

Locating and Isolating Neurological Disorders in MRI Datasets Using Hardware-Accelerated Delaunay Triangulation

A. M. Adeshina

Faculty of Information Science and Technology, Multimedia University, Malaysia
codedengineer@yahoo.com, am.adeshina@mmu.edu.my (corresponding author)

S. O. Kareem

High Performance Computing Research Laboratory, Nigeria
kareem.so@hpc.com.ng

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ABSTRACT

Parkinson's disease and stroke are among the deadliest progressive neurological disorders affecting movement. Researchers have attributed the increasing prevalence of Parkinson's disease to the aging global population, making it the fastest-growing neurodegenerative disease. Interdisciplinary research in computer science and bioengineering frequently finds alternative and improved techniques that can greatly assist in the diagnosis and management of Parkinson's disease. Studies to date still confirm that Parkinson's disease is challenging to diagnose, as there are no specific tests to confirm the disease, and many symptoms overlap with those of other neurodegenerative disorders, such as essential tremor, a condition that causes involuntary and rhythmic shaking similar to that observed in Parkinson's disease. Connectomes and artificial intelligence have recently been examined for computer-assisted disease diagnosis and therapy management. Connectomes map and analyze neural linkages within the human nervous system, providing a viable approach for diagnosing brain diseases requiring detailed assessment of vascular structures. This study proposes a hardware-accelerated brain connectomic framework for locating and isolating possible neurological disorders in Magnetic Resonance Imaging (MRI) datasets using the Delaunay triangulation algorithm. The framework was implemented using the Microsoft .NET environment, primarily in C# and Visual Basic (VB), and integrated with hardware acceleration for enhanced processing. The connectomic framework was evaluated using Magnetic Resonance (MR) brain images from the Department of Surgery, University of North Carolina, United States, which mostly contained healthy datasets and certain brain abnormalities. Notably, the framework was not only able to successfully depict the connectomes of the datasets but also achieved processing times of less than 17 s for datasets containing more than 300 images. Moreover, the connectomic framework is considered resourceful in revealing the vascular structures in MR brain images, irrespective of the captured neurological disorders, with all features optimized for web and browser compatibility.

Keywords-brain abnormalities; brain diagnosis; connectomes; hardware acceleration

I. INTRODUCTION

Brain structural connectivity describes the physical connections between different brain regions and can be further analyzed using techniques such as Diffusion Tensor Imaging (DTI) and Magnetic Resonance Imaging (MRI). To investigate these connections, Delaunay triangulation can be used to visualize structural connectivity data. First, brain regions of interest are identified, and their coordinates are extracted from the imaging data. These coordinates are then used as inputs for the Delaunay triangulation algorithm, which generates a set of non-overlapping triangles connecting the brain regions. The resulting network can be visualized in multiple ways, such as varying node size or edge thickness to represent connection

strength. 3-D visualizations can also be created to explore the spatial distribution of connectivity within the brain. This study therefore focuses on applying Delaunay triangulation in combination with Compute Unified Device Architecture (CUDA) to accelerate medical image visualization.

Stroke is a leading cause of death worldwide and a major contributor to long-term disability, particularly in developing countries. It results from vascular abnormalities in the brain's veins and arteries, which may arise from malformed, entangled, or ruptured blood vessels, leading to partial or complete disruption of cerebral blood flow. Stroke can be classified as either ischemic or hemorrhagic. Ischemic stroke occurs when arteries are blocked or narrowed by fatty deposits, resulting in

reduced blood supply to the brain, whereas hemorrhagic stroke is primarily caused by high blood pressure and occurs when blood vessels leak or rupture, leading to bleeding into or around the brain. Medical imaging plays a critical role in the accurate analysis and diagnosis of stroke-related brain abnormalities and in assessing neural connectivity in relation to vascular structures. However, some imaging approaches remain limited in their ability to reveal complex relationships between the structural and functional components of brain networks [1].

Neuroimaging is a computationally non-invasive approach used to observe the structure and function of the human nervous system. It is also used for quantitative assessment of brain abnormalities and other brain illnesses. Electroencephalography (EEG), Positron Emission Tomography (PET), and MRI are neuroimaging techniques used to explore and determine various activities in the brain. EEG measures the electrical activity of the brain using metal discs attached to the scalp. It is mostly used in the diagnosis of seizure disorders such as epilepsy. PET uses radioactive substances (tracers) injected into the body to measure metabolic and functional activity in brain tissues, enabling the identification of abnormalities associated with neurological disorders. MRI involves the use of computer systems, radio waves, and magnetic field technology to generate high-resolution images of brain structures and surrounding tissues, with the primary aim of analyzing brain anatomy and identifying abnormalities. PET, as a radiation-based technique, is highly sensitive to physiological and metabolic changes and is widely used in the assessment of brain function and cerebrovascular disorders. To assist neurologists in making accurate and efficient clinical decisions, the construction and visualization of brain networks through the concept of the connectome has been introduced.

A connectome is a term in the field of neuroscience that describes neuronal connections (networks) and the physical wiring or patterns that exist between different regions of the brain and how they communicate. This concept describes the brain as an electronic device, with wires represented by axons and dendrites, whereas the components are neurons, as shown in Figure 1. The connectome focuses on the assembly, mapping, and detailed analysis of neural linkages within the human nervous system. Recently, the connectome has been accepted as a viable method for diagnosing brain diseases that require critical analysis of vascular structures. The vascular structures of the brain can be connected through structural, functional, or effective connectivity. Structural connectivity describes the anatomical connectivity of neurons, which emphasizes physically connected neurons, whereas functional connectivity measures the interdependence of physiological activities across different brain regions. Effective connectivity is the direct influence of one neural entity on another, as well as the causal effect generated by the interaction of these entities. The brain connectome is derived from neuroimaging techniques and further analyzed through various methods, such as network analysis, graph theory, and the Delaunay algorithm (which is the most recent approach) to reveal the topological architecture of the human brain network.



Fig. 1. Brain connectome showing neural connectivity.

Recently, researchers have used advanced neuroimaging techniques to visualize and map complex networks of fiber tracts in the human brain. Authors in [2] used DTI to investigate the organization of white matter fiber tracts in the human brain and their relationship with cognitive function. They found that individual differences in the organization of fiber tracts were related to differences in cognitive performance. Authors in [3] provided a comprehensive review of the different types of white matter fiber tracts in the human brain and their clinical relevance, including their involvement in various neurological and psychiatric disorders. Authors in [4] used a machine learning approach to identify patterns of white matter fiber tract organization in individuals with Autism Spectrum Disorder (ASD) compared to typically developing individuals. They found that individuals with ASD had altered organization of several fiber tracts, including the corpus callosum and the superior longitudinal fasciculus. Authors in [5] used Delaunay triangulation to classify individuals based on their structural connectivity patterns. Similarly, authors in [6] investigated the relationship between white matter fiber tract organization and depression severity in individuals with major depressive disorder. They found that altered organization of several fiber tracts, including the cingulum and uncinate fasciculus, was associated with greater depression severity.

Hardware-accelerated visualization approaches utilize specialized hardware components, such as Graphics Processing Units (GPUs) and CUDA developed by NVIDIA, to support high computing performance, which has been successfully used to improve the performance of computer-assisted medical applications, mainly to speed up the rendering and display of complex visual data [7]. This approach is particularly useful for visualizations that require real-time interactivity or high frame rates, such as 3-D gaming, virtual reality, and scientific simulations. The use of hardware acceleration in visualization involves offloading computationally intensive tasks from the Central Processing Unit (CPU) to specialized hardware components. GPUs are designed to handle large amounts of data and perform parallel processing tasks efficiently, making them well-suited for visualizations that require real-time rendering and interactivity [8]. In neuroimaging, this approach intends to improve the shortcomings of tractography in medical

visualization. Although tractography can offer a higher level of accuracy and valuable information for medical diagnostic procedures, its high complexity and large size still pose significant challenges [7]. The hardware-accelerated approach in visualization has been the subject of numerous studies in recent years. Authors in [9] presented a review of GPU-accelerated visualization techniques and tools for large-scale scientific data. The researchers highlighted different methods and challenges of hardware acceleration in visualization and the limitations of existing techniques. This review covers both academic and industrial applications of hardware acceleration in visualization and provides insight into future research directions. Similarly, authors in [10] conducted a comprehensive survey of hardware acceleration techniques for interactive scientific visualization. The study discussed state-of-the-art approaches, their limitations, and directions for future research. The survey covers various hardware acceleration techniques such as GPU, Field-Programmable Gate Array (FPGA), and Application-Specific Integrated Circuit (ASIC)-based approaches and highlights their advantages and disadvantages. Authors in [11] conducted a comprehensive review of hardware-accelerated rendering techniques for volume visualization, discussing different approaches to hardware acceleration in volume rendering and their impact on performance and image quality. The review also covers different optimization techniques, such as data compression, which can be used in hardware-accelerated volume visualization.

Web technology has revolutionized the field of medical visualization by providing a platform to create interactive and immersive experiences that allow healthcare professionals and patients to explore medical data in real time. Medical visualization generally refers to the process of creating visual representations of medical data such as MRI scans, Computerized Tomography (CT) scans, and X-rays. One of the key benefits of using web technology in medical visualization is that it enables the creation of cross-platform applications that can be accessed from any device with an internet connection. This means that healthcare professionals and patients can access medical visualizations using desktop computers, laptops, tablets, and smartphones. Web-based medical visualization technologies have been shown to improve diagnostic accuracy and reduce the time required for diagnosis [12], alongside several efforts that have contributed to preparing brain datasets for effective clinical diagnosis of brain diseases [8]. Web-based 3-D visualization tools improve surgical outcomes and reduce the time required for surgical planning [13]. Because traditional chart-based tabular representations often fall short in conveying complex data intuitively, web-based real-time solutions are increasingly necessary for healthcare professionals [14].

II. MATERIALS AND METHODS

A. Development Environment

C# and Visual Basic (VB) programming environments were used to develop the application. The Visualization Toolkit (VTK) was used as the rendering engine. Hardware acceleration was achieved by integrating the framework with CUDA.

B. Proposed Framework

The method proposed in this study is classified into three main phases: data acquisition, visualization architecture, and connectomic visualization, as illustrated in Figure 2, which are discussed in the following subsections.

C. Data Acquisition

During this phase, MRI data were collected for conversion into digital numeric values that could be manipulated by a computer to produce anatomical and physiological structures of the brain for research, diagnostics, and treatment purposes. Magnetic Resonance (MR) brain images from the Department of Surgery, University of North Carolina, United States, consisting of about 109 datasets from volunteer patients, were used for this study. Permission was obtained to download and use the datasets for the study. The images were divided into five age groups; each age group (18–29, 30–39, 40–49, 50–59 and 60–74 years) comprised 20 subjects, equally divided by gender, as reported by authors in [15]. The adjunct information that accompanied the datasets served as guidance during the evaluation of the framework. The majority of the subjects were healthy volunteers, whereas a number presented certain conditions such as hypertension, diabetes, Waldenström's macroglobulinemia, stroke, and penetrating brain injury [7].

D. Visualization Architecture

The proposed visualization architecture is divided into four stages, with each stage integrated into one system, as shown in Figure 3. Dataset fragmentation, analysis, and classification to enhance the image before processing are handled within the proposed architecture.

E. Dataset Preprocessing

This phase receives raw data that are susceptible to noise, outliers, and inconsistencies from the database. Preprocessing techniques are responsible for the removal of noise (image artifacts and geometric distortion), improving the quality of images (image artifacts and low contrast), and producing an image suitable for further processing through correction for motion artifacts, adjustment of image intensity, and removal of non-brain tissues. To enhance the reliability of medical images, preprocessing algorithms are expected to transform the datasets into a suitable format by matching intensity values to array values and adapting data to a projective plane [7]. This phase was designed to read the data through an image reader and convert them to Extended Markup Language (XML) image data.

F. Enhancing / Accelerating Hardware

At this stage, the preprocessed data were analyzed to reconstruct the structural connectivity of the brain. This process involves mapping the location and orientation of white matter tracts, identifying functional brain networks, and analyzing the connectivity between brain regions. To ensure efficient memory throughput and reduce processing time, this stage was integrated with CUDA, which has been shown to be efficient in solving the computational overhead in image visualization because of its memory technology that contains thousands of cores, capable of trillions of operations per second.

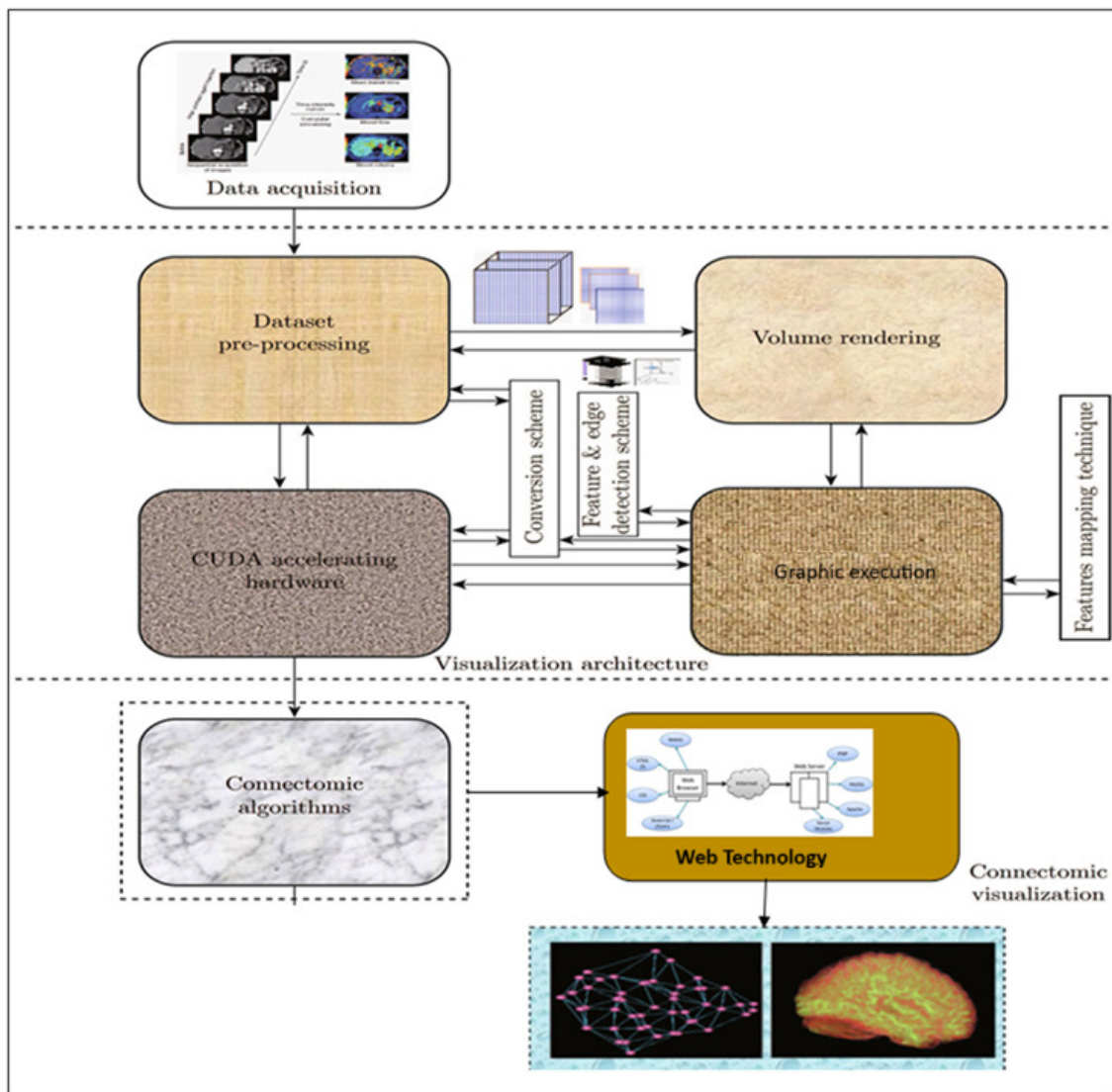


Fig. 2. Connectomic framework.

G. Graphic Execution and Volume Rendering

The essence of this phase was to integrate quality control measures into the process to ensure that the acquired data were of high quality and met the criteria for this study, which involved reviewing the images for artifacts, checking the data for completeness and accuracy, and ensuring that the data met scanner safety criteria. We ensured that the analysis and classification of fragmented data were performed through classification sampling, shading and lighting, composition, and rendered image output for each dataset. Color and opacity mapping were performed at the classification and sampling stages, whereas interpolation and gradient computation were performed at the shading and lighting stages, respectively.

In the graphic execution phase, the Delaunay triangulation algorithm was activated, and codes were developed to transform stacks of 2-D medical data into 3-D visual representations through surface rendering, volume rendering, and virtual endoscopy.

H. Connectomic Visualization

Algorithms for the visualization architecture were employed, and extended connectomic algorithms were used to create brain networks that met the objectives of this phase. Similarly, the Delaunay triangulation concept was applied in developing the connectomic algorithms.

Delaunay triangulation considers the highest point on triangle T , along with two distant points, t_1 and t_2 within the triangle. The study considered two scenarios. The first scenario occurs when t_d is situated within the interior of the triangle. The second scenario occurs when t_d falls on the edge, which necessitates the addition of an edge from t_d to t_k and to the third vertex t_l of the other triangle incident on line $t_i t_j$. This addition splits the two triangles connected to line $t_i t_j$ into four triangles. However, legalizing all edges in this scenario requires edge flipping.

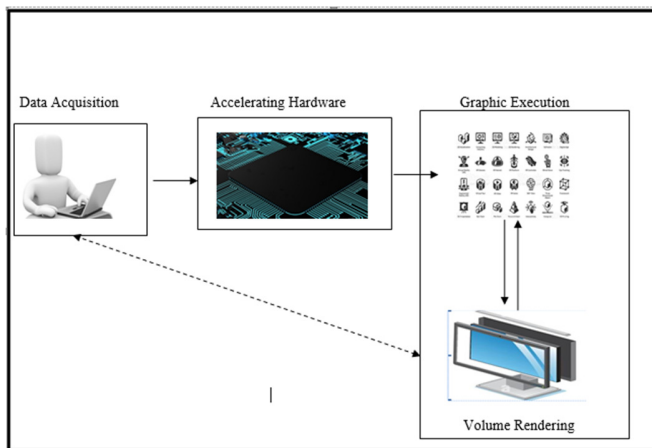


Fig. 3. Visualization architecture.

The algorithm identifies the highest point on triangle T , which is designated as t_0 and located at the rightmost position with the highest y -coordinate. The algorithm then locates the other two points, t_1 and t_2 , which are farthest away from T in the plane and are within triangle $t_0t_1t_2$. The Delaunay triangulation of T with a single triangle is initialized, and a random permutation of t_1, t_2, \dots, t_n is computed. A location within triangle t_d was selected, which may lie either in the interior of the triangle or on its edge, as shown in Figure 4.

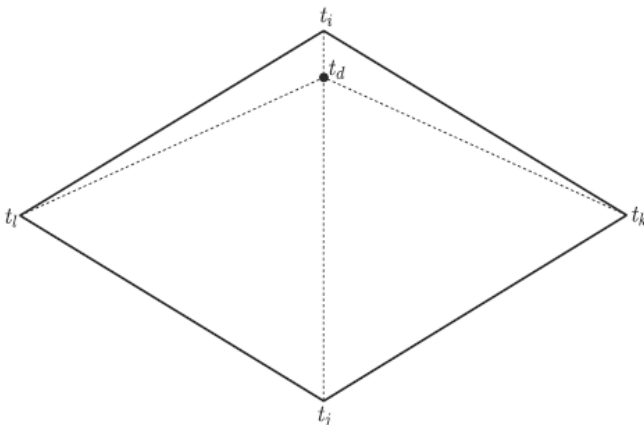


Fig. 4. Location of t_d at the edge of the triangle.

If t_d falls in the interior of the triangle, the triangle $t_it_jt_k$ is split into three triangles by adding edges from t_d to the three vertices, followed by normalization of the edges. However, if t_d falls on the edge of the triangle, the edges from t_d are added to t_k and then to the third vertex t_l , as shown in Figure 4, thus splitting the two triangles incident on line t_it_j into four triangles. The second case also requires normalization by flipping the edges at a later stage.

1. Web-Based Visualization

This phase of the proposed framework focused on a web-based approach for visualizing structural brain connectomes using the Delaunay triangulation algorithm. Web technology has greatly facilitated the sharing and visualization of structural

brain connectome data and the exploration of human brain connectivity patterns. One popular technique for visualizing structural brain connectomes is the Delaunay triangulation algorithm, a computational geometry algorithm that constructs a triangulated surface from a set of points. An overview of this phase is shown in Figure 5.

The following procedures were adopted to ensure that all features in the framework were optimized and compatible with web and browser usage:

1. Acquire brain connectome data: The first step is to acquire structural brain connectome data (or transform 2-D/3-D datasets for use) through any of the neuroimaging techniques; the data can be in any file format.
2. Preprocess the data: The data acquired from step one are processed to remove noise and artifacts and to extract the connectivity information between different brain regions.
3. Represent the data as points: The connectivity information derived from step two is represented as a set of points in 3-D space, where each point represents a brain region and the distance between points represents the strength of connectivity between the regions.
4. Apply Delaunay triangulation algorithm: At this stage, the Delaunay triangulation algorithm is applied to the set of points to construct a triangulated surface, where each triangle represents a connection between two brain regions.
5. Create interactive visualization: At this final stage, the triangulated surface is visualized in an interactive 3-D environment within a web browser. This stage permits the user to enhance the visualization using features such as color coding to represent connectivity strength and highlight specific regions or connections of interest.

Algorithm 1 outlines the main steps for web-based connectomic visualization.

Algorithm 1: Web Connectomic Visualization

- 1.0. Begin
- 2.0. Acquire preprocessed connectome
- 3.0. Preprocess the data
- 4.0. Represent the data as points
- 5.0. Apply Delaunay triangulation algorithm
- 6.0. Create interactive visualization
- 7.0. Display the visualization
- 8.0. End

A visualization architecture that integrates preprocessing, graphic execution, hardware acceleration, and volume rendering using the Delaunay triangulation algorithm is hosted on a server. This server acts as a dedicated platform, managing software applications that respond to requests from clients. It receives incoming network requests from client user agents and sends the processed results back over the internet. The client, which may be a mobile device or a standalone system with a

Network Interface Card (NIC), displays the final output. To facilitate user interaction, the data acquisition phase is performed at the client end, allowing users to input the required datasets through the web-based interface.

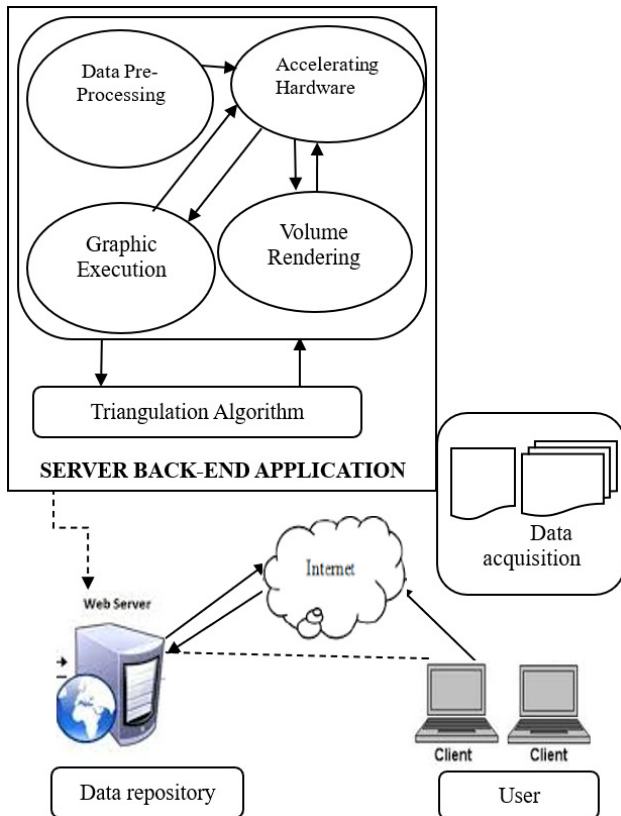


Fig. 5. Web-based connectomic visualization framework.

III. RESULTS AND DISCUSSION

To confirm the performance of our framework, MR brain images from the Department of Surgery, University of North Carolina, United States, containing mostly healthy datasets and certain brain abnormalities, were used for the evaluation. The voxel dimensions are important factors that influence image quality because of their relationship with pixel size and slice thickness. Similarly, the physical dimensions of the datasets determine how the image is displayed on the screen, whereas

voxel spacing provides information about the 3-D spatial distribution of the data.

The output of our experiments, in reference to the performance of our connectomic visualization algorithm in creating nodes from the datasets, is shown in two planes: the raw plane, displaying the 2-D image, and the connectome plane, displaying the 3-D connectome image, as shown in Figure 6(a-i). The rendering process, final output, and processing time were determined based on the dataset specifications, which include the number of images in the datasets, voxel dimensions, physical dimensions and origin, voxel spacing, scalar range, and data size.

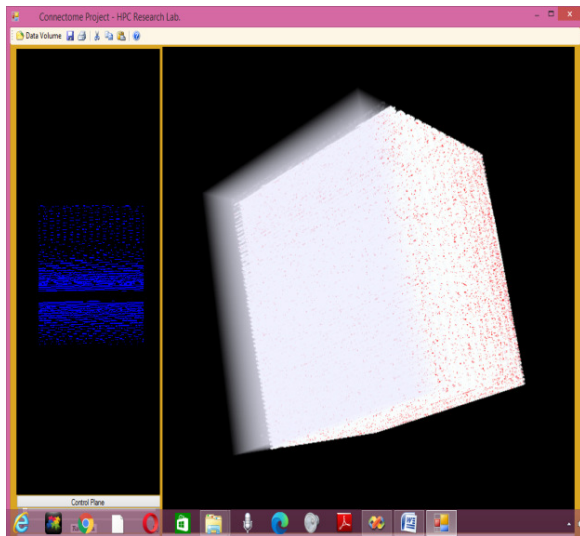
The main goal of this study is to develop a web-based application capable of clearly and efficiently identifying links between brain structures by representing cortical regions as nodes and fiber tract tips as edges. According to the results shown in Figure 6(a-i), the framework is interactive and can produce multiple nodes and edges from a given dataset. Table I presents sample results for the processing time of the datasets with respect to the number of images in the datasets and other relevant information.

Based on the clinical information that accompanied the dataset, the results displayed in Figures 6(a) and 6(i) correspond to normal patients, free from any observable neurological disorder. In contrast, Figures 6(b-f) show patients with minor stroke, asymmetrical head due to suture closure, or tiny intracranial acoustic tumors. The output for the patient shown in Figure 6(g) corresponds to Waldenström's macroglobulinemia, whereas Figure 6(h) is noted to be completely abnormal.

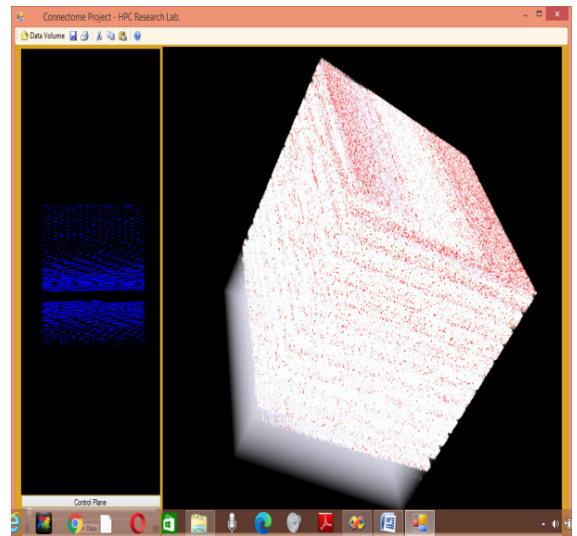
MRI-based connectomics has assisted in the effective analysis of brain connectivity, supporting the understanding of both normal and abnormal brain development and enabling precise surgical diagnosis and treatment. The complete mapping of the neural connections involves two steps: segmentation of the brain region into nodes and identification of connectivity measures that serve as edges in the network. Our framework was evaluated in terms of processing speed, as shown in Fig. 6(a-i), where the Delaunay triangulation algorithm, in conjunction with CUDA architecture, was able to establish network connection nodes and edges for volumetric datasets. The proposed framework is capable of processing 304 datasets in 16.16 s.

TABLE I. PROPERTIES AND PROCESSING TIME OF MRI DATASETS

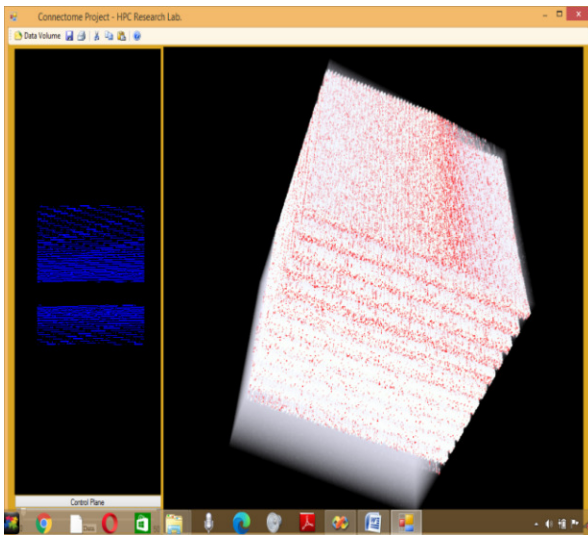
S/N	Number of images	Voxel dimensions	Physical dimensions	Physical origin	Voxel spacing	Scalar range	Data size (B)	Processing time (s)
1	304	256×256×304	256×256×304	0,0,0	1×1×1	0-2,227	2	16.16
2	304	256×256×304	256×256×304	0,0,0	1×1×1	0-2,227	2	12.50
3	304	256×256×304	256×256×304	0,0,0	1×1×1	0-2,598	2	11.96
4	315	256×494×315	256×494×315	0,0,0	1×1×1	0-255	1	14.02
5	304	256×256×304	256×256×304	0,0,0	1×1×1	0-4,095	2	12.75
6	304	256×256×304	256×256×304	0,0,0	1×1×1	0-2,579	2	16.21
7	304	256×256×304	256×256×304	0,0,0	1×1×1	0-1,385	2	11.94
8	351	128×180×351	128×180×351	0,0,0	1×1×1	0-255	1	06.57
9	334	38×159×334	38×159×334	0,0,0	1×1×1	0-0 / 0-255 / 0-71	1	08.06



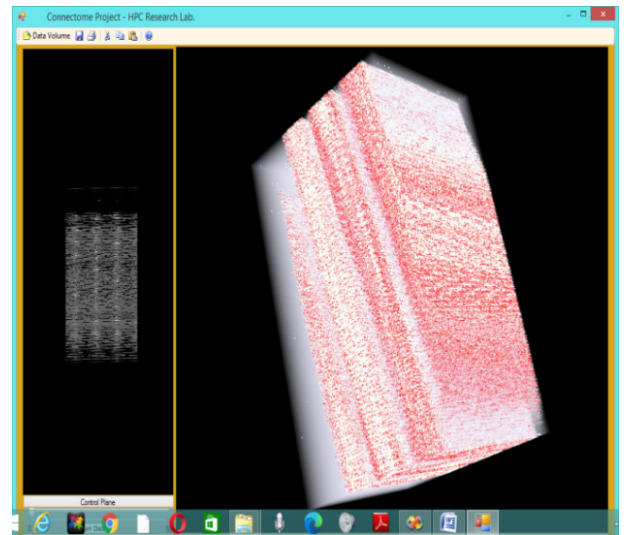
(a)



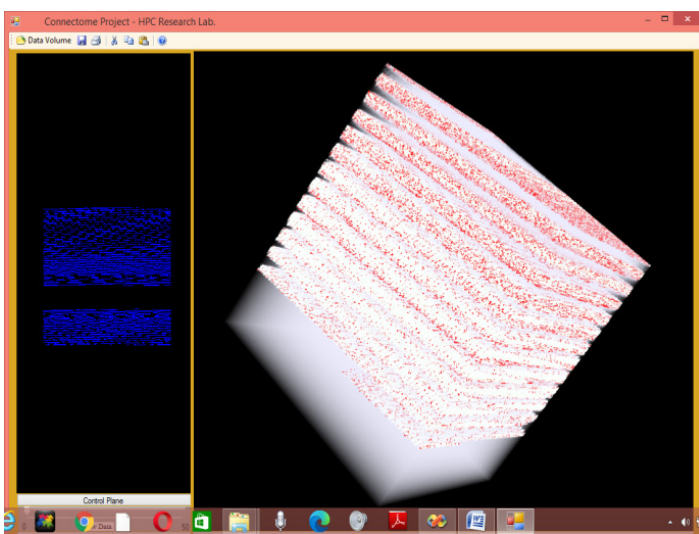
(b)



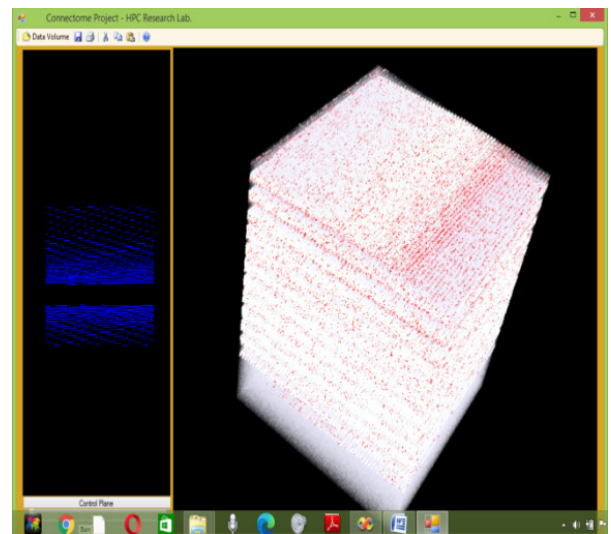
(c)



(d)



(e)



(f)

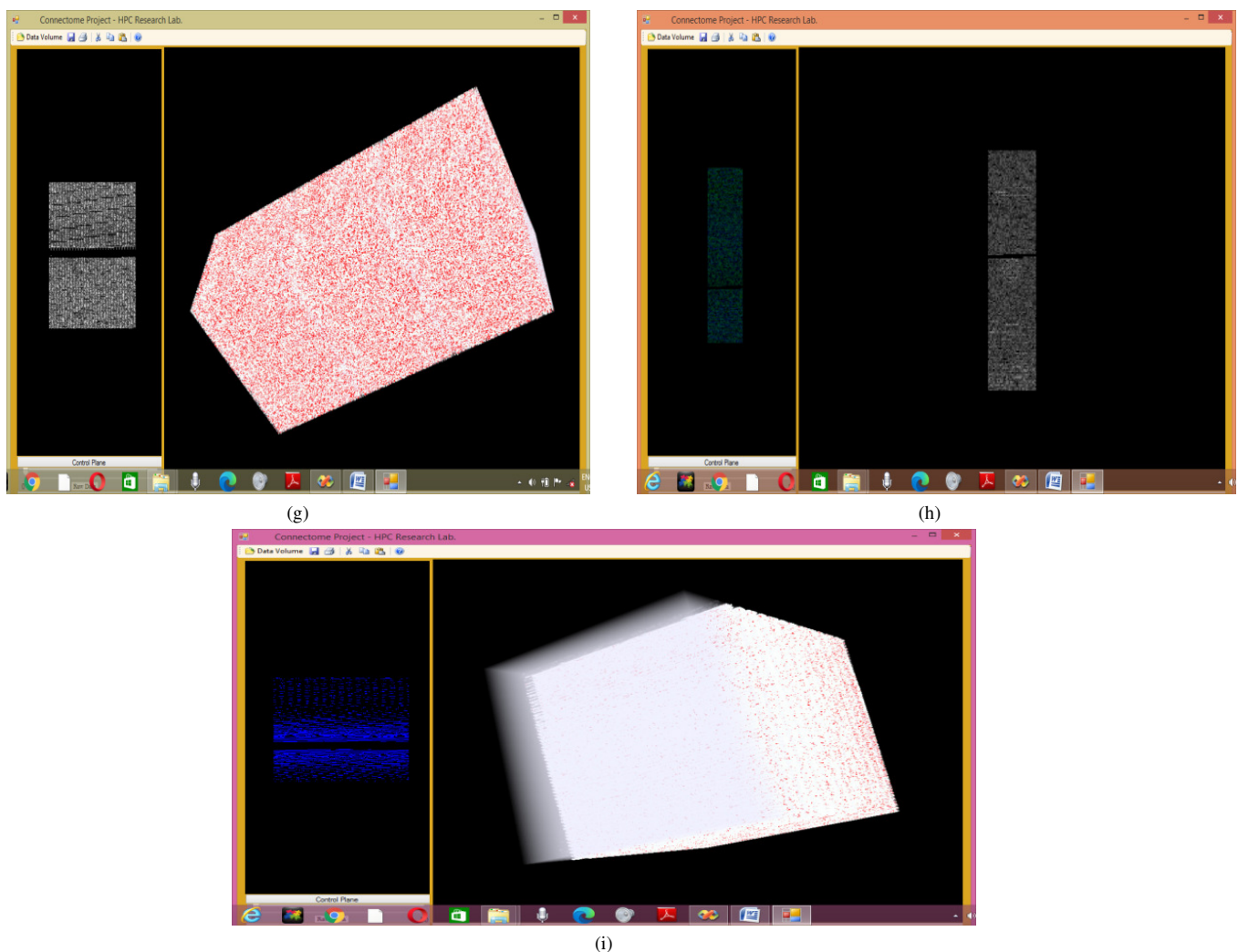


Fig. 6. Representative connectomic outputs of the processed MR datasets

IV. CONCLUSION

Imaging research focuses on the development of new techniques to create images that convey both abstract and concrete information. This study focused on the development of a structural brain connectome using the Delaunay triangulation algorithm. We adopted a web server–client approach to facilitate remote access from distant locations, which represents an improvement compared with previous studies on brain structural connectomes. This web capability can assist in extracting nodes and edges from brain datasets through connected clinical networks, using volume rendering to map these nodes and edges onto the brain surface. To ensure reliability and improve processing time, the framework was integrated with Compute Unified Device Architecture (CUDA) technology, which leverages the high processing capacity of Graphics Processing Units (GPUs). More significantly, compared with previous studies, our framework includes features that facilitate operations such as image bisecting, rotation, and coloration of nodes and edges, providing useful functionality for remote medical systems.

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