A Review: An Efficient Approach to Detect and Analyse Heart Tumor Using Parallel Data Modelling

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Abstract:- *The parallel computing systems are widely used in order to enhance and analyze complex systems. The proposed system provides the mechanism to analyze the Heart tumor through the applications of the parallel system. The proposed system utilizes the Gauss seidel method in order to analyze total number of iterations which are required in order to determine the abnormal cell growth within the Heart. The MRI dataset will be used in proposed technique. The parabolic equations will be used in order to determine the position of the cells in the Heart and their growth. The progress of the expectation scheme is the mixtures of the parallel algorithms, open source software on Linux environment and distributed multiprocessor system. The paper ends with a closing observation on the parallel performance assessments and mathematical study in decreasing the execution time, communication cost and computational complexity.*

Keywords: USI, Fundus Images, Heart Tumours, Classification, Deep Learning (DL),Risk Predicion.

1. INTRODUCTION

Cardiac or heart tumours are anomalous and unrestrained explosions of cells or valves. The Cardiac or heart made of neurons cells or valves; these cells or valves are liable for Cardiac or heart usual activities. The Cardiac or heart generally creates new cells or valves only when they are necessary to interchange old or smashed ones. Most cells or valves restore themselves by distributing to make more cells or valves. Usually, this turnover takes place in an organized and precise manner. If, for some reason, the development becomes out of control, the cells or valves will endure to divide, evolving into an inflammation, which is called a tumour. Cardiac or heart tumour can be defined as an unexpected evolution of cells or valves inside the Cardiac or heart or the skull, which can either be cancerous or non-cancerous.

Primary and precise detection of Cardiac or heart tumour is significant for realizing effective remedy and treatment scheduling. However the Diagnosis is a very inspiring assignment due to the huge modification and intricacy of tumour description in images, such as size, shape, location and intensities and can only be accomplished by proficient neuro radiologists. In the contemporary earlier numerous research works have been done for the analysis and treatment of Cardiac or heart tumour. Curing cancer has been a major goal of medical researchers for decades, but development of new treatments takes time and money.

Parallel computing is a type of computation in which many calculations are carried out simultaneously,[1] operating on the principle that large problems can often be divided into smaller ones, which are then solved at the same time. There are several different forms of parallel computing: bit-level, instruction-level, data, and task parallelism. Parallelism has been employed for many years, mainly in high-performance computing, but interest in it has grown lately due to the physical constraints preventing frequency scaling.[2] As power consumption (and consequently heat generation) by computers has become a concern in recent years, parallel computing has become the dominant paradigm in computer architecture, mainly in the form of multi-core processors.

- In the simplest sense, parallel computing is the simultaneous use of multiple compute resources to solve a computational problem:
  - A problem is broken into discrete parts that can be solved concurrently
  - Each part is further broken down to a series of instructions
  - Instructions from each part execute simultaneously on different processors
  - An overall control/coordination mechanism is employed

1.1 Types of Parallelism

Bit-level parallelism

From the advent of very-large-scale integration (VLSI) computer-chip fabrication technology in the 1970s until about 1986, speed-up in computer architecture was driven by doubling computer word size—the amount of information the processor can manipulate per cycle.[21] Increasing the word size reduces the number of instructions the processor must execute to perform an operation on variables whose sizes are greater than the length of the word.

For example, where an 8-bit processor must add two 16-bit integers, the processor must first add the 8 lower-order bits from each integer using the standard addition instruction, then add the 8 higher-order bits using an add-with-carry instruction and the carry bit from the lower order addition; thus, an 8-bit processor requires two instructions to complete a single operation, where a 16-bit processor would be able to complete the operation with a single instruction.

Instruction-level parallelism

A computer program, is in essence, a stream of instructions executed by a processor. Without instruction-level parallelism, a processor can only issue less than one instruction per clock cycle (IPC < 1). These processors are known as subscalarprocessors. These instructions can be re-ordered and combined into groups which are then executed in parallel without changing the result of the program. This is known as instruction-level parallelism. Advances in instruction-level parallelism dominated computer architecture from the mid-1980s until the mid-1990s.

Task parallelism

Task parallelisms is the characteristic of a parallel program that "entirely different calculations can be performed on either the same or different sets of data". This contrasts with data parallelism, where the same calculation is performed on the same or different sets of data. Task parallelism involves the decomposition of a task into sub-tasks and then allocating each sub-task to a processor for execution. The processors would then execute these sub-tasks simultaneously and often cooperatively. Task parallelism does not usually scale with the size of a problem.

2. LITRATURE REVIEW

Breward et al. (2004) [6] proposed a multiphase model which describes the vascular tumour growth in which the blood vessel density is manifestly considered. The model described in this paper is able to produce the image of tumour structure that is found in vivo in certain cases. Their framework can be easily altered to include the effect of other phases. In this paper they present a mathematical model to describe the growth of a vascular tumour.

They suppose that our tumour consists of three phases, namely tumour cells or valves, blood vessels and extracellular material. They formulate their one-dimensional mathematical model by applying conservation of mass and momentum to each of the three phases. They explicitly track the pressure within the tumour, and include vessel death if the pressure the cells or valves exert on the vessel exceeds a threshold value. In this paper they represent graphs showing how the width of the tumour changes with time and how the volume fraction of blood vessels changes through the tumour mass using various variables.

Harpold et al. (2007) [7] presented an historical description of the repetitive comparisons of theory and reality, which have allowed the liberal improvement of a relatively simple bio-mathematical model. In this paper they discussed only gliomas, but there is certainly a important overlap with recent mathematical modelling struggle concerning other cancers. With the inevitable and connected advancements in imaging, it is clear that the progress in modelling will continue to transform our understanding of in vivo tumour dynamics. They believe that increased understanding of tumour growth dynamics will lead to enhancement in the diagnosis and treatment of these diseases.

Norma Alias and Mohd Said (2007) [4] aims on the implementation of parallel algorithm for the simulation of Cardiac or heart tumours growth using one dimensional parabolic equation, designed on a distributed parallel computer system. The result of finite difference approximation using explicit, Crank-Nicolson and fully implicit methods are presented graphically. The implementation of parallel algorithm based on parallel computing system is used to capture the growth of Cardiac or heart tumour. Parallel Virtual Machine (PVM) is considered important as communication platform in parallel computer systems. The parallel performance measurement will be analysed from the look of speedup, efficiency, effectiveness and temporal performance.

Both Crank-Nicolson and the fully implicit method are relevant to capture the real life problem. As a result, they choose Crank-Nicolson method to be applied in the mathematical model to visualise the growth of Cardiac or heart tumour for 30 days. This is because of its stability and accuracy. They used Gauss Seidal Red Black algorithm in solving the finite difference equation to implement parallel algorithm. They proposed that 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 separates arrays among local processors to reduce the communication. The data structure has to be divided where given set of ranges designated to particular processors must be physically sent to those processors for processing to be done.

Wilfred D. Stein et al. (2008) [8] developed the regression expansion equation based on the model that the PSA level decreases exponentially but there is also self-standing exponential regrowth of the tumour reflected in the measured PSA level. PSA is one of the highest quality model for metastatic cancer, and for evaluating new strategies for disease assessment. They explained the use of mathematics to describe tumour kinetics has been widely explored in prostate cancer because of the sensitivity and specificity of the tumour marker PSA.

Two derivations, PSA doubling time (PSA-DT) and PSA velocity (PSAV), have received special attention. The PSA-DT rests on the assumption that increases in PSA follow first-order kinetics and hence an exponential growth curve, so that a plot of the log of the PSA versus time produces a slope that should remain constant provided the patient is not receiving an effective therapy. PSA-DT has been advanced as a method to discern disease aggressiveness. PSA-DT is a mathematical estimate of the rate of tumour growth.

Mahlet Aseefa et al. (2009) [9] developed mathematical models for the growth of gliomas within central nervous system. The model focuses on two key parameters; the spread of glioma cells or valves to tissues within the central nervous system, and the net proliferation rate of glioma cells or valves. According to them, this model considers the location of the tumour within the CNS because tumour cells or valves are known to diffuse at a faster pace in white portion as compared to grey portion. As a result, more accurate prediction of patient's longevity and the time period of tumour's inevitability recurrence can be made.

3. PROPOSED WORK

After reviewing the literature it was found that as we increase the number of processors the efficiency of the system decreases and efficiency is directly proportional to speed up. Mathematical model using the one dimensional parabolic equation regarding the growth of Cardiac or heart tumours has been used in past years. Higher order equation of parabolic and elliptic type could be used for the parallel system optimization in terms of numerical analysis and parallel performance evaluations.

PROBLEM DEFINITION As we increase the number of processors the efficiency of the system decreases so that in order to improve speed and performance we have to use more number of processors as efficiency is directly proportional to speedup. We can also extend the visualization or prediction of human tumour growth in multi dimension parabolic equation.

We try to find out a more accurate prediction of patient's longevity and the time period of tumour's inevitability recurrence can be made. This accuracy will make doctor's to make more accurate diagnosis and treatment of glioma results in extending patient's survival. There are various ways to implement fast numerical simulation under consideration are some explicit methods called IADE, AGE and Brian. Any of this method is chosen as the comparison method.

4. OBJECTIVE

There are following objectives associated with the proposed approach.

1. To study existing techniques to detect heart tumors.
2. To develop an efficient approach to detect heart tumor using parallel data modelling.
3. To implement the proposed approach.
4. To evaluate and compare the proposed approach with existing using following parameters:
   Error rate, Clarity, Detection time.

5. CONCLUSION

From the created environment it is clear that the proposed system is producing better results as compared to the existing system. The simulation is created in MATLAB and charts will be prepared in CHART DESIGNED software tool. The simulations will show that the proposed system will give better results in terms of time and number of infected cells or valves detected. Through the proposed method it will be easy to detect the tumour at earliest stage and hence warn the persons about the disease so that cure can be taken in time.

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