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An Investigation towards Challenges in medical image processing

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Article History	Abstract
Received: Revised: Accepted: CC License	*Imaging is important in today's healthcare since it is used at every stage of the clinical process, from diagnosis and treatment planning to surgery and follow-up investigations. Large data volumes provide issues for medical image processing because most imaging modalities have gone completely digital with ever-increasing resolution. This work, address difficulties in the range of Kilo- to Terabytes related to bioimaging, virtual reality in medical visualisations, bioimage management, and neuroimaging. Algorithms for image processing and visualisation must be modified due to the growing volume of data. With the aid of graphical processing units, scalable algorithms and sophisticated parallelization strategies have been created. This publication provides a summary of them. Although these methods are managing the difficulty from Kilo to Terabyte, the Petabyte level is quickly approaching. Medical image processing is still an important area of study because of this.* ***Keywords:** Image processing, Scalable algorithms, large medical imaging, Visualization of medical.*

Introduction

The term "data" is widely used to describe a wide range of applications across several fields, regardless of the format. The data may take the kind of text, images, audio files, or video clips, for example. Image data is the most widely used sort of data since it better represents the information. The majority of real-time applications, including remote sensing and healthcare, process and analyse data using visual data.

The picture data are ideal for sensitive applications since they are efficient for acquiring, processing, and analysing. Medical pictures are widely used in the healthcare industry to provide improved analytics and diagnosis. Depending on the condition, several imaging methods can be used to provide medical images. Medical professionals examine the medical photos and make the necessary diagnosis. This work focuses on medical picture quality enhancement and Content-Based picture Retrieval (CBIR) systems. Medical image analysis is a broad research area.

Since that medical images directly affect people's lives, improving their quality is extremely important. Basically, factors like noise, low contrast, lighting, and so on have an impact on the quality of photos. The primary problem with medical images is noise, which has a negative impact on any system used for analytical analysis of medical images.

The effectiveness of the image analysis system is dependent on the quality of the medical image, which is of utmost importance. However, when the programme handles a large volume of image data, getting the required image becomes a major challenge. In light of these research concerns, this work uses a Soft Computing (SC) technique to address problems including improving the quality of medical images and retrieving images from a large image collection.

[1] When it comes to automation and optimisation issues, the Soft Computing method is quite important. The need for enormous storage arises from the continuous increase in the use of image data. Finding the necessary data at the appropriate time is therefore crucial. [2] Applications built using the Soft Computing methodology raise the system's efficacy and quality. As previously said, picture quality enhancement and CBIR are two important concerns in the field of medical image processing that are taken into consideration in this research work. [3] The first problem is addressed in the research phase one, while CBIR for medical imaging is covered in the next two stages.

A Medical Image Integrated Possessions Assisted Soft Computing Techniques (MIPSCT) for Optimised Image Fusion is presented in the first phase of this study. [4] The final phase of the research provides a soft computing strategy in digital image processing employing Artificial Neural Networks (ANN) and Genetic Algorithm Framework (GAF). [5] The mid-phase of the research suggests a soft computing assisted heuristic learning approach for the computation of data processing.

[6] Standard performance metrics such the Absolute Mean Error (AME), Peak Signal-to-Noise Ratio (PSNR), accuracy, sensitivity, contrast ratio, matching rate, error rate, selectivity, and so forth are used to assess the performances of all the suggested approaches. [7] The suggested works perform well when the obtained outcomes are compared to the current methodologies.

Examples of large medical imaging

Medical image management and image data mining

PACS is one area where there has been a "explosion" of data obtained. Most clinical modalities, including plain x-rays, CT scans, MRIs, and ultrasounds (US), as well as optical imaging methods like endoscopy and microscopy, have gone digital and are now providing copious volumes of imaging data into PACS systems. [8] The systems have to manage many TB annually, which is considered a logistical challenge. "Information logistics" is the term used in medical informatics to describe the process of getting the correct information to the right location at the right time. [9] In the field of information logistics, several benchmarks have already been accomplished.

However, when it comes to medical images, retrieval from PACS archives is still dependent on alpha-numerical annotations, which can include the patient's name, the date of acquisition, the diagnosis written in natural language, or some research meta-data.

Recent research has also addressed CBIR-PACS integration. [10] CBIR-based techniques are still not available for use in normal radiology procedures today, nevertheless. Lack of (i) translational cooperation between biomedical and engineering experts, (ii) effective representation of medical content by low-level mathematical features, (iii) thorough system evaluation, and (iv) appropriate integration tools are potential barriers to the use of CBIR in medicine.

An online graphical user interface (GUI) built from standardised IRMA input/output (I/O) templates. [11] The IRMA-based application supporting screening mammography is the largest in terms of data volume. It currently contains 10,517 high-resolution digital photographs with replicates in various sample sizes, all annotated using ground truth. [12] Up to 54 MB of uncompressed data can be obtained from a single macrography, depending on the imaging device vendor. The Kilo-to-Terabyte step already applies in this case.[13] Therefore, all performance-related concerns are still outstanding and unresolved. [14] A sophisticated case-based reasoning approach for medical diagnosis and treatment will be made possible by fusing visual information with natural language-based access to medical case records. [15] Thus, the next challenge in medical informatics is to interface image processing with computerised text interpretation.

Bioimaging

For example, a single (3D t)-dataset obtained using fluorescence microscopy can readily contain several gigabytes of raw data. [16] Merely capturing two of these datasets daily results in an approximate annual mean data amount of 1,001 to 1,500 GB, rendering the visual examination of this data unfeasible. Not only are these data logistically challenging to handle, but their sheer number necessitates automated analysis in place of eye inspections. [17] Since biomolecular systems are inherently dynamic, the main difficulty lies in quantitatively and consistently analysing motion.
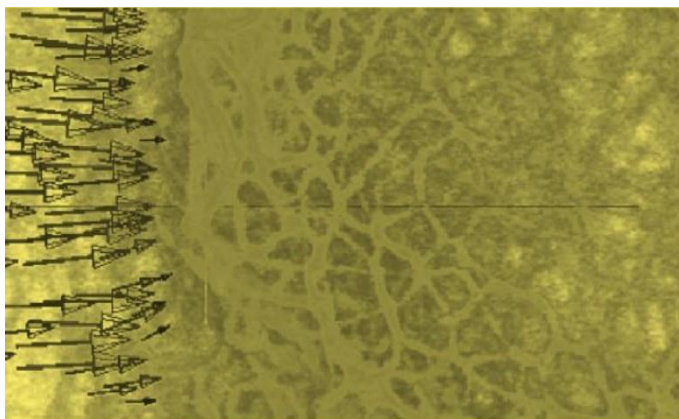

Fig. 1 Cytoskeletal filaments of a living cell superimposed with motion vectors

As a result, many strategies for monitoring molecular or cellular structures have been created; early research in this regard dates back to the 1970s.

Approaches based on cross correlation and particle flow are presented to evaluate polymer transport and turnover in fluorescent speckle microscopy (FSM). Micro-tubule tracking methods include the use of hidden Markov model (HMM) and active contours, as well as speckle-based techniques. In order to track fluorescent structures, a global reduction technique using simulated annealing was devised in. A registration-based technique is devised to trace the continuous translocation of intermediate filaments towards the nucleus (Fig. 1).

Cell motility is influenced by structures known as focal adhesions (FAs). FAs must be tracked and segmented in order to analyse their dynamics. It is common practise to phrase motion estimate as an ill-posed problem. The solution necessitates regularisation using a priori knowledge of the generally predicted features of the motion field in addition to measurements on the picture data.

Virtual reality in the visualisation of medicine

With its primary hypothesis being that better comprehension may be attained faster through the use of real-time, stereoscopic displays and direct user involvement, virtual reality (VR) technology has long been seen as a promising option for a more effective analysis of massive data. Part VII of Hansen and Johnson's Visualisation Handbook provides general overviews of VR-based visualisation. To enable an understandable trial-and-error investigation, interactive data handling is a fundamental idea of VR-based data analysis. The rich user interface that virtual reality (VR) technology offers, allowing us to mix interactive exploration and immersive feeling, is one of this approach's main advantages.

Virtual reality (VR) has gained recognition as a useful tool for analysing simulated technical and physical processes, although attitudes in the medical community are not entirely clear. VR is still relatively new to the practical practise of medical imaging. Speaking with radiologists during interviews revealed that they have received thorough training in the extraction of three-dimensional (3D) information from two-dimensional (2D) slices of CT, MRI, and PET data. Additionally, pre-processing raw data is necessary for the VR presentation of medical pictures, adding a cost element to radiologists' everyday tasks. In contrast, things are very different when it comes to research-related activities. Scientists recognise that virtual reality (VR) can provide valuable insights into intricate and vast medical data. Additionally, VR-based visualisation has demonstrated its influence on interdisciplinary discussions between medical specialists and researchers from other domains.

One example of active research in the medical profession that can benefit from VR-based visualisation and interaction tools is diffusion tensor imaging (DTI). The most sophisticated technique for evaluating white matter fibre routes in a living human brain is currently offered by DTI. In this way, measuring the brain's water diffusivity allows for an estimation of the fiber's path. Each voxel's effective diffusion tensor can be computed using the DTI data. The components of the diffusion tensor can be used to calculate the parameters such as mean diffusivity, principal diffusion direction, or anisotropy of the diffusion ellipsoid. Compared to deterministic tractography, the probabilistic method takes into consideration the degree of uncertainty in the predicted white matter fibre paths and makes it possible to depict the overall fibre architecture of the human brain more clearly.

The domain scientists can directly analyse their findings in three dimensions interactive visualisation of probabilistic fibre tracts (Fig. 2). It is possible to significantly lessen the mental strain that was previously necessary for evaluating 2D slices or for filling in uncertainty information in static charts. In order to allow

for a 3D representation of the fibre tract while still displaying its main orientation and the degree of uncertainty, distinct probability values are coded with different colours and transparency. It is possible to intuitively expose relevant regions of the probabilistic fibre pathways and correlate them with anatomical landmarks by employing specialised 3D visualisation and interaction techniques. This makes it possible to examine the anatomical features right next to fibre networks with greater accuracy. Domain experts have claimed that the visualisation provides far more valuable insight than typical visualisation methods since it combines anatomical information from a reference brain with overlaying fibre tracking results in 3D.
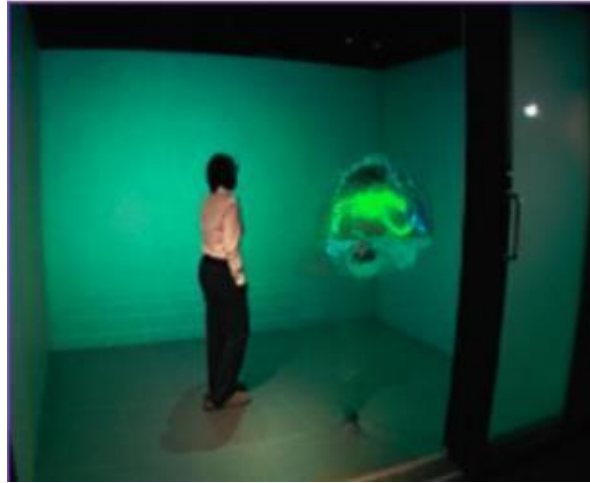

Fig. 2 Interactive exploration of probabilistic tractography data in a CAVE virtual environment

Immersion-based virtual reality technology has become more significant in the last few years. Simulators that are operated on today's high speed computers are getting more and more complex due to their ever-increasing performance. Since most modern simulations are based on erratic 3D processes, standard visualisation approaches are insufficient for analysing them. Because VR technology enables the interactive visualisation and exploratory study of complicated, time-variant computational fluid dynamic (CFD) data directly in 3D space, it holds the potential to streamline this analysis process. Virtual reality (VR) technology has been effectively used in the field of computational engineering research for nearly twenty years. Bryson et al.'s Virtual Windtunnel was among the earliest instances.

One team is studying the aerodynamics of nasal respiration, while the other is studying artificial blood pump computational analysis. Researchers can identify and extract essential flow patterns from their datasets substantially more profitably by using VR for direct engagement with the data in 3D space (Fig. 4) and the Virtual Windtunnel paradigm applied in a cave automated virtual environment (CAVE)-like setting (Fig. 3).
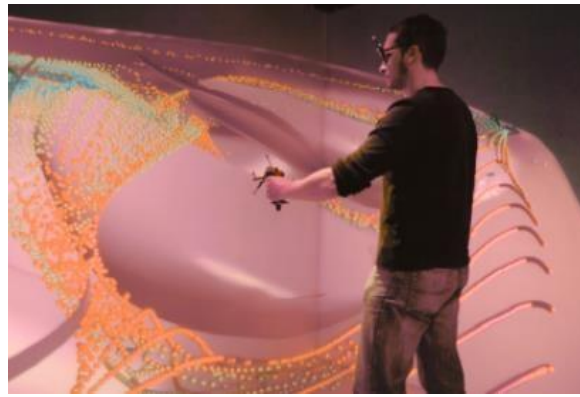
Fig. 3 The Virtual Windtunnel: Interactive exploration of the flow field inside a human nasal cavity by real-time particle tracing in 3D space
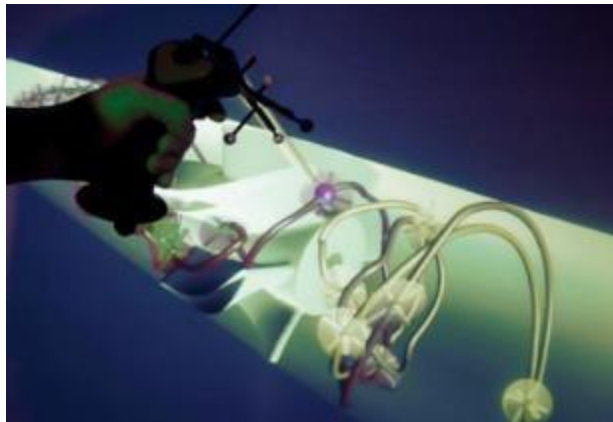

Fig. 4 (*Color online*) Direct interaction with "virtual *red* blood cells"flowing through a simulated artificial blood pump allows an intuitive navigation in space and time. Here, the domain expert picks a particlein order to navigate to a specific point in time

Neuroimaging

1 320 histological cuts produce a fresh data collection of the human brain with a volume reaching to GB. Every incision is 100 µm thick and scanned using 3 569 2 700 pixel polarised light imaging (PLI). When 32 or 8 bits per pixel are used, the total memory for all scanned photos is 47.4 GB or 11.9 GB. Reconstructed nerve fibre routes from PLI scans are stored in an additional large data set. Rebuilding nerve fibres using PLI is similar to DTI. On the other hand, PLI offers an exceptionally high resolution that is currently unattainable using in-vivo methods. Additionally, a microscope is used to scan the polarised histological slices, obtaining many TB of volume per data set. Analysis of the architecture of nerve fibres in the human brain is made possible by micron resolution, which satisfies nerve fibre resolution.

data sets with two different 1D transfer functions

With these massive volumes of data, interactive navigation and visualisation are difficult tasks to do. A specialised 3D navigator has been created to view particular brain regions in real-time alongside the

associated nerve fibre data. A multi-modal approach can be used to integrate PLI scans with interactive visualisation of nerve fibres. This is a combination of several volume data sets. In order to accomplish this goal, several data sets are simultaneously loaded into the memory of the graphics processing unit (GPU) or central processing unit (CPU), requiring memory space for each set. Using two distinct transfer functions, (figure 5) displays a multi-modal ray casting from two volume data sets (MTI and PET from a head) integrated in a single 3D representation. The brain's images are mixed with previously reconstructed neural fibres to create a three-dimensional vision. A three-dimensional representation of the reconstructed nerve fibres from 36 PLI scans of a small brain region measuring $27.39 \times 22.72 \times 3.20$ mm3 is shown in (figure 6)
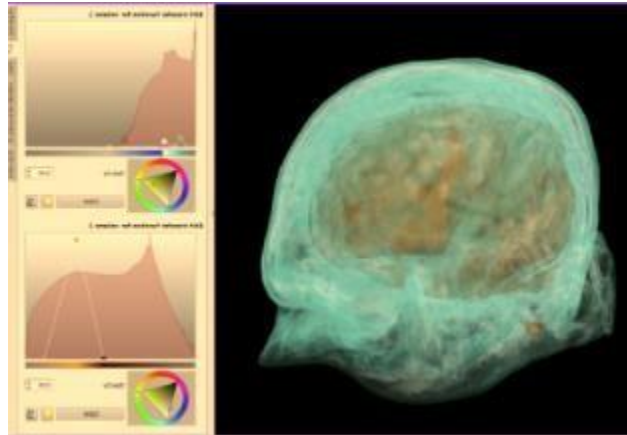

Fig. 5 (*Color online*) Multi-modal ray casting visualization of MRI (*blue*) and PET (*ocher*)
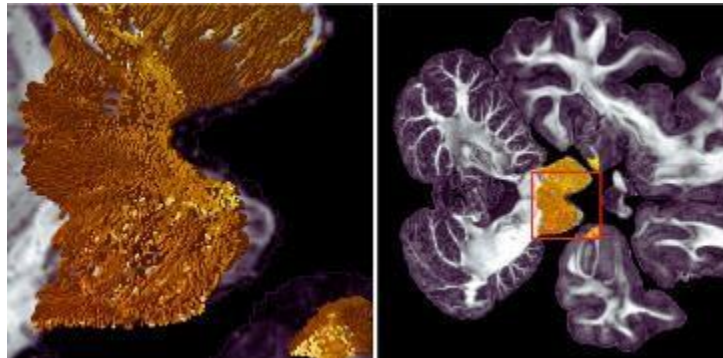

Fig. 6 (*Color online*) 3D visualization of 20 816 reconstructed nerve fibers

Software Strategies for Handling Massive Data

The increasing volume of data necessitates the adjustment of image processing and visualisation methods. The artificial blood pump dataset, for instance, has 30 GB of data total since it has a 3.6 million cell tetrahedral grid for each of 200 time steps. Standard visualisations can easily manage such quantities of

data. But interactive, real-time post-processing and data rendering on immersive, high-resolution displays is a difficult undertaking that calls for the advancement of computer graphics, data management, and improved parallelization techniques. It is anticipated that future datasets in this subject would grow to TB scale.

To shorten processing times and improve memory economy, parallel approaches must be used to create scalable algorithms. Bricking and decomposition were integrated with a hierarchical data structure in recent study.

In this instance, interactive representation of massive volumes of data comprising billions of samples is examined. Various programming approaches are employed for data management: (i) decomposition methods to obtain a multi-resolution subset of the data, (ii) streaming methods to obtain the appropriate viewing data. Volume data is broken down into smaller bricks using decomposition procedures, which are then processed further. Using a streaming method, runtime viewing data is fetched asynchronously. The visualisation pipeline receives only this visible data, and it uses a GPU-based ray casting process to produce the desired 3D view.

Aside from the logistical challenge, the biggest drawback of working with Giga- to Terabyte volume data is the runtime performance. The user is unable to wait for responses from the application. Therefore, in order to achieve a satisfactory real-time response, current research focuses on sophisticated parallelization approaches. Different hardware architectures, involving one or more computers, CPUs, and GPUs, are needed for these techniques. A number of programming languages have been created to facilitate these architectures:

1. By moving the programme from the CPU to the GPU, a number of algorithms have increased in efficiency developments in GPU architecture. This indicates that 240 to 480 massively parallel processing cores on the graphic card are employed in place of four to eight parallel CPUs. The graphic card industry has created a number of languages to write algorithms that run on the GPU, such as:

   - The processing engine found in NVIDIA graphics processing units is called Computer Unified Device Architecture, or CUDA. A C-like programming language called C for CUDA was created specifically for NVIDIA graphics cards.

   - A framework called Open Computing Language (OpenCL) operates on heterogeneous platforms made up of CPUs, GPUs, and other processors. Task-based and data-based parallelism are used by OpenCL to enable parallel computation. The common language for general-purpose programming on any graphics device is called OpenCL.

2. Parallel computing, often known as grid computing, is the process of running several nodes of a cluster of interconnected computers at the same time across a fast local area network (LAN). Special software interfaces, such as the message passing interface (MPI), control the communication between the processes.

Conclusion

Comprehensive programming methodologies have been summarised and current research in medical image management and data mining, bioimaging, virtual reality in visualisation, and neuroimaging has been discussed. Scalable programmes must be created to handle giga- to terabytes of image data and various parallel hardware architectures. With the introduction of contemporary programming languages, such as C for CUDA, OpenCL, and Qt-Threaded, process threading on multiple CPUs and GPUs is now supported. The next stage, which will take us from Tera- to Petabyte, is almost here. Up to 100 TB of data are generated by high-throughput next-generation sequencing for a single study (30 repeats). Whole body MRI is becoming more and more common in translational medical research. Given an eight bit grey scale resolution, 256 256 pixel slices, and 8 mm slice thickness, a single scan will produce roughly 16 MB, and the cohort as a whole will be roughly 3 PB. In the future, managing Tera- to Petabytes of biomedical image data will be a logistical challenge for PACS, CBIR, and HIS. The development of real-time applications that are accepted by doctors will depend heavily on data compression, decomposition, and parallelization techniques.

Abbreviation

CBIR   - Content-Based picture Retrieval

SC   - Soft Computing

MIPSCT   - Medical Image Integrated Possessions Assisted Soft Computing Techniques

ANN   - Artificial Neural Networks

GAF   - Genetic Algorithm Framework

AME   - Absolute Mean Error

PSNR   - Peak Signal-to-Noise Ratio

GUI   - graphical user interface

CFD   - computational fluid dynamic

GPU   - graphics processing unit

CPU   - central processing unit

LAN   - local area network

MPI   - message passing interface

Competing interests

The authors declare that they have no competing interests.

Consent for publication

Not applicable

Ethics approval and consent to participate

Not applicable

Availability of data and materials

Not applicable

Authors' contribution

Author A supports to find materials and results part in this manuscript. Author B helps to develop literature part.

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