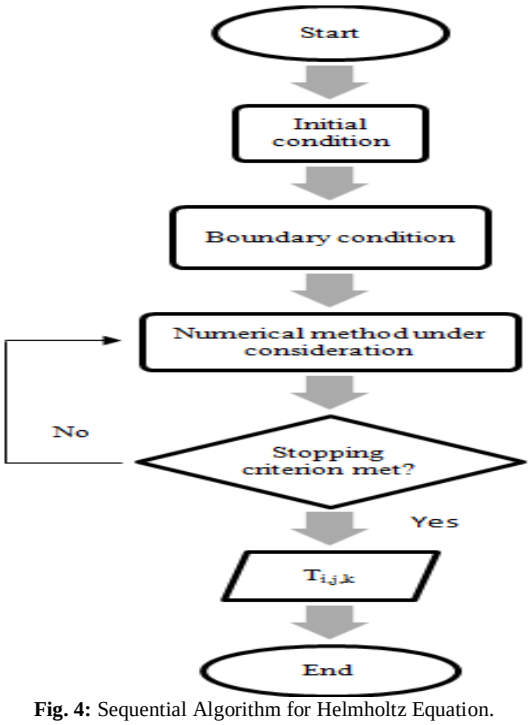


Fig. 4: Sequential Algorithm for Helmholtz Equation.

5.1. Numerical analysis

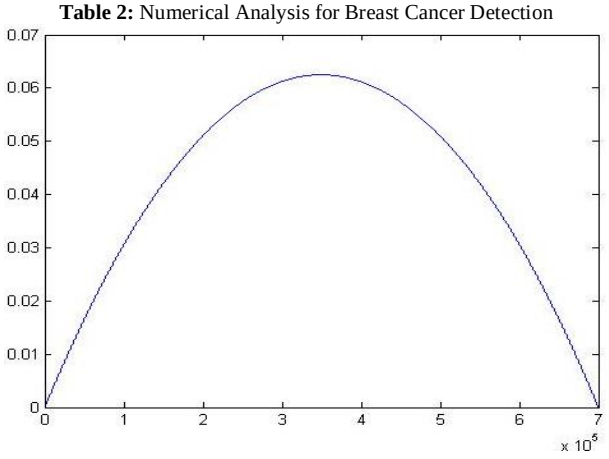
AGE, RBGS and Jacobi methods are highlighted in the current study. It also highlights certain numerical analyses such as time execution, number of iteration, computational complexity, maximum error and RMSE. The results for numerical analysis are as follows.

Table 1: Numerical Analysis for Some Numerical Methods

m=700000; tol=1e-10	AGE	RBGS	JACOBI
Time Execution (s)	67.39038	118.6026	226.0142
Number of iteration	47	872	3468
Computational Complexity (+,-, ×, ÷)	564 940	3488 5232	6936 10404
Max Error	9.979834304E-11	9.992250134E-11	9.999928869E-11
RMSE	4.032204252E-12	4.592445613E-12	5.009908068E-12

The results of numerical analysis as illustrated in Table 1 indicate that AGE is faster than Jacobi and RBGS iterative method regarding convergence. It also shows that the method of RBGS proved to be better than Jacobi method [28]. The table also shows that both RBGS and Jacobi method express higher number of iteration and computational complexity. Moreover, the AGE proved to be an alternative method to solve breast cancer growth problem as it produces a smaller maximum error and RMSE in comparison to the other methods. Figure 5 illustrates the graph for the affected breast tissues using AGE method which resulted from the MATLAB distributed computing.

Table 2: Numerical Analysis for Breast Cancer Detection



6. Parallel algorithm

Figure 4 illustrates the parallel algorithm. It shows the communication activities among the server (master) and processors (slaves). A set of ranges assigned to particular processor for computing the solution are send through the process of data structure decomposition. Parallel computing has the privilege of having the same task on multiple processors been executed simultaneously. This is an advantage as the time execution of computational complexity can be reduced.

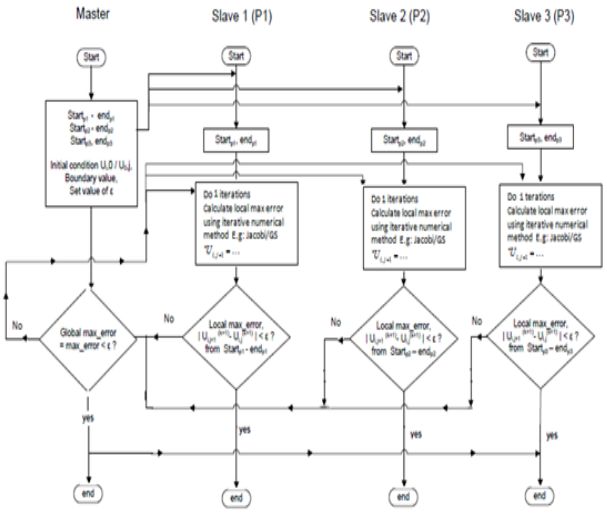


Fig. 5: The Parallel Algorithm for Helmholtz Equation.

6.1. Parallel performance evaluation

Table 2 illustrates parallel algorithm of some numerical methods and their speedup, efficiency, effectiveness and temporal performance. The parallel performance measurements of parallel algorithm have been enhanced using an increasing number of processors. Based on the Amdahl's Law, when the number of processors increases up to the certain level, the speedup accordingly increases. Thus, there is a strong relation between the efficiency is perfor-

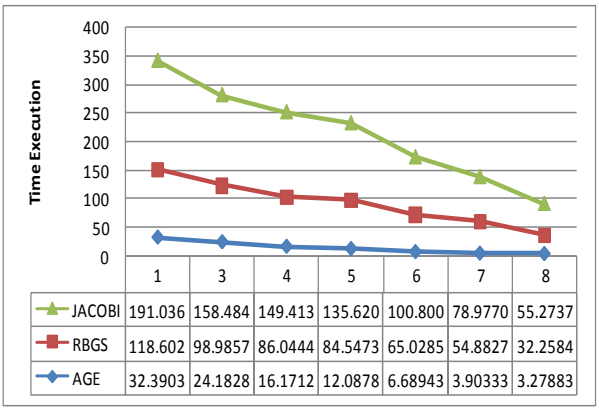
mance and the speedup. Based on these facts, it is said that the speedup determines the formula of the effectiveness.

Table 3: Parallel Performance Evaluation

Numerical Methods	Parallel Analysis	Number of Processors						
		1	3	4	5	6	7	8
AGE	Time Execution (s)	57.390381	30.836849	26.32646	22.182816	19.4912	17.01832	15.422043
	Speedup	1	1.8610974	2.1799506	2.5871549	2.9444252	3.3722706	3.7213216
	Efficiency	1	0.6203658	0.5449876	0.517431	0.4907375	0.4817529	0.4651652
	Effectiveness	0.0174245	0.0201177	0.0207011	0.0233258	0.0251774	0.0283079	0.0301624
	Temporal performance	0.0174245	0.0324287	0.0379846	0.0450799	0.0513052	0.0587602	0.0648423
RBGS	Time Execution (s)	118.60256	69.230378	59.325728	52.662173	46.736705	42.774046	39.179721
	Speedup	1	1.7131578	1.9991758	2.2521395	2.5376748	2.7727693	3.0271415
	Efficiency	1	0.5710526	0.499794	0.4504279	0.4229458	0.3961099	0.3783927
	Effectiveness	0.0084315	0.0082486	0.0084246	0.0085532	0.0090495	0.0092605	0.0096579
	Temporal performance	0.0084315	0.0144445	0.0168561	0.018989	0.0213965	0.0233787	0.0255234
JACOBI	Time Execution (s)	226.01423	140.63246	112.03611	95.153441	91.629567	83.5621	76.689095
	Speedup	1	1.6071271	2.0173338	2.3752607	2.4666081	2.7047457	2.9471495
	Efficiency	1	0.535709	0.5043335	0.4750521	0.4111013	0.3863922	0.3683937
	Effectiveness	0.0044245	0.0038093	0.0045015	0.0049925	0.0044866	0.004624	0.0048037
	Temporal performance	0.0044245	0.0071107	0.0089257	0.0105093	0.0109135	0.0119671	0.0130397

Figure 2(a) proves that the number of processors is responsible for decreasing the time of execution. The existence of domain decomposition that is distributed to each workstation and compute synchronously is responsible for the happening of this circumstance. Similarly, Figure 2(b) the influence of adding processors in increasing the speed up. It could be noticed from the distributed memory hierarchy the speedup increased while the time to access a cluster of workstations is reduced. Figure 2(c) that the number of processors increases when the efficiency decreases. Thus, speedup is closely related to efficacy as a performance. Effectiveness is reported to increase as the number of processors is growing which illustrated in 2(d). Thus, the formula of effectiveness strongly depends on the speedup where the former increases when the latter increases too. Figure 2(e) shows the relation between the number of processors and temporal performance. The number of processors versus the decreasing of execution.

(A)



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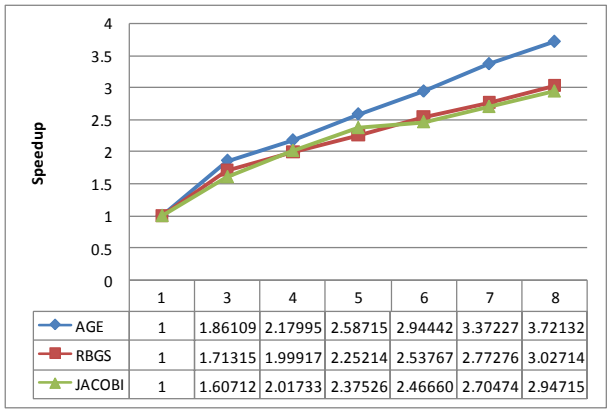
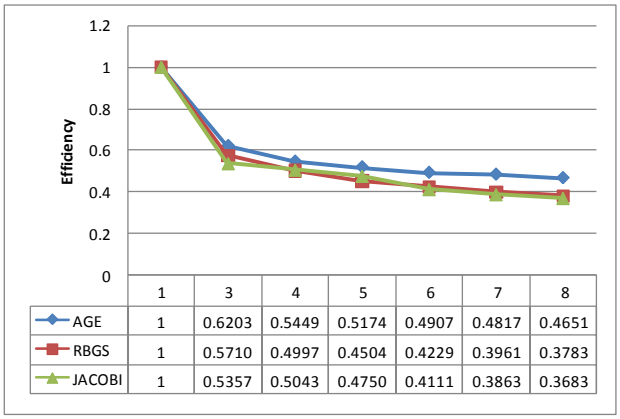


(C)



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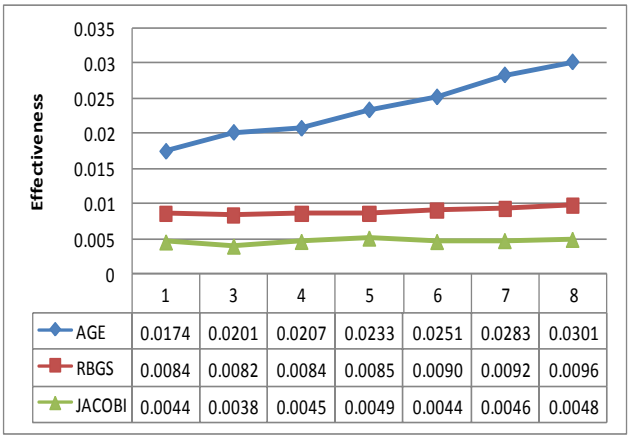
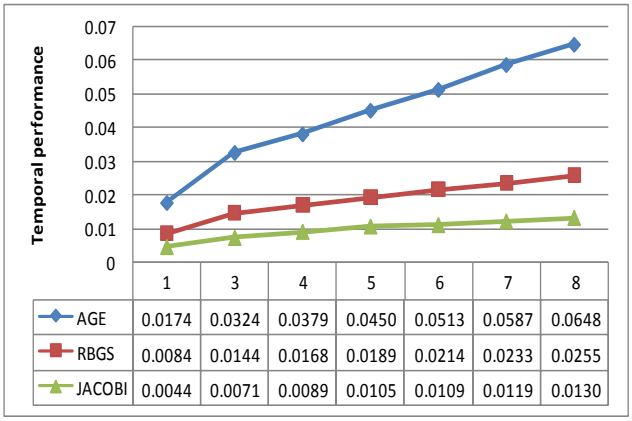


(E)



The analysis also shows that parallel algorithm is better than sequential algorithm in terms of validity and huge data size. In terms of the execution time, speedup, efficiency, effectiveness and temporal performance, the AGE proved to be better than RBGS and Jacobi methods. Compared with AGE's accuracy (2,2) and RBGS's accuracy (1,2), AGE is also more effective than the previously mentioned methods. In terms of computation, the AGE proved to compute at a half-time step compared to RBGS and Jacobi which are known as straight forward to one-time step. Finally, the acceleration parameter available in the AGE is effective in accelerating the computation converges in a faster base compared to RBGS and Jacobi method.

7. Conclusions

The current study highlights the importance of Helmholtz equation in the field of breast cancer growth in which it fully captures this type of growth. The method known as the AGE proved to be effective in handling this growth and that can be clearly noticed from the numerical analysis and parallel performance evaluation. AGE is also considered superior than other methods such as RBGS and Jacobi when it comes to number of iteration, time execution and maximum error. This method also used a half time step in computing the solution and considered an alternative method in this regard. When the data is a large sparse matrix, the results of the parallel implementation were better than those of the sequential algorithm. The shortcoming of the sequential algorithm represented by time consumption can be solved by the parallel algorithm. The current study recommends future research to work on this mathematical modelling of breast cancer growth that can be transformed into software. The development of software can be helpful in human-life line of the cancer patients. The study also recommends suture research to use smaller cell size to improve the resolution of the reconstructed bodies.

Acknowledgement

This work was supported in part by the Universiti Teknologi Malaysia, Malaysian Government and Ministry of Higher Education.

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