FAST PARALLEL VOLUME VISUALIZATION ON CUDA TECHNOLOGY

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ABSTRACT

In the medical diagnosis and treatment planning, radiologists and surgeons rely heavily on the slices produced by medical imaging scanners. Unfortunately, most of these scanners can only produce two dimensional images because the machines that can produce three dimensional are very expensive. The two dimensional images from these devices are difficult to interpret because they only show cross-sectional views of the human structure. Consequently, such circumstances require highly qualified doctors to use their expertise in the interpretation of the possible location, size or shape of the abnormalities especially for large datasets of enormous amount of slices. Previously, the concept of reconstructing two dimensional images to three dimensional was introduced. However, such reconstruction model requires high performance computation, may either be time-consuming or costly. Furthermore, detecting the internal features of human anatomical structure, such as the imaging of the blood vessels, is still an open topic in the computer-aided diagnosis of disorders and pathologies. This study proposed, designed and implemented a visualization framework named *SurLens* with high performance computing using Compute Unified Device Architecture (CUDA), augmenting the widely proven ray casting technique in terms of superior qualities of images but with slow speed. Considering the rapid development of technology in the medical community, our framework is implemented on Microsoft .NET environment for easy interoperability with other emerging revolutionary tools. The Visualization System was evaluated with brain datasets from the department of Surgery, University of North Carolina, United States, containing 109 datasets of MRA, T1-FLASH, T2-Weighted, DTI and T1-MPRAGE. Significantly, at a reasonably cheaper cost, *SurLens* Visualization System 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.

ABSTRAK

Dalam diagnosis perubatan dan perancangan rawatan, pakar radiologi dan pakar bedah bergantung pada hirisan yang dihasilkan oleh pengimbas pengimejan perubatan. Malangnya, kini kebanyakan pengimbas hanya boleh menghasilkan imej dua dimensi. Mesin yang dapat menghasilkan imej tiga dimensi adalah terlalu mahal. Imej dua dimensi yang terhasil ini adalah sukar untuk ditafsir kerana mereka hanya menunjukkan pandangan keratan rentas struktur manusia. Oleh itu, keadaan seperti ini memerlukan doktor pakar untuk menggunakan pengalaman mereka dalam tafsiran lokasi, saiz atau bentuk keabnormalan terutama sekali untuk set data yang besar. Sebelum ini, konsep membina semula imej dua dimensi ke tiga dimensi diperkenalkan. Walau bagaimanapun, model penyusunan semula itu memerlukan pengiraan berprestasi tinggi, sama ada memakan masa atau kos yang tinggi. Tambahan pula, mengesan ciri-ciri dalaman struktur anatomi manusia, seperti pengimejan saluran darah merupakan topik yang masih hangat dalam diagnosis berbantu komputer dan pathologi. Kajian ini mencadangkan, mereka bentuk dan melaksanakan rangka kerja visualisasi dinamakan *SurLens* dengan high performance computing menggunakan Compute Unified Device Architecture (CUDA) menggunakanplatform Microsoft.NET. Sistem Visualisasi ini telah divalidasi dengan menggunakan dataset daripada jabatan Pembedahan, Universiti North Carolina, Amerika Syarikat, yang mengandungi 109 dataset dari jenis MRA, T1-FLASH, T2 Berwajaran, DTI dan T1-MPRAGE. Pada kos yang rendah, *SurLens* Sistem Visualisasi mencapai pembinaan semula serta-merta dan pemetaan jelas ciri-ciri dalaman otak manusia dengan kebolehpercayaan yang tinggi utnuk menentukan lokasi kemungkinan berlaku sumbatan pada saluran darah otak tanpa perlu disegmentasi terlebih dahulu.

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λ -	Scale Factor
$f : \mathbb{E}^3 \rightarrow \Re$; -	Scalar Function
$f^n : \mathbb{E}^3 \rightarrow \Re^n$ -	n-Dimensional Vector Function
$f^{n^k} : \mathbb{E}^3 \rightarrow \Re^{n^k}$, -	A k-Ranked Tensor Function
π -	Plane
π' -	New plane
(S_{k-1}, S_k) -	Optical Depth
τ -	Extinction Coefficient
$[X, Y, Z]^T$ -	Vector Notation
2-D -	Two Dimensional
3-D -	Three Dimensional
ANN -	Artificial Neural Networks
ANSI -	American National Standard Institute
AOH -	Application Oriented Hypothesis
API -	Application Programming Interface
AR -	Augmented Reality
B -	Strength of the Magnetic (field in tesla)
BCC -	Body Centered Cubic
C# -	C-Sharp
CAD -	Computer-Aided Design
Cg -	C for Graphics
CIL -	Common Intermediate Language
Cos_α -	Product of the Vector of Light Source (a negative value)
CPU -	Central Processing Unit
CRT -	Cathode Ray Tube
CT -	Computed Tomography

CTF - Contrast Transfer Function
CUDA - Compute Unified Device Architecture
da - normal
DDR - Double Data Rates
DLL - Dynamic-Link Library
DoD - Department of Defense
DTI - Diffusion Tensor Imaging
DVR - Direct Volume Rendering
$d\Omega$ - Solid Angle
FCM - Fuzzy C-means
FDA - Federal Drug Administration
FDA - Food and Drug Administration
FEM - Finite Element Methods
FFTW - Fastest Fourier Transform in the West
FM - Frequency Modulation
fMRI - Functional Magnetic Resonance Imaging
FPGA - Field Programmable Gate Array
GB - Gigabyte
GLSL - Graphic Language Shading Language
GPGPU - General-Purpose Graphics Processing Unit
GPU - Graphic Processing Unit
h - Planck's Constant
H - Homography Matrix
h - Planck Constants ,
HIPAA - Health Insurance Portabiliity & Accountability Act
HLSL - High Level Shader Language
HPC - High Performance Computing
HSV - Human Visual System
HU - Hounsfield Units
$h\upsilon$ - Energy Carried by Each Photon

I -	Intensity
IV -	Integral Videography
k -	Boltzmann constant
KB -	Kilobyte
kNN -	k-Nearest Neighbour Rule
K_s -	Reflection Constant
L_c -	Light Intensity Curve
LM -	Linear Memory
LMIP -	Local Maximum Intensity Projection
LoD -	Level-of-Details
LUT -	Look Up Table
MDFT -	Multidimensional Discrete Fourier Transform
MIP -	Maximum-Intensity Projection
MPR -	Multiplanar Reformation
MPU -	Multi-Level Partition of Unity
MRA -	Magnetic Resonance Angiography
MRF -	Markov Random Field
MRI -	Magnetic Resonance Images
MRT -	Magnetic Resonance Tomography
MS -	Multiple Sclerosis
ɲ -	Emission Coefficient
n -	Direction
Ň -	Number of Photons
NL-means -	Non-Local Means Modes
NMRI -	Nuclear Magnetic Resonance Imaging
nvcc -	Nvidia CUDA Compiler
NVIDIA -	American Global Technology Company, California
O_c -	Colour Curve of Object
OpenGL -	Open Graphic Language
PCA -	Principal Component Analysis

PET - Positron Emission Tomography

Pixel - Picture Element

PVE - Partial Volume Estimation

R (x,n,υ) - Radiance

RAM - Random-Access Memory

R_c - Resulting Intensity Curve

Regs - Register

RF - Radio-Frequency

RGBA - Red Green Blue Alpha

s - Distance

SIMD - Single Instruction Multiple Data

SIMT - Single Instruction, Multiple Thread

SMs - Streaming multiprocessor

SPECT - Single-Photon Emission Computed Tomography

SPs - Streaming Processors

SVM - Support Vector Machine

SVR - Singular Value Decomposition

s_x, s_y, s_z - Scale Factors along x, y, z axes

T - Temperature measured in Kelvin

T1-FLASH - T1-Fast Low Angle Shot Magnetic Resonance

T1-MPRAGE - T1-Magnetization Prepared Rapid Gradient Echo

TA - Tensor Approximation

Tcl - Tool Command Language

T_s - Transformation Matrix for Scaling

U_i - Points on Plane

U_i' - New sets of points on Plane

V - Vanishing Point

V(x,y,z) - Discrete regular volume buffer

V(x,y,z,d) - Three dimensional data

VDVR - Verifiable Direct Volume Rendering

VTK -	Visualization Toolkit
W_a -	Weight of Ambient
W_d -	Weight of Diffuse
WHO -	World Health Organization
W_s -	Weight of Specular
X, Y, Z -	Coordinates Notation
XML -	Extensible Markup Language
Z -	Ground Plane
α_k -	Opacity
γ -	Gyromagnetic Ratio of the nucleus in rad/T/s
δE -	Radiant Energy interval $d\upsilon$ around dt
θ_k -	Transparency of the Material
υ -	Frequency through a in
χ -	Absorption Coefficient
$\psi(x,n,\upsilon)$ -	Photon Number Density

CHAPTER 1

INTRODUCTION

1.1 Background Study

Throughout the history of humankind, visual imagery is seen as an appropriate way to communicate both abstract and concrete ideas to realization. Visualization is a way of making a form of mental vision, image or picture of something that is not visible, present to the sight or an abstraction, visible to the mind (The Oxford English Dictionary, 1989). Visual images are created through visualization, serving as models through which future things emerge. Some of the ancient uses of visualization are the European cave painting, the introduction of geometry by the ancient Greek and the description of locations in form of map.

Visualization spans through a wide spectrum of knowledge domain, however, it can be broadly categorized into scientific and information. Scientific visualization focuses on physical data such as meteorology, human body and earth while information visualization focuses on abstract, non-physical data such as financial data, bibliographic sources and statistical data (Teyseyre & Campo, 2009).

Volume Visualization is a domain within scientific visualization concerned with the representation, manipulation, modeling and rendering of volumetric datasets. Such volumetric datasets are represented as a 3-D discrete regular grid of volume elements (called voxels), stored in a discrete regular volume buffer V(x,y,z) (Kaufman, 1991). Medicine, Engineering, Geology and Pharmacology are among those fields that are massively benefiting from volumetric datasets. With the evolution of modern

technology, volume visualization has been extensively pushed into many applications, especially with arose consequence production of enormous data from medical community. Such creation of great amount of data has created more challenges and difficulties for the extraction of valuable information, analysis and its explanation in an intuitive way. Undoubtedly, CPU, as a functional processing device has high clock speed, facilitating its competencies for general-purpose tasks, but CPU has no parallel processing capabilities (Qin et al., 2012). Consequently, parallel computing is an alternative promising platform to accelerate visualization of medical volumetric datasets.

1.2 Brain Anatomy and Abnormalities

The relevance of brain in human being cannot be over-emphasized. Whereas, brain does not only exist in human being, it exists as well in other mammals. However, human brain is about three times larger, with around one hundred billion neurons (Kasthuri & Lichtman, 2010). Human brain is the center of nervous system controlling all activities of the human body, from self-control, reasoning, planning to vision, with all features greatly pronounced, enlarged and developed. Skull houses many brain slices. To perceive the complexity of the brain, each of the slices that made up the skull exists in certain measured thickness (ranges from 1 - 5mm) with each slice having distances in-between (ranges from 1 - 5mm) relative to image acquisition device employed.

Blood vessels, blood flows and the fluids surrounding the brain may contain different types of abnormalities. *Vascular abnormalities* may occur in the brain whenever abnormalities involve *arteries* or *veins*. In certain cases, there could be *blockages* in one of the blood vessels in the brain, depriving the brain of its functional flow of blood and oxygen. Vascular abnormalities are deadly medical cases that usually lead to *stroke*. Among other life-threatening abnormal conditions in the brain are *brain lesions*, as a result of abnormal tissue area in the brain, *brain tumor*, *hypertension*, *diabetes*, *walderstrom's macroglobulinemia* and *penetrating brain injury*.

Brain tumor is an abnormal growth of tissue in the brain. It may originate within the brain itself (primary tumor) or from other part of the body and travels to the brain

(secondary or metastatic tumor). While there are about two hundred and twenty (220) types of brain tumor classifications, brain tumor ranges from least aggressive, the benigns, which are non-cancerous, to the most aggressive, the malignants that are cancerous. However, most medical institutions use World Health Organization (WHO) standards for their classification. *Glioblastomas* is a malignant tumor that originates from the brain (primary tumor). Patients with *Glioblastomas* live an average of 12 - 14 months, although the medical communities hope for its medical long-term transfer into a more chronic disease for increase in life span of patients to 10-15 years. However, there is unlikely development of such cure within short expected time frame (Bredel, 2009). In the diagnosing procedures of most of these brain abnormalities, medical community has benefited immensely from the image modalities techniques such as MRI and CT.

Magnetic Resonance Images (MRI) sprung up in few decades ago and its significance is clearly noticed specifically in its ability to assign distinguishing intensity values to different levels of tissue densities. MRI is a non-invasive medical diagnostic technique for imaging human interior anatomical structures. MRI machine signal scans points-by-points into the patient's brain anatomical structures, creating a map, which it captures in *binary codes (1, 0)* and stored as 2-D datasets using mathematical function called *Fourier Transform*. MRI technique utilizes strong magnets and pulses of radio waves to manipulate the natural magnetic properties in the human body. Considering the fact that MRI does not use X-ray techniques unlike CT, there are no known biological risks involved when a patient is exposed to MRI scan. Moreover, it produces better images of organs, soft tissues and the interior structure of bones than those of other brain scanning technologies such as Computed Tomography (CT) and Positron Emission Tomography (PET).

The conventional MRI techniques include *axial*, *coronal* or *sagittal* orientation of *T1-weighted*, *T2-weighted* and *T*2-weighted*. However, a number of specialized MR imagery is available for special purposes. *Magnetic Resonance Angiography (MRA)* is primarily designed for imaging *blood vessels* of the brain, to generate images of the *arteries* for *stenosis (abnormal narrowing), occlusion or aneurysms*. *Diffusion Tensor Imaging (DTI)* is for determination of *magnitude and direction* of water; based on the principle of diffusion, the movement of water molecules from the region of higher

concentration to the region of lower concentration. The *T1-Fast Low Angle Shot Magnetic Resonance (T1-FLASH)* for *glioma tumor* and *lesions*, the *T1-Magnetization Prepared Rapid Gradient Echo (T1-MPRAGE)* which is for detecting *metastatic brain tumors*, are other specialized MR techniques employed in medical diagnosis.

1.3 Motivation

The physical world around us is in three-dimensional (3-D); yet traditional cameras and imaging sensors are only able to acquire and show two-dimensional (2-D) images that lack the depth information (Geng, 2011). The 2-D cross-sectional images produced from imaging techniques such as CT and MRI scanners are generally difficult to analyze. With this, the practice of surgical pathology involving the use of microscope to view tissue mounted on glass slides still persist significantly over many decades. In such usual cases of handling huge information embedded in each pixel of 2-D images, analyzing to deduce the position relationship between focus of infection and three dimensional geometry, estimating size and shape of focus of infection (Wu et al., 2010) usually require mental visualization of medical professionals based on their experience and expertise. This procedure is tedious, time-consuming and prone to error. Figure 1.1 and Figure 1.2 illustrate the conventional pathologist's procedure of analyzing scanned images of patients and the visualization-assisted procedures respectively.

Feature detection and local mapping of internal features are still open topics in the computer-aided diagnosis of biological disorders and pathologies. Although volume rendering has recorded good ability in depicting internal data features, however, locating object boundaries and revealing internal data features of interest are still challenging task due to the usual occlusion of features of interest by other volume structures (Kirmizibayrak et al., 2011; Gabor, Tornai & Cserey, 2010). Implicit visibility of tiny features, through allocation of transparency based on scalar values and assigning of transparency based on localized gradient magnitude for region of interest, are challenging issues. The difficulties of setting proper mapping functions to convert

original volumetric data to renderable color and opacity values limit the application of volume rendering (Guo, Mao & Yuan, 2011).

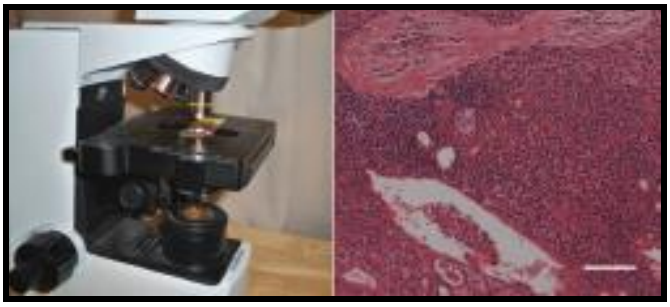

Figure 1.1: Conventional pathologists' slides viewing microscope (Jeong et al., 2010)

Figure 1.2: Clinical support with visualization

Medical visualization systems are developed to transform large and complex stacks of datasets into effective visual presentations for immediate medical diagnosis and therapy procedures. Volume rendering can be implemented to produce quality images, however, this technique still has a major outstanding drawback of "timely" generation of

such images (Yun & Xing, 2010). These medical scanners usually produce hundreds of 2-D slices requiring intense algorithm optimization. A computer-assisted brain diagnosis system that could effectively serve its purpose must be able to achieve not only fast generation of 3-D model of datasets but also the entire streams of datasets' processing within an interactive speed. The promise of computer-based surgical planning is to provide better surgical results with fewer procedures, decreased time in the operating room, lower risk to the patients (increased precision of technique, decreased infection risk), and lower resulting cost (Kumar & Rakesh, 2011).

Most of the previously developed medical visualization systems have shortcomings in:

1. reconstructing 2-D sequence of human organ, soft tissue and lesions sectional images to 3-D model, (Geng, 2011; Wu et al., 2010).
2. detecting, mapping and isolating abnormalities / tumor for surgery and/or disease diagnosis procedure, (Kirmizibayarak et al., 2011; Gabor, et al., 2010; Guo et al., 2011).
3. handling mass data within a considerable interactive speed, extensive application interoperability and at a low resulting cost (Yun & Xing, 2010; Kumar & Rakesh, 2011).

Thus, the main concentration of this study is to reconstruct sequence of 2-D imagery into 3-D model capable of clearly detecting, mapping and isolating abnormalities / tumor in MR imagery within a considerable interactive speed, extensive application interoperability and at a low resulting cost for optimum use in medical diagnosis and therapy treatment.

1.4 Research Questions

This study aims to solve the following research questions:

1. How to reconstruct 2-D sequence of brain MRI into 3-D model?
2. How to detect, map and isolate brain abnormalities / tumor for surgery and/or disease diagnosis procedures?
3. How to handle mass volume of volumetric brain MRI datasets within a considerable interactive speed, extensive application interoperability and at a low resulting cost?

1.5 Research Objectives

The objectives for this research are as follows:

1. To propose new approaches for brain volume visualization by introducing
   - a framework for reconstructing sequence of 2-D cross-sectional images to 3-D model,
   - a feature and edge detection scheme that can allocate transparency based on scalar values and assign transparency based on localized gradient magnitude for edge detection of region of interest in the data volume,
   - a technique with automatic local feature mapping scheme that can isolate abnormalities / tumor and reveal internal features of brain blood vessels,
   - algorithms within the framework that are robust enough to handle mass volumetric data within a considerable interactive speed, extensive application interoperability and at a lower resulting cost.
2. To design and implement a visualization system (*SurLens*) based on the proposed approaches.
3. To compare the volume visualization results of *SurLens* with existing approaches.

1.6 Scope of the Research

This research focuses on the design of *SurLens* framework and the implementation of *SurLens* volume visualization system. The study is limited to reconstructing and locating abnormalities / tumor in Magnetic Resonance (MR) Imagery of the brain in 3-D model. Focus is on obtaining quality 3-D images, sufficient enough to reveal detail internal information of datasets using the MRI datasets from the department of Surgery, University of North Carolina, Chapel Hill, United States. The study concentrates on Magnetic Resonance Angiography (MRA) datasets, however, Diffusion Tensor Imaging (DTI), T1-Fast Low Angle Shot Magnetic Resonance (T1-FLASH) and T1-Magnetization Prepared Rapid Gradient Echo (T1-MPRAGE) would also be considered. The development of the proposed visualization system would be within C# programming language environment, built on top of visualization toolkit (VTK) libraries and on parallel computing platform, Compute Unified Device Architecture (CUDA).

1.7 Organization of the thesis

To disseminate the findings of this research, concise investigation is presented into the field of visualization, human brain anatomy and its associated abnormalities.

In order to properly draw attention of the readers to some of the fundamentals of this research, Chapter 2 commences with general introduction of volume visualization and volumetric image datasets. Datasets pre-processing techniques and medical volume visualization as a whole is reviewed. Parallel processing procedures, specifically CUDA technology and previously proposed software components in this domain are extensively reviewed and presented. Strengths and weaknesses of previously proposed frameworks, schemes, algorithms and techniques are presented. The chapter describes and compares ten (10) recently proposed volume visualization frameworks in their entirety, in justification of the newly proposed framework, schemes, algorithms and techniques in this study.

Chapter 3 discusses the procedural research methodology, numerical computations and data structures used in the development of *SurLens* visualization system. The framework, schemes, algorithms, techniques and data collection for the development of *SurLens* visualization system are presented. Chapter 4 focuses on the designs and implementation of the proposed *SurLens* Visualization system for volumetric brain MRI datasets.

Evaluation results and discussion in comparison with two (2) notable, previously developed visualization systems are presented in Chapter 5 while Chapter 6 concludes the research, summarizes the major contributions of the study and presents the future works.

CHAPTER 2

VISUALIZATION OF VOLUMETRIC DATASETS

2.1 Introduction

Visualization is a phenomenon existing in our day-to-day life. Over a thousand years ago, visualization has been used in the data plots, maps and scientific drawings. As far back as 1137 A.D, visualization was used to draw the map of China and the very famous map of Napoleon's invasion of Russia in 1812 (Owen, 1993). Visualization could be defined as a tool or method for interpreting image data, fed into a computer and for generating images from complex multi-dimensional data sets (McCormick, DeFanti & Brown, 1987). Informally, visualization engages the human vision and the processing power of human mind in the transformation of data or information into visual images referred to as pictures.

Visualization has received many descriptive terminologies over the years. Scientific visualization was first fundamentally used in 1987 (Rosenblum et al., 1994) and its seen as a representation of numerical data in a way that extrapolates meaningful information to understand or analyze interesting feature the data might hold. Data visualization is a more general term that implies treatment of data sources beyond the sciences and engineering. This encompasses marketing, business and financial data. More often, the term information visualization is becoming more pronounced. It is used to describe visualization of abstract information such as hypertext documents on the

World Wide Web, directory or file structures on a computer or abstract data structures (InfoVis, 1995).

Visualization is also seen as a method of extracting meaningful information from complex dataset through the use of interactive graphics and imaging (Kaufman, Cohen & Yagel, 1993), hence, computer graphics and image processing (or imaging) are tools for visualization. Computer graphics is the creation of images using computer, which encompasses 2-D paint techniques, drawing or rendering techniques. The output of computer graphics is an image. With image processing, we can define techniques to transform (rotate, scale, shear), extract, analyze and enhance images. Visualization focuses on exploring, transforming, viewing data as image in order to gain understanding and insight into the data. Computer graphics is used as a tool to produce the output for visualization. However, this study specifically tread the path of volume visualization, which is typically identified with the rendering, modeling, manipulation and representation of datasets (Kaufman, 1991; Kaufman, 1996).

Volume visualization is an important diagnostic tool in modern medicine. With computer imaging techniques such as Computed Tomography (CT) and Magnetic Resonance Imaging (MRI), internal information of a living patient is captured. The information is captured in form of slice-planes or cross-sectional images of patient which could be compared to the conventional photographic X-ray. A slice consists of a series of number values representing the attenuation of X-rays (in case of CT) or the relaxation of nuclear spin magnetization (MRI) (Krestel, 1990). However, with applied and sophisticated mathematical techniques, the slice-planes could be reconstructed and gathered into a volume of data.

Generally, with the slices, the series of number values are arranged in either a matrix pattern or regular array. However, with huge amount of information data in the slice, it is not possible to understand the data in its raw form, even with a trained eye. This is where the gray scale value comes in. Computer only understands 0’s and 1’s, whereas, human being cannot firmly relates the codes to meaningful information, possible solution is to represent the number values in 2-D cross-section that could be more useful with human vision system. Hence, such representation requires understanding the way medical imaging device scans.

This chapter reviews visualization of volumetric datasets and presents earlier frameworks from which medical volume visualization can be facilitated. After outlining broad collection of volumetric data acquisition methodologies, varying volume rendering techniques are described. The chapter extrapolates image reconstruction approaches, direct volume visualization techniques; possible optimization procedures specifically parallel processing approaches and their outstanding issues, which crystalize the research direction for this study. The weaknesses and strengths of each of the previous techniques are discussed. The strengths and weaknesses of ten (10) recently proposed volume visualization frameworks in entirety, including their proposed schemes, algorithms and techniques, are presented and compared in justification of the proposed framework, schemes, algorithms and technique in this study.

2.2 Volume Visualization

Volume visualization is a sub-field of scientific visualization that extracts meaningful information from volumetric data using interactive graphics and imaging, and it is concerned with volume data representation, modeling, manipulation, and rendering (Suter et al., 2011). Volume visualization is an important tool for visualizing and analyzing data sets with its extensive application into such areas as biomedicine, computational fluid, finite element models, computational chemistry and geophysics. Magnetic Resonance (MR) Imagery and Computed Tomography (CT) are both imaging techniques benefiting optimally from volume visualization. Such numerical simulations and sampling devices create images of the human body for clinical diagnosis while volume visualization presents such datasets for viewing and clinical analyzing of the anatomical structures. Over recent years, volume visualization is continually evolving as visualization approaches, especially with the advent of faster processing devices. One of the challenges depriving the usage of volume visualization is the memory system to support volume processing (Suter et al., 2011; Ma, Murphy & O'Mathura, 2012).

Two-dimensional (2-D) data is represented as X and Y axes. These are mere flat structures in horizontal and vertical axes. Any image we have in this form, if turned to

its other sides, will become a line. Hence, a 2-D structure has corners or vertices and sides in two planes and cannot provide detail information embedded in image data. However, the 2-D representation can be re-represented in three-dimension (3-D), using mathematical models which has X and Y planes (just as 2-D image) but a Z-axis inclusive, this gives the image more features such as rotation. This third axis added faces to the 3-D structures, making the data available for real world simulation of the imaged object.

Since, there is a one-to-one correspondence between the pixel value in the image scan and a specific tissue of a patient, the numbers could be assigned a specific gray scale value. Displaying the data on the computer screen at this stage will emerge the structures in the patient's data. The emerged structures are as a result of the interaction of the human visual system with data spatial organization and the chosen gray-scale values. With this approach, its being possible to translate what computer represents as series of numbers into the corresponding cross-section of human body; the skin, the bone and the tissue. A more useful result could be made available for diagnosis by extending the 2-D into 3-D technique. In this case, the image slices are gathered as a volume of data. With 3-D technique, we can reveal the entire anatomical structure of a living patient without the intervention of surgery.

With the inability of the medical image scanners to present human anatomical structures in 3-D format, reconstruction procedure is the alternative. Reconstruction is a reverse engineering technique of 2-D MR imagery to 3-D. This is achieved in the medical diagnosis and disease management using the combination of computer graphics and image processing tools, the resulting 3-D data could serve as information for *opinion making and intervention planning* on a living patient without any prior mandatory surgical operation.

2.3 Volumetric Image Datasets

The first step towards volume visualization is the acquisition of volumetric data. Typical set of data samples is represented as $V(x,y,z,d)$, in the case of a three- dimensional data,

with *d* representing the data property at a location determined by *x,y,z.* To describe value at any *d* continuous location, *zero-order (the Nearest Neighbor), first-order (trilinear also called piecewise function)* and *higher-order interpolation* are possible options. The region of constant value that surrounds each sample in *zero-order interpolation* is known as a *volume cell* (commonly interchangeably referred to as *voxel (volume element)* or *grid location* or *sample points*) with each voxel being a rectangular cuboid having six faces, twelve edges and eight corners (Kaufman, 1996). Dataset is a collection of volume elements. However, there is variation in the spatial and intensity resolution of images produce by different medical imaging devices. This section presents some of the commonly used tools for volume data acquisition.

It is important to discuss the *topology* or *geometry* in which *volumetric data* must be. Data samples may exist as *scalar data*, holding such values as temperature, pressure and density, or exist as *vector* (e.g. velocity) or *tensor* (e.g. Finite Element Methods (FEM) modeling). Typically, a volume dataset *V* is a set of element (Winter, 2002) defined as:

$V = \{ \upsilon_i(x, y, z) \mid i = 1,2,...,n \}$

(x, y, z) is a point in 3-D space, $\mathbb{E}^3$

$\upsilon_i(x, y, z)$ could be scalar, vector or tensor, which is defined as follows:

- a scalar function $f : \mathbb{E}^3 \rightarrow \Re$;
- an n-dimensional vector function, $f^n : \mathbb{E}^3 \rightarrow \Re^n$, or
- a k-ranked tensor function, $f^{n^k} : \mathbb{E}^3 \rightarrow \Re^{n^k}$,

Scalar and *vector* functions are representation of special cases of tensor functions with ranks 0 and 1 respectively. Usually in volume visualization, a total function is given by a physical or simulated object and then sampled at discrete points which is stored as discrete set of elements resulting in the formation of the defined dataset V. Figure 2.1 is the representation of volumetric data in Cartesian grid.

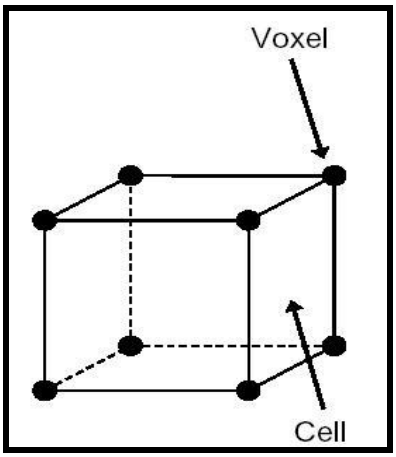

Figure 2.1: Volumetric Data in Cartesian Grid

Speray & Kennon (1990) categorized volume *dataset V* into *structured* and *unstructured* based on the topology of the *dataset*. In line with such categorization, the topology of structured data is well defined in each of its three orthogonal planes. This category includes cartesian, rectilinear and curvilinear grids. Unstructured grids are complex and difficult to use because their structures are not implicitly defined by data arrangements. However, *rectilinear grids* can be defined in *computational space* and classified as being *regular* or *irregular* in structure. If the spacing between samples along each axis is constant along the three orthogonal axes (x, y, z), which is mostly the case, the *dataset V* is called *isotropic.* In certain cases, there might be separation along each axis in the dataset sample but different between the axes, the *dataset V* is referred to as *anisotropic*. Hence, if *V* is defined on a *regular grid*, a *3-D array* (commonly referred to as *volume buffer, 3-D raster or cubic frame buffer*) is used to store the values and *V* is referred to as *array of values* $V(x, y, z)$ defined only at grid locations. Figure 2.2 shows the different data structure grids.

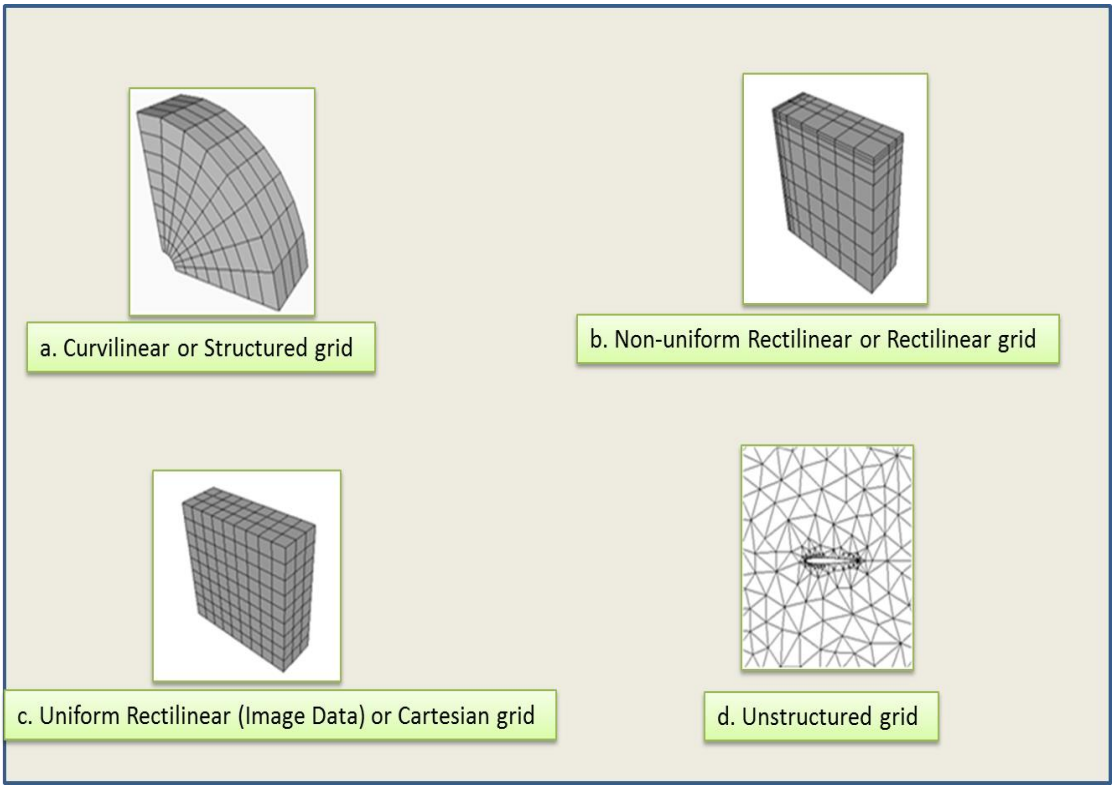

Figure 2.2: Data Structure Grids

2.4 Medical Imaging Modalities

Volume visualization became feasible with the revolution in image acquisition for extensive medical diagnosis and pre-treatment planning. The medical science that uses electromagnetic radiation, ultrasonography or radioactivity for evaluation of body tissues in case of injury or disease is referred to as *diagnoses medical imaging*. However, electromagnetic radiation can either be ionizing or non-ionizing. This section gives a brief overview and concepts of some of medical imaging modalities.

X-ray is the oldest imaging technique widely used throughout the world. It is an ionizing radiation technique discovered by the German physicist in 1895 by Wilhelm Conrad Röntgen (Yang, Guang-Zhong & Firmin, 2000). The discovery of Röntgen in that century drives the use of electromagnetic radiation in the form of ionizing radiation (gamma and X-rays) in an unprecedented speed for diagnostic radiology. The basic

principle for using X-ray involves passing of beam of X-rays, produced by an X-ray tube to selected parts of the body. There was an attempt to reconstruct images from projections as at 1940, this was even planned before the advent of modern computer technology. Gabriel Frank achieved this with the plan of describing the basic idea of modern tomography including such concepts as sonograms and optical back projection (Hsieh, 2002). About 16 years later, Allah M. Cormack furthered the research objectives with some experimental works based on reconstructive tomography.

$$\text{CT Number} = (\mu - \mu_{water} / \mu_{water} - \mu_{air}) \times 1000 \quad (1)$$

In 1967, the first CT scanner was developed by Godfrey N. Hounsfield in England at the Central Research Laboratory of EMI, Ltd (Hounsfield, 1973). Hounsfield investigation on pattern recognition techniques shows that if X-ray is passed through a body from different directions, this would result in its' internal body reconstruction. In his trials in 1969, test objects were scanned with isotope source that required a scan time of 9 days per image (Kalender, 2006).

Research usage of any of the image modalities depends on the intended image area to extract. Some could successfully extract certain information called "*Morphological Information*" while others are very useful in extracting "*physiological or functional information*". *X-ray*, *CT* and *MRI* are typical examples of former while *PET* and *SPECT* are examples of the later. However, such specific features and functionalities justify their usage in medical community. Section 2.4.3 explains specific clinical relevancies of these image modalities.

2.4.1 Computed Tomography

Computed tomography (CT) is a widely adopted imaging modality with many clinical applications from *diagnosis* to *procedure planning* (Merck, 2009). Computed Tomography is a technique of X-ray photography in which a single plane of a patient is scanned from various angles in order to provide a cross-sectional image of the internal structure of that plane (Hsieh, 2002). Conventional radiography uses the relative

distribution of X-ray intensities for its measurement. It involves sending of uniform intensity X-ray through a patient from an X-ray source of intensity I_o and corresponding exiting of the X-ray with intensity *I (x, y)* from the other side, which then interact with a radiography film sheet. The different paths through the material will alternate the X-rays by varying amounts, based only on the mass attenuation coefficient (μ), since the *distance (d)* is the same on all point of the radiography film (Shabaneh et al., 2004). CT uses attenuation as the judgments of its measurements as the X-ray is scanned through the patients.

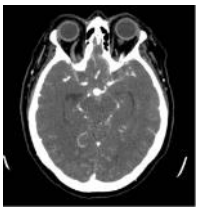

Figure 2.3: An example of a CT slice, a head scan (Lundström, 2007)

The patient is scanned using an X-ray source from one side of the plane and the detector placed on the opposite side is used to measure the attenuated X-ray, which is recorded by computer. After the first scan through the plane, the X-ray source and the detector rotate with a particular predefined amount for another translational scan. Hence, an X-ray technique involves passing electromagnetic radiation through the body. This is usually presented as CT Number, expressed in "*Hounsfield Units*" or "HU" named after Godfrey Hounsfield. A *positive CT* indicates a tissue is more attenuating than water while a *negative CT* denotes a tissue with lower density than water.

2.4.2 Magnetic Resonance Imaging

Magnetic Resonance Imaging (MRI) technique has been one of the primary tools employed in medical diagnosis since the first publication of human body image in 1977 (Damadian, Goldsmith & Minkoff, 1977). MRI imaging technique is completely

different from that of Computed Tomography as it uses energy sources as its imaging procedure rather than ionizing radiation technique of X-ray. In the early years of existence of MRI, it was referred to as *Nuclear Magnetic Resonance Imaging (NMRI)* since it was developed from knowledge gained in the study of nuclear magnetic resonance (Amruta, Gole & Karunakar, 2010). The term NMRI is sometimes still in use when discussing non-medical devices of the same NMRI principle. However, in medical imaging, magnetic resonance tomography (MRT) may sometimes be interchangeably used for MRI. The procedure requires the usage of a strong magnetic field for spin alignment of hydrogen nuclei (photons) in the body.

The spin synchronizes as the radio-frequency (RF) pulse matches the nuclear resonance frequency of the photons. As the pulse is removed, different relaxation times are measured, that is, the times for the spins to go out-of-sync (Lundström, 2007). The density and chemical surroundings of the hydrogen atoms determine the measured value. Whilst some vectors will form alignment towards the direction of the main magnetic field, a slight majority will align themselves in the slightly lower energy state associated with the direction of the main magnetic field (Geoffrey et al., 2008). MRI creates its images as a result of the difference between two populations of vectors leading to the equilibrium net magnetic vectors. We could therefore say that, with MRI, a body is prepared for radio signal transmission on the FM bandwidth. The relative distribution of the vectors aligned within or against the main magnetic field is described by *Boltzmann distribution* as in equation (2).

The value of *k* is the *Boltzmann constant*, *T* is the *temperature* measured in *kelvin*, *h* is the *Planck constants*, γ is the *gyromagnetic ratio* of the nucleus in *rad/T/s* and *B* is the *strength of the magnetic field in tesla*, $\prod$ is a constant approximately equal to 3.14159. The number of spins in the lower energy level and the number of spins in the upper energy level are denoted by $n\uparrow$ and $n\downarrow$ respectively.

$$n\uparrow / n\downarrow = \exp(-\Delta E / kT), \text{ with } \Delta E = h\gamma B/2\prod \quad (2)$$

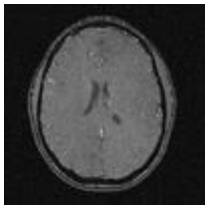

Figure 2.4: An example of an MRI slice, brain's Scan

2.4.3 Clinical Applications / Relevancies

MRI is the only chemically sensitive in-vivo imaging technique with high-resolution soft tissue contrast that allows physicians to peer deep inside the human body, producing clinically relevant images of soft tissue lesions and functional parameters of the body organs, without the use of invasive procedures or ionizing radiation such as X-rays (Cosmus & Parizh, 2011). However, with the knowledge gained in the course of this study, some of the clinical applications of CT and MRI, as being proven by researchers, solemnly depend on the required medical examination on the patient and in certain cases, the image modalities are seen to be complementary to each other in the diagnosis procedures.

With CT scan, hermiated disc, spinal stenosis, fractures in the spin can be detected. It has also proven very useful in cartilage invasion and anatomy of the surrounding tissues. MRI has ability to demonstrate and characterize soft tissues hence useful in heart, muscles, brain, spinal cord, some head and neck tumors. Consequently, CT and MRI are mostly used image modality. In order to benefit optimally from CT and MRI, their combinatory techniques were introduced to create more impact features in medical imaging such as PET / CT and PET / MRI. Meanwhile, Magnetic Resonance Imaging (MRI) is the most recently applied technique, most commonly used in radiology to visualize the structure and functions of the body for many reasons among which is, it provides detailed images of the body in any plane with higher discrimination (Sun, Bhanu & Bhanu, 2009).

2.5 Dataset Pre-Processing Techniques

Pre-processing stage in volume visualization is to enhance the visual appearances of the images and the manipulation of the datasets' structures, to convert them from their acquired representation to spatial representation required and appropriate for visualization. However, a lot of caution needs to be exercised with image enhancements' procedures as poorly embarked approach may introduce image artefacts or even lead to loss of information in the datasets.

Segmentation, a key step and a large research area in visualization, is usually performed at the pre-processing step of volume visualization. As a matter of fact, different organs or tissues of an acquired volumetric data might have the same density or intensity hence segmentation stage and not only classification becomes essential. The fundamental principle guiding volume visualization is based on the fact that empowering the user to see a certain structure, using only classification is not always possible (Meißner et al., 2000). Though acquisition methods usually demand different level or extent of required segmentation but most methods require semi-automatic approach which invariably increases the overall processing time of datasets in volume visualization. Studies have shown that segmentation of brain MR is a compulsory, difficult and time consuming stage for volume visualization because of variable imaging parameters, overlapping intensities, noise, partial voluming, gradients, motion, echoes, blurred edges, normal anatomical variations and susceptibility artefacts (Lladó et al., 2012; Sha & Sutton, 2001).

This section reviews previous datasets pre-processing techniques and highlights the significant contribution of *SurLens* Dataset Pre-processing approach.

2.5.1 Filtering, Enhancement, Detection & Extraction

One of the key processes in the pre-processing is the removal of noise from MRI data. Some of the techniques used for MRI de-noising include non-linear filtering methods (Muhamed et al., 2011; Gupta, Anand & Tyagi, 2012) spectral subtraction (Liu et al.,

2012), wavelet-based thresholding (Agrawal & Sahu, 2012), anisotropic non-linear diffusion filtering (Zhang & Ma, 2010; Perona & Malik, 1990), Markov Random Field (MRF) models (An & An, 1984), wavelet models (Nowak, 1990), non-local means modes (NL-means) (Buades, Coll & Morel, 2005), and analytical correction schemes (Sijbers, 1998). Despite the fact that there are quite a substantial number of state-of-the-art methods for de-noising, accurate removal of noise from MRI is still a challenge; as all these methods are almost the same in terms of computation cost, de-noising, quality of de-noising and boundary preserving, which has retained MRI de-noising as an open issue that needs better improved methods (Bandhyopadhyay & Paul, 2012). Hence, de-noising methods at this current state of research are not reliable enough to fully support pre-processing stage of volume visualization. The main challenge in de-noising MRI is to preserve the edges and the details, at the same time to reduce noise in uniform regions (Diaz et al., 2011).

Edge detection or extraction is an important step in MRI data pre-processing. There are three steps in edge detection process (Senthilkumarn & Rajesh, 2008), the image filtering, the image enhancement, and the image detection. Image filtering is required in pre-processing because the target MRI images might have been corrupted through a number of circumstances like impulse noise, Gaussian noise, being common situations. More filtering procedures to reduce noise may results in loss of the strength of the edges (Senthilkumarn & Rajesh, 2009). Image enhancement emphasizes pixels where there is a significance change in local intensity values and is usually performed by computing gradient magnitude (Wen, Zhang & Jiang, 2008) while image detection usually based on threshoding criterion (Paulinas & Usinskas, 2007).

Quite a number of operators are usually used for image filtering, enhancement, and detection such as Sobel, Prewitt, Roberts, Laplacian of Gaussian, Zero-cross and cunny (usually refers to as Gaussian) operators. Among these set of techniques, Sobel operators' produces best sharpness and clear edges (Ponraj et al., 2011). Though Sobel operator has been proven to produce superior qualities compared to other techniques, it has also been confirmed inaccurate and sensitive to noise (VenuGopal & Naik, 2011). Therefore, since image filtering, enhancement, detection and extraction technique play a key role in the development of a reliable medical visualization framework, a better and a

contributing approach must be considered during the pre-processing stage of a volume visualization framework in order to improve accuracy and noise sensitivity interference.

As one of our contributions to this field, we have therefore designed and implemented a new algorithm for image filtering, enhancements, detection and extraction, actualized at the graphic execution phase of our framework, which is the main entry point of datasets into volume visualization. This is an improved and better approach tackling accuracies of image filtering, enhancements, detection and extraction by enabling the datasets to be processed at the main entry point of volume visualization in order to avoid any unwanted noise sensitivity. We do not observe any shortcoming of this design hence it is noted as an improvement over all the previously pre-processing approaches.

2.5.2 Volume Segmentation

Brain MRI segmentation has been attracting attention for a while considering its significance in the medical image analysis and diagnosis. As each of the points in the image scan corresponds to a particular point in the human body structure, during segmentation process, each point in the scanned image and its correspondence to the tissue or organ is identified. A number of segmentation algorithms have been proposed in the past. Clustering-based (Kannan & Pandiyarajan, 2009), region-growing (Welinski & Fabijanska, 2011; Deng et al., 2010), active contour-based (Tanoori et al., 2011), watershed-based (Freitas et al., 2011) and morphological-based segmentation (Li et al., 2011) have been previously applied to brain MRI volume segmentation. Sethian (1999), Ben-Zadok, Riklin-Raviv & Kiryati (2009) and Cremers et al., (2007) have made appreciable contribution in the boundary-based segmentation procedures.

One of the notable studies in this regard is that of Bezdek, Hall & Clarke (1993). Bezdek et al. (1993) made a thorough review on MRI segmentation using pattern recognition techniques. The study categorized brain MRI segmentation algorithms into supervised methods and unsupervised strategies. Supervised segmentation strategy is based on some prior information or knowledge to perform segmentation while

unsupervised strategy performs brain MRI segmentation with no prior knowledge or information. The supervised methods are listed to include Bayes classifiers with labeled maximum likelihood estimators, the k-nearest neighbour rule (kNN) and artificial neural networks (ANN) while the unsupervised methods include Bayes classifiers with unlabelled maximum likelihood estimators or the fuzzy C-means (FCM) algorithms.

Though segmentation is usually performed at the pre-processing stage of volume visualization, being a key and a large research area, some studies separated the usual pre-processing stages distinctly from segmentation. Clarke et al. (1995) reviewed both pre-processing and segmentation methods of soft brain tissue. In the same vein, Styner et al. (2008) reviewed semi-automated and automated multiple sclerosis (MS) lesion segmentation approaches, analyzing MS lesions, pre-processing steps and segmentation approaches. More recently, Lladó et al. (2012) presented a review of brain MRI with the goal of helping diagnosis and follow-up of multiple sclerosis lesions in brain MRI.

In order to enhance the visual appearance of the brain MRI images, any possible artefacts will need to be removed. Removal of the contained artefacts could be done at this stage, done partly or delayed until the final entry point of the dataset into volume visualization phase, this depends on the design of the volume visualization framework. Whichever of the approach being adopted in the framework design, there must be adequate provision set aside in case of unexpected introduction of certain level of artefacts during the pre-processing phase.

Skull stripping is another important pre-processing step since fat, skull, skin and other non-brain tissues may cause mis-classifications in some approaches due to the intensity similarities with brain structures (Detta & Narayana, 2011). Some of the components of the brain require a particular MRI technique for their diagnosis, hence, without thorough skull stripping it might be difficult to have the intended structures' of study visible with volume visualization algorithms.

In cases where studies need to be carried out on more than one components structure of the brain e.g. tissue and fat, alignment of the soft brain images would be required. Aligning all the images from different modalities or MR images is known as registration (Zitova & Flusser, 2003). The precise steps involve include feature

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