

Automated Medical Visualization: Application of Supervised Learning to Clinical Diagnosis, Disease and Therapy Management

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Abstract

The rapid advancement in high performance computing, ultrafast computing, autonomous technologies and complexity of biomedical data for visualization and image guidance play a significant role in modern surgery, redefining the ways in which surgeons perform their surgical procedures. Undoubtedly, several notable efforts have been recorded towards the development of a reliable computer-assisted medical visualization; unfortunately, aligning medical volume visualization applications with Artificial Intelligence features still remains challenging. Brain tumour diagnosis requires an enhanced, effective and accurate 3-D visualization system for navigations, references, diagnoses as well as documentations. With this study, a 3-D, high-performance artificial intelligence-enabled medical visualization framework was designed and implemented using automated machine learning features (AutoML), leveraging the auto-selective capabilities of machine learning to help specialists in the identification of the most appropriate regions of interest with their associated hyper parameters to optimizing performances, while simultaneously attempting to maximizing the reliability of the resulting predictions. C# and Compute Unified Device Architecture (CUDA) within the Microsoft.NET environment, in side-by-side comparison with VB.NET were used for the implementation. The framework was evaluated for rendering processing speed using the brain datasets obtained from the Department of Surgery, University of North Carolina, United States. Interestingly, the framework achieves 3-D visualization of the human brain, reliable enough to detect and locate possible brain tumour within high interactive speed and accuracy. Furthermore, in comparison with other previously proposed medical visualization systems, the framework was able to significantly highlight automatically, with greater accuracy, the features in brain datasets without any manual intervention.

Keywords: Brain Tumour, Compute Unified Device Architecture (CUDA), Medical Visualization

1. Introduction

Visualization has spanned all the way through a wide continuum of knowledge domain to the path of visual imagery to communicate both abstract and concrete ideas to realization throughout the history of humanity and the creativity that led to the creation of machines that outperform human capabilities in terms of workload, effectiveness, precision, endurance, strength and repetitiveness. Visualization is generally categorized into scientific and information visualization. Scientific visualization has traditionally been playing a role of visually revealing structural and material details so as to help in understanding the scientific phenomena that focuses on physical data such as spatial dataset like airflow simulation, meteorology, human body and earth data, while information visualization focuses on abstract, non-spatial datasets, indispensable and non-physical data such as financial data, bibliographic and statistical data. The aim of visualization is to produce images to communicate message and information visually to users (McMahon & Wallace, 2015).

Volume visualization is the manipulation, representation, modeling, interpretation, rendering, and displaying of complex scientific volumetric datasets of medical image data that used to create two-dimensional (2-D) representations from scalar datasets, defined on three-dimensional (3-D) overview. It usually focuses on single-subject data example, applying visualization techniques to MRI and CT dataset of a single patient for diagnosis, or of a single study participant to explore and transforms large and complex stacks of datasets into effective visual presentations for immediate medical diagnosis and therapy procedures. The target is an automated computer-assisted diagnosis with high precision. The automatic and effective 3-D framework for brain tumour of MR image classification using machine learning for automatic feature extraction and feature selection was to reduce data complexity during the pre-processing stages. Such will in turn assist physicians and neurologists in the interpretation of the possible location, size and shape of the abnormalities or tumours (Adeshina & Hashim, 2016). The need for complete automations in many areas of life is becoming significant as the world is rapidly tilting towards full automation for better precision. Undoubtedly, computer-assisted applications would benefit more in terms of reliability due to unforeseen human-error with full automations of medical visualization applications

2. Related Works

Medical Visualization has been receiving huge contributions and persistent effort towards the development of highly resourceful medical visualization applications. Some studies have solely concentrated on producing quality output through obvious mappings of the brain datasets features; this is to give the medics more assurances of correct diagnosis, while a number of studies concentrated on achieving fast processing. We however, have a few of those studies only focusing on accurate visualization output through automation and also quality of output with fast processing.

In 2013, a volume visualization framework using Compute Unified Device Architecture (CUDA), augmenting the widely proven ray casting technique in terms of superior qualities of images, was developed (Adeshina et al., 2013). The framework was evaluated with 109 MRA brain datasets obtained from the Department of Surgery, University of North Carolina, United States. Uniquely, at a reasonably cheaper cost, SurLens framework achieves immediate reconstruction and obvious mappings of the internal features of the human brain, reliable enough for instantaneously locate possible blockages in the brain blood vessels without any prior segmentation of the datasets.

Kwang et al. (2015) considered many uses of GPU architecture in mobile devices towards providing more realistic image processing, and various high specification features to satisfying users. Apparently, mobile devices have been tremendously developed for fast computing acceleration following the strong parallelism of GP-GPU processing. Kwang's teams, proposed GP-GPU architecture for stream processing architecture which has the advantage of high parallelism useful in enhancing image processing capabilities. High resolution 3-D brain visualization is automatically obtained through brain reconstruction in a template space.

Contributions of Gholipour et al. (2017) would have been a breakthrough but it suffers from low robustness when dealing with pathological brains with spina bifida. The team proposed a Convolution Neural Network (CNN) based on fetal brain segmentation method in a Coarse-to-Fine fashion to reduce false positives and to obtain high-resolution volume reconstruction of MR images of fetuses through automatic fetal brain localization, segmentation and robust reconstruction as well as template-space alignment. This was with the intention of achieving efficient and accurate fetal brain reconstructions for potential clinical translation. Similarly, there have been reported researches on parallelizing segmentation algorithms using GPUs such as the contributions received from Yang and Ranka (2018). The researchers used register combiners to perform thresholding, and basic convolutions on two-dimensional color images. The study achieved GPU implementation with NVIDIA Geforce4 demonstrated a 30% speedup over a CPU implementation on 2.2 GHz Intel Pentium 4 CPU.

A novel method that automatically converts 2-D to 3-D was presented in 2017 (Kanchan & Mathur, 2017). The study achieved the reconstructions using the Multi-Time Frame (MTF) squeeze model and determination of gradient map related to each depth level. Similarly, Bharathi & Vasuki (2018) dealt with the 2-D to the 3-D reconstruction of images using edge information.

The study used the edge information to group the images into coherent regions based on Region of Interest boundary by MTF squeeze function estimation of depth levels. The method was compared with edge, and depth with fusion, and seems better than most of the previously proposed methods. Description of the estimation of depth levels was achieved by using the MTF Squeeze model and determination of gradient map related to each depth level (Sang-Hyun, & Kyung-II, 2015).

Wang and his team presented a medical image segmentation technique based on an active contour model, dealing with the problem of intensity in homogeneities image segmentation (Wang et al., 2020). The group also proposed an automatic feature extraction technique for brain tumour detection based on Gaussian mixture model (GMM) using MR images. In this method, using Principal Component Analysis (PCA) and Wavelet-based Functions, the performance of GMM feature extraction was improved. An accuracy of 97.05% for T1-weighted and T2-weighted images and 94.11% for FLAIR-weighted MR images were achieved.

More recently, there were several attempts towards aligning Deep Learning (Huff et al., 2021), Dual Tree Complex Wavelet Transform and Non-Subsampled Contour Transform (Alseelawi et al., 2022), 3-D Mixed Reality (Wierzbicki et al., 2021) etc into visualization applications. Unfortunately, most of the studies were not able to successfully lure supervised learning seamlessly into medical visualization feature extraction stages. Strategically integrating medical solutions with auto selectivity, using appropriate AI routines and subroutines, would significantly improve the quality of the outputs of the medical visualization solution to a competitive level.

Therefore, this study focuses mainly on improving those original contributions of SurLens Visualization System (Adeshina et al., 2012), also considering all significant efforts towards its improvement afterwards as being documented in Adeshina et al. (2013), Adeshina et al. (2014) and Adeshina & Hashim, (2015) to more resourceful stage.

3. Methodology

The framework was developed using C-sharp (C#) because of its versatility and for the fact that it offers a gentle learning curve. Similarly, due to the C# object oriented ability in the Microsoft.NET ecosystem compared with the VB.NET. Compute Unified Device Architecture (CUDA) is a type of heterogeneous programming platform that involves running code on two different platforms, the host and the device, permitting computational acceleration of intensive applications by leveraging GPU power for the parallelizable portion of the computation. Meanwhile, non-sequential, multi-threaded tasks are executed on the GPU, which then returns its results to the CPU. A GPU has many single cores that allow parallel computations through thousands of cores at the same time. The GPU runtime requirement for both libraries is CUDA and the resulting processing time is usually less compared to running on CPU.

3.1. Data Acquisition

The brain datasets used were originally obtained from the Department of Surgery, University of North Carolina, Chapel Hill, United States, and from the Swedish National Infrastructure for Computing. The datasets were converted into (.vti) format. The datasets run the image data transformation schema, scaled to extent scalar data elements to correlate the intensity values with the array values and fit the data to the projective plane, structure data into model, view, and display coordinate systems.

3.2 Dataset Preprocessing

Data preprocessing is an integral step as the quality of data and the useful information that can be derived from it directly affects the ability of our framework to learn. Therefore, it is extremely important that we pre-processed our data before feeding it into our model. Within this phase, data cleaning, data integration, data reduction, and data transformation were achieved, while data discretization was done to transform the lost variable information during the datasets preparation. The purpose of preprocessing phase is to prepare the data to minimize or eventually eliminate those small data associated with experimental error in a manner appropriate for input classification.

3.3 Volume Rendering

Volume rendering using computer graphics in scientific visualization is a set of techniques used to display a 2-D projection of discretely sampled 3-D data sets. A typical 3-D dataset is a set of 2-D slices acquired by CT, MRI scanners. They are usually acquired in a regular pattern (eg, one slice per millimeter) and have a regular number of pixels.

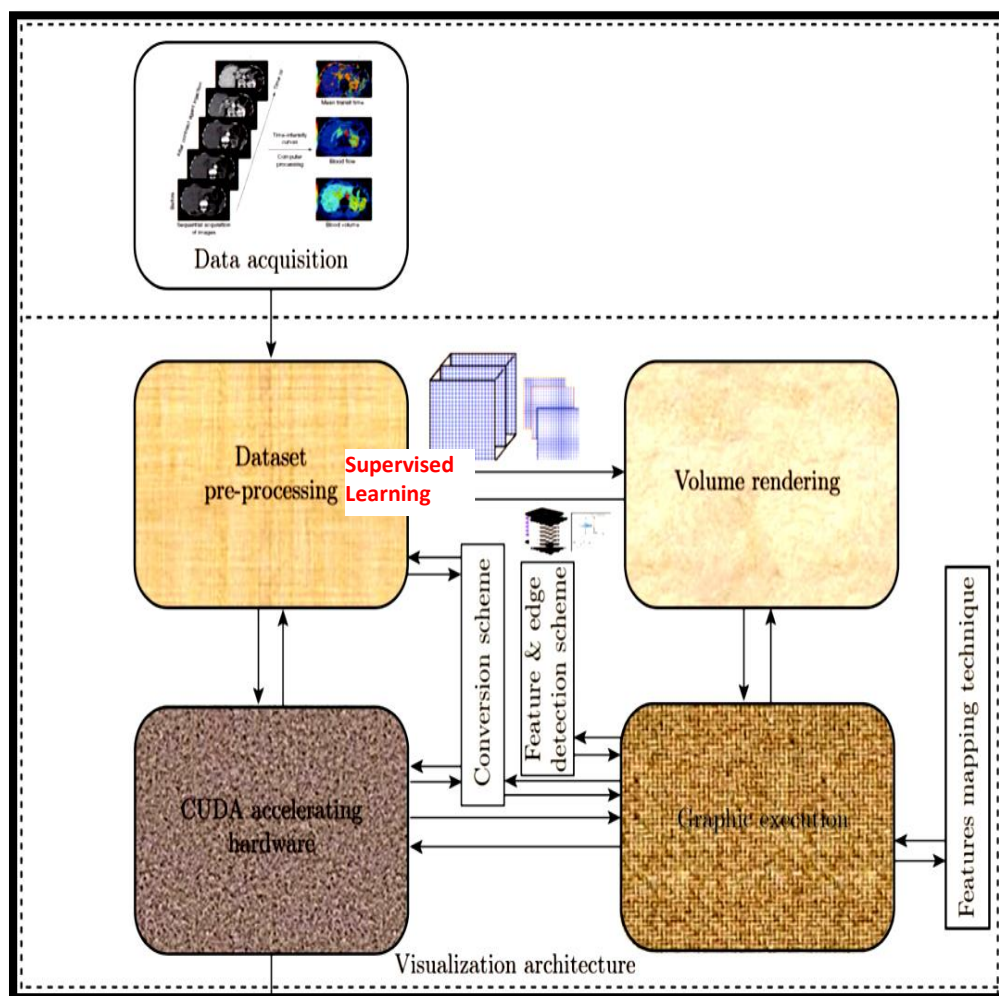


Fig. 3.1: Overview of the Proposed Framework

3.4 CUDA-Accelerated Hardware

Compute Unified Device Architecture (CUDA) is a parallel computing platform designed to work with the Application Programming Interface (API) model. It has proven to be effective in addressing computational overhead in image visualization based on its memory technology, which contains thousands of cores capable of trillions of operations per second. A powerful memory system has a great influence on the performance of volume visualization in transistor power, amplification, switching of electronic signals and power supply. The integration of CUDA in the study is to ensure efficient memory throughput and processing time through simultaneous access of different memory components: shared memory, local memory, and global memory (Adeshina et. al, 2011).

3.5 Graphic Execution

This phase is responsible for analyzing and classifying fragmented data for compatibility purposes. Analyze data for compatibility and map data to a geometric shape. Color mapping and opacity enhancement was done in the classification and sampling stages of this phase, while interpolation and gradient calculation was done in the shading and interpolation stages of the phase.

4. Implementation

The framework was implemented using C-sharp (C#) in a Microsoft .NET environment for easy interaction with other innovative tools, and in comparison, side-by-side with VB.NET development environment on a computer system with an Intel (R) COM (TM) processor. i3-4010 at 1.7GH, 4.00 RAM, 64-bit OS and X64 based-CPU. The Unified Compute Device Architecture (CUDA), which serves as the bedrock for hardware acceleration was integrated to ensure efficient memory bandwidth during the compilation process. The implementation methodology is shown in Fig. 4.1. The framework is AI-enabled using *AutoML* for feature selection, and parameter extraction to produce high-quality 3-D images that are sufficient to reveal detailed information of medical image datasets. It was carefully designed to provide instant insight imaging for clinical diagnosis and aid decision-making procedures. Image guidance and visualization techniques proposed are to aid in the location of regions of interest (tumour location in the brain) for accurate preoperative guidance for enhanced and improved crucial clinical diagnosis and therapy management. Algorithms for each of the phases are presented accordingly.

Phase 1: Data Pre-Processing Algorithm

1. *Begin*
2. *Read the raw dataset from the data store.*
3. *Link pointer to Structural Data Model*
 - 1.1. *Classify datasets*
2. *Link pointer to Display Coordinate Systems*
 - 2.1. *Classify data*
3. *Call class Partition*
4. *Call Class AutoSL*
 - 4.1. *Process Datasets semantically*
 - 4.2. *Process Homogeneously with ROI extracts*
 - 4.2.1. *Process non-overlapping regions using ROI*
5. *End*

Phases 2: Colour Curve Visualization Algorithm

1. *Begin*
2. *Use AI feature*
 - 2.1. *Set colour Curve*
 - 2.2. *Set Opacity*
3. *Sum color*
4. *Cover contributions from the re-sampled locations*
5. *Use colors and opacity*
 - 5.1. *Enhance Volume element*
 - 5.2. *Separate Volume elements*
 - 5.3. *Classify volume elements*
6. *Call the interaction class to display the final pixel color*
7. *End*

Phase 3: 3-D Auto Visualization Algorithm

1. *Begin*
2. *Enter CUDA phaseLink*
 - 2.1. *Fragment data into block(s) with CUDA.*
 - 2.2. *Maximize the memory throughput for orthogonal viewing directions*
 - 2.3. *Analyze data for compatibility use*
 - 2.4. *Estimate surface normals using neighborhood of voxels*
 - 2.5. *Render window with 3-D volume*
3. *End*

Phases 4: Setting Event Interactivity Algorithm

1. *Begin*
2. *Shade and Interpolate*
3. *Setting event with mouse and keyboard*
4. *Establishing relationship with trackball effect*
5. *End*

5. Results and Discussion

The medical imaging systems designed is to transform large and complex datasets into effective visual presentations for immediate medical diagnosis and therapeutic procedures. The proposed framework was tested using datasets acquired using Magnetic Resonance Imaging machine. The tests were performed on a computer with a 4-core Intel® Core i5-8265U processor at 1.6 GHz and 4 GB of system memory. The results of our experiments showed that the proposed framework is able to aid in accurate, timely imaging and detection of brain tumours, and in determining the exact location, size and shape of the tumour, within a reliable and efficient measurements. Therefore, the proposed framework is important for brain tumour detection using MR imaging. The results of the speed experiments are shown in the Table 5.1 , Table 5.2 and Table 5.3.

Diagnosis of a brain tumour is quite difficult due to the variety of shape, size, location and appearance of the tumour in the brain. The overwhelming availability of medical imaging techniques supports the creation of rich information that the radiologists, surgeons, or physicians can analyze for disease diagnosis and therapy management. 3-D imaging technology is rapidly expanding in the field of medical imaging to understanding the anatomy of the brain, and other internal organs, which are easier in 3-D. Experiments were performed and the average speed with the datasets MRA, Normal_MRA, T1-FLASH, Normal_T1-FLASH, T1_MPRAGE, and Normal_T1_MPRAGE were recorded. The time taken in seconds was recorded to observe the difference in rendering processing time of the selected random sample of readings.

The observed rendering processing time was influenced by a number of factors, among which is the number of images, voxel size, physical size, inter-voxel spacing and the ability to overcome the contention of inter-voxel spacing, the level of pixel presence. The nature of the abnormality and their heterogeneous intensity levels are also significant. The pixel sizes depend on both the field of view and the image matrix. Voxel size is related to the

pixel size and the thickness of the slices, an important component of image quality. Many Magnetic Resonance (MR) artefacts are explained using the errors in the underlying spatial coding of the Radio Frequency (RF) signals originating from the image voxels. Tumour and healthy tissue can be well observed using intensity contrast information with a machine learning tool. The difference in tumour size and location of brain tumours varies from slice to slice in different patients. The AI-supported medical imaging system proposed recorded a clearer and more interesting contrast of the brain, and abnormalities and tumours can be identified and isolated from normal cells in the datasets used for the experiments.

Table 5.1: The Result of MRA Datasets for Speed Experiment

S/N	No of images	Voxel Dimension	Physical Dimension	Voxel Spacing	Voxel Speed CPU 4GB	
					2-D	3-D
047_MRA	128	448x448x128 Voxels	230x230x102.401	0.513393x 0.513393x 0.800004	0.3 sec	0.9 sec
054_MRA	128	448x448x128 Voxels	230x230x102.4	0.513393x 0.513393x 0.799999	0.4 sec	0.10 sec
069_MRA	128	448x448x128 Voxels	230x230x102.4	0.513393x 0.513393x 0.800002	0.3 sec	0.9 sec
097_MRA	176	448x448x176 Voxels	180.714x230x140.801	0.513393x 0.513393x 0.800003	0.4 sec	0.10 sec
098_MRA	176	448x448x176 Voxels	180.714x230x140.8	0.513393x 0.513393x 0.800003	0.4 sec	0.10 sec
Normal008-MRA	128	448x448x128 Voxels	230x230x102.4	0.513393x 0.513393x 0.799998	0.3 sec	0.10 sec
Normal105-MRA	176	448x448x176 Voxels	180.714x230x140.8	0.513393x 0.513393x 0.799998	0.3 sec	0.10 sec
Normal108-MRA	128	448x448x128 Voxels	230x230x102.4	0.513393x 0.513393x 0.799998	0.3 sec	0.10 sec
Normal109-MRA	176	448x448x176 Voxels	180.714x230x140.801	0.513393x 0.513393x 0.800003	0.3 sec	0.10 sec
Normal077-MRA	128	448x448x128 Voxels	230x230x102.4	0.513393x 0.513393x 0.800002	0.3 sec	0.9 sec

Table 5.2: The Result of T1-FLASH Datasets for Speed Experiment

S/N	No of images	Voxel Dimension	Physical Dimension	Voxel Spacing	Voxel Speed CPU 4GB	
					2-D	3-D
047 T1-FLASH	178	176x256x176 Voxels	176x256x176	1x1x0.9999999	0.2 sec	0.5 sec
054 T1-FLASH	176	176x256x176 Voxels	176x256x175.999	1x1x0.999996	0.3 sec	0.5 sec
067 T1-FLASH	176	176x256x176 Voxels	176x256x176	1x1x1	0.3 sec	0.5 sec
Norrmal001_ T1-FLASH	256	170x256x256 Voxels	170x256x256	1x1x1	0.3 sec	0.5 sec
Norrmal002_ T1-FLASH	176	176x256x176 Voxels	176x256x176	1x1x1	0.3 sec	0.6 sec
Norrmal004_ T1-FLASH	176	176x256x176 Voxels	176x256x176	1x1x1	0.3 sec	0.6 sec
Norrmal007_ T1-FLASH	176	176x256x176 Voxels	176x256x176	1x1x1	0.3 sec	0.6 sec
Norrmal008_ T1-FLASH	128	176x256x176 Voxels	176x256x176	1x1x1	0.3 sec	0.5 sec
Norrmal009_ T1-FLASH	176	176x256x176 Voxels	176x256x176	1x1x1	0.3 sec	0.6 sec
Norrmal010_ T1-FLASH	176	176x256x170 Voxels	176x256x176.999	1x1x0.999994	0.2 sec	0.5 sec

Table 5.3: The Result of T1_MPRAGE Datasets for Speed Experiment

S/N	No of images	Voxel Dimension	Physical Dimension	Voxel Spacing	Voxel Speed CPU 4GB	
					2-D	3-D
047T1_MPRAGE	128	208x256x256 Voxels	208x256x128	1x1x0.9999 999	0.2 sec	0.4 sec
054T1_MPRAGE	128	208x256x128 Voxels	208x256x128	1x1x1	0.2 sec	0.5 sec
084T1_MPRAGE	160	208x256x160 Voxels	208x256x160	1x1x1	0.3 sec	0.6 sec
Norrmal028_ T1_MPRAGE	128	170x256x256 Voxels	208x256x128	1x1x1	0.2 sec	0.5 sec
Norrmal030_ T1_MPRAGE	128	208x256x128 Voxels	208x256x127.999	1x1x0.9999 94	0.3 sec	0.6 sec
Norrmal031_ T1_MPRAGE	128	208x256x128 Voxels	208x256x128	1x1x1	0.3 sec	0.5 sec
Norrmal035_ T1_MPRAGE	128	208x256x128 Voxels	208x256x128	1x1x1	0.3 sec	0.5 sec
Norrmal036_ T1_MPRAGE	128	208x256x128 Voxels	208x256x128	1x1x1	0.3 sec	0.5 sec
Norrmal037_ T1_MPRAGE	128	208x256x128 Voxels	208x256x128	1x1x1	0.3 sec	0.6 sec
Norrmal039_ T1_MPRAGE	128	208x256x128 Voxels	208x256x128	1x1x1	0.3 sec	0.5 sec

6. Conclusion and Future Work

The rapid advancement of technology in the medical community requires greater efforts for easy availability and interoperability with other revolutionary tools. Imaging research focuses on the development of new techniques for preoperative planning and intra-operative guidance, as well as clinical diagnosis. The purpose of visualization is to create images that convey both abstract and concrete messages. In medical imaging, especially neurosurgery, computed-assisted medical solutions are resourceful in locating areas of interest such as tumour, eloquent areas, blood vessels, among others in relation to each other. Due to the fact that human brain is very complex, analyzing the structure of tumours in this area is a difficult process, and tumour detection is a challenging task due to intensity overlap between tumour and normal tissue, deformation of nearby healthy tissues, and large heterogeneity of the tumours in terms of shape, location, size and appearance.

The development of new technologies, especially artificial intelligence and machine learning has a significant impact on the medical field and has provided an important support tool for many medical fields, including medical imaging. In this paper, we proposed, designed and implemented artificial intelligence-enabled medical visualization framework for human brain structure visualization using a supervised machine learning (*AutoML*) facilitating automatic feature selection and feature extraction for edge detection within a volume using parallel computing capability. In the supervised *AutoML* used, the classifier automatically separates healthy from unhealthy tissues with sufficient resolution to distinguish tumours from its background.

Compute Unified Device Architecture (CUDA)-enabled GPUs and their supporting architecture have been used to accelerate compute-intensive applications by leveraging GPU power for the parallelizable portion of the computation. Meanwhile, non-sequential multi-threaded tasks are executed on the GPU which then returns its result to the CPU. The framework also uses RGBA for its gradient to display the visualization with respect to the image density ratio, and was able to correctly map scalar values to opacity and color transfer function to clearly isolate distinct features in the volume as well as contrast agents, to obtain a better delineation of the tumour to be identified so that they are isolated from the normal cell in the datasets. The proposed framework focuses on visualization for brain tumour to visualize the internal structures of the brain in 3-D. This is to be able to clearly study the human brain which will greatly help the radiologist and surgeon for immediate and efficient medical analysis, diagnosis and treatment planning with collaborative speed, high contrast and accuracy for effective visual analysis. Interestingly, our framework achieves instant 3-D visualization of the human brain structure, reliable enough to detect and locate possible brain tumour with high interactive speed and accuracy, automatically.

In future work, further investigations on why certain datasets with the same number of images have slight differences in processing time would be looked into. Furthermore, improving the accuracy of the classification by exploring the selective classifier scheme would be studied. Such study may focus on combining more than one classifier and feature selection techniques with real and clinically-based datasets covering different scenarios.

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