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High Performance Simulation for Brain Tumours Growth Using Parabolic Equation on Heterogeneous Parallel Computer System

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ABSTRACT

Brain tumour is one of the prevalent cancers in the world that lead to death. Based on the present knowledge of the properties of gliomas, mathematical models have been developed by researchers to quantify the proliferation and invasion dynamics of glioma within anatomically accurate heterogeneous brain tissue. This paper focuses on the implementation of parallel algorithm for the simulation of brain tumours growth using one dimensional parabolic equation, designed on a distributed parallel computer system. The numerical finite-difference method is focused on a design of a platform for discretising the parabolic equations. The result of finite difference approximation using explicit, Crank-Nicolson and fully implicit methods will be presented graphically. The implementation of parallel algorithm based on parallel computing system is used to capture the growth of brain tumour. Parallel Virtual Machine (PVM) is emphasized as communication platform in parallel computer systems. The software system functions to enable a collection of heterogeneous computers to be used as synchronized and flexible concurrent computational resource. The parallel performance measurement will be analysed from the aspect of speedup, efficiency, effectiveness and temporal performance.

Keywords: Parallel computer system, parallel virtual machine, mathematical model, brain tumour growth, Crank-Nicolson method.

ABSTRAK

Barah otak antara barah utama yang menyumbang kepada peningkatan kematian disebabkan kanser. Fenomena ini menarik minat pengkaji daripada pelbagai bidang untuk mendalaminya, termasuklah ahli-ahli matematik. Terdapat beberapa model matematik telah dibangunkan berdasarkan pengetahuan tentang ciri-ciri sel barah dan pertumbuhannya. Kajian ini fokus kepada penggunaan teknik algoritma selari dalam meyelesaikan dan menggambarkan pertumbuhan sel barah otak menggunakan persamaan

parabolik satu dimensi. Kaedah penghampiran beza terhingga, dikaji dan digunakan dalam pendiskretan persamaan parabolik. Kaedah tersirat, tak tersirat, dan Crank-Nicolson untuk penghampiran beza terhingga dianalisis dan hasilnya ditunjukkan dalam bentuk graf. Dalam kajian ini, algoritma selari dilaksanakan menggunakan sistem pengkomputeran selari. Mesin Selari Ingatan Maya iaitu PVM digunakan sebagai platfom komunikasi dalam sistem komputer selari. PVM merupakan satu perisian yang membolehkan sekumpulan komputer heterogenus digunakan sebagai satu sumber pengiraan yang bekerjasama secara teratur dan fleksibel serta dihubungkan oleh satu sistem rangkaian. Prestasi algoritma selari juga dianalisis dari aspek kecepatan, kecekapan, keberkesanan dan masa pelaksanaan.

Katakunci: Sistem pengkomputeran selari, mesin maya selari, permodelan matematik, pertumbuhan barah otak, kaedah Crank-Nicolson.

INTRODUCTION

The human body is made up of many types of cells. Each type of the cells has special functions. Most of the cells in the body grow and then divide in an orderly way to form new cells as they keep the body healthy and working properly. The cells will divide often and without any order when they lose the ability to control their growth. The extra cells from a mass of tissue are called tumours.

Brain tumour is one of the prevalent cancers in the world and is one of the leading causes of death from cancer. The brain tumours can be benign (not cancerous) or malignant (cancerous). Mathematical modelling of biomedical phenomena (Murray 2003) can be extremely helpful in analyzing factors that may contribute to the complexity intrinsic in insufficiently understood developmental process disease. Based on present knowledge of the properties of gliomas, a mathematical model has been developed to quantify the proliferation and invasion dynamics of gliomas within anatomically accurate heterogeneous brain tissue. The implications of the model would be of considerable interest to not only for neuro-oncologists attempting to improve the treatment of gliomas but also to those interested in the study of other diseases for which medical imaging plays a part of the assessment of the disease (other cancer as well as developmental diseases).

MATHEMATICAL MODEL

The mathematical model has been developed to detect the growth and the extension of theoretical glioblastomas cells in a matrix that accurately describes the brain's anatomy to a resolution of 1 cu mm. By defining a virtual human brain with the anatomical distribution of grey and white matter

(the two primary tissue components of the brain) to a resolution of 1 cu mm, the differential motility of glioma cells in grey and white can be modeled. The glioma cells migrate more rapidly in white than in grey matter (Giese & Westphal, 1996; Silbergeld & Chicoine, 1997), the motility coefficient dependence on the local tissue composition. The model can be written mathematically as:

(1)

where $c(x, t)$ is the concentration of glioma cells at any position **x** and time t, ρ is the units of per day and represents the net rate of growth of tumour cells, including proliferation, loss and death, D denotes the units of cm^2 per day and represents the diffusion coefficient of cells in brain tissue, $D(x) = D_g$ (constant for x in grey matter) and $D(x) = D_w$ (constant for x in white matter).

As noted, the diffusion coefficient in white matter is larger then that in grey matter: $D_w > D_g$. ∇ represents the spatial gradient. The diffusion term describes the active migration of the glioma cells using a simple Fickian diffusion (Murray 1993) where cells move from regions of higher to lower densities. Tumour cells are assumed to grow exponentially.

The boundary condition simply requires that glioma cells are not allowed to migrate outside of the brain tissue. Assume that the tumour has grown to about 4000 cells as a local mass before it begins to diffuse. We used the growth rate, $\rho \approx 0.012$/day (Alvord & Shaw 1991; Swanson 1999; Swanson *et al.*, 2000) and diffusion coefficient, $D \approx 0.0013 cm^2$/day (Swanson 1999; Swanson et al. 2000) in the model as suggested for high-grade gliomas [Swanson, Alvord & Murray 2000].

NUMERICAL SIMULATION AND DISCUSSIONS

THE STANDARD FORM

The model equation is a parabolic equation and it can be solved using numerical finite difference methods. From equation (1),

(2)

Let $D(x) = D$ as a constant, the non-dimensionalizing process in shown as:

with dimensionless variables:

Then,

and

Equation (2) transforms to

Let ,

Applying the function of a function rule to the left side,

Let , (3)

The finite-difference approximation to equation (3) can be written as,

$$\frac{c_{i,j+1}-c_{i,j}}{\Delta t} = \frac{1}{(\Delta x)^2}\left[(1-\theta)\left(c_{i-1,j}-2c_{i,j}+c_{i+1,j}\right)+\theta\left(c_{i-1,j+1}-2c_{i+1,j+1}\right)\right]+\alpha c_{i,j}$$

$$c_{i,j+1}-c_{i,j} = \lambda\left[(1-\theta)\left(c_{i-1,j}-2c_{i,j}+c_{i+1,j}\right)+\theta\left(c_{i-1,j+1}-2c_{i,j+1}+c_{i+1,j+1}\right)\right]+\alpha c_{i,j}$$

$$c_{i,j+1}-c_{i,j} = \lambda(1-\theta)c_{i-1,j}-2\lambda(1-\theta)c_{i,j}+\lambda(1-\theta)c_{i+j}+\lambda\theta c_{i-1,j+1}-2\lambda\theta c_{i,j+1} + \lambda\theta c_{i+1,j}+\alpha c_{i,j}$$

$$\therefore \quad -(\lambda\theta)c_{i-1,j+1}+(1+2\lambda\theta)c_{i,j+1}-(\lambda\theta)c_{i+1,j+1} = \lambda(1-\theta)c_{i-1,j}+\left[1+\alpha+2\lambda(1-\theta)\right]c_{i,j}+\lambda(1-\theta)c_{i+1,j} \tag{4}$$

For $0 \le \theta \le 1$. $\theta = 0$ gives the explicit scheme, $\theta = \frac{1}{2}$ the Crank-Nicolson, and $\theta = 1$ a fully implicit backward time-difference method. The equation (4) can be written in the matrix form:

$$\begin{bmatrix} p & s & & & \\ s & p & s & & \\ & \ddots & \ddots & \ddots & \\ & & s & p & s \\ & & & s & p \end{bmatrix}\begin{bmatrix} u_{1,j+1} \\ u_{2,j+1} \\ \vdots \\ \vdots \\ u_{N-1,j+1} \end{bmatrix} = \begin{bmatrix} r & q & & & \\ q & r & q & & \\ & \ddots & \ddots & \ddots & \\ & & q & r & q \\ & & & q & r \end{bmatrix}\begin{bmatrix} u_{1,j} \\ u_{2,j} \\ \vdots \\ \vdots \\ u_{N-1,j} \end{bmatrix}$$

where $p = (1 + 2\lambda\theta)$, $s = -\lambda\theta$, $r = [1 + \alpha + 2\lambda(1 - \theta)]$ and $q = \lambda(1 - \theta)$.

SOLUTION USING THE FINITE-DIFFERENCE METHOD

The linear system from the problem statement has been solved for three finite-difference approximations: explicit, Crank Nicolsan, and fully implicit methods using Gauss-Seidel iterative method with C programming under Linux environment. When $\theta = 0$, it gives the explicit method, when $\theta = \frac{1}{2}$, it gives the Crank-Nicolson method and when $\theta = 1$ it gives the implicit method. The results from the sequential algorithm using C programming are shown in Table 1, where $\partial x = \frac{1}{200}, \partial x = \frac{1}{10}$ for 3 days.

TABLE 1. The results for three finite-different methods

Methods / Grid	Explicit $\theta = 0$	Crank-Nicolson $\theta = 0.5$	Fully Implict $\theta = 1.0$
1	4146.96	4593.47	4646.61
2	9004.30	8268.93	8214.44
3	10055.12	10620.65	10424.19
4	12626.83	11817.62	11568.04
5	12354.69	12270.09	12028.38
6	12354.69	12270.09	12028.38
7	12626.83	11817.62	11568.04
8	10055.11	10620.65	10424.19
9	9004.30	8268.93	8214.44
10	4146.96	4593.47	4646.61

Table 1 summarised the number of tumour cells that had been computed using three finite-difference methods. The data for the Crank-Nicolson and fully implicit methods are quite similar compare to the data that compute using explicit method.

The graphs visualise the pattern of the brain tumour growth using explicit method (Figure 1), Crank-Nicolson (Figure 2) and the fully implicit method (Figure 3). It can be concluded that the explicit method is not suitable to solve the mathematical model since the curve is not smooth and cannot capture the real image of the tumour cells. The step size in time must be small in order for the explicit method to work properly. The problem will occurr as we make the grid size small, the number of computation increase and the round off errors will also increase. The Crank Nicolson implicit and the fully implicit method showed a smooth curve and relevant to visualise the growth of the tumours. The implicit method has an advantage over the explicit method, since the step size can be made larger without worrying about excessive buildup of round off error.

Both Crank-Nicolson and the fully implicit method are relevant to capture the real life problem. As a result, Crank-Nicolson method will be chosen to be applied in the mathematical model to visualise the growth of brain tumour for 30 days. This is because of its stability and accuracy.

PARALLEL ALGORITHM

GAUSS SEIDEL RED BLACK ITERATIVE METHOD

To implement the parallel algorithm in solving the finite difference equation, Gauss Seidel Red Black (GSRB) algorithm is used. The iterative method

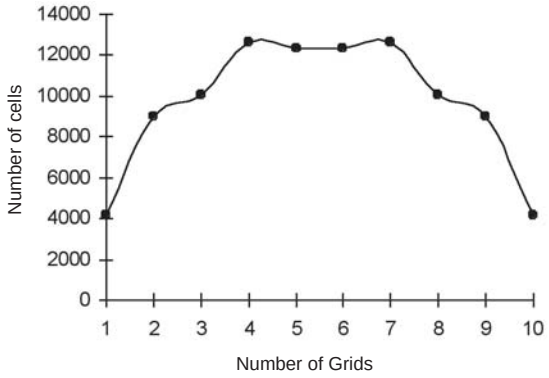

FIGURE 1. Graph for explicit method

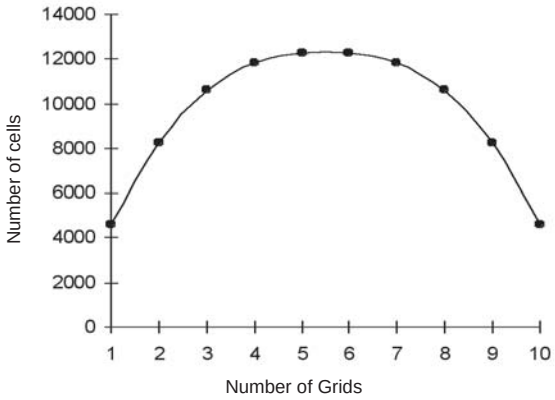

FIGURE 2. Graph for Crank-Nicolson

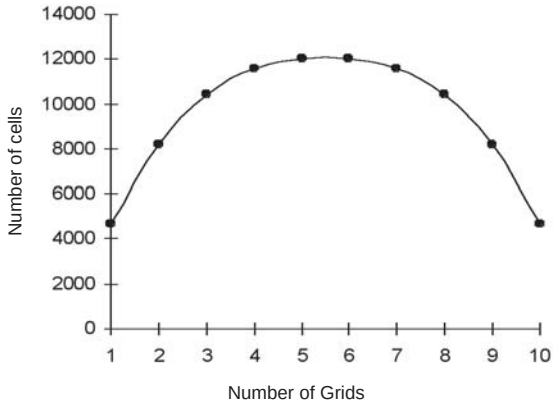

FIGURE 3. Graph for fully implicit method

contains 2 sub domain, Ω^R and Ω^B. There is communication between Ω^R and Ω^B. The calculation of this method is shown by the equation (5) and (6),

i. Grid calculation at Ω^R:

$$u_i^{(n+1)} = \frac{1}{2} r \left\{ u_{i-1}^{(n+1)} - 2u_i^{(n+1)} + u_{i+1}^{(n)} \right\} + b_i, \qquad i = 1.3.5,\ldots,m. \tag{5}$$

ii. Grid calculation at Ω^B:

$$u_i^{(n+1)} = \frac{1}{2} r \left\{ u_{i-1}^{(n+1)} - 2u_i^{(n+1)} + u_{i+1}^{(n)} \right\} + b_i, \qquad i = 2,4,6,\ldots,m-1 \tag{6}$$

The GSRB iterative using parallel computing shows convergence very fast compared to the parallel algorithm using Gauss Seidel (GS) iterative. GSRB is a data decomposition approach that divides arrays among local processors to minimize the communication. The data structure has to be decomposed where given set of ranges assigned to particular processors must be physically sent to those processors for processing to be done. The result must be sent back to whichever processors responsible for coordinating the final result.

The simple GS update strategy may be appropriate in a sequential program and often preferred over Jacobi strategies because they allow solutions of comparable accuracy to be obtained using less iteration. However, for the solution of large sparse matrix problem, the GSRB parallel algorithm is more suitable to be implemented compared to the GS.

THE VISUALIZATION OF THE BRAIN TUMOUR GROWTH USING CRANK-NICOLSON

The number of cancer cells is computed by using parallel algorithm with PVM. The tumour is assumed growing to about 4000 cells as a local mass before it begins to diffuse and the model equation (1) applies in order to avoid simulating a case of gliomatosis cerebri for which tumour cells have invaded throughout the brain without a single dominant tumour mass (Swanson, Alvord & Murray 2002). The boundary condition simply requires that glioma cells are not allowed to migrate outside of the brain tissue.

The concentration gradient of brain tumour cells is represented by the curves in Figure 4 for every 5 days within 1 month. The graph has shown that in the first 5 days, the tumour cells only proliferate to form a small dense lesion. After 20 days, the tumour cells become highly diffusive. The tumour cells have diffused to more than 160,000 after 30 days.

Since that the glioma are diffuse tumour, only a small portion of actual tumour can be predicted. The length of the growth area that consist of tumour cells is only 0.167cm within 30 days. From the graph of the growth of brain tumour, we can also conclude that the tumour grow slowly and quickly diffusing.

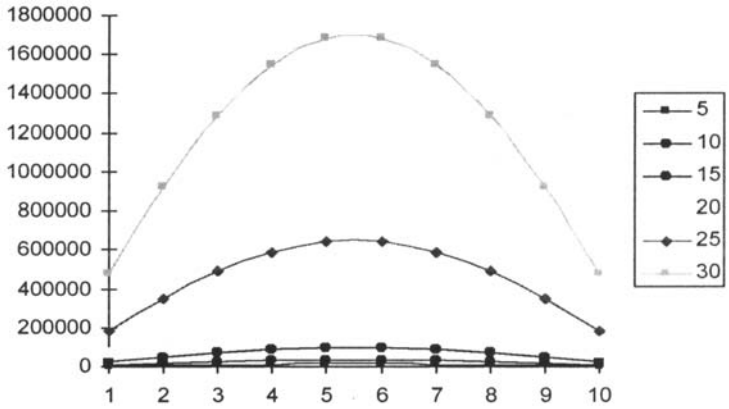

FIGURE 4. The growth rate of brain tumour

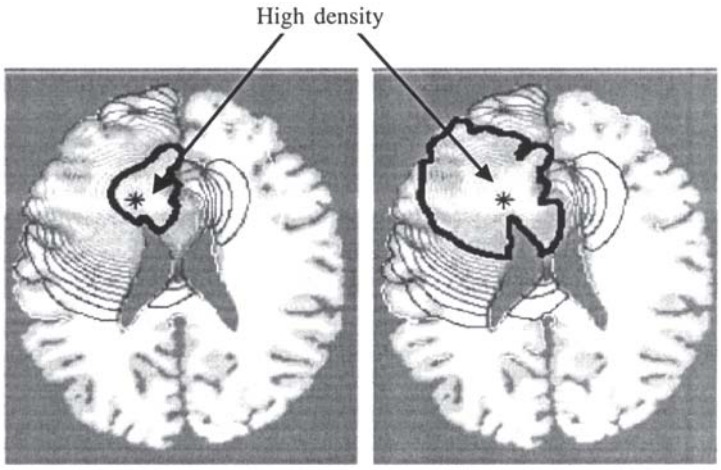

FIGURE 5. Detection of brain tumour growth using CT scan

Figure 5 is the results in British Journal of Cancer (2002) 86, 14-18, written by KR Swanson, EC Alvord Jr and JD Murray. The section of the virtual human brain in the figure above is in horizontal planes. The left column of the human brain section represents the tumours at diagnosis using CT-detectable tumours with average diameter of 3cm, while the right represents the same tumours at death. The CT (or CAT) scan is a series of detailed pictures of the brain. The pictures are created by a computer linked to an X-ray machine and denoting the high density area of tumour cells. The elapsed time between diagnosis and death for this virtual glioma is approximately 158 days.

The results that is presented using PVM programming shown in Figure 4 is only a small area, about 2.78% of the tumour at death. For the detection of the growth of cancer cells in human brain using parallel computing, the area can be predicted broadly by using the different net proliferation rate, ρ and diffusion coefficient, D. The various area of the human brain has the different value for ρ and D.

Analysis of the Performance of PVM

The parallel performance measurements such as time execution, speedup, efficiency, effectiveness and temporal performance are analyzed to proof parallel algorithms is significantly better than the sequential algorithms. The parallel implementation of an algorithm involves the division of total workload into a number of smaller tasks, which can be assigned to different processors and executed concurrently, which allows the large problems of iterative methods converge faster to the solution. The analysis of the executive time by parallel programming helps to understand the barriers of high performance computing and how improvement can be done by increasing the number of processors. As the cluster gets larger, it becomes more important and efficient for solving real-life problems.

In the PVM implementation of the modeling codes there is a master task and there are a large sparse problem number of worker tasks. The main job of master task is to divide the region domain into sub-domains and distribute them to worker tasks. The worker tasks perform execution computation and communication after each time step.

TABLE 2. Time, convergence and count for parallel and sequence algorithm

	Gauss Seidel Red-Black with PVM	Gauss Seidel with Sequence Algorithm
Time (microsecond)	50820	632821
Convergence	1.09139e-11	4.18368e-11
count	64	74

Table 2 shows that the executive time, convergence and number of iterations for solving the mathematical model using parallel GSRB algorithm with PVM and sequential GS algorithm. The execution time for parallel GSRB with PVM is about 10 times faster than sequential GS algorithm. This shows that parallel algorithm is significantly better than sequence algorithm. Besides that, parallel GSRB is more convergence compare to its sequential algorithm. The iteration for GSRB algorithm to be converging is only 64 while the GS with sequence algorithm perform 74 iterations for convergence.

Amdahl's law states that the speed of a program is the time to execute the program while speedup is defined as the time it takes a program to execute in serial (with one processor) divided by the time it takes to execute in parallel (with many processors). The formula of speedup for a parallel application is given as

,

where *Time*(1) denotes execution time for a single processor and *Time*(*p*) is the execution time using *p* parallel processors.

Figure 6 shows the speedup graph is the straight linear and as well as the number of processors increases, *p*. It is because the distributed memory hierarchy reduces the time consuming access to a cluster of workstations. According to Amdahl's Law, the speedup increases with the number of processors increase up to the certain level.

The efficiency of a parallel program is a measure of processor utilisation. Figure 7 depicts the efficiency decreases with the increasing of number of processors, *p*. The decrease of efficiency contributed by the factors of poor load balance when imbalance workload distributed among the different processors. It is also contributed by the idle time, time startup and waiting time for all processors to complete the computations. Efficiency is the speedup divided by the number of processors used.

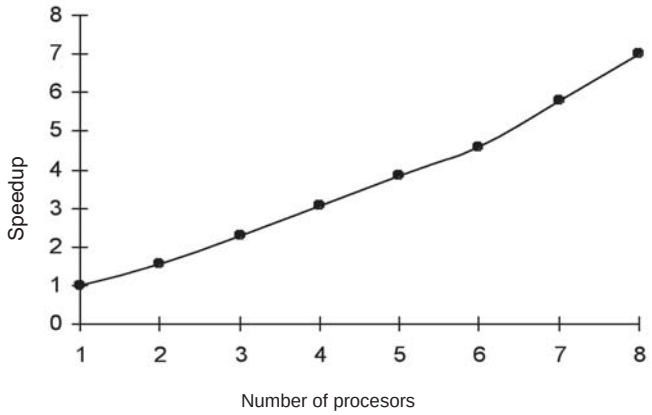

FIGURE 6. The speedup vs. number of processors

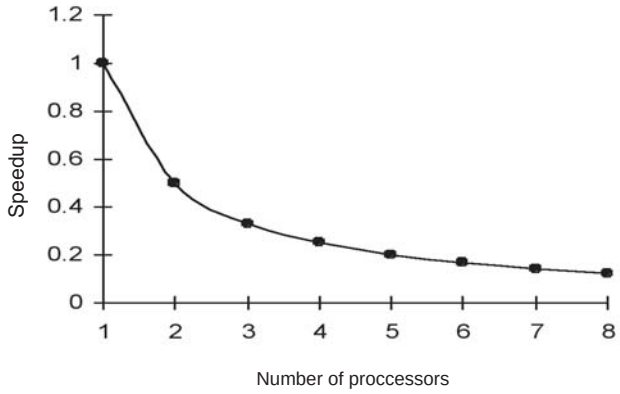

FIGURE 7. Efficiency vs. number of processors

Effectiveness is used to calculate the speedup and the efficiency. The effectiveness is

where p is number of processors and $Time(t)$ is execution time using p parallel processors.

Figure 8 shows that the effectiveness increase when the number of processors are increased. The formula of effectiveness depends on the speedup. When the speedup increases, the effectiveness will also increase. Furthermore, the use of the number of processors is added to make the graph increase. The graph does not show the straight line because there is a communication between eight of the processors.

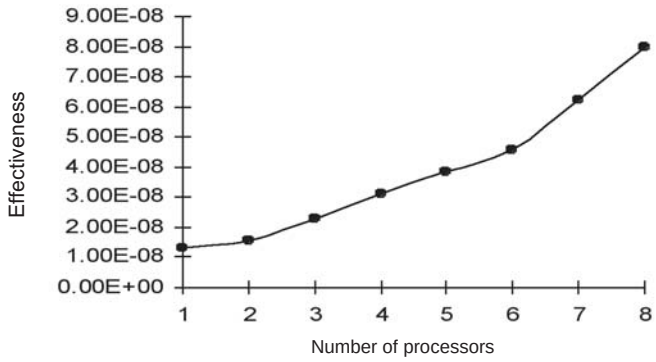

FIGURE 8. Effectiveness vs. number of processors

Temporal performance is a parameter to measure the performance of a parallel algorithm which is

Figure 9 shows that the temporal performance is increased with the increasing number of processors. The graph below shows a straight line because of the execution time is decreasing extremely versus the number of processors.

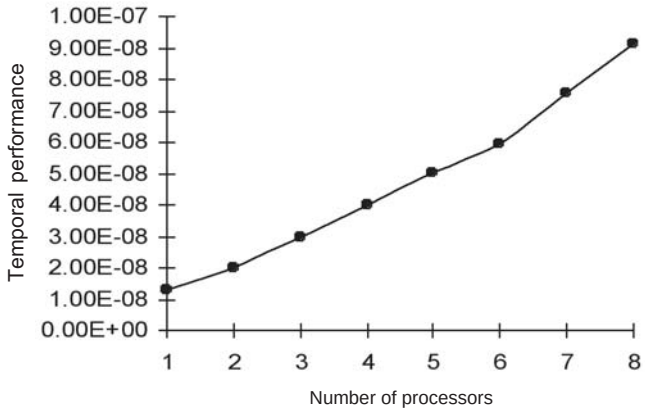

FIGURE 9. Temporal performance vs. number of processors

CONCLUSIONS

A mathematical model using the one dimensional parabolic equation regarding the growth of brain tumours has been presented. The explicit, Crank-Nicolson and fully implicit methods are used in solving the equation. The graphical results show that the Crank-Nicolson and fully implicit methods are more relevant to describe the growth of tumour cells, compared to the explicit method. Since the Crank Nicolson method is well known of its unconditional stability and good accuracy, this method is choosen to visualise the growth of brain tumors for 30 days.

The analysis of the performance measurements such as time execution, speed up, efficiency, effectiveness and temporal performance proved that parallel algorithm is significantly better than the sequential algorithm especially in terms of the execution time. The Gauss Seidel Red Black is effective iterative method and found to be well suited for parallel implementation on the PVM where data decomposition is run synchronously and concurrently at every time level.

Finally, the development of mathematical model in visualising the growth of human brain tumour can be easily extended into multiple dimensions parabolic equation. More processors could also be used in solving the mathematical model in order to improve the speed and performance on a distributed parallel computer systems.

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