

Project summary

In this project we developed a detailed algorithm to visualize the tumors in the MRI images.

In this process we had gone through various image processing techniques Digital Image Representation, Basic Image processing tasks, Statistical analysis of an image Segmentation Histogram thresholding. 3D representation is using Volume rendering, Marching Cube Algorithm etc

Aim of the project:

Cancer detection in the preliminary stages with the help of Magnetic Resonance Imaging (MRI) For better understanding of the cancer stage result 2D images are combined to form a 3D view of the cancer.

Literature survey:

- Recent advancement in biomedical image processing using Magnetic Resonance Imaging (MRI) makes it possible to detect and localize brain tumors with ease. We aim to classify brain scans into eight (8) different categories with seven (7) indicating different tumor types and one for normal brain. The proposed classification approach is validated using Leave 2-Out cross-validation technique.-
Muhammad Nasir, Asim Baig and Aasia Khanum
- MRI brain imaging technique is widely used to visualize the anatomy and structure of the brain. The detection of tumour requires several processes on MRI images which includes image preprocessing, feature extraction, image enhancement and classification. The final classification process concludes that a person is diseased or not. segmentation algorithms are reviewed and their advantages- **D.SELVARAJ, R.DHANASEKARAN**
- wavelet domain denoising for removal of Rician noise from MR images.- **Sayali SavajiPP, Parul AroraP**
- MRIbased brain tumor segmentation studies are attracting more and more attention in recent years due to non-invasive imaging and good soft tissue contrast of Magnetic Resonance Imaging (MRI) images. With the development of almost two decades, the innovative approaches applying computer-aided techniques for segmenting brain tumor are becoming more and more mature and coming closer to routine clinical

applications.- **Jin Liu, Min Li, Jianxin Wang , Fangxiang Wu, Tianming Liu, and Yi Pan**

- Despite intensive research, segmentation remains a challenging problem due to the diverse image content, cluttered objects, occlusion, image noise, non-uniform object texture, and other factors. This paper presents an efficient image segmentation approach using K-means clustering technique integrated with Fuzzy C-means algorithm.- **Eman Abdel-Maksoud , Mohammed Elmogy , Rashid Al-Awadi**

Later developed algorithm is applied on to the MRI slices to identify the cancer. Since Doctors had only the 2D Image Data to visualize the tumors in the MRI images, which never gave the actual feel of how the tumor would exactly look like, it is necessary to view the cancer in 3D. In order to have the complete information of the cancer, the signature in all three dimensions is required. Therefore these images are processed to extract the 3D signature of the cancer. Among all the methods, the proposed algorithm segmented the image well by retaining the edge pixels which gives perfect volume of the tumor in terms of pixels.

Technical report submitted to UGC Minor Research Project

**ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE
IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS**

UGC Minor Research project sanction F. No. MRP-6175/15 dated 28-01-2015

(Technical report No. AITAM/ECE/UGC/Minor Res proj/ YSR/2017/Mar)

Y.SRINIVASA RAO

Principal Investigator



**Department of Electronics & Communication Engineering
Aditya Institute of Technology and Management (A)
Tekkali, Srikakulam-532201, A.P., India**

ACKNOWLEDGEMENT

It is indeed with a great sense of pleasure and immense sense of gratitude that I acknowledge the help of these individuals. I am highly indebted to the **University Grants Commission – S.E.R.O, Hyderabad** for considering my proposal and providing financial assistance.

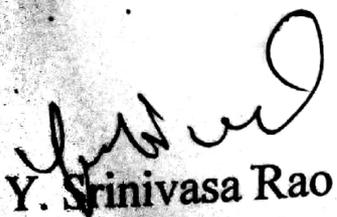
I am highly indebted to **Prof. V. V. Nageswara Rao**, Director of **Aditya Institute of Technology And Management (A)** and **Dr.K.B.Madhu sahu**, Principal for the facilities provided to accomplish this project.

I would like to thank **Dr.G.Sateesh Kumar**, Head of the Department, Dept. of **ECE** for his constructive criticism throughout the project.

My heartfelt thanks are due to **Dr. R.Madhu**, Asst. Prof, Dept. of **ECE**, **JNTUK, Kakinada** and **Dr.M.N.V.S.S Kumar**, Assoc. Prof., **AITAM** for their great support throughout the project.

I express my gratitude to all teaching and nonteaching staff of our department for their cooperation and keen interest throughout the project.

Finally, I express my heartfelt thanks to all of my friends and family members who helped me in successful completion of this project


Y. Srinivasa Rao

Principal Investigator

CERTIFICATE

This is to certify that the present work titled "**ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS**" is carried out by me and was not submitted for partial / full financial assistance to any other funding agency.


(Mr. Yenni Srinivasa Rao)
Principal Investigator

Chapter I

1.1 Introduction to Brain tumors :

Most analysis in developed countries has exposed that the death rate of individuals suffering from tumor has exaggerated over the past 3 decades. Today one in every of the foremost causes for the rise in fatality among kids and adults is tumor. Brain tumor is a pathology appearing in the intracranial anatomy due to abnormal and unstructured augmentation of cells. It is a very aggressive and life-threatening condition, which must be promptly diagnosed and cured to prevent mortality.

Brain tumors are of various sizes, locations and positions. They even have overlapping intensities with normal tissues. Neoplasm may be benign or malignant will occur in several elements of the brain and may or may be primary tumors. So it is very essential to identify tumors before reaching uncontrollable stage. The mechanism used to identify the tumors is MRI.

MRI is a sophisticated medical imaging technique provides made data concerning the human soft-tissue anatomy it's largely employed in radiology so as to see the structure and performance of the physical body. It produces the elaborated pictures of the body in any direction. Significantly, MRI is useful in neurological (brain), musculoskeletal, and oncological (cancer) imaging because it offers much distinction between the various soft tissues of the body. This MRI image contains lots of information along with tumor.

In this project an attempt is made to identify the tumor by developing a new hybrid algorithm based on Expectation-Maximization, Histogram and object based thresholding methods. The result obtained from this algorithm is in 2D format. For higher understanding of the tumor stage these 2D images are combined to create a 3D view of the tumor.

1.2 Aim of the project:

Cancer detection in the preliminary stages with the help of Magnetic Resonance Imaging (MRI) For better understanding of the cancer stage result 2D images are combined to form a 3D view of the cancer.

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

1.3 Applications of the project:

Cancer research

Cancer diagnosis

1.4 Literature survey:

- Recent advancement in biomedical image processing using Magnetic Resonance Imaging (MRI) makes it possible to detect and localize brain tumors with ease. We aim to classify brain scans into eight (8) different categories with seven (7) indicating different tumor types and one for normal brain. The proposed classification approach is validated using Leave 2-Out cross-validation technique.- **Muhammad Nasir, Asim Baig and Aasia Khanum**
- MRI brain imaging technique is widely used to visualize the anatomy and structure of the brain. The detection of tumour requires several processes on MRI images which includes image preprocessing, feature extraction, image enhancement and classification. The final classification process concludes that a person is diseased or not. segmentation algorithms are reviewed and their advantages- **D.SELVARAJ, R.DHANASEKARAN**
- wavelet domain denoising for removal of Rician noise from MR images.- **Sayali SavajiPP, Parul AroraP**
- MRIbased brain tumor segmentation studies are attracting more and more attention in recent years due to non-invasive imaging and good soft tissue contrast of Magnetic Resonance Imaging (MRI) images. With the development of almost two decades, the innovative approaches applying computer-aided techniques for segmenting brain tumor are becoming more and more mature and coming closer to routine clinical applications.- **Jin Liu, Min Li, Jianxin Wang , Fangxiang Wu, Tianming Liu, and Yi Pan**
- Despite intensive research, segmentation remains a challenging problem due to the diverse image content, cluttered objects, occlusion, image noise, non-uniform object texture, and other factors. This paper presents an efficient image segmentation approach using K-means clustering technique integrated with Fuzzy C-means algorithm.- **Eman Abdel-Maksoud , Mohammed Elmogy , Rashid Al-Awadi**

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

- This project proposes a medical image denoising algorithm using discrete wavelet transform. The presence of noise in biomedical images is a major challenge in image processing and analysis. Denoising techniques are aimed at removing noise or distortion from images while retaining the original quality of the image.- **Shashikant Agrawal, Rajkumar Sahu**
- There is a growing interest in using multiresolution noise filters in a variety of medical imaging applications. We review recent wavelet denoising techniques for medical ultrasound and for magnetic resonance images and discuss some of their potential applications in the clinical investigations of the brain.- **Aleksandra Pi_zurica, Alle Meije Wink, Ewout Vansteenkiste, Wilfried Philips and Jos B.T.M. Roerdink**
- In the past, many researchers in the field of medical imaging and soft computing have made significant survey in the field of brain tumor segmentation. Both semiautomatic and fully automatic methods have been proposed.- **Nelly Gordillo , Eduard Montseny , Pilar Sobrevilla**
- A novel hybrid method using Gaussian Mixture Model based Hidden Markov Random Field (HMRF) with Expectation Maximization (EM) has been proposed which segments tissues from MR brain images efficiently and helps to separate out tumour area easily.- **Saurabh Shah and N C Chauhan**
- An algorithm is presented for fully automated brain tumor segmentation from only two magnetic resonance image modalities. The technique is based on three steps: (1) alternating different levels of automatic histogram-based multi-thresholding step, (2) performing an effective and fully automated procedure for skull-stripping by evolving deformable contours, and (3) segmenting both Gross Tumor Volume and edema. The method is tested using 19 hand-segmented real tumors which shows very accurate results in comparison to a very recent method (STS) in terms of the Dice coefficient. Improvements of 5% and 20% respectively for segmentation of edema and Gross Tumor Volume have been recorded.- **Mohamed Ben Salah, Idanis Diaz, Russell Greiner, Pierre Boulanger, Bret Hoehn, and Albert Murtha.**

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

- With the development of computer image processing technology, three-dimensional (3D) visualization has become an important method of the medical diagnose, it offers abundant and accurate information for medical experts. Three-dimensional (3-D) reconstruction of medical images is widely applied to tumor localization; surgical planning and brain electromagnetic field computation etc.- **Megha Borse, S.B. Patil, B.S.Patil**
- We propose an effective and efficient approach to 3D reconstruction of brain tumor and estimation of its volume from a set of two dimensional (2D) cross sectional magnetic resonance (MR) images of the brain. In the first step, MR images are preprocessed to improve the quality of the image. Next, abnormal slices are identified based on histogram analysis and tumor on those slices is segmented using modified fuzzy c-means (MFCM) clustering algorithm. Next, the proposed enhanced shape based interpolation technique is applied to estimate the missing slices accurately and efficiently. Then, the surface mesh of the tumor is reconstructed by applying the marching cubes (MC) algorithm on a set of abnormal slices. The large number of triangles generated by the MC algorithm was reduced by our proposed mesh simplification algorithm to accelerate the rendering phase. Finally, rendering was performed by applying Phong lighting and shading model on the reconstructed mesh to add realism to the 3D model of the tumor.- **Megha P. Arakeri and G. Ram Mohana Reddy**
- This project presents method for 3D image reconstruction, which is one of the most attractive avenues in Computed tomography (CT) and Magnetic Resonance Imaging (MRI) are modern and valuable diagnostic methods in a wide range of medical applications. Segmentation of anatomical regions of the brain is the fundamental problem in medical image analysis. In this paper brain tumor segmentation method has been developed and validated segmentation on 2D MRI Data. And morphology or other functions. Finally, work was carried over to calculate the area of the tumor of single slice of MRI data set and then it was extended to calculate the volume of the tumor from multiple image MRI data sets.- **NAVEENKUMAR.R, SANJAY D.S**

- In this study, we have proposed a three-dimensional (3D) model reconstruction system for breast tumors. This developed system uses multispectral breast magnetic resonance images as input and detects the contour of the tumor in different sections using an active contour method — multispectral gradient vector flow snake (MGVFS) method. - **Sheng-Chih Yang, Cheng-Yi Yu, Cheng-Jian Lin, Hsueh-Yi Lin, Chi-Yuan Lin**

1.5 Methodology:

To reduce the computational cost and improve the accuracy rate for tumor 3d reconstruction, the following steps are applied in the proposed algorithm, which is briefly described in this section. The block diagram of proposed work is shown in Fig. 1.

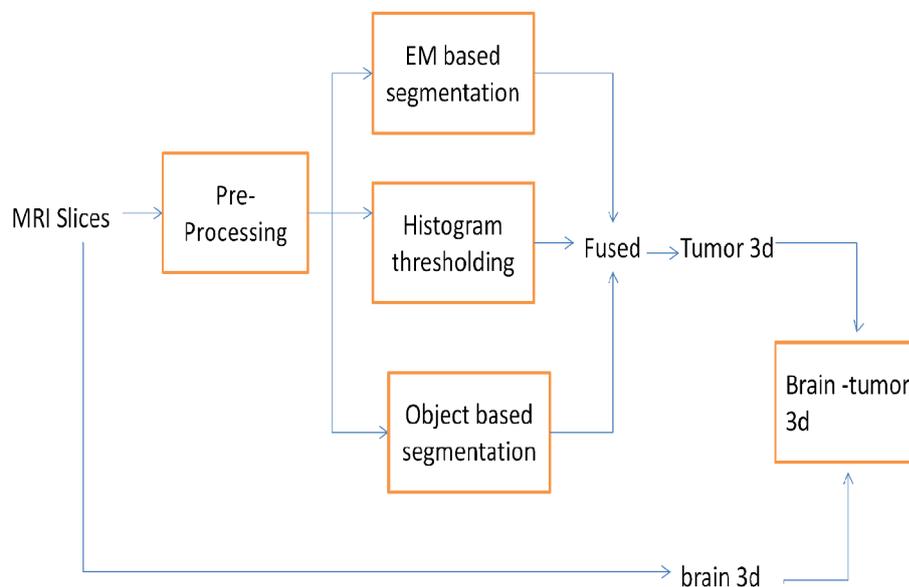


Fig. 1.1 flowchart of proposed algorithm

1.6 Organization of the project:

The project is organized as follows. Chapter 1 provides the introductory part, aims, applications, Literature review and methodology. Basics of image processing discuss in chapter 2. Wavelet denoising various segmentation techniques and different kinds of algorithms are discussed in Chapter 3. Chapter 4 provides Volume Visualization methods & proposed methodology. Simulation results are presented in Chapter 5.

Chapter II

2.1 Introduction

Digital image processing is the process that uses the computer algorithms to perform processing on digital images. It has many advantages over analog image processing. Digital images are usually obtained by converting continuous signals to digital format. They are viewed using diverse display media including digital printers, computer monitors and so on. The frequency with which information is transmitted, stored, processed and displayed in the digital visual format is increasing rapidly. The design of engineering methods for efficiently transmitting, maintaining and even improving the visual integrity of this information is heightened. The objective of this chapter is to give an idea of image processing by examining some of the principal areas in which it is applied. The principal approaches discussed in this chapter include digital image representation, overview of the tasks contained in an image processing system and reconstruction of an image using the magnitude and phase information of the Fourier transformed image. Description of the image statistics such as average brightness, standard deviation, Signal to Noise ratio (SNR), Mean Square Error (MSE) etc., used in image processing are also discussed.

2.2 Digital Image Representation

An image is defined as a two dimensional function, $f(x, y)$, where x and y are spatial coordinates. The amplitude of 'f' at any pair of coordinates (x, y) is called the intensity or gray level of the image at that point. An analog image is continuous with respect to x and y coordinates and also in amplitude. Converting such an image to digital form requires that the coordinates, as well as the amplitude be digitized (Sohi et al 2000). Digitizing the coordinate values is called sampling and digitizing the amplitude values is called quantization. Thus, when x , y and the amplitude values of function, f , are all finite discrete quantities, then an image is a digital image. Fig. 2.1 illustrates the relationship between an analog image and a digital image.

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

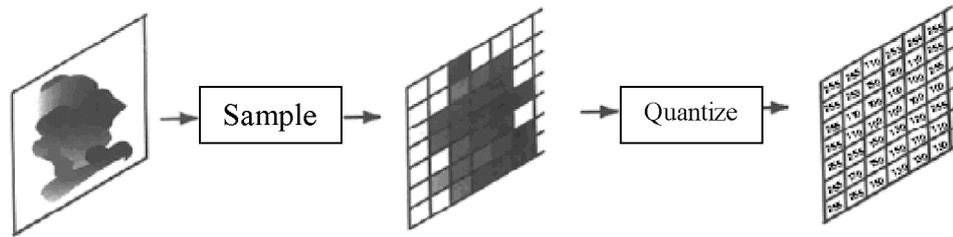


Fig. 2.1 Relationship between an analog image and a digitized image

If an image $f(x, y)$ is divided into M rows and N columns, then the intersection of a row and a column is termed as a pixel or picture element. Each picture element will have a location and a value. Pixel is the term most widely used to denote the elements of a digital image. The image shown in Fig. 2.2 has been divided into $M=16$ rows and $N=16$ columns. The value assigned to every pixel is the average brightness of the pixel rounded to the nearest integer value. The process of representing the amplitude of the 2D signal at a given coordinate as an integer value with L different gray levels is usually referred to as amplitude quantization or simply quantization.

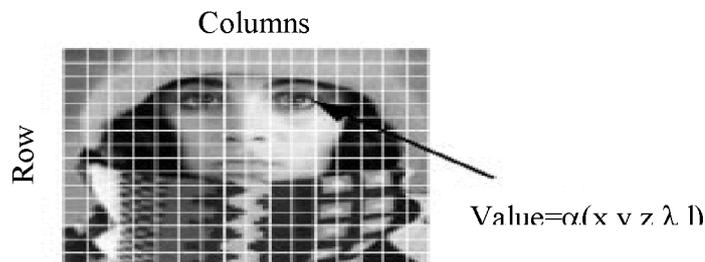


Fig. 2.2 Digitization of a continuous image

The main difference between the conventional coordinate system and the image coordinate system is that the origin is at $(x, y) = (1, 1)$ which is at the top left hand side of the image. This coordinate convention is such that the first component x increases downwards and the second component y increases to the right from the origin.

2.2.1 Types of Digital Images

- i) **Binary Images:** Each pixel in a binary image is either black or white. Binary images are also called as bi-level or two-level. Since there are only two possible values for each pixel, it requires only one bit per pixel. Such images can therefore be very efficient in terms of storage. Images for which a binary representation may be suitable includes text

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

(printed or handwriting), fingerprints or architectural plans. Binary images often arise in digital image processing as masks or as the result of certain operations such as segmentation, thresholding and dithering. The names black and white (B&W), monochrome or monochromatic are often used for this concept.

- ii) Grayscale Images:* Grayscale image is an image in which each pixel is a shade of grey, normally varying from 0 (black) at the weakest intensity to 255 (white) at the strongest. Grayscale images are typically stored as 8 bits per sample i.e., each pixel can be represented by eight bits or exactly one byte which allows 256 intensities (i.e., shades of grey) to be recorded typically on a non linear scale. This is a very natural range for image file handling. Other grayscale ranges are used, but generally they are a power of 2. Such images arise in medicine (X-rays), images of printed works and indeed 256 different grey levels are sufficient for the recognition of most natural objects. Gray scale images are also called as intensity images.
- iii) True colour or RGB:* In RGB images, each pixel has a particular colour which is described by the amount of red, green and blue in it. Each of these components has a range of about 0–255, which gives a total of $256^3=16,777,216$ different possible colours in the image. Since the total number of bits required for each pixel is 24, such images are also called 24-bit colour images. Such an image may be considered as consisting of a “stack” of three matrices; representing the red, green and blue values for each pixel. This means that for every pixel, there correspond to three values.
- iv) Indexed:* Most colour images have only a small subset of the more than sixteen million possible colours. For convenience of storage and file handling, the image has an associated map or palette, which is simply a list of all the colours used in that image. Each pixel has a value which does not give its colour (as for an RGB image), but an index to the in the map. It is convenient if an image has 256 s or less. Then the index values will require only one byte each to store.

2.2.2 Gray level transformation

As discussed earlier in this chapter, a digital image is a matrix of digital numbers. i.e., there are a large number of digital numbers in any given image and these digital numbers or intensity values are filled in pixels. Statistically, all these numbers form an

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

ungrouped data set and such data set is difficult to understand spatially. Information extraction from such an ungrouped data set is also a difficult process and sometimes is not possible. Hence, it is necessary to convert or transform the ungrouped intensity values into grouped data using frequency distribution or Histogram method.

The image histogram is a valuable tool used to view the intensity profile of an image. The histogram provides information about the contrast and overall intensity distribution of an image (Cox I. et al, 1995). The image histogram is simply a bar graph of the pixel intensities. The pixel intensities are plotted along the x-axis and the number of occurrences for each intensity value represents the y-axis. A sample histogram of an image is shown in Fig. 2.3.

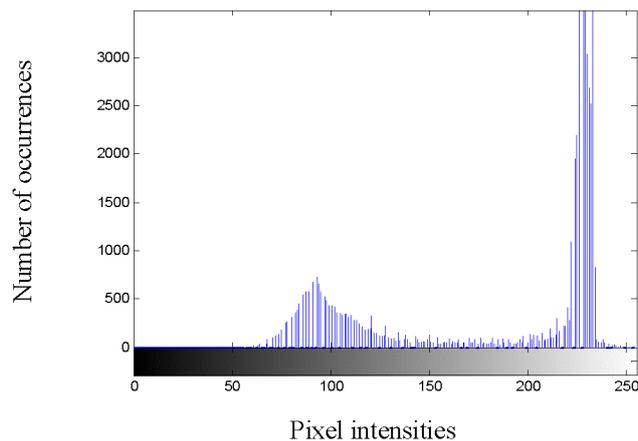


Fig. 2.3 Sample histogram of an image

The histogram of a digital image with L total possible intensity levels in the range $[0, G]$ is defined as the discrete function

$$h(r_k) = n_k \quad (2.1)$$

Where r_k is the k^{th} intensity level in the interval $[0, G]$ and n_k is the number of pixels in the image whose intensity level is r_k . The value of G is 255 for images of class uint8, 65535 for images of class uint16, and 1.0 for images of class double. It is to be noted that indices in MATLAB cannot be 0, so r_1 corresponds to intensity level 0, r_2 corresponds to intensity level 1, and so on, with r_L corresponding to level G (Gonzalez R. C., 2005). Also, note that $G=L-1$ for images of class uint8 and uint16. Often it is

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

useful to work with normalized histograms obtained simply by dividing all elements of $h(r_k)$ by the total number of pixels in the image which is denoted by n .

$$p(r_k) = \frac{h(r_k)}{n} = \frac{n_k}{n} \quad \text{for } k=1,2,3, \dots, L \quad (2.2)$$

From basic probability, $p(r_k)$ recognized as an estimate of the probability of occurrence of intensity level r_k .

2.3 Basic Image processing tasks

Fig. 2.4 shows basic operations that are generally carried out in image processing. The intension is to convey an idea of all the methodologies that can be applied to images for different purposes (Sohi D. S. et al, 2000).

i) Image acquisition is the process of sensing our surroundings and then representing the measurements that are made in the form of an image. The sensing phase distinguishes image acquisition from image creation. Acquisition can be accomplished using an existing set of data, and does not require a sensor.

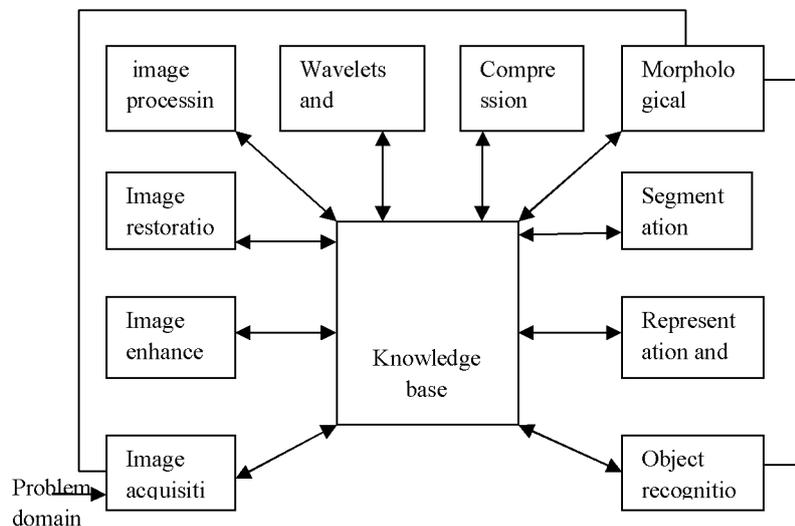


FIG 2.4 Schematic of an image

ii) Image enhancement is the step in which the principle objective is to process an image so that the result is more suitable than the original image for a specific application. The word “specific” is important because the processing techniques for the image depend upon the application. Image enhancement techniques can be divided into

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

two broad techniques namely, spatial domain methods, which operate directly on pixels, and frequency domain methods, which operate on the Fourier Transform (FT) of an image. Spatial domain methods include contrast stretching, contrast enhancement, brightness adjustment, dynamic range compression, image subtraction, image averaging, histogram operations such as histogram equalization, adaptive histogram equalization and various spatial filters such as smoothing filters, sharpening filters, derivative filters.

Frequency domain techniques are based on modifying the Fourier Transform (FT) of an image. The frequency domain methods include transform operations such as lowpass filtering, Highpass filtering, Bandpass filtering, Butterworth filtering, Histogram operations etc.

iii) Image restoration: The objective of restoration is to improve a given image in some predefined sense. Although there are areas of overlap between image enhancement and image restoration, the former is largely a subjective process while image restoration is an objective process in the sense that restoration techniques are based on mathematical or probabilistic models of image degradation. Restoration attempts to reconstruct or recover an image that has been degraded by using a priori knowledge of the degraded phenomenon. Thus, restoration techniques are oriented towards modeling the degradation and applying the inverse process in order to recover the original image (Russell et al, 2008). For example, noise removal of image blur by applying a deblurring function is considered as a restoration technique. There are two basic types of noise models: noise in spatial domain described by the noise Probability Density Function (PDF), and noise in frequency domain described by various Fourier properties of the noise (Bernd Jahne 2004). The parameters of periodic noise are typically estimated by analyzing the Fourier spectrum of the image. In case of noise in spatial domain, the parameters of the PDF may be known partially from sensor specifications, but it is often necessary to estimate them from sample images. The several spatial domain models for noise removal are Arithmetic mean filter, Median filter, Geometric mean filter, Harmonic mean filter, Minimum filter, Maximum filter, Wiener filter etc.

iv) **Morphological processing:** Morphology denotes a branch of biology that deals with the form and structure of animals and plants. The same word can be used in the context of mathematical morphology as a tool for extracting image components that are useful in the representation and description of region shape such as boundaries, skeletons and convex hull. In computer vision, it is about regions or shapes – how they can be changed and counted, and how their areas can be evaluated (Dougherty Edward, 1993). The morphological techniques for pre or post processing include filtering, thinning, and pruning. There are two fundamental morphological operations, dilation and erosion in terms of union (or intersection) of an image with a translated shape (structuring element).

Dilation is an operation that “grows” or “thickens” objects in a binary image. The specific manner and the extent of this thickness are controlled by a shape referred to as a structuring element. Erosion “shrinks” or “thins” objects in a binary image. As in dilation, the manner and extent of shrinking is controlled by a structuring element. Computationally, structuring elements typically are represented by a matrix of 0s and 1s. Sometimes, it is convenient to show only the 1s. In addition, the origin of the structuring element must be clearly identified.

v) **Segmentation:** Partitioning an image into its constituent regions or objects is called segmentation. The level of subdivision carried depends on the problem being solved. That is, segmentation should stop when the objects of interest in an application have been isolated. Segmentation is a basic requirement for identification and classification of objects in an image. Segmentation can be achieved from two basic properties of image intensity values: discontinuity and similarity. In the first category, the approach is to partition an image based on abrupt changes in the intensity such as edges in an image (Foresti G. L. et al, 1997). The principle approaches in the second category are based on partitioning an image into regions that are similar according to a set of predefined criteria (Cseke I., 1992). Thresholding is a fundamental approach to segmentation that is popular especially in applications where speed is an important factor. Another approach to segmentation is morphology, which produces closed well-defined regions.

vi) **Representation and Description:** After an image has been segmented into regions, the next step usually is to represent and describe the aggregate of segmented “raw” pixels in a form suitable for further computer processing. Representing a region involves two basic choices:

- a)* in terms of its external characteristics (its boundary) and
- b)* in terms of its internal characteristics (the pixels comprising the region).

Choosing a representation is only a part of the task of making data useful to a computer (Russell et al, 2008). The next task is to describe the region based on the chosen representation. For example, a region may be represented by its boundary and boundary may be described by the features such as its length and the number of concavities it contains. A region is a connected component and the boundary (also called the border or contour) of a region is a connected set of pixels in the region that have one or more neighboring pixels that are not in the region. Points not on the boundary or region are called as background points.

An external representation is selected when the interest is on shape characteristics. An internal representation is selected when principal focus is on regional properties such as colour and texture. The various representation approaches include: chain codes, polygonal approximations, signatures, boundary segments, skeletons. Chain codes are used to represent a boundary by a connected sequence of straight-line segments of specified length and direction. A boundary can be approximated with arbitrary accuracy by a polygon. For a closed curve, the approximation is exact when the number of segments in the polygon is equal to the number of points in the boundary, so that each pair of adjacent points defines an edge of the polygon. The idea of polygon approximation is to use the least vertices possible to capture the “essence” of the boundary.

A signature is a 1-D functional representation of a boundary and may be generated in various ways. One of the simplest ways is to plot the distance from an interior point to the boundary as a function of angle. The basic idea is to reduce the boundary representation to a 1-D function which presumably is easier to describe than

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

the original 2-D boundary. Signatures generated by the above approach are invariant to translation, but they do depend on rotation and scaling (Gonzalez R. C., 2005).

The length of a boundary is one of its simplest descriptors. The length of a 4-connected boundary is the number of pixels in the boundary minus 1. If the boundary is 8-connected, vertical and horizontal transitions are counted as 1 and diagonal transitions as $\sqrt{2}$. The shape of 1-D boundary representations (e.g., boundary segments and signature waveforms) can be described quantitatively by using statistical moments such as mean, variance and higher-order moments. Other descriptors such as Fourier descriptors, Regional descriptors etc. are also in existence (Quidu I. et al, 2000).

vii) Object recognition: The regions and/or boundaries are called as objects or patterns. Pattern recognition identifies objects from an image using object models which are known a priori. This assigns a label to an object based on its descriptors (Tommasini T. et al, 1998). Pattern recognition may be divided into two principal areas: decision-theoretic and structural (Mei Han et al, 2004). The first category deals with patterns described using quantitative descriptors such as length, area, texture and many of the other descriptors. The second category deals with patterns best represented by symbolic information such as strings etc. (Mignotte et al, 1998).

viii) Colour image processing: Image processing toolbox handles colour images either as indexed images or RGB (red, green, blue) images. The colour image processing includes the development of additional colour generation and transformation functions from one colour space to other. However, there are other colour spaces (also called colour models) such as NTSC, YCbCr, HSV, CMY, etc., whose use in some applications may be more convenient and/or appropriate than RGB.

ix) Compression: Image compression addresses the problem of reducing the amount of data required to represent a digital image. Compression is achieved by the removal of one or more of following three basic data redundancies:

- a) coding redundancy, which is present when less than optimal (i.e., the smallest length) code words are used;*
- b) inter-pixel redundancy, which results from correlations between the pixels of an image;*

c) psychovisual redundancy, which is due to data that is ignored by the human visual system (i.e., visually nonessential information).

x) **Wavelets** are the foundation for representing images in various degrees of resolution i.e, when digital images are to be viewed or processed at multiple resolutions, the Discrete Wavelet Transform (DWT) is the mathematical tool of choice. The DWT provides useful insight into an image's spatial and frequency characteristics. Wavelets can also be used in applications in which Fourier methods are not well suited like progressive image reconstruction etc.

DWT refers to a class of transformations that differ not only in the transformation kernels, but also in the fundamental nature of those functions (whether they constitute an orthonormal or biorthonormal basis). Like the Fourier transform, wavelet transforms can be used in tasks ranging from edge detection to image smoothing. One use of wavelet approximation is in data compression. In similarity with the other transforms, wavelet transforms can be used to transform data and encode the transformed data, resulting in effective compression. For example, JPEG 2000 is an image compression standard that uses biorthogonal wavelets.

xi) **Knowledge base:** Knowledge about a problem domain is coded into an image processing system in the form of knowledge database. This knowledge may be as simple as detailing regions of an image where the information of interest is known to be located, thus limiting the search that has to be conducted in seeking that information. Knowledge base is quite complex such as an interrelated list of all possible defects in a material inspection problem or an image database containing high-resolution satellite images of a region in connection with the change-detection applications.

In addition to guiding the operation of each processing module, the knowledge base also controls the interaction between each module. This is indicated in Fig. 4.4 by using double headed arrows between the processing modules and the knowledge base.

2.4 Statistical analysis of an image

In image processing, it is quite common to use simple statistical descriptions of images and sub images for performance analysis. The notion of a statistic is intimately connected to the concept of a probability distribution, generally the distribution of

signal amplitudes. For a given image (or a region), the probability distribution function and the probability density function of the brightness in that region can be defined. In this section, the computations for the estimation of image statistics with respect to a region in an image are given (Deutsch R., 1965).

i) Probability Distribution Function of the brightness

The probability distribution function, $P(a)$, is the probability that a brightness chosen from the region is less than or equal to a given brightness value 'a'. As 'a' varies from $+\infty$ to $-\infty$, $P(a)$ increases from 0 to 1. $P(a)$ is monotonic, non decreasing in 'a' and thus $dP/da \geq 0$.

ii) Probability Density Function of the brightness

The probability that brightness in a region falls between 'a' and 'a + Δa ', given the probability distribution function $P(a)$, can be expressed as $p(a)\Delta a$, where $p(a)$ is the probability density function

$$p(a)\Delta a = \left(\frac{dP(a)}{da} \right) \Delta a \quad (2.3)$$

Because of the monotonic, non decreasing character of $P(a)$

$$p(a) \geq 0 \text{ and } \int_{-\infty}^{\infty} p(a)da = 1 \quad (2.4)$$

For an image with quantized (integer) brightness amplitudes, the interpretation of Δa is the width of a brightness interval. By assuming constant width intervals, the brightness probability density function is frequently estimated by counting the number of times that each brightness occurs in the region to generate a histogram, $h[a]$. The histogram can then be normalized so that the total area under the histogram is 1 as shown in Eq. (2.4). In other way, the $p(a)$ for a region is the normalized count of the number of pixels, 'n', in a region that has a quantized brightness 'a' is

$$p(a) = \frac{1}{n} h[a] \text{ With } n = \sum_a h[a] \quad (2.5)$$

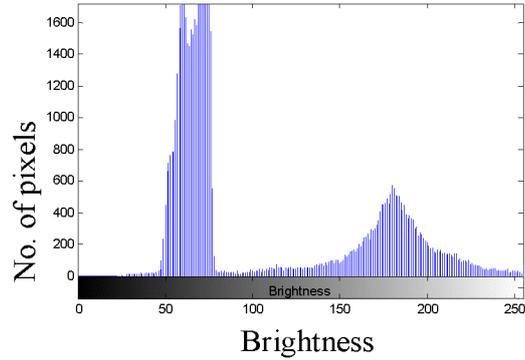


Fig. 2.5 (a) Original image

(b) Brightness histogram

The (un-normalized) brightness histogram of Fig. 2.5(a) which is proportional to the estimated brightness probability density function is shown in Fig. 2.5(b). The height in this histogram corresponds to the number of pixels with a given brightness. Both the distribution function and the histogram as measured from a region are a statistical description of that region. It should be emphasized that both $P(a)$ and $p(a)$ should be viewed as estimates of true distributions when they are computed from a specific region. That is, an image and a specific region can be viewed as one realization of the various random processes involved in the formation of that image and that region. In the same context, the statistics defined below must be viewed as estimates of the underlying parameters.

iii) Average

The average brightness of an image or a region in the image is defined as the sample mean of the pixel brightness within that region. The average, m_a , of the brightness over the n pixels within a region is given by

$$m_a = \frac{1}{n} \sum_{(m,n) \in r} a(m, n) \quad (2.6)$$

Alternatively, formulation based on the (unnormalized) brightness histogram, $h[a] = n \times p(a)$ with discrete brightness values a can be used. This gives

$$m_a = \frac{1}{n} \sum_a a \times h[a] \quad (2.7)$$

The average brightness, m_a , is an estimate of the mean brightness of the underlying brightness probability distribution.

iv) Standard Deviation

The unbiased estimate of the standard deviation, s_a , of the brightness within a region r with 'n' pixels is called the sample standard deviation and is given by

$$s_a = \sqrt{\frac{1}{n-1} \sum_{(m,n) \in r} (a(m,n) - m_a)^2} \quad (2.8)$$

By using the histogram, the above Eq. (2.8) can be written as

$$s_a = \sqrt{\frac{\left(\sum_a a^2 \times h[a] \right) - n \times m_a^2}{n-1}} \quad (2.9)$$

The standard deviation, s_a is an estimate of σ_a which is the underlying brightness probability distribution.

v) Coefficient-of-Variation

The dimensionless Coefficient-of-Variation (CV), is defined as

$$CV = \frac{s_a}{m_a} \times 100\% \quad (2.10)$$

vi) Percentiles

The percentile, $p\%$ of an unquantized brightness distribution is defined as that value of the brightness 'a' such that

$$P(a) = p\% \quad \text{or} \quad \int_{-\infty}^a p(\alpha) d(\alpha) = p\% \quad (2.11)$$

Three special cases are frequently used in digital image processing.

0% means the minimum value in the region

50% means the median value in the region

100% means the maximum value in the region

vii) Mode

The mode of the distribution is the most frequent brightness value. There is no guarantee that a mode exists or that it is unique.

**ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI)
DATA TO IDENTIFY BRAIN DISORDERS**

viii) Signal to Noise Ratio (SNR)

The SNR can have several definitions. The noise is characterized by its standard deviation, s_n . The characterization of the signal can differ. If the signal is known to lie between the two boundaries, $a_{\min} \leq a \leq a_{\max}$, then the SNR for a bounded signal is

$$\text{defined as } SNR = 20 \log_{10} \left(\frac{a_{\max} - a_{\min}}{s_n} \right) dB \quad (2.12)$$

If the signal is not bounded but has a statistical distribution, then two other definitions for a stochastic signal are

$$\text{If signal and noise are Inter-dependent, } SNR = 20 \log_{10} \left(\frac{m_a}{s_n} \right) dB \quad (2.13)$$

$$\text{If signal and noise are Independent } SNR = 20 \log_{10} \left(\frac{s_a}{s_n} \right) dB \quad (2.14)$$

Where m_a and s_a are defined in (2.14) and 2.16).

Statistical Parameter	Value (pixel intensity)
Average	102.9791
Standard deviation	13.2861
Minimum	23
Median	73
Maximum	255
Mode	73

Table 2.1 Image statistics from Fig 2.5(a).

Table 2.1 gives the list of statistical parameters and their values obtained for an image shown in Fig 2.5(a). Mean Square Error (MSE) and Peak Signal to Noise Ratio (PSNR) are the two parameters which are used in this thesis to evaluate the performance of the developed algorithms. These parameters are calculated for the original image and the image obtained after doing some processing. They are given as

ix) **Mean Square Error (MSE)**

$$MSE = \frac{1}{MN} \sum_{x=1}^M \sum_{y=1}^N \|f(x, y) - J(x, y)\|^2 \quad (2.15)$$

where $f(x,y)$ denotes the samples of the original input image and $J(x,y)$ denotes the samples of the processed image. M and N are number of pixels in row and column directions respectively.

x) **Peak Signal to Noise Ratio (PSNR)**

$$PSNR = 10 \log_{10} \left(\frac{MAX_I^2}{MSE} \right) = 20 \log_{10} \left(\frac{MAX}{\sqrt{MSE}} \right) \quad (2.16)$$

where MAX_I is the maximum pixel value of the original image. When the pixels are represented using 8 bits per sample, this value is 255.

2.4.1 Image Processing Applications

The field of digital image processing has experienced continuous and significant expansion in recent years (Bernd Jahne 2004). The usefulness of this technology is apparent in many different disciplines covering medicine through remote sensing. The advances and wide availability of image processing hardware has further enhanced the usefulness of image processing. Digital image processing applications include (Fig. 2.6)

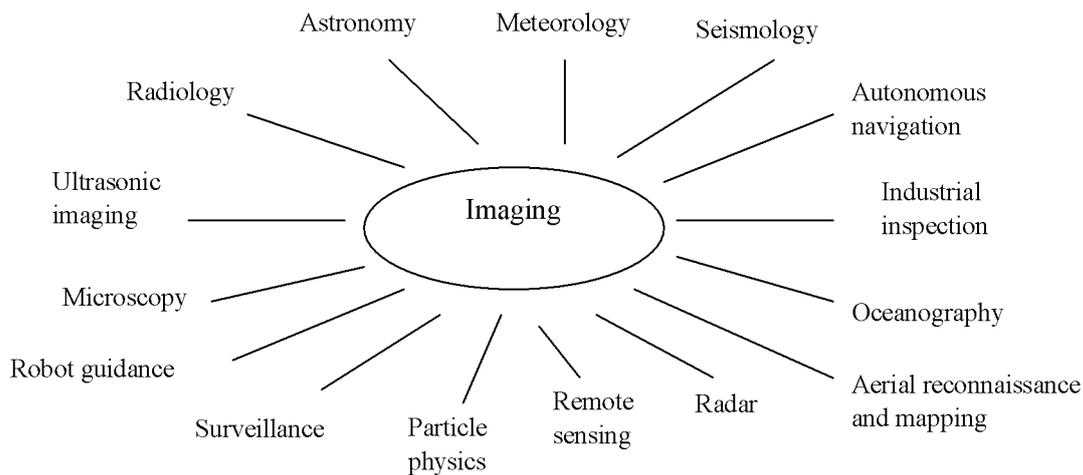


Fig.2.6.Image processing applications

**ANALYSIS OF THREE DIMENTIONAL MAGNETIC RESONANCE IMAGING (MRI)
DATA TO IDENTIFY BRAIN DISORDERS**

new gray value is calculated is a linear function of all the gray values in the mask, then the filter is called a linear filter. A linear filter can be implemented by multiplying all elements in the mask by corresponding elements in the neighbourhood, and adding up all these products. This process is nothing but convolution. Considering a 3x5 mask as illustrated in Fig. 2.7 (a) is considered. The mask values and their corresponding pixels are shown in Fig. 2.7 (b).

$m(-1, -2)$	$m(-1, -1)$	$m(-1, 0)$	$m(-1, 1)$	$m(-1, 2)$	$p(i-1, j-2)$	$p(i-1, j-1)$	$p(i-1, j)$	$p(i-1, j+1)$	$p(i-1, j+2)$
$m(0, -2)$	$m(0, -1)$	$m(0, 0)$	$m(0, 1)$	$m(0, 2)$	$p(i, j-2)$	$p(i, j-1)$	$p(i, j)$	$p(i, j+1)$	$p(i, j+2)$
$m(1, -2)$	$m(1, -1)$	$m(1, 0)$	$m(1, 1)$	$m(1, 2)$	$p(i+1, j-2)$	$p(i+1, j-1)$	$p(i+1, j)$	$p(i+1, j+1)$	$p(i+1, j+2)$

Fig. 2.7 (b) Mask values of the pixels

By performing the convolution process, on the above it can be written as

$$\sum_{s=-1}^1 \sum_{t=-2}^2 m(s, t) p(i+s, j+t) \quad (2.17)$$

where, $m(s, t)$ are the mask coefficients and $p(s, t)$ are the image pixel values

The process for performing linear spatial filtering is illustrated in Fig. 2.8. The spatial filtering process thus requires three steps:

- i)* Position the mask over the current pixel
- ii)* Form all the products of the filter elements with the corresponding elements of neighborhood
- iii)* Finally add up all the products

The above steps are repeated for all pixels in the image. Allied to spatial filtering is spatial convolution. The method for performing a convolution is the same that for filtering, except that the filter must be rotated by 180^0 before multiplying and adding.

Using the $m(i,j)$ and $n(i,j)$ notation as before, the output of a convolution with a mask for a 3×5 mask for a single pixel is

$$\sum_{s=-1}^1 \sum_{t=-2}^2 m(-s, -t) p(i + s, j + t) \quad (2.18)$$

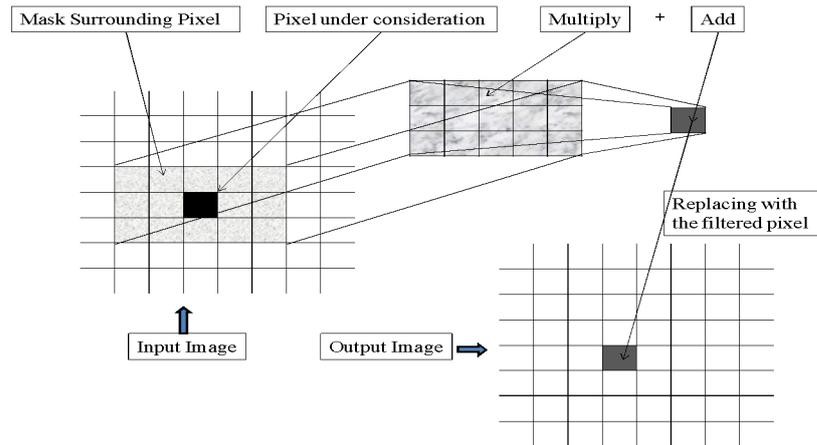
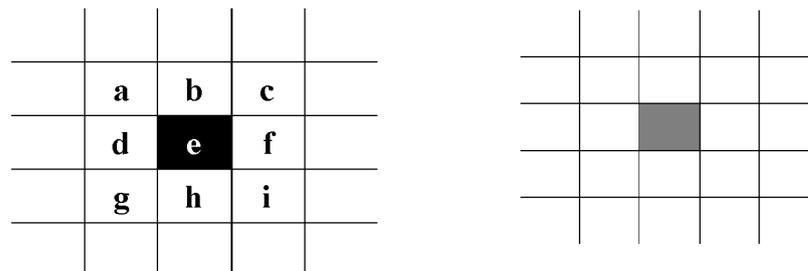


Fig. 2.8 Process for performing linear spatial filtering

The same result can be achieved with the following Eq. (2.19)

$$\sum_{s=-1}^1 \sum_{t=-2}^2 m(s, t) p(i - s, j - t) \quad (2.19)$$

Here, though the image pixels are rotated by 180° , this does not affect the result. The average filter performs spatial filtering on each individual pixel in an image using the gray level values in a square or rectangular window surrounding each pixel (Fisher R et al 2005). One important linear filtering is to use a 3×3 mask and take the average of all nine values within the mask. This value becomes the grey value of the corresponding pixel in the new image. This operation may be described using the following illustration shown in Fig



ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

$$\text{Average} = \frac{1}{y}(a + b + c + d + e + f + g + h + i)$$

Fig. 2.9 (a) A 3×3 mask

Here, e is the grey value of the current pixel in the original image and the average is the grey value of the corresponding pixel in the new image. There is an obvious problem in applying a filter i.e. when applying a mask it partly falls outside the image so there will be a lack of grey values to use in the filter function at the edge of the image Fig. 2.9 (b) (Tim Morris, 2004).

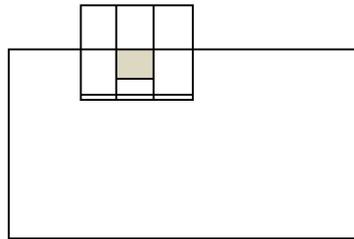


Fig. 2.9 (b) A mask at the edge of an image

There are number of different approaches to deal with this problem:

- i)* The first step is to ignore the edges. That is, the mask is only applied to those pixels in the image for which the mask will lie fully within the image. This means all pixels except for the edges are included and this results in an output image which is smaller than the original. If the mask is very large, a significant amount of information may be lost by this method.
- ii)* The second step is to “Pad” with zeros. All necessary values outside the image are assumed to be zeros. This gives us all values to work with, and will return an output image of the same size as the original, but may have the effect of introducing unwanted artifacts (for example, edges) around the image.
- iii)* The size of the image is extended by replicating the values in its outer border.
- iv)* The size of the image is extended by mirror reflecting it across its border.
- v)* The size of the image is extended by treating the image as one period of a 2-D periodic function.

Chapter III

3.1 Wavelet:

Wavelet may be seen as a complement to classical Fourier decomposition method. Suppose, a certain class of functions is given and we want to find ‘simple functions’, $f_0, f_1, f_3 \dots$ such that each

$$f(x) = \sum_{n=0}^{\infty} a_n f_n(x) \quad (3.1)$$

For some coefficients a_n . Wavelet is a mathematical tool leading to representations of the type (1) for a large class of functions f .

Definition (Wavelet): A wavelet means a small wave (the sinusoids used in Fourier analysis are big waves) and in brief, a wavelet is an oscillation that decays quickly. Equivalent mathematical conditions for wavelet are:

$$\int_{-\infty}^{\infty} |\varphi(t)|^2 dt < \infty \quad (3.2)$$

$$\int_{-\infty}^{\infty} \varphi(t) dt = 0 \quad (3.3)$$

A wavelet is a mathematical function used to divide a given function or continuous-time signal into different scale components. Usually one can assign a frequency range to each scale component. Each scale component can then be studied with a resolution that matches its scale. A wavelet transform is the representation of a function by wavelets. The wavelets are scaled and translated copies (known as "daughter wavelets") of a finite-length or fast decaying oscillating waveform (known as the "mother wavelet").

$$\varphi_{a,b}(t) = \frac{1}{\sqrt{|a|}} \varphi\left(\frac{t-b}{a}\right) \quad a, b \in R, a \neq 0 \quad (3.4)$$

where φ is a wavelet function, a , is a scaling parameter which measure the degree of compression or scale, and b , is a translation parameter which determines the time location of the wavelet. Wavelet transforms have advantages over traditional

Fourier transforms for representing functions that have discontinuities and sharp peaks, and for accurately deconstructing and reconstructing finite, non-periodic and/or non-stationary signals.

3.2 Discrete Wavelet Transform (DWT):

The Wavelet Series is just a sampled version of Continuous Wavelet Transform (CWT) and its computation may consume significant amount of time and resources, depending on the resolution required. If the function being expanded is a sequence of numbers, like samples of a continuous function $f(x)$, the resulting coefficients are called the Discrete Wavelet Transform (DWT) of $f(x)$. In this case, the series expansion of wavelet transform in one dimension is given below.

$$W_{\varphi}(j, k) = \frac{1}{\sqrt{M}} \sum_x f(x) \varphi_{j_0, k}(x) \quad (3.5)$$

$$W_{\chi}(j, k) = \frac{1}{\sqrt{M}} \sum_x f(x) \chi_{j_0, k}(x) \quad (3.6)$$

For $j \geq j_0$ and

$$f(x) = \frac{1}{\sqrt{M}} \sum_k W_{\varphi}(j, k) \varphi_{j_0, k}(x) + \frac{1}{\sqrt{M}} \sum_{j=j_0}^{\infty} \sum_k W_{\chi}(j, k) \chi_{j, k}(x) \quad (3.7)$$

3.3 Some Applications of Wavelets

Wavelets are a powerful statistical tool which can be used for a wide range of applications, namely

- a. Signal processing
- b. Data compression
- c. Smoothing and image denoising
- d. Fingerprint verification
- e. Biology for cell membrane recognition, to distinguish the normal from the pathological membranes
- f. DNA analysis, protein analysis
- g. Blood-pressure, heart-rate and ECG analyses

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

- h. Finance (which is more surprising), for detecting the properties of quick variation of values
- i. In Internet traffic description, for designing the services size
- j. Industrial supervision of gear-wheel
- k. Speech recognition
- l. Computer graphics and multiracial analysis

Many areas of physics have seen this paradigm shift, including molecular dynamics, astrophysics, optics, turbulence and quantum mechanics. Wavelets have been used successfully in other areas of geophysical study. Orthonormal wavelets, for instance, have been applied to the study of atmospheric layer turbulence. Wavelets have also been used to analyze seafloor bathymetry or the topography of the ocean floor. The use of wavelet analysis revealed patterns, trends, and structures that may be overlooked in raw data. Also, the use of methods like local oracles allowed for separation of data in regions of interest. Several other geophysical applications such as analysis of marine seismic data and characterization of hydraulic conductivity distributions have also been used. The usefulness of wavelets in data analysis is clear, particularly in the field of geophysics, where large and cumbersome data sets abound.

3.4 Advantages of Wavelets:

- a. One of the main advantages of wavelets is that they offer a simultaneous localization in time and frequency domain.
- b. The second main advantage of wavelets is that, using fast wavelet transform, it is computationally very fast.
- c. Wavelets have the great advantage of being able to separate the fine details in a signal. Very small wavelets can be used to isolate very fine details in a signal, while very large wavelets can identify coarse details.
- d. A wavelet transform can be used to decompose a signal into component wavelets.
- e. In wavelet theory, it is often possible to obtain a good approximation of the given function f by using only a few coefficients which is the great achievement in compare to Fourier transform.

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

- f. Most of the wavelet coefficients $\{d_{j,k}\}_{|j|,|k|\geq N}$ vanish for large N .
- g. Wavelet theory is capable of revealing aspects of data that other signal analysis techniques miss the aspects like trends, breakdown points, and discontinuities in higher derivatives and self-similarity.
- h. It can often compress or de-noise a signal without appreciable degradation.

3.5 Disadvantages:

- **Lack of shift invariance:** - this results from the down sampling operation at each level. When the input signal is shifted slightly, the amplitude of the wavelet coefficients varies so much.
- **Lack of directional selectivity:** - as the DWT filters are real and separable the DWT cannot distinguish between the opposing diagonal directions.

3.6 Segmentation

Segmentation of an object in an image is performed either by locating all pixels or voxels that form its boundary or by identifying them that belong to the object. In medical imaging, segmentation is an important analysis function for which lots of algorithms and methods have been built up. Variability of data is quite high in medical image processing especially for analyzing anatomical structure and tissue types hence segmentation techniques that provide flexibility, accuracy and convenient automation are of paramount importance. Segmentation subdivides an image into its regions of components or objects and an important tool in medical image processing. As an initial step segmentation can be used for visualization and compression. Through identifying all pixels (for two dimensional image) or voxels (for three dimensional image) belonging to an object, segmentation of that particular object is achieved. In medical imaging, segmentation is vital for feature extraction, image measurements and image display. Segmentation of the brain structure from magnetic resonance imaging (MRI) has received paramount importance as MRI distinguishes itself from other modalities and MRI can be applied in the volumetric analysis of brain tissues such as multiple sclerosis, schizophrenia, epilepsy, Parkinson's disease, Alzheimer's disease, cerebral atrophy, etc. Graph cuts is one the image segmentation techniques which is initiated by

interactive or automated identification of one or more points representing the 'object'. In this technique one or more points representing the 'background' are called seeds and serve as segmentation hard constraints whereas the soft constraints reflect boundary and/or region information. An important feature of this technique is its ability to interactively improve a previously obtained segmentation in an efficient way.

3.7 Histogram thresholding

The most uncomplicated image segmentation process is histogram thresholding since thresholding is fast and economical in computation. For segmenting background and objects, a threshold which is defined as brightness constant is used. Band thresholding, local thresholding, multi thresholding and semi- thresholding are some of the modifications of this technique. Single thresholds that can differ in image elements are known as local threshold whereas Single thresholds that can be applied to the complete image are known as global threshold. In order to determine the threshold automatically, threshold recognition approaches are exploited. Threshold recognition approaches can employ optimal thresholding, p-tile thresholding and histogram shape analysis. Optimal thresholding results in minimum error segmentation as the threshold as the closest gray-level corresponding to the minimum probability between the maxima of two or more normal distributions is established through this approach. For or multi band images multi-spectral thresholding is suitable. As a minimum between the two highest local maxima, in bi-modal histograms the threshold is verified. In the approach where based on the image histogram only one threshold is chosen for the complete image, then it is called global thresholding. It is assumed that the object in interest can be extracted from the background comparing image values having threshold value T (32,132) and the image has a bimodal histogram. In Figure 1, the bimodal histogram of an image $f(x, y)$ with selected threshold T has been illustrated.

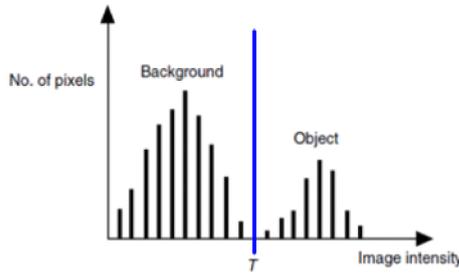


Figure 3.1. Bimodal histogram of an image $f(x, y)$ with selected threshold T .

The threshold image $g(x,y)$ can be represented as below:

$$g(x, y) = \begin{cases} 1, & \text{if } f(x, y) > T \\ 0, & \text{if } f(x, y) \leq T \end{cases} \quad (3.8)$$

The resultant image is a binary image from global thresholding where pixels that correspond to objects and background have value 1 and 0 respectively. Simple and rapid calculation is the main advantages of global thresholding. When thresholding relies on local properties of some image regions, then it is called local thresholding. It can be established in either of the two ways.

In the first way through dividing an image into sub images and calculating threshold for each sub image thresholding can be obtained. In the other way image intensities in the region of each pixel is studied and thresholding is obtained.

Image histogram can be made better through applying image preprocessing techniques. Image smoothing is one this preprocessing technique. Gaussian filter is one of the smoothing filters where based on a Gaussian function convolution mask coefficients are $g[i, j]$ for each pixel $[i, j]$.

$$g[i, j] = \exp\left(-\frac{i^2 + j^2}{2\sigma^2}\right) \quad (3.9)$$

Here σ refers to the spread parameter. Better image smoothing is implied through larger σ .

3.8 Object based thresholding

Thresholding is one of the frequently used method for image segmentation. This method is effective for images with different intensities. Using this method, the image is

partitioned directly into different regions based on the intensity values. Thresholding is defined mathematically

$$g(x, y) = \begin{cases} 1, & \text{if } f(x, y) > T \\ 0, & \text{if } f(x, y) \leq T \end{cases} \quad (3.8)$$

Let $f(x, y)$ be the input image and ‘T’ be the threshold value then the segmented image $g(x, y)$ is given by, Using the above Equation the image can be segmented into 2 groups. If we want to segment the given image into multi groups then we should have multi threshold point. Algorithm:

The algorithm for the thresholding is given by [Gonzalez *et al.* (2007)],

Step 1: Select an initial estimate for the global threshold, T.

Step 2: Segment the image using T in equation (1) to get 2 groups of pixels: G1 consisting of all pixels with intensity values $>T$ and G2 consisting of pixels with values $\leq T$.

Step 3: Compute the average mean intensity values m_1 and m_2 for the pixels in G1 and G2 respectively.

Step 4: Compute a new threshold value

Step 5: Repeat steps 2 through 4 until the difference between values of T in successive iterations is smaller than a predefined parameter ΔT

3.9 EM—a brief history

The name ‘EM’ was coined by Dempster, Laird and Rubin in a paper in 1976 and was published in the Journal of Royal Statistical Society in 1977. Because the idea behind the EM algorithm is very general, algorithms like it were formulated and applied in a variety of problems even before the paper was presented. However, it was in the paper presented by Dempster, Laird and Rubin that various ideas were synthesized and a general theory was developed. The various references to literature on an EM-type of algorithm can be found in.

The EM algorithm is a technique for maximum likelihood estimation in situations best described as incomplete data problems. It is so called because of its two important steps—Expectation (E step) and Maximization (M step). The EM algorithm seeks to iteratively compute the maximum likelihood estimates and it is very useful in situations

where algorithms such as Newton-Raphson, Prediction-Error, Sliding Window and Least-Squares turn out to be tedious and time consuming.

EM has specifically gained importance because in certain incomplete data situations, the maximum likelihood estimation can be difficult due to the absence of the data. If the same problem is converted to a complete data problem with additional unknown parameters, then the problem can be solved more easily using EM iterations. Although these incomplete data problems can arise in different situations, this thesis will study the incomplete data problems as applied to mixture models. In background modeling, the background data can be characterized as coming from a set of different probability distributions. This problem is an incomplete data problem in the sense that the class wise association of the data is unknown. Also the proportions of different classes are not known. Thus in these situations the EM algorithm can be applied to distribute the data into classes and to find the class proportions and parameters of distribution in a parametric mixture model.

3.10 The EM algorithm

The EM algorithm estimates the parameters of the mixture model iteratively, starting from some initial guess. Each iteration consists of the following two steps:

Step 1: (Expectation): This step tries to find the distribution of the complete data given the known values of the observed data and a current estimate of the parameters. The estimation step basically involves the formulation of a ‘ Q ’ function (to be described later), which is basically the estimation of the likelihood function of the complete data given the observed data and the current fit of parameters (i.e. the parameters obtained in the maximization step of the previous iteration).

Step 2: (Maximization): This step re-estimates the parameters to be those with maximum likelihood under the assumption that the distribution found in the estimation step is correct. The maximization step is so called because it maximizes the ‘ Q ’ function formulated in the estimation step to obtain a new set (fit) of parameters.

Each step is carried out in the above order until the terminating condition is reached. The terminating condition can be assumed to have been reached when the log likelihood function of the complete data does not show significant improvement over its previous

value. It can be shown that each successive iteration either improves the true likelihood or leaves it unchanged (if a local maximum has already been reached).

3.11 Mathematical formulation of EM

Let us suppose that for any practical situation:

x = Complete Data (observed plus unobserved),

y = Observed (incomplete) data,

z = Additional data which is missing (or is unobservable).

Also $f(y, \varphi)$ is the probability density function (pdf) of the observed incomplete data, where ' φ ' is the set of parameters that characterize the pdf. The problem is to estimate ' φ ' based on the incomplete information represented by the observed data, ' y '. The likelihood function, $\mathcal{L}(\varphi | y)$, for the parameter, ' φ ' given ' y ' can be formed as:

$$\mathcal{L}(\varphi | y) = f(y, \varphi). \quad (3.10)$$

Log-likelihood function, $\ln[\mathcal{L}(\varphi | y)]$ can be formed where ' \ln ' is the natural logarithm.

$$\ln[\mathcal{L}(\varphi | y)] = \ln[f(y, \varphi)]. \quad (3.11)$$

A log-likelihood function is considered because it makes the analysis and calculations easier without changing the optimization problem at all.

The maximum likelihood estimation problem is complicated by the fact that only the incomplete data is at hand. Thus in order to ease the problem, the incomplete loglikelihood function is converted to the *complete* log-likelihood function by adding the missing information, ' z .' The log-likelihood of the complete data, $\{y, z\} = \{x\}$, is defined as:

$$\ln[\mathcal{L}_c(\varphi | y, z)] = \ln[\mathcal{L}_c(\varphi | x)] = \ln[f(x | \varphi)], \quad (3.12)$$

where $\mathcal{L}_c(\varphi | x)$ is the likelihood function of the complete data.

Therefore the EM algorithm approaches the problem of solving the incomplete data likelihood function indirectly by proceeding iteratively in terms of the complete data loglikelihood function, $\mathcal{L}_c(\varphi | x)$. As the complete data is unobservable, it is replaced by its conditional expectation given the observed data, and the current fit of parameters, i.e.

$$\ln[f(x|\varphi)] = \ln[f(y|\varphi).f(z|y,\varphi)] \quad (3.13)$$

Starting from some initial guess of the parameters, ‘ φ^0 ,’ the EM algorithm iterates between the two steps, known as the ‘E’ and ‘M’ steps. These are described as follows:

E (Estimation) Step: This step forms the ‘ Q ’ function by estimating the log-likelihood of the complete data given the observed data and current fit of parameters. The current fit of parameters is the set of parameters that is obtained from the maximization step of the previous iteration. The ‘ Q ’ function is formulated as:

$$Q(\varphi, \varphi^k) = E_{\varphi^k} [\ln\{\xi_c(\varphi | x)\} | y, \varphi^k] \quad (3.14)$$

where ‘ φ^k ’ represents the current set of parameters and ‘ E_{φ^k} ’ represents the expectation of the log-likelihood of the complete function over ‘ φ^k ’.

M (Maximization) Step: This step maximizes the ‘ Q ’ function in Equation above, to get a new set of parameters, so that,

$$E \left[\frac{\partial [Q(\varphi, \varphi^k)]}{\partial \varphi} \right] = 0 \quad (3.15)$$

The new value of the parameter ‘ φ ’ is given by:

$$\varphi^{k+1} = \varphi^k + (I_m)^{-1} E \left[\frac{\partial [Q(\varphi, \varphi^k)]}{\partial \varphi} \right] \quad (3.16)$$

where ‘ I_m ’ is the information matrix, calculated at ‘ φ^k .’

Once the parameters, ‘ φ^k ,’ are obtained in the k^{th} iteration, the ‘E’ step is carried out again, and the ‘ Q ’ function is updated with these new parameters to form the new estimate of the log-likelihood of the complete data. The ‘M’ step is then carried again for the new updated ‘ Q ’ function to yield a more updated set of parameters, ‘ φ^{k+1} ,’ and the process is carried on until the difference, $\xi_c(\varphi^{k+1} | x) - \xi_c(\varphi^k | x)$, changes by a arbitrarily small amount. At this point, the most likely set of parameters is reached. This condition is often used as the terminating condition.

Chapter-IV

4.1 Volume Visualization

Volume visualization, which includes the representation, manipulation, and rendering of volumetric datasets, is a method of extracting meaningful information from volumetric datasets by using interactive graphics and imaging.

Advantages of volume visualization:

- Insensitivity to scene complexity.
- Insensitivity to object complexity.
- Viewpoint independence.
- Support sampled and simulated datasets.
- Can display inner information of an object.
- Boolean or block operations can be applied.

Volumetric dataset is represented as a 3D grid of voxel which is the element of volume.

4.1.1 Voxel

A voxel is the 3D counterpart of a pixel in 2D space. A voxel can be represented by a quadruple (x,y,z,v) . Cartesian coordinates (x,y,z) are its position in 3D space and “v” is some kind of characteristic associated to this voxel. The value “v” can be either a scalar or a vector. To represent density, temperature and penetrability etc., a scalar value is enough, while representing direction and strength of fluid or wind, a vector is needed. In this thesis, the value used in volumetric dataset is a scalar, e.g. bone density, only. There are two different representations of a voxel (Figure 4.1).

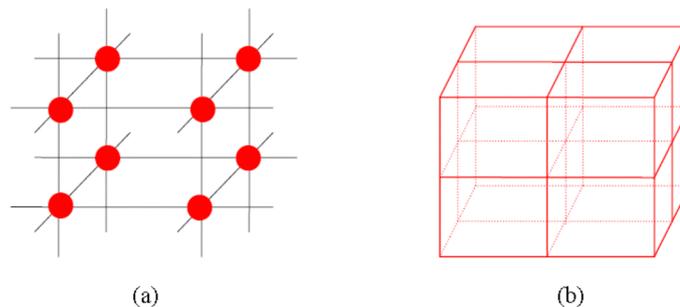


Figure 4.1 Voxel Representation. (a) As grid point; (b) As solid cube.

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

The first is that a voxel is a grid point in a 3D lattice without occupying any space. The other is that a voxel is a solid cube and all the voxels are packed to form the whole volumetric dataset. Those two representations are in fact the same. If we use the center of each cube as a voxel, the second representation can be converted to the first one.

If the scalar value is only either 0 or 1, the volume is called a binary volume. And if the scalar value can be any number in a range, this volume is called a gray-scaled volume. In this thesis, some manipulations treat the volumetric dataset as a gray-scaled volume such as in visualization part and some may take it as a binary volume such as in thinning and classification parts. If a voxel's value is 1 (for binary volume) or higher than a user-defined threshold (for gray-scaled volume), this voxel is also called a black, object or bone voxel in this thesis. A voxel with value 0 (for binary volume) or value smaller than a threshold (for gray-scaled volume) is also called a white, background or marrow voxel. In this thesis, the terms volume dataset and 3D digital image are also used interchangeably.

4.1.2 Volume Rendering

Volume rendering is a technique used to display a 2D projection of a 3D discretely sampled data set. A typical 3D data set is a group of 2D slice images acquired by a CT or MRI scanner. Usually these are acquired in a regular pattern (e.g., one slice every millimeter) and usually have a regular number of image pixels in a regular pattern. This is an example of a regular volumetric grid, with each volume element, or voxel represented by a single value that is obtained by sampling the immediate area surrounding the voxel to render a 2D projection of the 3D data set, one first needs to define a camera in space relative to the volume. Also, one needs to define the opacity and of every voxel. This is usually defined using an **RGBA** (for red, green, blue, alpha) transfer function that defines the RGBA value for every possible voxel value.

Volume rendering can be classified into indirect volume rendering (IVR) and direct volume rendering (DVR). IVR first constructs an iso-surface from the volumetric dataset, and then uses traditional surface-based rendering techniques to display the profile of objects. In IVR, the most famous method is the Marching Cube (MC)

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

algorithm [4]. Contrary to IVR, DVR does not need to convert volume element to surface element, but uses voxels directly. In DVR, the well known algorithms are Ray Casting (RC) approach, the forward projection approach, the splatting algorithm and the 3D texture mapping based projection technique.

A volume may be viewed by extracting surfaces of equal values from the volume and rendering them as polygonal meshes or by rendering the volume directly as a block of data. The Marching Cubes algorithm is a common technique for extracting a surface from volume data. Direct volume rendering is a computationally intensive task that may be performed in a several ways.

4.1.3 Direct Volume Rendering :

A direct volume renderer requires every sample value has to be mapped to opacity and a . This is done with a “transfer function” which can be a simple ramp, a piecewise linear function or an arbitrary table. Once converted to an **RGBA** (for red, green, blue, alpha) value, the composed RGBA result is projected on correspondent pixel of the frame buffer. The way this is done depends on the rendering technique. A combination of these techniques is possible. For instance, a shear warp implementation could use texturing hardware to draw the aligned slices in the off-screen buffer.

4.2 Marching Cube Algorithm

MC uses linear interpolation to setup triangle models of constant value surface (iso-surface) and uses normalized gradient of original data to calculate shading .

First a logic cube is defined by 8 voxels: four from one slice and four from a neighboring slice and a user defined constant value C is chosen. To determine how the iso-surface passes through the volume, divide-and-conquer method is used to create triangle patches in a logic cube. If one voxel's value is higher than C , this voxel is out of the surface and if its value is smaller than C , this voxel is inside the surface. Each voxel can be an “out” or “in” state, so totally there are $2^8 = 256$ situations in a logic cube. Considering the complementary case of one situation (i.e., each vertex's state changes to its opposite), the topology of triangles in this logic cube is not changed. And considering the rotational symmetry, some cases are in fact the same one. So the 256 situations can be reduced to 15 cases (Figure 4.2).

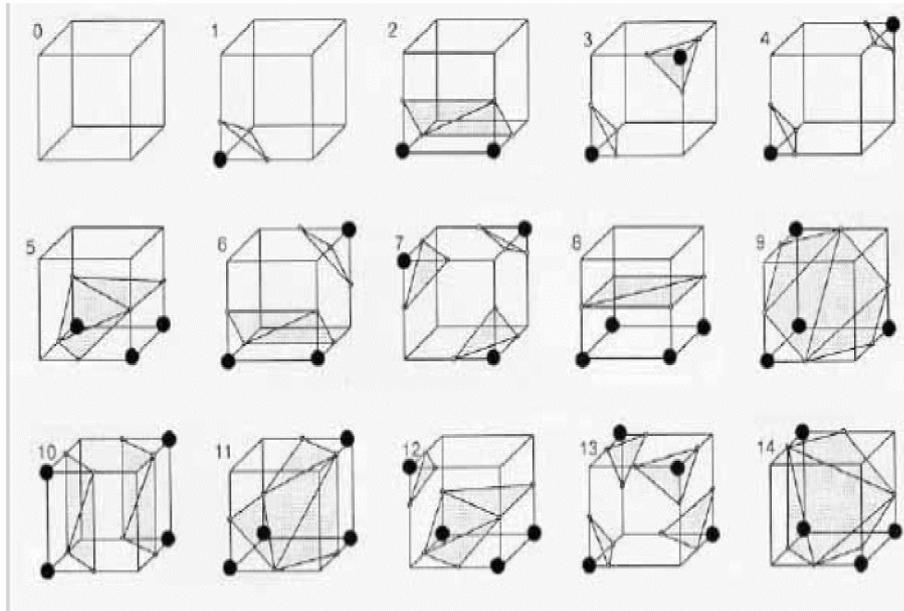


Figure 4.2 Triangulated Cubes

Courtesy of W.E. Lorensen and H.E. Cline

A look-up table is set up beforehand, which includes the 256 cases. In every entry, we can find edges which are intersected by the isosurface and these edges are output by a sequence that forms a front face. According to the inside or outside status of each vertex of a cube, an entry index is created, $\text{Index} = V_8 V_7 V_6 V_5 V_4 V_3 V_2 V_1$ (V_i is 0 or 1, instead of inside or outside of isosurface). We use this index to look up the pre-calculated table and find out which edges are intersected with the isosurface. The value of one of the vertices on such an edge must be smaller than the threshold and the other must be bigger than it. Using linear interpolation, the intersecting location can be found on the edge. Then, we store all the location information in a list and store each location's normal value into another list. The normal value is the linear interpolation of normal values of the two end vertices. And each vertex's normal value is computed using central differences.

$$\begin{aligned}
 g_x &= \frac{V_{x+1,y,z} - V_{x-1,y,z}}{2} \\
 g_y &= \frac{V_{x,y+1,z} - V_{x,y-1,z}}{2} \\
 g_z &= \frac{V_{x,y,z+1} - V_{x,y,z-1}}{2}
 \end{aligned}
 \tag{4.1}$$

Having locations and normal values of vertices of a triangle, this triangle can be shaded.

The MC method does not guarantee a continuous surface. “Holes” can be generated when two ambiguous faces meet. Nielson suggested the asymptotic decider method to settle this problem.

MC is such a commonly used method for generating iso-surface and lots of researches are carried on MC to improve its performance. In MC, the number of triangles generated is proportional to rendering time. Some researchers designed algorithms to reduce the number of triangles. Montani used midpoint of each edge as the intersection point of the iso-surface and the logic cube instead of linear interpolation, i.e., only to keep the topology. This method can reduce the number of generated triangles by merging output facets into large coplanar polygons. Although this approach is simpler than MC, it loses some precision. Shekhar presented a decimation method to down sample the volume data where the iso-surface is mostly flat and maintain high resolution at places with finer details. This approach balanced surface details and rendering time.

The disadvantages of MC are:

- It cannot represent partially transparent materials correctly.
- A binary decision has to be made on the position of the intermediate surface.
- False positives (introducing features that do not exist) and false negatives (losing tiny features) are introduced.
- Inappropriate for low-resolution sampling.

4.3 Proposed methodology

“3D Visualization of MRI images using MATLAB”. The goal of this work was to show the possibility of such reconstruction using a wide range program such as MATLAB. Solution is displayed through an example which does not allow virtual “entering” into the 3D structure, but enables slicing out desired volume to a size of one pixel of the original images. Tomographic layers at the appropriate depth will be displayed on both sides of chosen parallelepiped. Sets of images originating from two modalities were placed at disposal. Images used in this project originate from the

ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

device, having greater resolution. . Two sets were used, in both sagittal and transversal plain, with the emphasis on the latter one. The example displayed in this paper shows how a powerful tool like MATLAB can be used for 3D visualization of 3D tomographic images. It is mentioned that with further work on this realisation it could be possible to create the effect of entering the structure in such a way to observe inner volumes. MATLAB supports this function, but working with matrixes this large would be very time consuming for home computers.

The extraction of 3D objects and its visualization is one of the most important steps in the analysis of the pre processed medical image data, which can help in performing diagnosis, treatment planning, and treatment delivery. Thus in practice, radiation oncologists spend a substantial portion of their time performing the extraction of 3D objects and its visualization is one of the most important steps in the analysis of the pre processed medical image data, which can help in performing diagnosis, treatment planning, and treatment delivery.

The main steps to create 3D models and volume rendering from 2D slice images:

- 1) Create an empty space for 3D volume.
- 2) Each image pixel's x and y coordinate on 2D will be transferred to the empty space. The slice number with respect to the distance between each slice is taken as z coordinate. If a pixel is adjacent to another pixel, the 3D points will be connected together.
- 3) Repeat the previous 2 steps until all slices are done. All the points in the 3D space will be connected just like in the 2D slices.
- 4) 3D volume rendering. For the correct rendering of stacked image slices, since all 2D images are of the same dimension, Hence the 3D volume can hold all of them in a rectangular cube. Different degrees of interactive Control are provided for 3D tools in MATLAB, for the semiautomatic 3D propagation and rendering. In this way, we can perform a hierarchical volume rendering of the segmented slices.

Chapter-5

RESULTS

Firstly the 2D MRI slices are extracted from mha file. One of the MRI slice shown in Fig 5.1



Fig 5.1 MRI slice

These images are preprocessed for denoising using wavelet denoising method.

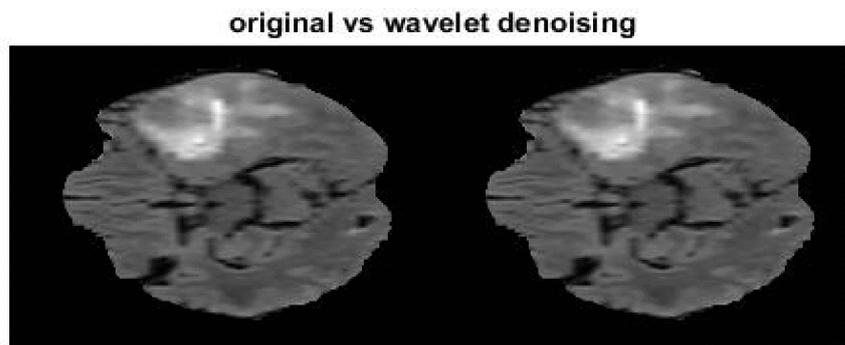


Fig 5.2 wavelet denoised MRI slice compared with extracted MRI

Now by applying existing segmentation methods object based thresholding, histogram thresholding, EM based segmentation and developed method caner is identified as shown in Fig 5.3, 5.4, 5.5 and 5.6 respectively.

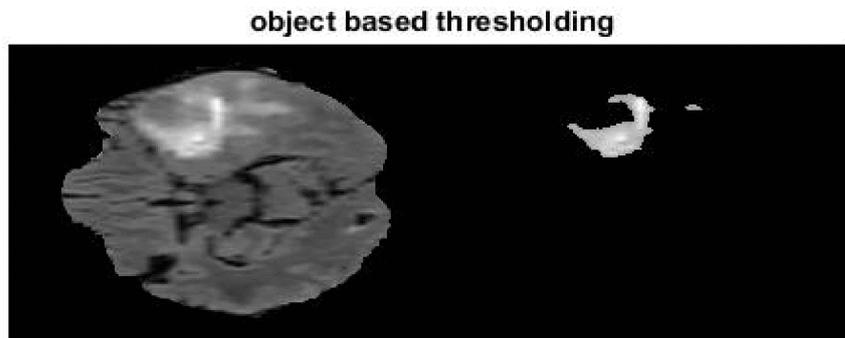


Fig 5.3 object based thresholding

histogram thresholding

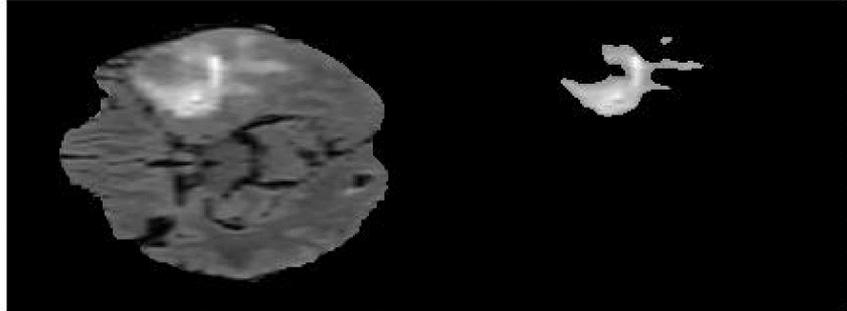


Fig 5.4 histogram based thresholding

EM based segmentation

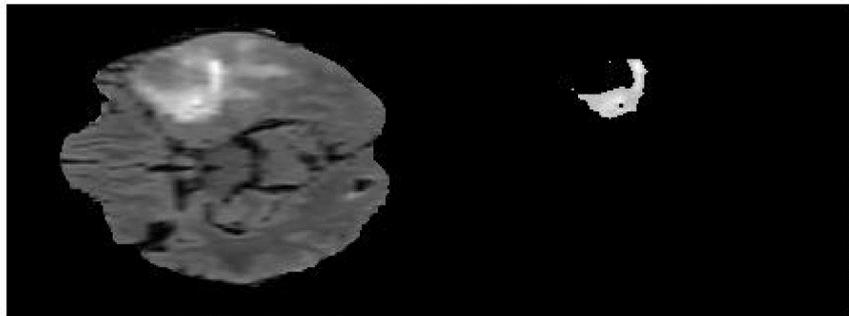


Fig 5.5 EM based segmentation

fused tumour

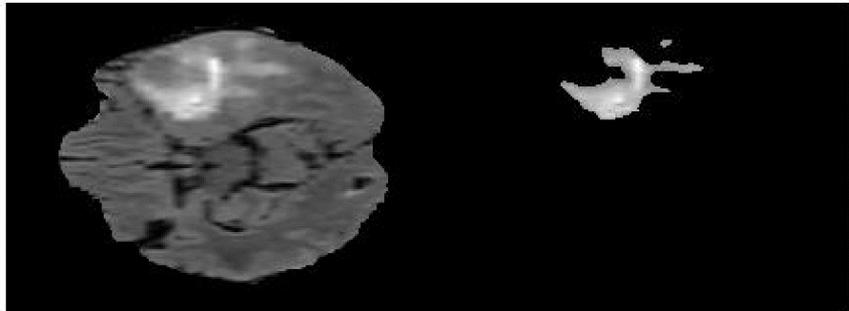


Fig 5.6 Proposed fusion based segmentation

All the information extracted is in 2D. So for better understanding of the cancer features like size, position etc. it is very essential to construct 3D view. The results for 3D view are shown in Fig. 5.7.

ANALYSIS OF THREE DIMENTIONAL MAGNETIC RESONANCE IMAGING (MRI) DATA TO IDENTIFY BRAIN DISORDERS

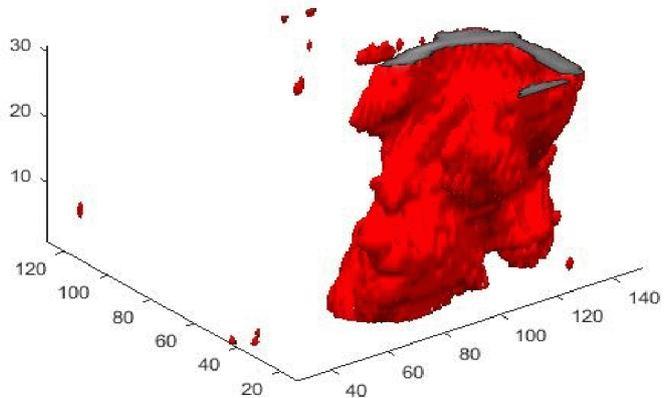


Fig 5.7 3D view of cancer

Later this 3D view of cancer is fused with original MRI slices for better view as shown in Fig. 5.8.

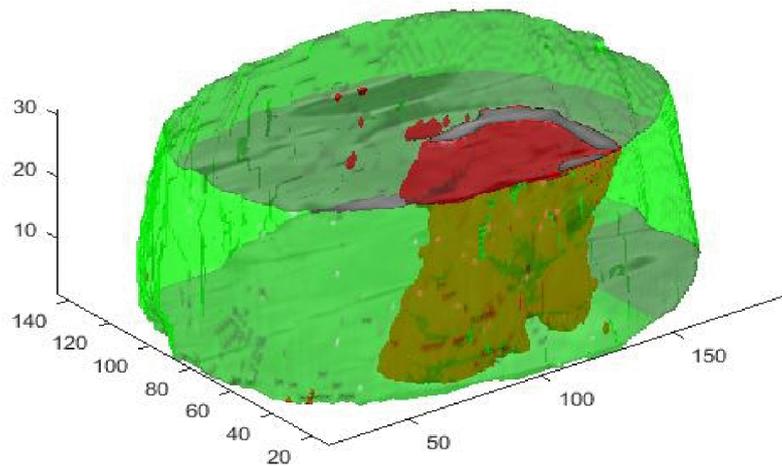


Fig 5.8 Brain-tumor 3d

The volume of the tumor in terms of pixels for existing segmentation methods and developed method is shown in Table 5.1.

TABLE 5.1 Volume of the cancel in terms of Pixels.

Method	EM based segmentation	Histogram based segmentation	Object based thresholding	Proposed Algorithm
Number of pixels in tumor	19759	40097	26301	42347

From the Table 5.1 it is found that, the developed method performed well by preserving the edges also.

Chapter-6

CONCLUSION

In this project a new hybrid algorithm based on Expectation-Maximization, Histogram and object based thresholding methods is developed to identify the cancer in the MRI slices. Initially 2D MRI slices are extracted from the dataset and these slices are denoised using wavelets. Later developed algorithm is applied on to the MRI slices to identify the cancer. Since Doctors had only the 2D Image Data to visualize the tumors in the MRI images, which never gave the actual feel of how the tumor would exactly look like, it is necessary to view the cancer in 3D. In order to have the complete information of the cancer, the signature in all three dimensions is required. Therefore these images are processed to extract the 3D signature of the cancer. Among all the methods, the proposed algorithm segmented the image well by retaining the edge pixels which gives perfect volume of the tumor in terms of pixels.

REFERENCES

- [1]. Muhammad Nasir, Asim Baig and Aasia Khanum “Brain Tumor Classification in MRI Scans Using Sparse Representation”, Springer International Publishing Switzerland 2014, A. Elmoataz et al. (Eds.): ICISP 2014, LNCS 8509, pp. 629–637, 2014.
- [2]. D.SELVARAJ, R.DHANASEKARAN “MRI BRAIN IMAGE SEGMENTATION TECHNIQUES - A REVIEW”, Indian Journal of Computer Science and Engineering (IJCSE), ISSN : 0976-5166 Vol. 4 No.5 Oct-Nov 2013.
- [3]. Sayali SavajiPP, Parul AroraP “Denoising of MRI Images using Thresholding Techniques through Wavelet” International Journal of Science, Engineering and Technology Research (IJSETR) Volume 1, Issue 3, September 2012.
- [4]. Jin Liu, Min Li, Jianxin Wang , Fangxiang Wu, Tianming Liu, and Yi Pan “A Survey of MRI-Based Brain Tumor Segmentation Methods” TSINGHUA SCIENCE AND TECHNOLOGY ISSN11007-02141104/101pp578-595 Volume 19, Number 6, December 2014.
- [5]. Eman Abdel-Maksoud , Mohammed Elmogy , Rashid Al-Awadi “Brain tumor segmentation based on a hybrid clustering technique” Egyptian Informatics Journal (2015).
- [6]. Shashikant Agrawal, Rajkumar Sahu “Wavelet Based MRI Image Denoising Using Thresholding Techniques” International Journal of Science, Engineering and Technology Research (IJSETR) Volume 1, Issue 3, September 2012.
- [7]. Aleksandra Pi_zurica, Alle Meije Wink, Ewout Vansteenkiste, Wilfried Philips and Jos B.T.M. Roerdink “A review of wavelet denoising in MRI and ultrasound brain imaging” CURRENT MEDICAL IMAGING REVIEWS 2005.
- [8]. Nelly Gordillo , Eduard Montseny , Pilar Sobrevilla “State of the art survey on MRI brain tumor segmentation” Magnetic Resonance Imaging (2013).
- [9]. Saurabh Shah and N C Chauhan “An Automated Approach for Segmentation of Brain MR Images using Gaussian Mixture Model based Hidden Markov Random Field with Expectation Maximization” VOLUME 2 ISSUE 4 17th August 2015.
- [10]. Mohamed Ben Salah, Idanis Diaz, Russell Greiner, Pierre Boulanger, Bret Hoehn, and Albert Murtha “Fully Automated Brain Tumor Segmentation Using Two MRI Modalities” Springer-Verlag Berlin Heidelberg 2013 ISVC 2013, Part I, LNCS 8033, pp. 30–39, 2013.

**ANALYSIS OF THREE DIMENSIONAL MAGNETIC RESONANCE IMAGING (MRI)
DATA TO IDENTIFY BRAIN DISORDERS**

- [11]. Megha Borse, S.B. Patil, B.S.Patil “LITERATURE SURVEY FOR 3D RECONSTRUCTION OF BRAIN MRI IMAGES” International Journal of Research in Engineering and Technology eISSN: 2319-1163 | pISSN: 2321-7308 Volume: 02 Issue: 11 | Nov-2013
- [12]. Megha P. Arakeri and G. Ram Mohana Reddy “An Effective and Efficient Approach to 3D Reconstruction and Quantification of Brain Tumor on Magnetic Resonance Images” International Journal of Signal Processing, Image Processing and Pattern Recognition Vol. 6, No. 3, June, 2013.
- [13]. Kamel Aloui and Mohamed Saber Naceur “3D Tumor Segmentation from Volumetric Brain MR Images Using Level-Sets Method” -20267
- [14]. NAVEENKUMAR.R, SANJAY D.S “MORPHOLOGICAL IMAGE PROCESSING APPROACH FOR 2D TO 3D RECONSTRUCTION OF BRAIN TUMOR FROM MRI IMAGES AND VOLUME CALCULATION OF TUMOR” Proceedings of 3rd IRF International Conference, 10th May-2014, Goa, India, ISBN: 978-93-84209-15-5.
- [15]. Sheng-Chih Yang, Cheng-Yi Yu, Cheng-Jian Lin, Hsueh-Yi Lin, Chi-Yuan Lin “Reconstruction of three-dimensional breast-tumor model using multispectral gradient vector flow snake method” Journal of Applied Research and Technology 13 (2015) 279-290.