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The Visualization of Three Dimensional Brain Tumors' Growth on Distributed Parallel Computer Systems

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Abstract: The main aim of this study is to visualize the brain tumors' growth in three-dimensional and implement the algorithm on distributed parallel computer systems. The Partial Differential Equations (PDE) to solve the mathematical problem will be discussed in this study. The growth of the brain tumor through angiogenic process is described as parabolic model in partial differential equations. The discretization of the three-dimensional parabolic equations for the brain tumor's growth mathematical model using a numerical finite-difference method will be implemented from the earlier study of two dimensional model and thus a parallelization of algorithm simulation to computational resources based on high-performance computing systems will be used to generate the growth of the brain tumor in three dimensional. The study also includes an observation of the behaviour of the cells graphically and Parallel Virtual Machine (PVM) is used to communicate the platforms involved in the computational clusters. A comparison of sequential and parallel algorithm will be discussed and this study will address the major issues of the parallel computers performance in terms of efficiency, effectiveness, speedup and temporality.

Key words: Partial differential equations, 3D parabolic equations, finite difference method, parallel virtual machine, parallel computing, brain tumor

INTRODUCTION

A brain tumor is a growth of abnormal cells or normal cells in an inappropriate place in the brain. A primary brain tumor is one that starts in the brain, rather than cancer in another part of the body that has spread to the brain. Primary tumors can be grouped into non-cancerous (benign) and cancerous (malignant).

Malignant brain tumors are commonly called brain cancer and they are usually invasive and life-threatening. Brain tumors also may be metastatic or secondary brain tumors. These tumors are formed from cancer cells that begin growing elsewhere in the body and travel to the brain, usually through the bloodstream. Metastatic brain tumors are always cancerous and commonly come from cancers of the lung or breast or from melanomas. They are more common than primary brain tumors.

The correlation between lateral ventricles deformations and tumor existence has been found useful in the brain MRI, in brain tumor detection and prediction. A new method has been proposed by Xiao *et al.* (2007) to analyze the deformation of ventricles, to retrieve the lateral ventricles deformation data for further statistical analysis and processing. In that method, the boundaries of the lateral ventricles are segmented firstly, pixels on the boundary are sampled and a nonlinear interpolation method based on Thin Plate Spline (TPS) is accomplished to create a more perfect template image for each specific case, followed by the application and performance evaluation between TPS with Radial Basis Function Neural Networks (RBF-NN) and Radon Transform (RT) on the extracted Skeleton of the boundary of the ventricles for locating the optimal orientation of the image through iterative image rotation. The reoriented ventricles are analyzed based on the displacement values obtained from the TPS of the sampled template and the diagnostic lateral ventricle. Their experimental results suggest that their method is effective and relevant in prediction of the location of tumor.

This study is to visualize or capture the growth of brain tumor in three-dimensional space and to develop or identify the three-dimensional brain tumor growth. The aim is to identify the discretization of the mathematical models which will be converted to standard form and to implement the algorithm to perform the iterative methods from the discretization of the mathematical model. One of the significant objectives of this study is to identify the right parallel algorithm or parallel programs for our three-dimensional brain tumor growth model.

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The most malignant form of brain cancer is glioblastoma (Andrew *et al*., 2007), which is responsible for 23% of primary brain tumors and has extremely poor outcome. They conducted experiments on the patterns of growth and dispersion of U87 glioblastoma tumor spheroids in a three-dimensional collagen gel to gain insight into glioblastoma invasion. They developed a continuum mathematical model of the dispersion behaviors with the aim of identifying and characterizing discrete cellular mechanisms underlying invasive cell motility.

The pennes equation is the most widely used (Pennes, 1948), among the various models proposed to the study of heat transfer in living tissues. The understanding of thermal life phenomena and temperature behavior in living tissues is required (Gautherie, 1980; Chato, 1989), in the contemporary clinical treatments and medicines such as cryosurgery, Cancer hyperthermia, cryopreservation and thermal disease diagnostics, etc. Liu (2001) presented an analytical explanation of the 3D Pennes equation using multidimensional green function. While this solution may be helpful in some exceptional cases, the difficulty of multidimensional heat transfer problems in many practical circumstances suggests the application of numerical techniques.

Numerical methods: The methods under consideration for this study are the finite-difference methods for three-dimensional parabolic equations for brain tumor growth. We will also use the method of discretization under the basis of Partial Differential Equations from Numerical methods (Tan Liang and Ang Keng, 2005). The discretization will produce a finite-dimensional equation which will later be converted to matrices form. The matrices will be solved using iterative methods, namely Gauss Seidel method by both sequential and parallel algorithms. Besides, a distributed parallel computing system with the communication platform of Parallel Virtual Machine (PVM) and C programming with Linux environment are applied.

Mathematical model: By using finite difference method, certain assumptions and using lattice scheme, we'll obtain the three dimensional parabolic equation of the tumor growth as:

$$\frac{\partial u}{\partial t} = -\nabla.W(u) + \nabla.(Q\nabla u) + \Gamma - Lu$$

where, in three dimensions, W = (P, R, S).

The model represented in the study is an extension to the model by Angelis and Preziosi (2000) from W = (P, R) (two dimensions) to W = (P, R, S) (three dimensions).

Table 1: Evidence based on medicine

Terms	Yes	No
Keep secret from family	50	50
Member of family that have similar illness	10	90
Other than hospital treatment	60	40
Age >40	70	30
Family support	80	20
Get consultation from expertise	80	20
Changing of emotion	70	30
Changing of personality	60	40
Changing of speech	70	30
Changing of hearing	60	40
Changing of daily routine	60	40
Changing of diet	60	40

Table 2: Evidence based medicine (Real data versus hospital data versus mathematics simulation)

Parameters	Level	Spheroid	Detect. lesion	Diagnosis	Death
Radius (mm)	Test	0.5	5.0	18.5	25.0
	Math	0.5	5.0	18.5	25.0
	Hosp	0.5	4.18	18.0	24.0
Volume-doubling	Test	6	45	70	105
time (days)	Math	6	38	70	105
	Hosp	6	40	70	105
Velocity (v)	Math	0.07	0.1289	0.2629	0.2371
(mm day^{-1})	Hosp	0.0111	0.11829	0.11829	0.11829
Growth rates (p)	Math	0.007	0.00015	0.0004	0.0003
(1/day)	Hosp	0.00833	0.00278	0.00278	0.001136
Cell No.	Data	10^6	10^9	10^{10}	10^{11}
	Math	1.62×10^6	3.95×10^9	4.19×10^{10}	1.07×10^{11}

Some sort of evidences based on medicine is shown in Table 1. The comparison of Real Hospital Data (Hosp) versus Real Data from Journals (Test) Vs Mathematic Simulation results (Math) have shown in Table 2. The reasons, to persuasive monitoring software to predict tumor growth are:

- 33.3% patients do not tell anybody about the disease
- 22.2% patients used prediction software to detect tumor growth while
- 11.1% used other electronic devices

PARALLEL COMPUTING SYSTEM

The definition of distributed memory is referred to the multiple processors operate independently but each has own private memory, data is shared across a communications networked using message passing paradigm. The world's largest supercomputers are used almost exclusively to run applications that are parallelized using Message Passing (Fig. 1).

Why parallel computing?

Emergence of computational science: Science includes mass number of researches involves analysis that is only restricted model problems and simple geometries. With

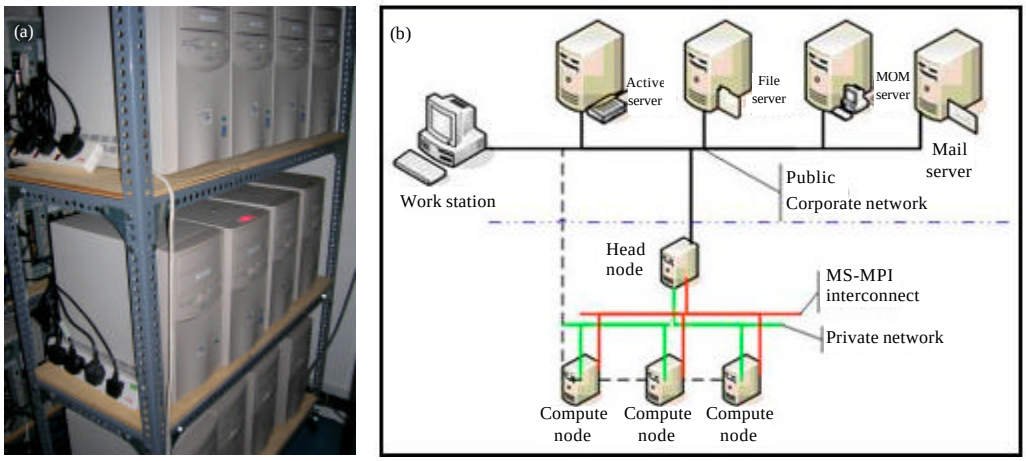

Fig. 1: (a) Parallel computing system and (b) Part of a parallel computing platform

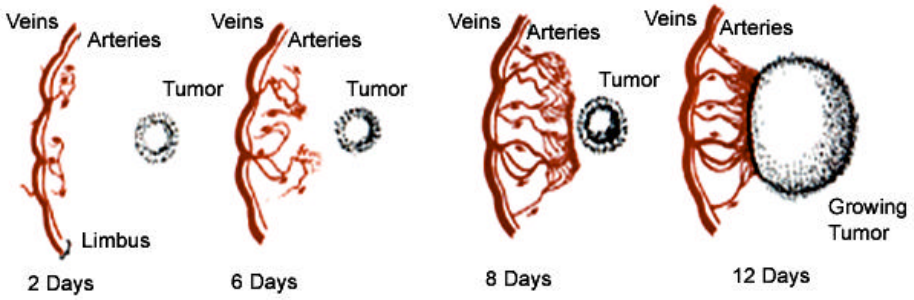

Fig. 2: Time depending growing tumor

parallel computing, the experiments which are rather expensive, dangerous, difficult to reproduce and sometimes impossible can be attained.

Sequential computing is slow: To get faster the system has to get smaller. However, there are many physical and mathematical limitations to be taken into account. Ultimately, parallel computing system is faster by definition since the No. of processors for a single CPU is increased.

This study predicts basically the growth of the tumor, $N_{ijk}(t)$ found in the node (i, j, k) in at time t, where, two mechanisms which govern the movement of the cells exists (Fig. 2).

- A diffusive-like phenomenon governed by a Brownian motion with probability which depends on the direction of the movement. In the study it's indicated for instance (since in three dimensions) with $Q_{i,i+1,j,k}$ the transition probability density per unit time that a cell diffuses from (i, j, k,) to (i+1, j, k)
- A transport-like phenomenon, which generates a drift of cells with a probability which again depends on the direction of motion. Since in three dimensions the motions involve are such that:

$P_{i,i+1,j,k}$: Transition probability density per unit time that a cell is transported along x from (i, j, k) to (i+1, j, k)

$R_{i,j,j+1,k}$: Transition probability density per unit time that a cell is transported along y from (i, j, k) to (i, j,+1, k)

$S_{i,j,j,k+1}$: Transition probability density per unit time that a cell is transported along z from (i, j, k) to (i, j, k+1)

Angelis and Peziosi (2000) assumed that the drift velocity has positive components. Since the three dimension model involves 3 nodes, i, j and k, one has to follow the following scheme:

Number of cells in (i, j, k) at time t+dt = (No. of cells present in (i, j, k) at time t)+(No. of cells drifting in along x from (i -1, j, k), along y from (i, j -1,k) and along z from

(i, j, k-1))−(No. of cells drifting away along x to (i+1, j, k), along y from (i, j+1, k) and along z from (i, j, k+1))+(No. of cells diffusing from neighbour-ing nodes)−(No. of cells diffusing away to neighbour-ing nodes)+(Generation of new cells)−(Death of cells). This leads to the following finite difference equations:

$$N_{i,j,k}(t+\Delta t) = N_{i,j,k}(t) + \Delta t$$
$$\begin{bmatrix} P_{i-1,i,j,k}N_{i-1,j,k}(t) + R_{i,j-1,j,k}N_{i,j-1,k}(t) + S_{i,j,k-1}N_{i,j,k-1}(t) - \\ P_{i,i+1,j,k}N_{i,j,k}(t) - R_{i,j,j+1,k}N_{i,j,k}(t) - S_{i,j,k,k+1}N_{i,j,k}(t) \\ +Q_{i-1,i,j,k}N_{i-1,j,k}(t) + Q_{i+1,i,j,k}N_{i+1,j,k}(t) + Q_{i,j-1,j,k}N_{i,j-1,k}(t) + \\ Q_{i,j+1,j,k}N_{i,j+1,k}(t) + Q_{i,j,k-1,k}N_{i,j,k-1}(t) + Q_{i,j,k+1,k}N_{i,j,k+1}(t) \\ -\left(Q_{i,i-1,j,k} + Q_{i,i+1,j,k} + Q_{i,j,j-1,k} + Q_{i,j,j+1,k} + Q_{i,j,k,k-1} + Q_{i,j,k,k+1}\right) \\ N_{i,j,k}(t) + \Gamma_{i,j,k} - L_{i,j,k}N_{i,j,k}(t) \end{bmatrix}$$

We applied a few assumptions to the scheme formed above then later we'll obtain the three dimensional brain tumor growth equation as:

$$\frac{\partial u}{\partial t} = -\frac{\partial (Pu)}{\partial x} - \frac{\partial (Ru)}{\partial y} - \frac{\partial (Su)}{\partial z} + Q\frac{\partial^2 u}{\partial x^2} + \frac{\partial Q}{\partial x}\frac{\partial u}{\partial x} + Q\frac{\partial^2 u}{\partial y^2} + \frac{\partial Q}{\partial y}\frac{\partial u}{\partial y} + Q\frac{\partial^2 u}{\partial z^2} + \frac{\partial Q}{\partial z}\frac{\partial u}{\partial z} + \Gamma - Lu$$

We applied the explicit method finite-difference scheme to perform discretization of the model and obtain the discretized model as:

$$\frac{N_{ij}(t+\Delta t) - N_{ij}(t)}{\Delta t} =$$
$$\begin{bmatrix} [P_{i-1}^{j}N_{i-1,j,k}(t) - P_i^{j}N_{ijk}(t)] + [R_i^{k}N_{i,j-1,k}(t) - R_i^{j}N_{ijk}(t)] \\ +[S_i^{k-1}N_{i,j,k-1}(t) - S_i^{k}N_{ijk}(t)] + [Q_{i-1}^{k}N_{i-1,j,k}(t) - (Q_{i-1}^{k} + Q_{i+1}^{k})N_{ijk}(t) \\ +Q_{i+1}^{k}N_{i+1,j,k}(t)] + [Q_i^{j-1}N_{i,j-1,k}(t) - (Q_i^{j-1} + Q_i^{j+1})N_{ijk}(t) \\ +Q_i^{j+1}N_{i,j+1,k}(t)] + [Q_i^{k-1}N_{i,j,k-1}(t) - (Q_i^{k-1} + Q_i^{k+1})N_{ijk}(t) \\ +Q_i^{k+1}N_{i,j,k+1}(t)] + \Gamma_{ijk} - L_{ijk}N_{ijk}(t) \end{bmatrix}$$

THREE DIMENSIONAL PARABOLIC EQUATIONS

There are two systems considered for a three dimensional parabolic equations, which are Cartesian coordinates and cylindrical polar coordinates.

However, in this study we are only interested to fine the approximations using the Cartesian coordinates systems.

Generally, one can write the weighted finite difference approximations to the three dimensional parabolic equations as:

$$\frac{\partial^2 u}{\partial x^2} + \frac{\partial^2 u}{\partial y^2} + \frac{\partial^2 u}{\partial z^2} = \frac{1}{(\Delta x)^2}\left[\theta(\delta_x^{\,2} + \delta_y^{\,2} + \delta_z^{\,2})u_{i,j,k}^{(p+1)}\right]$$
$$+(1-\theta)(\delta_x^{\,2} + \delta_y^{\,2} + \delta_z^{\,2})u_{i,j,k}^{(p)}$$
$$= \frac{1}{(\Delta x)^2}[\theta(u_{i-1,j,k}^{(p+1)} + 6u_{i,j,k}^{(p+1)} + u_{i+1,j,k}^{(p+1)} + u_{i,j-1,k}^{(p+1)} + u_{i,j+1,k}^{(p+1)}$$
$$+u_{i,j,k-1}^{(p+1)} + u_{i,j,k+1}^{(p+1)}) + (1-\theta)(u_{i-1,j,k}^{(p)} + 6u_{i,j,k}^{(p)} + u_{i+1,j,k}^{(p)}$$
$$+u_{i,j-1,k}^{(p)} + u_{i,j+1,k}^{(p)} + u_{i,j,k-1}^{(p)} + u_{i,j,k+1}^{(p)} + O((\Delta x)^2 + (\Delta y)^2 + (\Delta z)^2)$$

For our Brain tumor's three-dimensional parabolic equation, the mathematical simulations in C programming for the weighted finite difference approximations to the problem is developed as follows:

```
lelaran1=0;
round=2;
dt=1.5;
count=0;

for (jt=1;jt<=round;jt++) /*start jt loop */
{
   dt=dt+1.5;
   count=0;
   j1=tol;

   for(ijk = 0; (ijk < TIMESTEP)andand(j1>=tol) ; ijk++) /*start
   TIMESTEP*/
   {
                lelaran1++;
                count++;

for(i=start;i<=end;i++)
{
   for(j=1;j<=n;j++)
     {
        for(k=1;k<=h;k++)
          {
            if((i+j+k)%2==1) /*ganjil*/
            {

                Tjjnew[i][j][k] = Tjj[i][j][k]+dt*(-(P[i][j][k]+R[i][j][k]
                                  +S[i][j][k]+Q[i-1][j][k]+Q[i+1][j][k]+
                                  Q[i][j-1][k]+Q[i][j+1][k]+
                                  Q[i][j][k-1]+Q[i][j][k+1]+L[i][j][k])*
                                  Tjj[i][j][k]+(P[i-1][j][k]+Q[i-1][j][k])*
                                  Tjj[i-1][j][k]+Q[i+1][j][k]*Tjj[i+1][j][k]+
                                  (R[i][j-1][k]+Q[i][j-1][k])*Tjj[i]
                                  [j-1][k]+Q[i][j+1][k]*Tjj[i][j+1][k]+
                                  (S[i][j][k-1]+Q[i][j][k-1])*Tjj[i][j][k-1]+
                                  Q[i][j][k+1]*Tjj[i][j][k+1]+G[i][j][k]);


              }}}}

if (left != 0)    {
                  pvm_initsend( PvmDataDefault );
                  if(start%2==1)
        pvm_pkdouble( andTjjnew[start][1][1],m*(madd+2)/2, 2 );
                  if(start%2==0)
                  pvm_pkdouble( andTjjnew[start][1][0],m*(madd+2)/2, 2 );
                  pvm_send(left,10 );
               }

if (right != 0)  {
                  pvm_recv(right,10);
                  if((end+1)%2==1)
                  pvm_upkdouble( andTjjnew[end+1][1][1],m*(madd+2)/2, 2);
```

```
            if((end+1)%2==0)
            pvm_upkdouble( andTjjnew[end+1][1][0],m*(madd+2)/2, 2);
            pvm_initsend( PvmDataDefault );
    if(end%2==1)
            pvm_pkdouble( andTjjnew[end][1][1],m*(madd+2)/2, 2 );
            if(end%2==0)
            pvm_pkdouble(  andTjjnew[end][1][0],m*(madd+2)/2,  2  );

            pvm_send(right,20 );
    }

if (left != 0)    {
                    pvm_recv(left,20);
                    if((start-1)%2==1)
                    pvm_upkdouble( &Tjjnew[start-1][1][1], m*
                    (madd+2)/2, 2 );
                    if((start-1)%2==0)
                    pvm_upkdouble( andTjjnew[start-1][1][0],m*
                    (madd+2)/2, 2 );

            }
```

SEQUENTIAL ALGORITHM ANALYSIS

Based on the computation of present sequential programming, below is the time execution for 1 CPU using time h, No. of iteration and the convergence (stopping criteria) in LINUX environment (Fig. 3).

Flow chart of the parallel programming on distributed computing platform shown in Fig. 4.

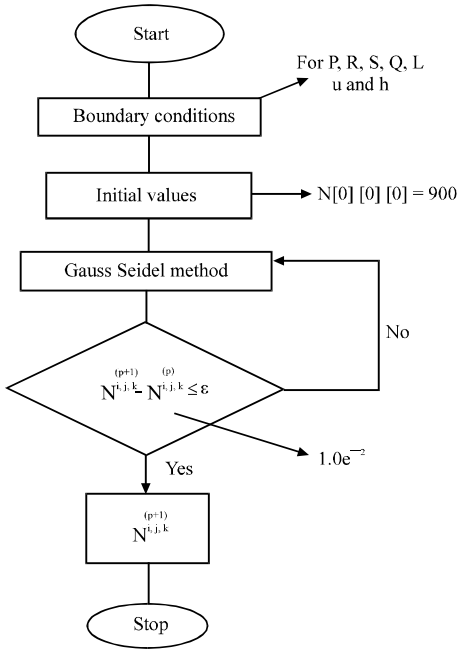

Fig. 3: The time execution for CPU. No. of CPU = 1. Time execution (sec) = 85.713708, No. of iteration = 200 and Convergence (stopping criteria) = 2.3911e-2

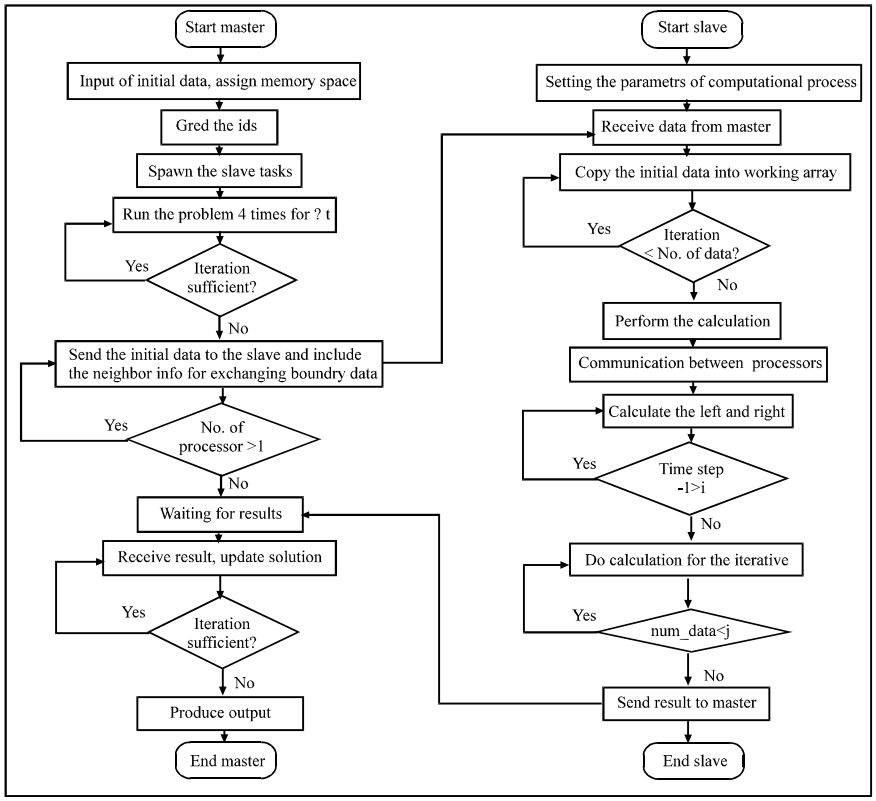

Fig. 4: Flow chart of the parallel programming on distributed computing platform (Parallel algorithm analysis)

THE VISUALIZATION OF THE BRAIN TUMOR GROWTH

The growth rates increase in the first 24 days consistently. After 24 days, the tumor cells become highly active in evolution. The tumor cell will grow more than 1000 cells after 30 days (Fig. 5).

By data experiment, the values used in solving the mathematical problem are:

- Drift coefficients of P R and S are 10^{-5}, 10^{-7} and 10^{-9}, respectively, while the diffusion coefficient, Q is 10^{-3}
- For each of the proliferation coefficient, Γ and death coefficient, L the values which have been taken are 10^{-2} and 10^{-8}

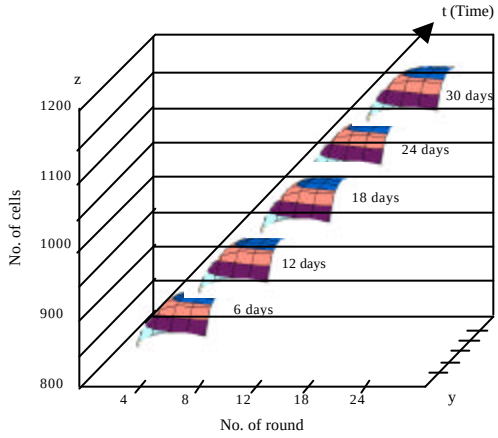

Fig. 5: Growth rate of brain tumor cells day by day

A heat capacity of 3000 J kg^{-1} °C and a density of 920 kg m^{-3} were used for both normal and cancerous tissue. The metabolic heat generation was 450 W m^{-3} and blood perfusion rate for normal tissue was considered to be 0.00018 mL/sec/mL and in the case of cancerous tissue, values of 29,000 W m^{-3} and 0.009 mL/sec/mL were used to account for the higher blood perfusion rates and metabolic heat generation, respectively. An effective thermal conductivity of 0.42 W m^{-1}, as estimated by Gautherie (1980) was used for both normal and cancerous tissue.

With COMSOL Multiphysics, we performed Finite Element Method simulations, a heat transfer coefficient of 5 W m^{-2} K was used as a convective boundary condition at the skin surface to account for natural convection.

RESULTS AND DISCUSSION

The 3D problem has been solved with numerical discretization scheme in this study (Fig. 6). The distinctive values for tissue properties and other parameters are applied as given by Gautherie (1980). The internal tissue temperature usually tends to stable within a short distance, as established in many studies (Gautherie, 1980). The distance between the head core and skin surface will exceed this depth for some particular issues, such as deeper heating, or more intense sources of heat. New bounded core is large enough in this case to abandon the pressure of the surface heating should be integrated into the estimate.

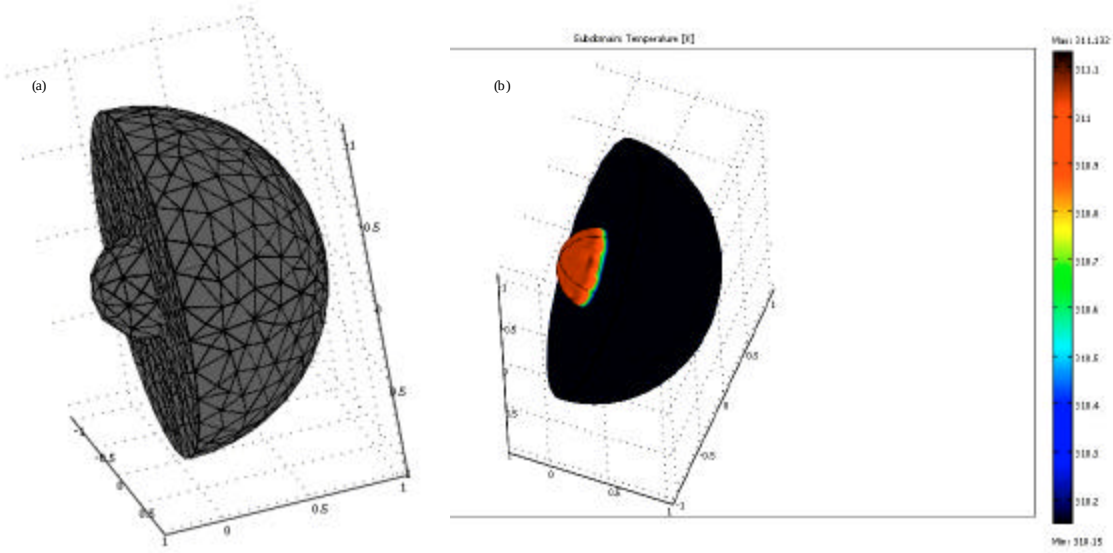

Fig. 6: (a) 3D model of the Mesh of brain tumor and (b) 3D sub-domain model of brain tumor visualization by heat detection

Table 3: Time execution, speedup, efficiency, effectiveness and temporal performances against different number of processors

No. of processor	Time execution (sec)	Speedup	Efficiency	Effectiveness	Temporal performance
1	0.0119850	1.000000	37.45312500	83.43763037	83.43763037
4	0.0025290	4.739027	20.77109875	468.46846580	395.41320680
8	0.0012420	50.649758	11.83382000	1008.36900000	805.15297910
12	0.0001712	70.005840	9.20621975	3076.42510000	5841.12149500
16	0.0001570	76.337580	8.18475670	2369.45610000	6369.42675200
20	0.0000160	83.062500	7.02568890	2298.36000000	6250.00000000

PERFORMANCE STUDY OF THE PARALLEL PROGRAMMING

The results provide engineers with information, data and techniques for fundamental design and analysis. And those will be benefited who needed for highly computational power with powerful performance and high-speed networks. A nice speedup can be obtained for all applications with 20 processors. The reductions in execution time often become smaller when a large number of processors are used. This phenomenon as stated in Amdahl's law, indicates that the number of processors increases, the communication cost (e.g., the latency for massage passing) and the cost for global operations will eventually become dominant over local computation cost after a certain stage. With the efficiencies of the parallel strategies it can able to process a large matrix such as above 100×100×100 grid for 3D.

The output based on the analysis from Table 3, the performance measurements of parallel computing were analyzed from the aspect of time execution, speedup, efficiency, effectiveness and temporal performance.

It shows that the time execution is decreasing when the number of processors increases. This is due to the task from the master had been divided into small parts to the slave. The more processors used mean the more slaves the master can divide its task.

From the speedup analysis in Table 3, when more processors are used, the faster the calculation is being executed.

From the efficiency analysis in Table 3, since the speedup are increasing when the number of processors increase, the efficiency will decrease because the task being done involve some problems with task distributing.

From the effectiveness analysis in Table 3, the effectiveness is increasing until the number of processors reaches 12 processors when it decreases as number of processors goes beyond 12 processors. This might due to some error communication within the processors.

From the temporal performance analysis in Table 3, as the number of processors increase, the overall performance of the parallel programming increase as well and also due to the fact that the temporal performance is inversely proportional to time execution.

CONCLUSIONS

The main aim of this study is being able to visualize the brain tumor growth in three-dimensional space. We had identified the three-dimensional parabolic equation described the brain tumor cells rate on the growth, in time, t and space, x, y and z the physical state of the system. The parabolic equations is derived using the numerical finite difference method and a weighted approximations equations has been formed to obtain the values of the volume of the tumor, $N_{i,j,k}$. To solve the equations, we will use the iterative methods namely Gauss-Seidel method and to do that we had developed the sequential C programming. The Red Black Gauss Seidel GSRB is found suitable for parallel implementation on the parallel virtual machine (Norma and Ping, 2006). Thus a scheme of GSRB also will be implemented in order to solve the equations.

The parallel computing with PVM system is a well suite performance tools in solving the grand challenge of mathematical problem (Norma and Ping, 2006). Therefore in this research, we will construct the parallel programming for the equations and analyze it in terms of its speed up, efficiencies, effectiveness and the temporal performance (Michael Quinn, 1994).

Suggestions would be to use other iterative methods such as Successive Over-Relaxation method (SOR), Alternative Group Explicit (AGE), Iterative Alternating Decomposition Explicit (IADE) method and make comparisons for the accuracy of the data and pre-conditioner method to increase the accuracy and convergence. Besides that other suggestions would be to compare the data with the real data from medical institutions to check the validity of the visualizations obtained in this research. Other than that, suggestions would be to develop a compilation of comparisons and analysis of the brain tumor growth in all three dimensions. This could include the performance of the PVM as well and the speed of convergence system is different range of values are obtained.

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