SLANTLET TRANSFORM-BASED SEGMENTATION AND α -SHAPE THEORY-BASED 3D VISUALIZATION AND VOLUME CALCULATION METHODS FOR MRI BRAIN TUMOUR

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I would like to dedicate this work for

my beloved wife "Hala" and lovely kids

"Malak & Hussein"

for being patience, supportive, and understanding.

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Thanks to Allah SWT for everything I was able to achieve and for everything I tried, but I was not able to achieve.

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ABSTRACT

Magnetic Resonance Imaging (MRI) being the foremost significant component of medical diagnosis which requires careful, efficient, precise and reliable image analyses for brain tumour detection, segmentation, visualisation and volume calculation. The inherently varying nature of tumour shapes, locations and image intensities make brain tumour detection greatly intricate. Certainly, having a perfect result of brain tumour detection and segmentation is advantageous. Despite several available methods, tumour detection and segmentation are far from being resolved. Meanwhile, the progress of 3D visualisation and volume calculation of brain tumour is very limited due to absence of ground truth. Thus, this study proposes four new methods, namely abnormal MRI slice detection, brain tumour segmentation based on Slantlet Transform (SLT), 3D visualization and volume calculation of brain tumour based on Alpha (α) shape theory. In addition, two new datasets along with ground truth are created to validate the shape and volume of the brain tumour. The methodology involves three main phases. In the first phase, it begins with the cerebral tissue extraction, followed by abnormal block detection and its fine-tuning mechanism, and ends with abnormal slice detection based on the detected abnormal blocks. The second phase involves brain tumour segmentation that covers three processes. The abnormal slice is first decomposed using the SLT, then its significant coefficients are selected using Donoho universal threshold. The resultant image is composed using inverse SLT to obtain the tumour region. Finally, in the third phase, four original ideas are proposed to visualise and calculate the volume of the tumour. The first idea involves the determination of an optimal α value using a new formula. The second idea is to merge all tumour points for all abnormal slices using the α value to form a set of tetrahedrons. The third idea is to select the most relevant tetrahedrons using the α value as the threshold. The fourth idea is to calculate the volume of the tumour based on the selected tetrahedrons. In order to evaluate the performance of the proposed methods, a series of experiments are conducted using three standard datasets which comprise of 4567 MRI slices of 35 patients. The methods are evaluated using standard practices and benchmarked against the best and up-to-date techniques. Based on the experiments, the proposed methods have produced very encouraging results with an accuracy rate of 96% for the abnormality slice detection along with sensitivity and specificity of 99% for brain tumour segmentation. A perfect result for the 3D visualisation and volume calculation of brain tumour is also attained. The admirable features of the results suggest that the proposed methods may constitute a basis for reliable MRI brain tumour diagnosis and treatments.

ABSTRAK

Pengimejan Resonans Magnetik (MRI) merupakan komponen utama yang penting dalam diagnostik perubatan yang memerlukan analisis imej yang teliti, cekap, tepat dan diyakini untuk pengesanan, segmentasi, visualisasi dan pengiraan isipadu tumor otak. Sememangnya tumor mempunyai pelbagai bentuk, lokasi dan keamatan imej yang sangat merumitkan bagi pengesanannya. Tentunya, adalah amat berfaedah jika sekiranya hasil pengesanan dan segmentasi tumor otak yang sempurna dapat diperolehi. Walaupun terdapat beberapa kaedah yang tersedia, namun pengesanan tumor dan segmentasi masih lagi belum dapat diselesaikan sepenuhnya. Sementara itu, kemajuan visualisasi 3D dan pengiraan isipadu tumor otak adalah sangat terhad kerana ketiadaan kebenaran mutlak. Oleh itu, kajian ini mencadangkan empat kaedah baharu iaitu pengesanan hirisan MRI tidak normal, segmentasi tumor otak berdasarkan jelmaan Slantlet (SLT), visualisasi 3D dan pengiraan isipadu tumor otak berdasarkan teori bentuk Alpha (α). Di samping itu, dua set data baharu beserta dengan kebenaran mutlak telah dicipta untuk mengesahkan bentuk dan isipadu tumor otak. Metodologi ini melibatkan tiga fasa utama. Dalam fasa pertama, ia dimulai dengan pengekstrakan tisu otak, diikuti dengan pengesanan blok yang tidak normal dan mekanisma penalaan halus, dan berakhir dengan pengesanan hirisan yang tidak normal berdasarkan blok tidak normal yang telah dikesan. Fasa kedua melibatkan segmentasi tumor otak yang merangkumi tiga proses. Pertama, hirisan tidak normal diuraikan menggunakan SLT, kemudian pekalinya yang signifikan dipilih menggunakan ambang sejagat Donoho. Imej yang terhasil dibentuk menggunakan SLT songsang untuk mendapatkan kawasan tumor. Akhirnya, dalam fasa ketiga, empat idea asli dicadangkan untuk menggambarkan dan mengira isipadu tumor. Idea pertama, ia melibatkan penentuan nilai α optimum secara automatik menggunakan satu formula baharu. Idea kedua adalah untuk menggabungkan semua titik tumor bagi kesemua hirisan tidak normal menggunakan nilai α tersebut untuk membentuk satu set tetrahedron. Idea ketiga adalah untuk memilih tetrahedron yang paling sesuai menggunakan nilai α di atas sebagai nilai ambang. Idea keempat adalah untuk mengira isipadu tumor berdasarkan tetrahedron yang terpilih. Dalam usaha untuk menilai prestasi kaedah-kaedah yang dicadangkan, satu siri eksperimen dijalankan menggunakan tiga set data piawai yang merangkumi 4567 hirisan MRI daripada 35 pesakit. Kaedah-kaedah tersebut dinilai dengan menggunakan amalan piawai serta ditanda araskan dengan teknik-teknik terkini yang terbaik. Berdasarkan eksperimen, kaedah-kaedah yang dicadangkan telah menghasilkan keputusan yang sangat menggalakkan dengan kadar ketepatan 96% bagi pengesanan keabnormalan hirisan dan 99% sensitiviti dan spesifisiti untuk segmentasi tumor otak. Keputusan yang sempurna juga dicapai bagi visualisasi 3D dan pengiraan isipadu tumor otak. Ciri-ciri yang mengkagumkan daripada keputusan ini mencadangkan bahawa kemungkinan kaedah-kaedah yang dicadangkan ini boleh dijadikan asas yang dipercayai bagi diagnosis tumor otak MRI dan rawatan.

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1D	-	One dimensional
2D	-	Two dimensional
3D	-	Three dimensional
ANFIS	-	Adaptive Network-Based Fuzzy Inference System
ANN	-	Artificial Neural Network
AR	-	Approximate Reasoning
BET	-	Brain Extraction Tool
BPNN	-	Back-Propagation Neural Networks
BRATS	-	Brain Tumour Segmentation
BSE	-	Brain Surface Extractor
CAD	-	Computer Aided Diagnostics
CF	-	Classification Forest
CHNN	-	Competitive Hopfield Neural Network
CNS	-	Central Nervous System
CSF	-	Cerebrospinal Fluid
CT	-	Computed Tomography
DT	-	Delaunay Triangulations
DWT	-	Discrete Wavelet Transform
EM	-	Expectation Maximization
FACT	-	Fully Automated Calibration Technology
FCM	-	Fuzzy c-Means
FHNN	-	Fuzzy Hopfield Neural Network
FKNN	-	Fuzzy Kohonen Neural Network
FLAIR	-	Fluid-Attenuated Inversion-Recovery

FLBPA	-	Fuzzy and Learning Back Propagation Algorithm
FN	-	False Negative
FP	-	False Positive
FP-ANN	-	Forward Back-Propagation Artificial Neural Network
FPCM	-	Fuzzy Probabilistic c-Means
GB	-	GigaByte
GBM	-	GlioBlastoma-Multiform
GC	-	Graph Cut
GHz	-	Gigahertz
GM	-	Gray Matter
GMM	-	Gaussian Mixture Models
GSFCM	-	Generalized Spatial Fuzzy c-Means
GTR	-	Gross Total Resection
HG	-	High-Grade
HH	-	High-High frequency band
HL	-	High-Low frequency band
HNN	-	Hopfield Neural Networks
HSOM	-	Hierarchical Self-Organizing Map
HWA	-	Hybrid Watershed Algorithm
IARC	-	International Agency for Research on Cancer
IBSR	-	Internet Brain Segmentation Repository
I-HF	-	Inter-Hemisphere Fissure
ISLT	-	Inverse Slantlet Transform
k-NN	-	k-Nearest Neighbors
LCC	-	Largest Connected Component
LG	-	Low-Grade
LH	-	Low-High frequency band
LL	-	Low-Low frequency band
LS-SVMs	-	Least Squares Support Vector Machines
MICCAI	-	Medical Image Computing and Computer Assisted Intervention
MLP	-	Multilayer Perceptron

MMC	-	Modified MacDonald
MRF	-	Markov Random Field
MRGM	-	Modified Region Growing Method
MRI	-	Magnetic Resonance Imaging
NN	-	Neural Network
PBT	-	Probabilistic Boosting Trees
PCA	-	Principal Component Analysis
PD	-	Proton Density
PET	-	Positron Emission Tomography
PSNR	-	Peak Signal-to-Noise Ratio
RF	-	Radio Frequency
ROI	-	Region of Interest
RW	-	Random Walker
SBRG	-	Seed-based region growing
SGLDM	-	Spatial Gray Level Dependence Method
SLT	-	Slantlet Transform
SOFM	-	Self-Organizing Feature Map
SOM	-	Self-Organizing Map
SOP	-	Standard Operating Procedure
SPECT	-	Single Photon Emission Computed Tomography
SVM	-	Support Vector Machines
TN	-	True Negative
TP	-	True Positive
UNNCK-M	-	Unsupervised Neural Network Clustering k-Means
VD	-	Volume Distribution
WAT	-	Watershed Algorithm
WCT	-	Wavelet Co-occurrence Texture features
WM	-	White Matter
WM	-	Weighted Median
WST	-	Wavelet Statistical Texture features
WT	-	Wavelet Transform

LIST OF SYMBOLS

A	-	The special area of the products of opposite sides
a_0, a_1, b_0, b_1, c_0, c_1, d_0, and d_1	-	Filters-bank parameters of
a_1 and a_2	-	The tumour area in two slices
C_1, C_2, C_3, …, C_8	-	The blocks name of current mask
C_i	-	The center of current mask
D(A,B)	-	The coefficient value of Dice
d_1 and d_2	-	The two longest orthogonal diameters of the tumour
F	-	Set of all pixels in an MR image
f	-	First tumour slice
H×W	-	Size of MR image
I(x,y)	-	MRI slice
i×i	-	Size of SLT image (ROI)
I_{mage_test}	-	ROI name
J(A,B)	-	The coefficient value of Jaccard
M×N×K	-	M and N are the MR image size and K is the slice number
n	-	Last tumour slice
N	-	The total number of MR images in the dataset
n_i	-	The number of occurrences the tumour in the slice “i”
P( )	-	Homogeneity predicates defined on groups of the connected pixels
P_i	-	The probability distribution (frequency of occurrence) of the tumour in the slice “i”
P_i	-	The center of preceding mask

s	-	Number of tumour slice
S_i	-	The center of succeeding mask
SLTfilter	-	SLT filter matrix
$SLTfilter^T$	-	SLT transposing filter matrix
SLTimage	-	SLT image matrix
Sub_1, Sub_2, …, Sub_n	-	Connected subsets
t	-	Slice thickness
T_1, T_2, and T_3	-	First, second, and third threshold
V	-	The volume of the tetrahedron
W×W	-	Size of non-overlapping blocks in MRI slice
w_k	-	Is all coefficients in SLT matrix
α	-	Alpha
π	-	3.14
σ	-	Standard deviation
ε	-	Donoho universal threshold
$g_i(n)$, $f_i(n)$ and $h_i(n)$	-	SLT filters-bank
μ_i	-	The mean values
σ_1^2 and σ_2^2	-	Variances of two classes probabilities isolated by threshold "t"
ω_1 and ω_2	-	Two classes probabilities isolated by threshold "t"
ω_i	-	Class probabilities

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CHAPTER 1

INTRODUCTION

1.1 Overview

This chapter rationalizes the urgent necessity of systematic research to detecting and segmenting the brain tumour in Magnetic Resonance Images (MRI). Brain tumour being the most common brain diseases affects and devastates many human lives (Siegel *et al*. 2012). According to the estimation of International Agency for Research on Cancer (IARC), every year over 126,000 people are diagnosed with brain tumour with a mortality rate above 97,000 (Ferlay *et al.* 2010). Despite many dedicated research efforts to overcome brain tumour related problems, higher survival rate of brain tumour patients is far from being achieved. Lately, multi-disciplinary approaches involving the knowledge of medicine, mathematics and computer science are adopted for better understanding of the disease and to discover more effective methods for cure.

MRI and Computed Tomography (CT) scans of human brain are the most common tests used to detect the presence and identify the location of brain tumour for selected specialised treatment option (Polidais 2006; Jeena and Kumar 2013). Presently, available options for brain tumour treatment include surgery, radiotherapy,

and chemotherapy. The choice for the treatment options are based on the size, shape, type, and grade of the tumour. It also depends on whether or not the tumour is exerting pressure on vital parts of the brain (Horská and Barker 2010; Tommaso 2012). Actually, the treatment options is critically decided by the factors such as the extent to which the tumour has spread to the other parts of the Central Nervous System (CNS) or body, the possible side effects on the patient relating to the treatment procedure and the overall health of the patient (Merchant *et al.* 2010).

Certainly, precise detection of the brain abnormality type is a great necessity to reduce diagnostic errors and to schedule a correct treatment plan. In this regard, Computer Aided Diagnostics (CAD) remarkably improved the detection accuracy. The CAD system not only renders an alternative opinion to support the image interpretation of the radiologist but also reduces the image reading time significantly. Brain segmentation for abnormality detection in MRI slices is the most tedious task due to its complex anatomy and problems inherent to the nature of the image (Hutchison and Mitchell 2011; Moghaddam and Soltanian-zadeh 2011; Reddy *et al.* 2012). The heterogeneous and diffuse manifestation of pathology in medical images often prohibits the employment of computational methods. Primarily, several classes for tumour types possess a variety of sizes and shapes (Prastawa *et al.* 2004; Louis *et al.* 2007). Appearance of tumour at different locations in the brain with varying image intensities is another factor that makes automated brain tumour image detection and segmentation difficult (Polidais 2006). Diffusive growth of tumours often makes their resection highly difficult. Usually, surgery is performed to achieve a Gross Total Resection (GTR) because the extent of surgical resection in turns determines the longevity of the patient (Lacroix *et al.* 2001; Stippich 2007; Merchant *et al.* 2010).

Precise determination and comparison of tumour volume on preoperative and postoperative MR images are prerequisite for the resection extent determination. The estimation of preoperative and postoperative tumour volumes are often depend on the surgeon's impression or on the measurement of its largest axis along x, y and z direction (Lacroix *et al.* 2001; Merchant *et al.* 2010). Consequently, accurate

volume calculation of tumour is not executed routinely. Definitely, the visualization of the tumour on MR images greatly diverges due to presence of varieties of tissues inside the tumour area and its diffuse expansion. Thus, the selection of different segmentation techniques is essential to differentiate the cancerous tissue from the surrounding healthy tissues. This assists to determine the correct tumour volume. Besides, the segmented tumours must be visualized distinctly to obtain their explicit shape and location in the brain.

1.2 Designations

The human brain being the central functional unit controls the entire human body parts. It is a highly specialised organ that allows human being to adapt and endure varying environmental conditions. In addition, the brain enables a human to articulate words, execute actions, bring about thoughts and feelings (Natarajan *et al.* 2012; Deepak *et al.* 2013). Under certain conditions due to mysterious reasons the brain cells grow and multiply in an uncontrolled manner. In this situation, the mechanism that controls normal cells is unable to regulate the growth of the brain cells. The abnormal mass of brain tissue is medically termed as the brain tumour. The tumour occupies the space inside the skull, intervene the regular activity of brain and enhances the brain pressure. This increased brain pressure causes some shift of the brain tissues, pushes them against the skull and responsible for the nerves damage of the other healthy brain tissues (Louis *et al.* 2007; Natarajan *et al.* 2012; Shally and Chitharanjan 2013; Salankar and Bora 2014).

Varieties of imaging modalities such as CT (Al-Kadi 2010), MRI (Wong *et al.* 2012), Single Photon Emission Computed Tomography (SPECT) (Bronnikov 2012) and Positron Emission Tomography (PET) (Wright 2010; Lartizien *et al.* 2012) are used to inspect brain tumours. Figure 1.1 shows an image slice through the human brain obtained via CT, MRI, SPECT and PET techniques to render different

information about the brain function and anatomy.

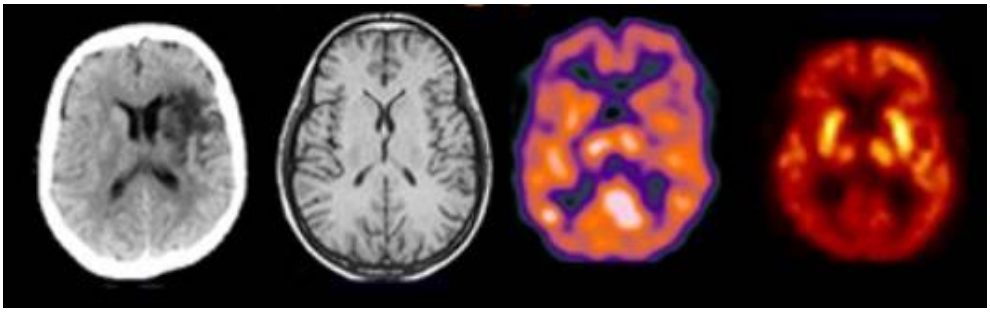


Figure 1.1 Human brain slices with different imaging modalities. From left to right: CT, MRI, SPECT and PET (Wright 2010)

Damadian invented the MRI in 1969 and first used it to investigate the human body (Damadian *et al.* 1977). Eventually, MRI became the most preferred imaging technique in radiology because it allows the visualization of internal structures in greater details. MRI reveals superior distinction among soft tissues within the body. This makes MRI suitable to generate better quality images for the cancerous tissues, brain, heart, and muscle than X-rays or CT methods (Novelline and Squire 2004; Fu *et al.* 2010; Abdullah *et al.* 2011).

Figure 1.2(a) illustrates a patient's head that is examined in a clinical diagnosis using three planes, including axial plane, coronal plane, and sagittal plane. Figure 1.2(b) to (d) depicts the brain MR images from various planes.

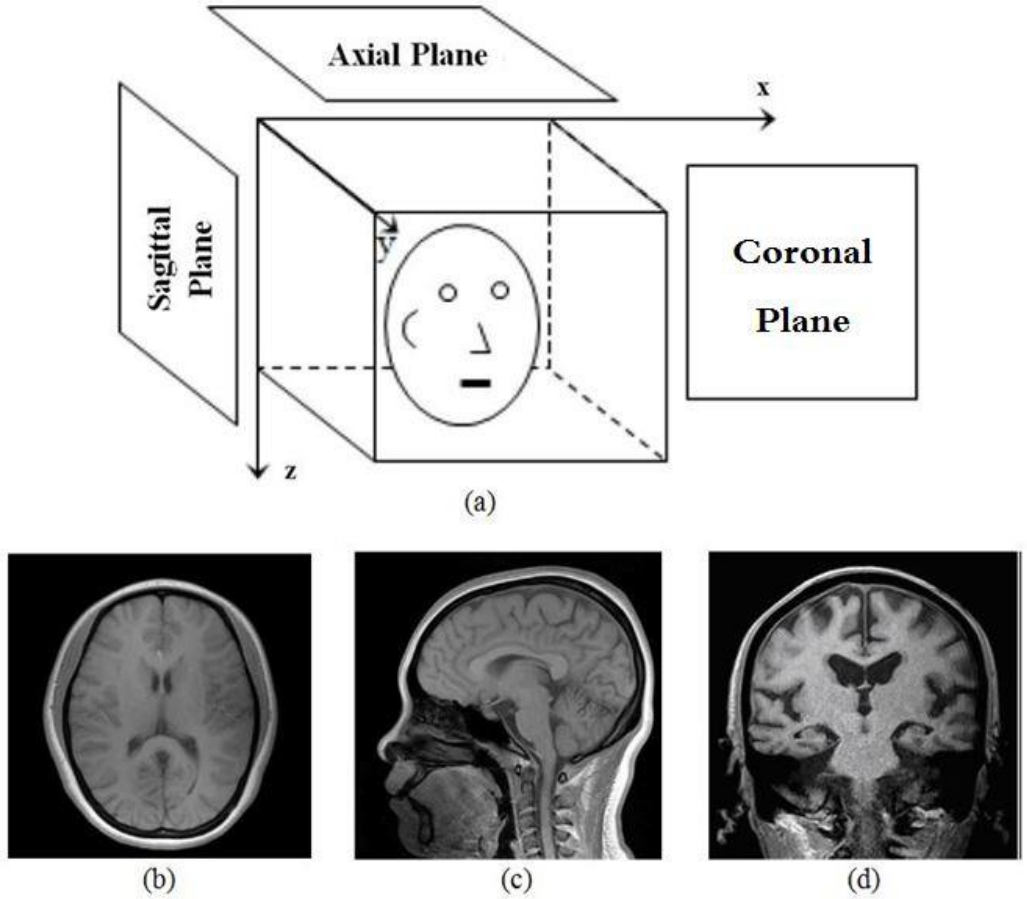


Figure 1.2 MR brain image from patient's head (a) The setup, (b) Axial plane view, (c) Sagittal plane view, and (d) Coronal plane view (Lorenzen *et al.* 2001)

MRI is represented via pixels grids with "H" rows and "W" columns. Every pixel of an MR image corresponds to a voxel (i.e. Volume element) whose value symbolizes the tissue and MR signal, respectively. The volume of a voxel depends on MR image parameters including slice thickness and pixel spacing. Normally, an MR image acquires more than one slice, which leads to an image sequence (H×W×K) with "K" slices. Figure 1.3 displays a typical MR image sequence of (512×512×9) having (5.5 mm) spacing between slices and (0.9375 mm×0.9375 mm) distance between each two pixels in the image slice.

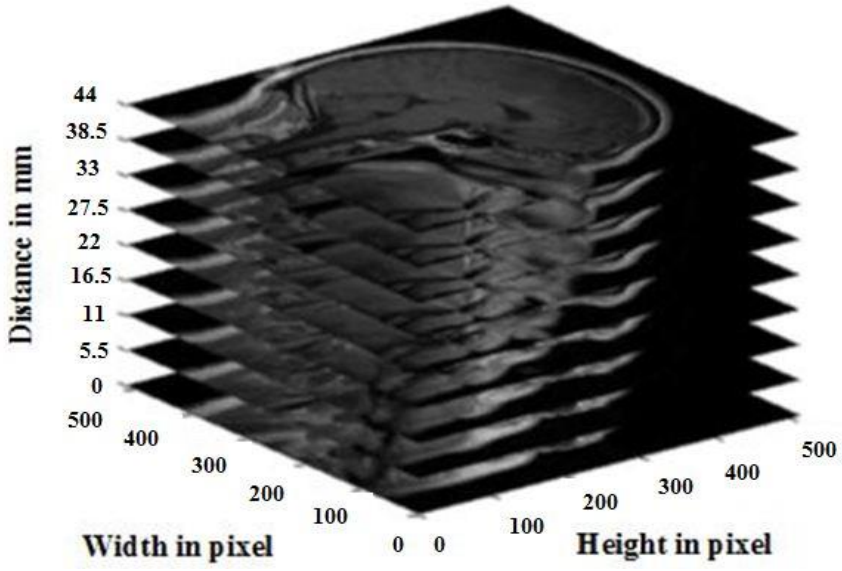


Figure 1.3 MR image sequence (Brown and Semelka 2011)

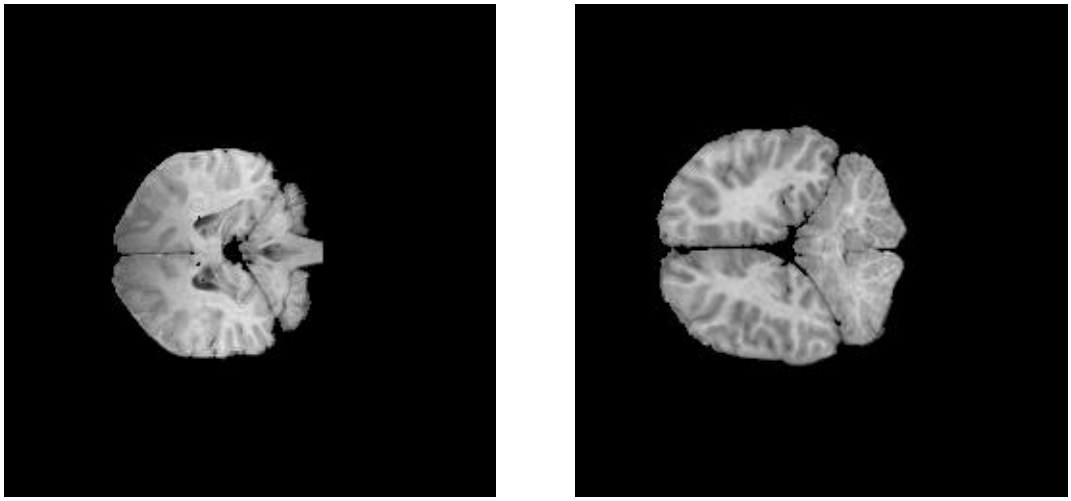
1.3 Background of Research

The medical brain images provide valuable and detailed information regarding normal and abnormal brain tissues. Currently, MR images are the most common test for diagnosing and confirming the presence of brain tumour (Horská and Barker 2010; Joshi 2010; Mehmood *et al.* 2013). Practically, brain MR images include both normal and abnormal image slices. Despite extensive research, the classification of brain MR image abnormality remains challenging (Padma and Sukanesh 2011; Elaiza *et al.* 2011a; Al-Badarneh *et al.* 2012). The resoans are due to variation of possible complex locations, size, shapes, and image intensities for different types of brain tumours (Kikinis *et al.* 1996; Xu *et al.* 2002; Veloz *et al.* 2011; Roy *et al.* 2013).

Radiologists analyse the brain MRI slices by visual inspection to detect and identify the presence of tumour or abnormal tissue (Amrutal *et al.* 2010; Salankar

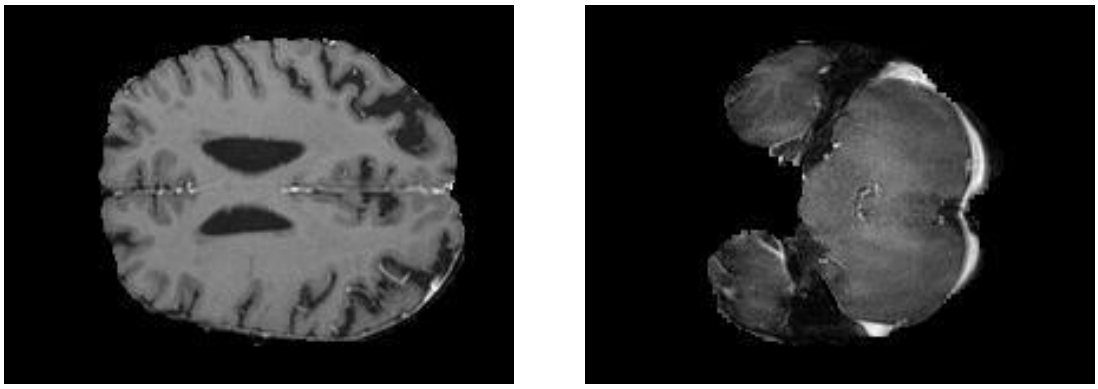
and Bora 2014). These diagnoses are based on the location, shape, and image intensity of different types of brain tumours. Clinically, radiologists analyse the brain image slice by slice visually for tumour detection and identification. Such effort is labour intensive, expensive and often erroneous, especially involving a large number of image slices. Furthermore, the sensitivity of the human eye and brain to elucidate such images reduces with the increase of number of cases, particularly when only a small number of slices contain information of the affected area (Salankar and Bora 2014). Therefore, a powerful and reliable tool needs to be developed to automate the tumour localization so that precise detection and segmentation of the abnormal tissue is feasible.

Figures 1.4 and 1.5 display a normal MRI slices of patients. Figure 1.6 illustrates an abnormal MRI slice at different locations, size, shapes, and image intensities for brain tumours in the same patient.



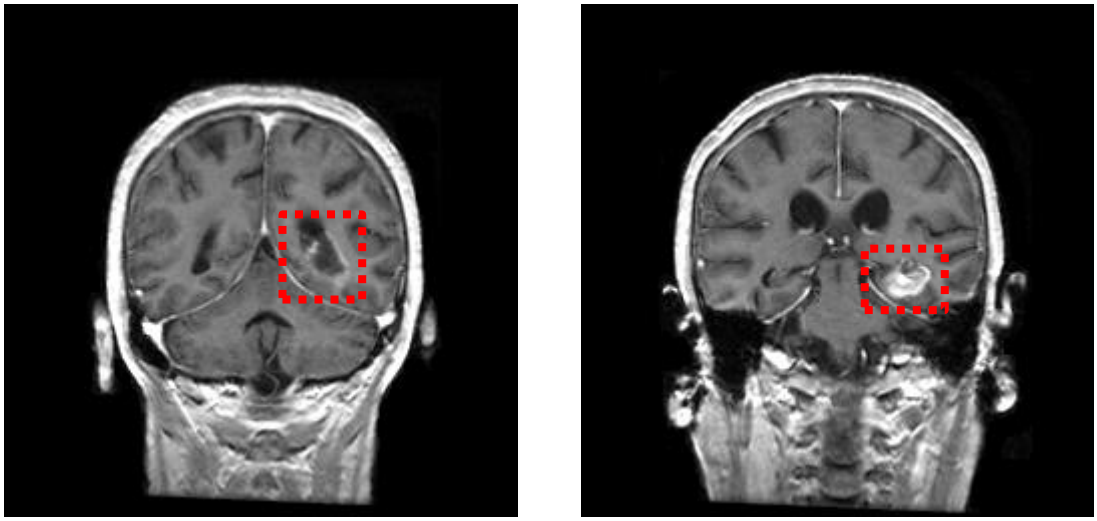
(a) **(b)**

Figure 1.4 Normal MRI slices from IBSR (10Normals_T1) dataset, (a) Slice 22 of patient Normal_4, and (b) Slice 16 of patient Normal_15



(a) **(b)**

Figure 1.5 Normal MRI slices from challenge MICCAI (BRATS2012-BRATS-1) dataset, (a) Slice 119 of patient BRATS_HG0010, and (b) Slice 54 of patient BRATS_HG0008

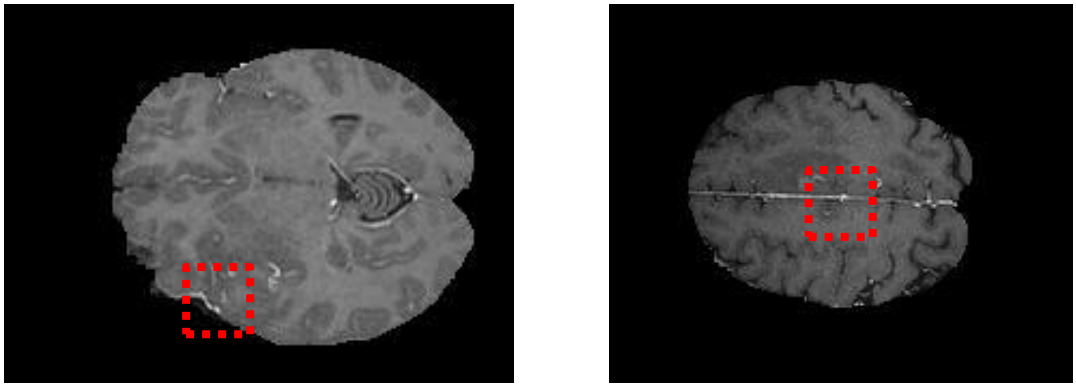


(a) **(b)**

Figure 1.6 Abnormal MRI slices at different locations with varying size, shapes, and image intensities of brain tumour (red rectangle) from IBSR (536_T1) dataset of MRI scan 536_32, (a) Slice 22, and (b) Slice 26

Anatomically, MR brain images consist of non-cerebral tissues such as skull, skin, bone, muscle, eye-balls, and dura together with cerebral tissues including White Matter (WM), Gray Matter (GM), Cerebrospinal Fluid (CSF) and tumour (if

present). Separation of these types of these tissues and localization or segmentation of tumours from cerebral tissues poses a severe challenge. Present outcome is far from being satisfactory and radical improvement is necessary (Xu *et al.* 2002; Harati *et al.* 2011; Bauer *et al.* 2011; Wang *et al.* 2011; Veloz *et al.* 2011; Hamamci *et al.* 2012). Figure 1.7 illustrates the separation complexity of the healthy tissues from the cancerous one for challenge MICCAI (BRATS2012-BRATS-1) dataset reflecting the intensity homogeneity and inherent complexity.



(a) **(b)**

Figure 1.7 Abnormal MRI slices in the presence of tumour inside the red square in terms of intensity homogeneity from challenge MICCAI (BRATS 2012-BRATS-1) dataset, (a) Slice 85 of patient BRATS_HG0004, and (b) Slice 127 of patient BRATS_HG0007

Of late, several segmentation algorithms are extensively implemented towards diverse medical imaging modalities (Moon *et al.* 2002; Sasikala *et al.* 2006; Zacharaki *et al.* 2008; Singh *et al.* 2009; Soesanti *et al.* 2011; Mustaqeem *et al.* 2012; Gang *et al.* 2013; Sinha and Sinha 2014). These techniques used dissimilar tactics to integrate the earlier available information with automatic segmentation. The performance of such techniques is decided by both the interaction plan and automatic computation scheme. Moreover, the performance evaluation varies from application to application because different medical images enclose entirely different complex anatomical structures. Thus, these methods face difficulties in managing the peripheral concavities, fragile edges, and noises of the medical image.

Brain tumour being a well-known serious disease with absolute complexity, the diffusive growth of tumours often makes their resection highly intricate. Usually, surgery is performed to achieve a GTR because the extent of surgical resection determines the longevity of the patient (Lacroix *et al.* 2001). Indisputably, the graphical visualization is an essential part of brain tumour detection and analysis. Still, accurate brain tumour visualization remains a formidable task. It is crucial to improve the degree of resection for the abnormal tissues while preserving normal tissues (González-Navarro *et al.* 2012; Yee Lau *et al.* 2014). Methods are available to visualize the brain tumour, but the major problem with these methods is the inability to visualize the boundaries of the tumour accurately in the details. In addition, their inability to separate the healthy tissues from the unhealthy one leads to the assessment and calculation of wrong tumour volume (Lee 2009; González-Navarro *et al.* 2012; Yee Lau *et al.* 2014). Figure 1.8 shows an example of the 3D visualization method of tumour patient, where the actual border is not seen and the tumour does not reveal the difference between healthy and unhealthy tissues.

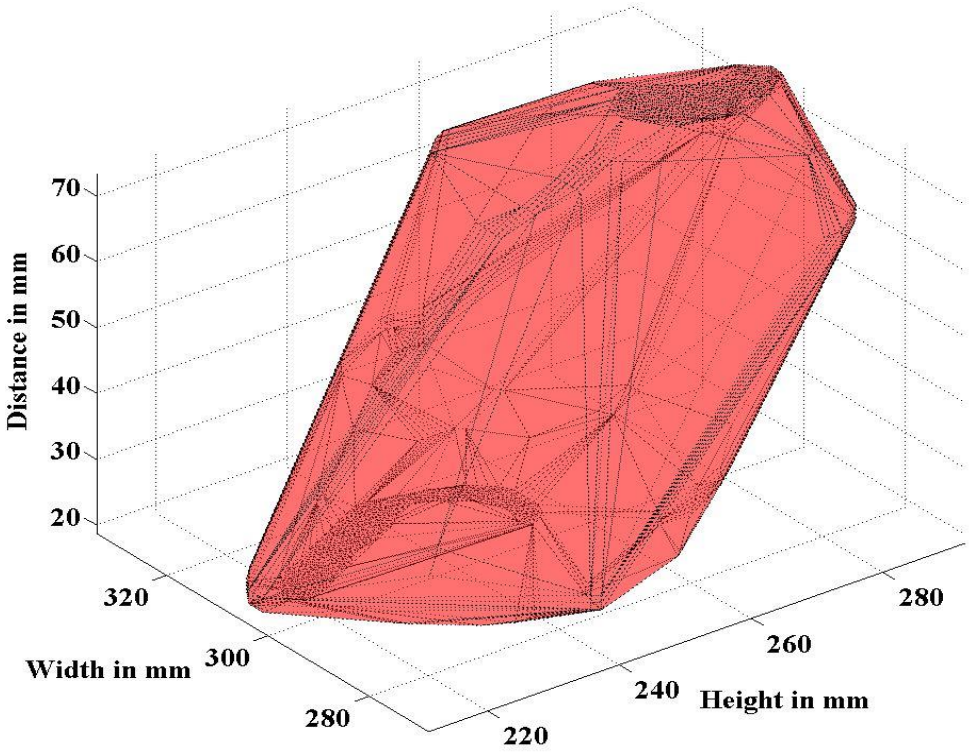


Figure 1.8 3D brain tumour visualization of MRI scan 536_32 in IBSR (536_T1) dataset using Matlab's Meshing Point Clouds function

The estimation of preoperative and postoperative tumour volumes are frequently decided by the surgeon's impression or on the measurement of its largest axis along x, y and z direction (Lacroix *et al.* 2001). Precise determination of the brain tumour extent for excised and advanced treatments requires careful calculation and systematic observation of the therapeutic effects on the tumour (Salman *et al.* 2005; Siegel *et al.* 2012; Dang *et al.* 2013). Typically, this is performed by measuring the volume of the tumour from 3D scans. Although, numerous methods for the estimation of the tumour volume are available, but the actual 3D shape of the tumour is seldom displayed. Conversely, each scientific research must evaluate and gauge their result. However, research is not yet perfected to extract the tumour from the brain and measure its volume to validate and evaluate the result given by other related method of brain tumour volume calculation. Simultaneously, there are methods to calculate the brain tumour volume manually. Some of them include Frustum Model (Shally and Chitharanjan 2013), Meshing Point Clouds (Iglesias *et al.* 2011), Trace method (Chong *et al.* 2004; Salman *et al.* 2005) and Modified MacDonald (MMC) method (Dang *et al.* 2013). However, the results obtained from these methods are not very accurate and often neglects the ground truth. Thus, it is indispensable to uncover an innovative method to gauge and validate the proposed method of tumour volume calculation.

In short, cancer is considered as the disease of the century. Despite the introduction of various methods and calculations the accurate determination of the tumour volume remains unsuccessful and many obstacles still exist that does not allow the full recovery. Moreover, overcoming the uncertainty of these methods in determining the actual volume, the brain tumour shape and the errors in drug dose calculations that lead to wrong dose (over or under) which would finally lead to jeopardizing the human life remain the future challenges. These performance limitations necessitate continued research efforts to mitigate the identified challenges.

In view of the above rationale, present thesis posed the following research questions to provide solutions to the challenges regarding abnormality detection of

MRI slices, brain tumour segmentation, 3D visualization and volume calculation of brain tumour and finally the creation of a new ground truth.

The main issues are how to detect, segment, visualise, and calculate the volume of the brain tumour in MR images with a high reliability?

The specific research questions that need to be answered are:

i) Is it possible to determine brain abnormality accurately?
ii) How to develop a new method to overcome the earlier limitations associated with MRI images brain tumour detection, segmentation, visualization, and volume calculation?
iii) Can the proposed method perfectly segment the brain tumour in MRI images?
iv) Does the new method capable to extract suitable features from the abnormal cerebral tissues which can be used to represent the brain tumour(s) in the MR images?
v) How to determine the brain tumour(s) volume accurately using the extracted features?
vi) Is it possible to represent and visualize the brain tumour in a 3D presentation?
vii) How accurate and reliable the 3D visualization and computed volume of a brain tumour?
viii) How to validate and evaluate the 3D visualization and computed volume of a brain tumour?
ix) How to create a new ground truth for reliable assessment and implementation of the proposed methods?

1.4 Problem Statements

It is an urgent necessity to build an understanding on the brain tumour detection and subsequent analyses with systematic processing steps, including abnormality detection in MRI slices, segmentation, 3D visualization and volume calculation of brain tumour. Despite numerous available methods satisfactory results on brain tumour detection and segmentation are far from being acquired. Consequently, surgery and diagnostics remain a dispute. Different approaches are proposed for the all previous processing steps. In addition, creation of a new ground truth is mandatory. The entire brain tumour detection scheme mainly depends upon appropriate preprocessing methods in terms of accuracy and reliability. A new fully automatic detection system for brain tumour need to be introduced by taking the following views of the latest developments:

1. Clinically, detection of MRI brain slices' abnormality is painstaking, voluminous and time-consuming (Singh and Kaur 2012; Kumari 2013; Salankar and Bora 2014). This is due to two main reasons: (1) homogeneity between healthy tissues and cancerous cells, which is very difficult to distinguish even by naked eyes, let alone the machines and, (2) large number of slices involved during the examination - the figure varies whose relies on the type and severity of illnesses (Selvaraj *et al.* 2007; Abdullah *et al.* 2011; Salankar and Bora 2014). Thus, many attempts are made to automate the process. However, its performance is rather less impressive and room for improvement is still wide open. Besides, another pressing issue is to localize a tumour or cancerous cell found in the abnormal slice, automatically, which is never being of research interest thus far. Therefore, an effective solution for the above problems not only would equip the doctor with the state of the art, but would also ensure a successful implementation of subsequent procedures, including segmentation, visualization, and volume estimation of tumours in a more precise manner.

2. Definitely, the brain tumours segmentation in MRI is a challenging and difficult task (Elaiza *et al.* 2011b; Hamamci and Unal 2012; Weizman *et al.*

2014) because of the variety of possible shapes, locations, and image intensities. The pathology identification, detection of the disease and comparison between normal and abnormal tissues require assorted mathematical algorithms for features extraction, modeling, and measurement in the images. Lately, several useful segmentation algorithms were proposed (Moon *et al.* 2002; Zacharaki *et al.* 2008; Farmaki *et al.* 2010). However, due to the nature of tumour, the accuracy of the algorithms is far from satisfactory (Dass and Devi 2012; Shin 2012; Roy *et al.* 2013).

3. Another pressing issue on tumour treatment is accurate 3D visualization of the tumour. However, research interest in this area is very limited (Wu *et al.* 2008; Lee 2009; González-Navarro *et al.* 2012; Wakchaure *et al.* 2014). Unfortunately, the accuracy of their works is challengeable due to the absence of the ground truth to validate their results (Wakchaure *et al.* 2014). Also, most of the tumour shapes generated by the methods are far from satisfactory because they only provide gross shape of the tumour, let alone to distinguish between the healthy tissues and cancerous tissues (Wakchaure *et al.* 2014).

4. In the cancer treatment, the tumour volume plays a significant role in determining the recommended therapy (Shi *et al.* 1998; Nelson 2001; Dubey *et al.* 2009; Shally and Chitharanjan 2013; Mehmood *et al.* 2013). In spite of several methods for tumour volume calculation such as Meshing Point Clouds, Frustum Model, Trace Method and Modified MacDonald (MMC) the detection accuracy and reliability remains debatable due to the absence of the ground truth to validate the findings (Lau *et al.* 2005; Shally and Chitharanjan 2013). Actually, these methods fail to determine the actual size of the tumour (Shally and Chitharanjan 2013). Therefore, a precise volume calculation method is required to overcome these drawbacks.

5. For any scientific research, it is obligatory to have a ground truth so that the work can be validated (Salman *et al.* 2005; Quinn *et al.* 2013; Weizman *et al.* 2014). Regarding the 3D visualisation and volume calculation of MRI brain tumour, to the best of the author's knowledge, there is no ground truth available thus far.

1.5 Research Goal

The goal of this thesis is to develop a new MRI brain tumour detection system, which includes brain tumour detection, segmentation, 3D visualisation and volume calculation, with a higher degree of accuracy than the existing one.

1.6 Objectives of the Study

In order to achieve the above mentioned goal, the following objectives need to be accomplished:

1. To detect the abnormal slices of the MR brain images.
2. To propose a new segmentation technique using the Slantlet Transform (SLT) that can precisely localise the brain tumour from cerebral tissues.
3. To develop new techniques for 3D visualization and volume calculation of the brain tumour based on the Alpha (α) shape theory.
4. To create two ground truth s for 3D visualisation and volume calculation of MRI brain tumour, respectively.

1.7 Research Scope

This study is a synthesis of a complete process of the previous works. A novel approach to MR image classification into normal and abnormal MRI slices and segmentation of the brain tumour will be developed. Finally, it will provide a full automatic system for 3D visualization and volume calculation of human brain

tumour. Computer experiments will be performed to test the proposed system on three standard datasets. The first two datasets are obtained from the Internet Brain Segmentation Repository (IBSR) created by the Center for Morphometric Analysis, Massachusetts General Hospital (USA), named IBSR (10Normals_T1) without any brain tumour and IBSR (536_T1) with brain tumours. They are used by several researchers for brain tumour detection worldwide. The third dataset called challenge MICCAI (BRATS2012-BRATS-1). The Multimodal Brain Tumour Segmentation (BRATS) challenge was the 15th international conference on Medical Image Computing and Computer Assisted Intervention (MICCAI 2012) held in France (2012). This datasets provides a large number of brain tumour MRI scans in which the brain tumour regions have been manually delineated.

This study will mainly focus on T1-weighted High-Grade (HG) brain tumour in three planes (axial, coronal, and sagittal plane) for MR image segmentation, 3D visualization and volume calculation of elevated category. However, the Low-Grade (LG) tumour and tumour classification either benign or malignant are beyond the scope of the present thesis. In addition, another MRI pulse sequences such as T2-weighted, PD-weighted (Proton Density), and Fluid-Attenuated Inversion-Recovery (FLAIR) are not within the scope.

1.8 Significance of the Study

The aforesaid diagnosis errors developed, the reason to form the foundation for the work presented here. It is strongly believed that complete automatic brain tumour detection system can improve both the false positive and the false negative diagnosis rates. The motivation of conducting this PhD study is to propose state-of-the-art, optimized and innovative techniques for the brain tumour detection. Proposed techniques should be capable to provide promising performance in an undesirable situation such as separating the MRI slices into normal and abnormal,

precise segmentation for the brain tumour by reducing segmentation error, resolve problems associated with tumour volume calculation, and visualize the brain tumour in 3D shape, and give a new way to create a new ground truth. In light of the above mentioned issues, the results of this research will contribute to what is currently known about brain tumour detection systems. Nonetheless, the significance of this study is not only limited to knowledge enrichment, but also to the development of a new method for future implementation and brain tumour diagnosis and cure.

1.9 Thesis Outline

This thesis is organized as follows. The rest of the chapters begin with a brief description highlighting the aims of each chapter and ends with a short summary. Each chapter is developed to be self-contained, but there exists cohesion among the chapters in order to ensure the free flow of presentation and understanding of the thesis content. It should also be borne in mind that mathematical notations and definitions are introduced at various points to render a consistency and better understanding of the presentation.

Chapter 2 provides an in-depth overview of relevant literatures on MR images of brain tumour detection, segmentation, 3D visualization, and volume calculation. It is emphasised that the brain tumour in MR images is still an emerging research area with very little literatures. Subsequently, a thorough discussion is provided on various approaches used so far in the brain MR image segmentation. The limitations of the existing methods and the need to develop a new method for detecting abnormal MRI slices, segmentation, visualization and volume calculation of brain tumour problems are underscored.

Chapter 3 presents a clear roadmap of this study to guide the reader for quick grasp of the detailed research framework. The advantages of using the popular dataset in the newly developed methods are emphasized. The layout of the entire research framework, strategies, and procedures are highlighted.

Chapter 4 discusses the proposed methods in details. It covers the cerebral tissue extraction, slice abnormality detection, segmentation, 3D visualisation and volume calculation of the MRI brain tumour.

Chapter 5 provides the experimental results, detailed analyses, and discussions. It explains the qualitative and quantitative measurements that are carried out for the performance evaluations and implementation of the method for every single phase such as detection of the MRI slices abnormal, segmentation of brain tumour, brain tumour 3D visualization and volume calculation. The qualitative measurements are based on visual human inspections, while the quantitative measurements are performed using standard approaches. In addition, every process is benchmarked against the best and up-to-date techniques for segmentation and volume calculation found in the literature.

Chapter 6 concludes by emphasizing the major contributions, significant findings, and recommended future directions of the present thesis.

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