BRAIN MAGNETIC RESONANCE IMAGE
TUMOUR SEGMENTATION
WITH
LATERAL VENTRICULAR DEFORMATION

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To My Parents Cai Ping Lu and Fan Chao Xiao
ABSTRACT

This thesis addresses some of the challenging issues on brain magnetic resonance (MR) image tumour segmentation caused by the weak correlation between magnetic resonance imaging (MRI) intensity and anatomical meaning. With the objective of utilising more meaningful information to improve brain tumour segmentation, an approach which employs lateral ventricular deformation as an additional feature for segmentation is proposed. This is motivated by potential performance improvement in the general automatic brain tumour segmentation systems which are important for many medical and scientific applications.

In this thesis, several important problems in the brain MR image tumour segmentation are reviewed. Based on the observations that brain lateral ventricles are compressed by tumours, this research investigates the correlation between lateral ventricular deformation and tumour location. It focuses on the design and implementation of a feature extraction component which transforms lateral ventricular deformation into an additional feature for improving accuracy of brain tumour segmentation.

Observations of the experimental results provided by the feature extraction component suggest that the obtained data is relevant to the location of brain tumour. Comparative tumour segmentation experiments using both supervised and unsupervised segmentation methods on eight brain MR image cases shows
that, in some cases where lateral ventricular deformation caused by the compression from brain tumours can be transformed to an additional feature, segmentation accuracy can be improved. Compared to common brain tumour segmentation systems, the key advantage of this system is that the feature of lateral ventricular deformation provides segmentation methods with an additional feature which is anatomically relevant to brain tumour in addition to the MRI intensity values.
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CHAPTER 1: INTRODUCTION

Never regard study as a duty, but as the enviable opportunity to learn to know the liberating influence of beauty in the realm of the spirit for your own personal joy and to the profit of the community to which your later work belongs.

--- Albert Einstein

1.1. Motivation

Brain tumour is an abnormal intracranial growth caused by cells reproducing themselves in an uncontrolled manner. In the United States alone, there were around 16,500 new cases of brain tumour in the year 2000, which accounted for 1.4 percent of all cancers, 2.4 percent of all cancer deaths, and 20 to 25 percent of paediatric cancers. It was estimated that there are approximately 13,000 deaths per year as a result of brain tumours [Greenlee et al., 2000].

Magnetic resonance imaging (MRI) is regarded as a powerful visualisation technique that allows images of internal anatomy to be acquired in a safe and non-invasive manner. It provides much greater contrast between different soft
tissues of the body than computed tomography (CT), making it particularly useful in assisting diagnosis, especially in evaluating brain tumours.

Automatic brain tumour segmentation in magnetic resonance (MR) image is an important image processing step for both medical practitioners and scientific researchers. For example, it can be applied in assessing tumour growth and treatment responses, enhancing computer-assisted surgery, planning radiation therapy, and constructing tumour growth models.

Within general MR image segmentation systems, two of the most important components are feature extraction and segmentation. Feature extraction provides the measurement data on which the segmentation component relies. With the features that are extracted from the images, such as MRI intensities and other calculated features, e.g., edge, texture, the segmentation component then produces separation of tumour and non-tumour regions.

Large amounts of research efforts have been made in developing effective segmentation methods in the past years, however, such methods have failed to achieve the accuracy level comparable to visual analyses performed by human experts. In addition, brain tumour-affected MR images contain many properties that make common methods used in automated systems inaccurate. One of the most challenging problems that hinder the development of accurate automatic systems is that MR image lacks strong association between actual anatomical meaning and MRI intensity, especially for brain tumour. Therefore, in addition to MRI intensities, other calculated features which are relevant to anatomical meaning are desirable for the brain tumour segmentation tasks.
One such feature studied in this research is the brain lateral ventricular deformation. It can be easily observed that in some MR image cases, although lateral ventricles may be irregular in size, shape and location, they will be compressed when cerebral tumour or oedema is present. In most cases, shrinkage within the lateral ventricular area is in a direction opposite to that of the tumour growth. To understand the correlation between brain tumour growth and brain lateral ventricular deformation, some pivotal questions that need to be answered are:

- Is it possible to develop methods to estimate deformation of brain lateral ventricles?
- Can quantitative correlations between deformation of lateral ventricles and the existence of brain tumours be obtained?
- Can the results obtained through measuring lateral ventricular deformation be used for brain tumour segmentation?
- How far can the results of automated tumour segmentation be improved after including lateral ventricular deformation information as additional parameters?

To answer the above questions, an idea of transforming lateral ventricular deformation into feature to be used for tumour segmentation is therefore investigated in this thesis. In order to implement this idea, multidisciplinary studies of brain tumours, lateral ventricles, deformation-based morphometry (DBM), brain MR image segmentation methods and common MR image
segmentation systems along with the feature extraction component have been conducted.

1.2. Objectives of the Thesis

The primary objective of this research is to develop methods and algorithms to enhance accuracy of brain tumour segmentation in MR images. The main research activities specifically focus on investigating and improving feature extraction of information on the brain lateral ventricular deformation. This additional feature is then used as one of the inputs to the general segmentation methods to improve brain tumour segmentation results. Some of the issues this research aims to address are summarised as follows:

1. Identifying major challenging issues in brain MR image tumour segmentation;

2. Studying the properties of lateral ventricles and brain tumour from both anatomical and MRI-visualisation aspects, and investigating the correlations between the compression of soft tissue structures due to existence of brain tumours and deformation observed in lateral ventricles;

3. Identifying problems related to the quantitative measurement or estimation of lateral ventricular deformation;

4. Investigating suitable methods for converting lateral ventricular deformation to feature;

5. Designing and implementing a practical system which is capable of transforming this deformation into a quantifiable feature;
6. Applying the additional feature to tumour segmentation methods and evaluating the overall accuracy of the tumour segmentation.

1.3. Structure of the Thesis

The rest of the thesis is organised as follow.

Chapter 2 (Background) introduces some of the background information relevant to this research. More specifically, general knowledge on medical imaging and MRI are presented to the readers, in addition to some of the challenging issues in both normal MR image segmentation and brain MR image tumour segmentation. Existing work on medical image segmentation and common MR image segmentation system are also reviewed in this chapter, and the importance of feature extraction component in the system is highlighted.

Chapter 3 (Using Lateral Ventricular Deformation for Brain Tumour Segmentation) develops the idea of improving brain tumour segmentation accuracy by using a feature transformed from lateral ventricular deformation based on the observations of correlations between lateral ventricular deformation and brain tumours. By discussing several key factors, main tasks and challenging issues with respect to the extraction of the feature of lateral ventricular deformation, this chapter provides a guideline for the design and implementation of this feature extraction process.

Chapter 4 (Lateral Ventricular Deformation Feature Extraction Component Design) implements the idea of improving brain tumour segmentation accuracy
by using lateral ventricular deformation information and presents the design of the feature extraction component.

Chapter 5 (*Implementation of Feature Extraction Component*) presents details on the actual implementation of each step of the lateral ventricular deformation extraction process following the component design. Experimental results obtained at each step are also evaluated and discussed in detail.

Chapter 6 (*Brain Tumour Segmentation with Lateral Ventricular Deformation*) demonstrates a system for brain tumour segmentation integrating the feature derived from lateral ventricular deformation analysis. Extensive experiments are conducted using both supervised and unsupervised pattern recognition methods; moreover, the results generated using both supervised and unsupervised methods (with and without deformation feature) are compared to those produced by medical experts (ground truth). The comparison study shows that accuracy of the results produced with the deformation feature is significantly higher than the one produced without employing the feature.

Chapter 7 (*Conclusions and Future Work*) summarises the work in this thesis and outlines possible future research directions. Some of the limitations of the approach presented in this thesis are also discussed.
CHAPTER 2: BACKGROUND

The invariable mark of wisdom is to see the miraculous in the common.

--- Ralph Waldo Emerson

This chapter provides an introduction to some concepts, terms and techniques related to magnetic resonance imaging (MRI), previous work on medical image segmentation and common magnetic resonance (MR) image segmentation system structure. Background information on brain tumours are provided, followed by the discussion of challenges and some related work in automatic brain MR image tumour segmentation.

Explanations of other relevant concepts, techniques and strategies employed at various stages of this research have been spread throughout this thesis. To avoid redundancy, their background details are not collected under any particular chapter, but can be found at the relevant parts within the remainder of the thesis instead.
2.1. Medical Imaging and Magnetic Resonance Imaging

Medical imaging refers to the techniques and processes for creating images of the human body (or parts thereof) for clinical purposes or medical science [Bushberg et al., 2001; Gonzalez and Woods, 2002; Sprawls, Online]. Various acquisition technologies and energy sources can be used to produce different types of medical images [Sprawls, Online; Bushberg et al., 2001], known as modalities in medical imaging [Pham et al., 2000; Bushberg et al., 2001]. These modalities include electron microscopy, medical radiography (projection radiography and fluoroscopy), MRI, nuclear imaging (gamma cameras and positron emission tomography (PET)), photoacoustic imaging, digital infrared thermography, computed tomography (CT) and medical ultrasonography [Bushberg et al., 2001; Sprawls, Online]. Each modality has its own applications in medicine. For example, because ultrasound is less harmful than ionising radiation to a growing foetus, medical ultrasonography is normally preferred for obstetric patients [Bushberg et al., 2001].

Medical images may be acquired in the continuous domain such as on X-ray (one traditional medical radiographic imaging technique) film, or in discrete space such as in MRI. Images in continuous domain and discrete space are referred to as analogue and digital images, respectively. In 2-dimensional digital images, the location of each measurement is called a pixel, and in 3-dimensional images, it is called a voxel [Pham et al., 2000]. For simplicity, ‘pixel’ is used for both 2- and 3-dimensional images throughout this thesis.
MRI is an imaging technique [Bushberg et al., 2001; Gonzalez and Woods, 2002] primarily used in radiology to visualise the structure and function of the body. MRI is based on the principles of nuclear magnetic resonance (NMR), a spectroscopic technique developed by scientists (including the University of Nottingham Nobel Laureate Professor Sir Peter Mansfield and the University of Illinois Nobel Laureate Professor Paul Christian Lauterbur who made NMR capable of producing images of biological body) to obtain microscopic chemical and physical information about molecules. The term magnetic resonance imaging is now used in preference to nuclear magnetic resonance imaging (NMRI) due to some of the negative connotations associated with the word “nuclear” in the late 1970’s [Hornak, Online]. MRI provides much greater contrast between the different soft tissues of the body than CT, making it particularly effective in neurological (brain), musculoskeletal, cardiovascular, and oncological (cancer) imaging [Bushberg et al., 2001; Rinck, 2001].

MR image contrast is basically created by the differences of the strength of the recovered NMR signal [Bushberg et al., 2001]. The basic mechanism of the MR scanner uses the approach of aligning magnetisation vectors of hydrogen atoms through application of an external magnetic field. Two of the most commonly used MRI visualisations are T1- and T2-weighted images. T1 and T2 respectively refer to the relaxation time associated with recovery of longitudinal magnetisation and phase coherence in the transverse plane of the specific tissues being imaged [Westbrook et al., 2005]. An alternative visualisation option in MRI is proton density (PD) image, where scanning parameters are adjusted in
such a manner as to eliminate the effects of T1 and T2 relaxation time, thus producing an image which is dependent primarily on the density of protons in the specific imaging volume [Brown and Semeka, 2003].

Since areas with high fat content have a short T1 relaxation time relative to water, T1-weighted MR images focus mainly on visualising fat. On the other hand, areas with high water content have a short T2 relaxation time relative to areas of high fat content. Image contrast is created by using a selection of image acquisition parameters that weights input signals by their respective T1 and T2 relaxation times [Westbrook et al., 2005]. Throughout this thesis, the term “MRI intensity value” is referred to as MR image greyscale or contrast value which alternatively denotes the strength of signal acquired from MRI scanner.

With respect to actual image contrasts observed, T1-weighted imaging causes nerve connection of white matter (WM) to appear white, and congregations of neurons of grey matter (GM) to appear from light grey to grey, while cerebrospinal fluid (CSF) appears dark. The contrast of WM, GM and CSF is reversed in the case of T2-weighted imaging [Brown and Semeka, 2003].

One variation, also known as fluid-attenuated inversion recovery (FLAIR), is a heavily T2-weighed imaging technique that dampens the ventricular CSF signal. The strongest signals are usually collected from certain brain abnormalities. Therefore, CSF and abnormalities appear black and bright, respectively. Although FLAIR is similar to T2-weighted imaging, it allows better abnormality visualisation since signal of free water is suppressed [Hashemi et al., 1995].
To visualise abnormalities through MRI better, another T1-weighted technique known as contrast enhanced T1-weighted (CE-T1) imaging, which makes use of injected contrast agents, is often used. This technique is devised to enhance lesion detection through MR images. The contrast agent compounds usually cause the T1 time of tissues surrounding abnormality areas to decrease temporarily, resulting in bright regions to be observed at locations that contain blood cells moving through the blood-brain barrier (BBB) [Brown and Semeka, 2003]. Presence of this type of enhanced area has been found to be useful for improving the detection of tumours [Brown and Semeka, 2003].

The above-mentioned MRI modalities are often combined together to facilitate a more accurate analysis. The use of the combination of multiple visualisation techniques is referred to as multi-spectral imaging\(^1\) [Clarke et al., 1995; Rinck, 2001; Brown and Semeka, 2003] where more than one measurement is made at each location in the image [Pham et al., 2000]. By providing means for observing additional correlations between anatomical and various functional metrics within different modalities of MR images, multi-spectral MRI techniques offer medical practitioners more information to characterise and discriminate various tissues based on physical and biochemical properties [Brown and Semeka, 2003].

\(^1\) Multi-spectral imaging is also known as vector, multi-channel or multi-modal imaging [Pham et al., 2000; Brown and Semeka, 2003].
Figure 2.1: Multi-spectral MR Images (axial view). T1-weighted images (first 3 rows), CE-T1-weighted images with contrast agent (middle 3 rows), and T2-weighted images (bottom 3 rows) (Images courtesy of University Malaya Medical Centre, Malaysia\(^2\)).

\(^2\) Images were produced from a Siemens 1.5-Tesla MRI scanner.
Figure 2.1 provides an example of multi-spectral images that include T1-, CE-T1- and T2-weighted brain MR images in axial view. The slices within modalities are ordered from left to right, then top to bottom. This order corresponds to moving from the top to the bottom of the head.

2.2. Medical Image Segmentation

In computer vision, the task of segmentation is to partition a digital image into multiple segments [Gonzalez and Woods, 2002]. The goal of segmentation is to simplify and/or change the representation of an image to be more meaningful and easier to analyse. More precisely, image segmentation is the process of assigning a label to every pixel in an image such that pixels with the same label share similar visual characteristics and properties [Shapiro and Stockman, 2001].

The result of image segmentation is a set of segments, regions or contours extracted from the image. Pixels within one region are similar to each other in terms of some characteristics or computed properties, such as colour, greyscale, contrast or texture. Adjacent regions are significantly different with respect to the same characteristic(s) [Shapiro and Stockman, 2001].

Segmentation is one of the indispensable steps within the analysis and processing of medical images. The primary objective of medical image segmentation methods is to aid diagnosis process. In other words, these methods are used to assist medical practitioners in evaluating medical imagery or recognising abnormal findings in a medical image [Suri et al., 2002]. Accurate medical image segmentation is useful in both clinical and scientific applications.
which include enhanced visualisations, high-throughput and consistent volume measurements, research into structural shape and variations, image-guided surgery, and change detection in images acquired at different times [O’Donnell, 2001].

In medical image segmentation, structures of interest include organs, parts of pathology, abnormalities (such as brain tumour) and normal structures. This has led to the development of a wide range of segmentation methods addressing specific problems in medical applications. Some methods proposed in the literature are extensions of methods originally proposed for generic image segmentation [Suri et al., 2002]. In contrast to generic segmentation, methods for medical image segmentation are often application-specific; as such, they often utilise prior knowledge about particular objects of interest and other structures in the image [Shapiro and Stockman, 2001; Suri et al., 2002].

Previous work on medical image segmentation can be roughly divided into two broad categories: single medical image segmentation, where only one image is employed as input data; and multi-spectral images such as MR images where different modalities are available [Clarke et al., 1995]. While the focus is placed on the recent methods and applications used in MR image segmentation, some early literature on medical image segmentation are reviewed.
2.2.1. Literature Review on Single Image Segmentation

Methods for single medical image segmentation can be further divided into four general sub-categories: thresholding-based, edge-based, seed growing, and those that fall outside these previous sub-categories [Clarke et al., 1995].

Thresholding-based is the simplest and the most intuitive single image segmentation approach, where one or more criteria is usually based on image contrast selected as thresholds in order to arrange the image pixels into one or more categories [Gordon et al., 1996; Sahoo et al., 1988]. However clinical application of thresholding-based segmentation methods is severely hindered if the image contrast value is not strongly associated with the anatomical meaning in medical images [Prastawa et al., 2005].

Edge-based segmentation methods take advantage of edge detection to delineate regions, but they often suffer from incorrect detection of edges due to noise, over- and under-segmentation, and variability in threshold selection in the image edge [Dellepiane, 1991]. Although improved results have been obtained through a combination of edge-detection (the Marr-Hildreth operator) with morphological filtering [Bomans et al., 1990], boundary tracing [Ashtari et al., 1990] and employing neighbourhood information [Singleton et al., 1997], the complexity observed in medical images, especially when pathology exists, makes precise detection of boundaries between two structures rather challenging.

Seed growing segmentation methods require an operator to empirically select seeds and thresholds first. Pixels around the seeds are examined and included in the region if they fall within pre-determined thresholds, and each of the added
pixels then becomes a new seed for the following iteration. The process is continued until the image is completely segmented [Cline et al., 1987]. Results obtained through seed growing segmentation techniques are dependent on the selected operator settings for the seeds [Pohlman et al., 1996].

A few of the other single image segmentation methods include statistical models such as Markov random field (MRF) methods [Dubes and Jam, 1989]. Although segmentation results can be improved by applying these methods, their practical implementation is limited due to the difficulties in selecting parameters or defining specific functions. More recent research has demonstrated that segmentation results can be improved by combining some of the above-mentioned methods with other image processing approaches [Gibbs et al., 1996; Zhu and Yan, 1997].

It can be summarised that although single image segmentation methods may be applicable in some medical image cases, their effectiveness is generally limited to relatively simple structures or pathology due to the fact that the information provided by a single image may not be enough for complex applications. For more challenging medical image segmentation tasks, limiting input data to that of single image generally fails to obtain robust results [Clarke et al., 1995].

2.2.2. Literature Review on Multi-spectral Image Segmentation
The most distinctive difference between single and multi-spectral medical image segmentation is that the latter uses multi-dimensional input dataset created by
multiple image data, thus allowing multi-spectral images measured at each location to be processed or analysed simultaneously by segmentation methods [Clarke et al., 1995; Pham et al., 2000]. Using MR image as the representative, the remainder of this section focuses on classifying and generalising some of the existing multi-spectral medical image segmentation methods, and summarising their common properties.

Pattern recognition techniques are generally considered as the most effective for segmenting multi-spectral images [Clarke et al., 1995]. Most literature in pattern recognition classifies its methods into unsupervised and supervised learning [Clarke et al., 1995; Duda et al., 2001]. As an application of pattern recognition, multi-spectral MR image segmentation methods are similarly sub-categorised.

The difference between supervised and unsupervised methods is the need for training in the former. Supervised methods use operator input for segmentation. They normally train the core algorithms or functions by repeatedly predicting values and comparing these predicted values with actual values obtained, thereby altering the original predicting algorithms or functions in order to make the following prediction more accurate [Duda et al., 2001]. In image segmentation, training is normally done by selecting pixels or regions of the images [Clarke et al., 1995]. Unsupervised methods, also called clustering methods, partition data into subsets without employing an explicit training process [Duda et al., 2001].

Clustering methods are commonly viewed as an instance of unsupervised learning where no training data is required. The most common unsupervised
methods employed for multi-spectral MR image segmentation include $k$-means$^3$ [Coleman and Andrews, 1979; Taxt et al., 1992; Gerig et al., 1992], and its fuzzy equivalent, the most widely used fuzzy c-means (FCM) [Dunn, 1973; Bezdek, 1980; Gerig et al., 1992; Hall et al., 1992]. By applying unsupervised clustering methods, relatively satisfying segmentation results have been obtained in the past [Gerig et al., 1992; Hall et al., 1992].

More effective systems based on the use of FCM and knowledge-based rules have been developed, such as a system that focuses on the segmentation of tumors not enhanced by contrast agent through previous methods [Fletcher-Heath et al., 2001]. Furthermore, the FCM algorithm has been consistently improved in order to obtain better segmentation results [Yeung and Wang, 2002; Shen et al., 2003; Wang et al., 2004; Chuang et al., 2006; Cai et al., 2007; Hung et al., 2008].

Expectation maximisation (EM) [Dempster et al., 1977] is another clustering algorithm which has been used frequently in multi-spectral image segmentation [Lei and Sewchand, 1992; Liang et al., 1994; Kapur et al., 1996; Tsai et al., 2005; Rouaini et al., 2006]. The EM algorithm applies the same clustering principles as that of FCM and $k$-means algorithms with the underlying assumption that the input image data follow a Gaussian mixture model (GMM). In the work presented by [Kapur et al., 1996], EM was successfully employed to perform brain MR image tissue segmentation with intensity properties modelled by the probability density function (PDF).

$^3$ K-means algorithm is also known as ISODATA [Coleman and Andrews, 1979].
In fact, FCM, \( k \)-means and EM clustering algorithms are not the only choices available for implementing unsupervised multi-spectral medical image segmentation. For example, [Sammouda et al., 1996] examined three methods to perform unsupervised brain MR image segmentation: Hopfield neural networks, Boltzmann machines and the \( k \)-means algorithm. [Capelle et al., 2004] developed interesting frameworks that utilise pixel dependencies on a pair of T1- and T2-weighted MR images so as to perform segmentation. These systems are based on the underlying assumption that the previous tissue classes of anatomical significance within the brain can be represented by GMM.

Another approach uses a method called fuzzy connectedness (FC) to calculate the relative affinity of neighbouring pixels through an assessment of their spatial closeness and the similarity of their pixel intensity values [Hata et al., 2005]. The FC algorithm builds its estimation of the region of interest (ROI) starting with a single pixel as seed point and thresholding value for an automatically computed fuzzy scene. Although only T2-weighted images were used in the experiments [Hata et al., 2005], FC algorithm can be applied in multi-spectral image segmentation.

In general, for multi-spectral medical images, unsupervised segmentation methods have the advantage of avoiding the human operation variability associated with manual training data [Clarke et al., 1995]. Normal structure segmentation on multi-spectral MR images using unsupervised segmentation methods generally creates satisfactory results [Clarke et al., 1995; Pham et al., 2000]. However, due to the fact that cluster is not a well defined concept [Everitt,
more accurate pathology segmentation may require patient-specific training which is not available for unsupervised segmentation methods.

There are a number of important pattern recognition techniques that have been developed in the past which are based on supervised methods (also known as classification methods or classifiers). The advantage offered by supervised methods is that relevant patterns in the data are automatically discovered based on prior knowledge, rather than through manual experimentation and intuition [Duda et al., 2001].

Three of the most frequently used supervised pattern recognition techniques employed for medical image segmentation in the past include the maximum likelihood (ML) [Vannier et al., 1985; Clarke, 1991; Mitchell et al., 1994], $k$-nearest neighbours ($k$-NN) algorithms [Agartz et al., 1992; Mitchell et al., 1994] and artificial neural networks (ANN) [Clarke, 1991; Hall et al., 1992]. The ML method is categorised as being parametric because the training of the maximum likelihood (ML) classifiers consist of optimising the parameters with the input data, therefore it can be useful when the input data distributions for the different classes are well known [Clarke, 1991; Ozkan et al., 1993]. Nevertheless, this is not always the case for multi-spectral images [Clarke et al., 1993; Clarke et al., 1995]. The $k$-NN algorithm does not rely on predefined input data distributions, but rather on the actual distribution in the training samples themselves, and is categorised as a nonparametric method [Clarke et al., 1993; Duda et al., 2001]. ANN, another nonparametric method, feeds the features through a series of nodes, where mathematical operations are applied to the input values at each
node and a classification is made at the final output nodes. The training process in ANN is actually the process of determining the values of the parameters for these mathematical operations to minimise the prediction errors at the output nodes [Duda et al., 2001].

For multi-spectral medical image segmentation, in addition to the medical imaging intensity values, other calculated data such as edge [Bomans et al., 1990; Ehricke, 1990; Waks and Tretiak, 1990], texture [Ehricke, 1990; Schad et al., 1993; Fleagle et al., 1994] and neighbouring pixel intensities [Evans et al., 1994] have been utilised. The additional data is often referred to as high-level features. Although texture and neighbouring pixel intensities are not suitable for pixel classification due to the fact that they are statistical features necessarily calculated from multiple pixels [Clarke et al., 1995], further information provided by them can be utilised to assist segmentation.


In the most recent work presented by [Iscan et al., 2009], two other features based on wavelet transform and moment [Gonzalez and Woods, 2002] were utilised to assist medical image segmentation. In order to form the feature set, 2-dimensional continuous wavelet transform (CWT) and the moments of the grey-
level histogram (MGH) were computed. A novel incremental supervised neural network (ISNN) classification method is also proposed for the segmentation of medical images to allow multiple features to be utilised more efficiently.

### 2.2.3. Challenges in General MR Image Segmentation

The MRI techniques introduced in Section 2.1 are useful in differentiating brain anatomical structures. However, inherent technical limitations of the MRI process introduce uncertainties into MR image. Three primary factors associated with general MR images which make accurate MR image segmentation a challenging task are local noise, intensity inhomogeneity, and intensity non-standardisation.

Noise corrupts the MR signal of each pixel. One major source of noise is the ambient electromagnetic field collected by the radiofrequency (RF) detectors during the process of acquiring the MR signal. Another is often attributed to the emission of electromagnetic signal from object being imaged. The noise in MR images is often modelled as a Gaussian function which is independent of the underlying tissue types. Estimation of noise strength can be represented by its signal to noise ratio (SNR) [Worth et al., 1998; Sled et al., 1999]. A simulation of this effect is illustrated in Figure 2.2.

Intensity inhomogeneity is also known as intensity distribution bias. It refers to the gradual intensity variation which causes a shading effect over the image domain [Sled et al., 1999; Pham et al., 2000], even though there is no anatomic variation over the actual region being imaged. This is usually the result of factors (such as radio-frequency non-uniformity, static field inhomogeneity, etc.)
associated with imaging instrumentation (such as the strength of the magnet and the type of receiver coil used in the MRI scanner) or the resultant physical movement of the patient undergoing the scan [Hou, 2006]. This variation in intensity within a set of slices can lead to inaccuracies of 10% to 20% relative to ideal intensity values [Sled et al., 1999]. The effect of the deviation at each pixel of an MR image is illustrated in Figure 2.3.

Figure 2.2: Local noise simulated on an MR image [The Whole Brain Atlas, Online]: (a) original image; (b) image with noise of SNR=10; (c) image with noise of SNR=5.

Figure 2.3: Intensity inhomogeneity simulated using BrainWeb [BrainWeb, Online]: (a) original image; (b) image with 40% intensity inhomogeneity; (c) illustrated shading effect caused by intensity inhomogeneity.
Another challenging problem in segmenting MR images is intensity non-standardisation. Intensities of MRI do not have a fixed meaning, not even within the same MRI modality, for the same body region, or for images obtained on the same scanner with the same patient [Nyul and Udupa, 1999]. This indicates that the same tissue type may have different scales of signal intensity within a set of different images. This variation in different MR images poses problems for intensity based segmentation methods, especially when models associating fixed anatomical meaning with intensity distribution in the image are applied. Figure 2.4 demonstrates the effect of intensity non-standardisation on two T1-weighted images acquired using the same MRI scanner.

![Figure 2.4: Intensity non-standardisation in a controlled situation. Two slices from two different patients at approximately the same area of the different patients, acquired by using the same MRI scanner and modality (Images courtesy of University Malaya Medical Centre).](image)

There are a number of other less significant factors that pose challenges to MR image segmentation. These include partial volume averaging, inter-slice intensity variations [Simmons et al., 1994], geometric distortions, anisotropic pixels, the ‘Gibbs-ringing’ effect [Gering, 2003], misalignment within image series and motion artefacts due to patient movement [Gering, 2003]. These factors will
not be discussed in this thesis as they have only minimal effects in the MR images used for experiments in this research.

2.2.4. Common MR Image Segmentation Systems

To address the previously discussed challenges in MR image segmentation, automatic MR image segmentation systems are typically designed as a combination of several components of pre-processing, feature extraction, segmentation and classification. Figure 2.5 shows a common MR image segmentation system consisting of the most fundamental components [Clarke et al., 1995].

Due to the previously discussed inherent technical limitations of the MRI process, uncertainties are often introduced into MR images. The MR image pre-processing techniques used in MR image segmentation systems are mainly concerned with reducing the detrimental effects of the artefacts and improving the quality of the data for the subsequent components. Some fundamental considerations should be taken into account when selecting a particular image pre-processing technique. These include the amount of information loss, the SNR gain, edge and fine detail degradation and computational complexity and time-consumption. It might be the case that optimising one of these would compromise the others [Clarke et al., 1995]. Therefore, with the consideration of the problems and the context of each particular system, methods to be applied in this component need to be tactically selected or designed.
Figure 2.5: Structure of a common MR image segmentation system.

Feature extraction component consists of steps for extracting and selecting features and provides input data for image segmentation method. Features extracted from the images can also be used to derive other features. For example, texture feature is normally computed based on MRI intensity features. Directly extracted features such as MRI intensities are referred to as low level features, while calculated features, such as edge, texture, image moment and deformation of certain normal structures, are considered as high level features. Generally the feature extraction process breaks down the problem of segmentation into the grouping of feature vector data or feature set. Selecting features is the process of choosing relevant features by reducing redundant data,
rather than using all the raw information in the images [Schad et al., 1993]. It is very important in cases where the dimensionality of the extracted feature data is posing computational burdens [Schad et al., 1993; Clarke et al., 1995]. However in normal MR image segmentation tasks, the dimensionality of input feature data is limited, therefore the step of selecting feature is normally not present in common MR image segmentation systems, while extracting relevant features is the key to successful segmentation [Clarke et al., 1995].

With feature data obtained from feature extraction component, segmentation and classification components divide MR images into several regions based on the similarity of characteristics and label them [Shapiro and Stockman, 2001]. In some systems, segmentation is followed by classification component to label the regions according to different tissue types, while others integrate segmentation and classification into one single component [Clarke et al., 1995]. Because MRI is a multi-spectral medical imaging technique, MR image segmentation methods can also be divided into two categories: single image segmentation, where only one image is used as input image data [Cline et al. 1987; Ashtari et al., 1990; Bomans et al., 1990; Clarke et al., 1995; Gibbs et al., 1996; Zhu and Yan, 1997; Gonzalez and Woods, 2002]; multi-spectral MR image segmentation, where a more sophisticated method is performed on multi-spectral MR images [Clarke et al., 1995]. Within pattern recognition methods, supervised ones [Vannier et al., 1985; Bomans et al., 1990; Ehricke, 1990; Waks and Tretiak, 1990; Clarke, 1991; Hall et al., 1992; Agartz et al., 1992; Ozkan et al., 1993; Schad et al., 1993; Fleagle et al., 1994; Mitchell et al., 1994; Vinitski et al., 1997; Kaus et al., 2001;
Zhang et al., 2004; Ruan et al., 2007; Gong and Brady, 2008; Iftekharuddin et al., 2008; Iscan et al., 2009] incorporate a training process to learn a model by repeatedly predicting and comparing data values; unsupervised methods [Bezdek, 1980; Gerig et al., 1992; Hall et al., 1992; Lei and Sewchand, 1992; Taut et al., 1992; Pal and Pal, 1993; Liang et al., 1994; Clarke et al., 1995; Kapur et al., 1996; Sammouda et al., 1996; Clark et al., 1998; Fletcher-Heath et al., 2001; Ho et al., 2002; Yeung and Wang, 2002; Shen et al., 2003; Capelle et al., 2004; Wang et al., 2004; Hata et al., 2005; Tsai et al., 2005; Chuang et al., 2006; Rouainia et al., 2006; Cai et al., 2007; Hung et al., 2008] partition data into subsets without employing an explicit training process [Duda et al., 2001].

2.3. Brain MR Image Tumour Segmentation

Brain tumours are any kind of intracranial mass of tissue and are caused by abnormal and uncontrolled cell division. More than 120 types of brain tumours have been identified and classified by the World Health Organisation (WHO) [Louis et al., 2007]. They are normally found in the brain itself, the cranial nerves, the brain envelopes, skull, pituitary and pineal gland. They can be also formed due to spread of cancers in other organs [Open Genomics, Online]. Primary brain tumours are commonly found in posterior cranial fossa and anterior two-thirds of the cerebral hemispheres in children and adults, respectively [Open Genomics, Online].

MR image tumour segmentation is an important process for medical practitioners on assessing tumour growth and treatment responses. However, it is a time consuming process. In addition, manual intervention in the process of
brain MR image tumour segmentation is prone to subjective interpretations as well as to inevitable human errors. For example, it was estimated that the average variability of accuracy is from 18% to 40% when different individuals perform the same brain tumour segmentation task; and 5% to 35% when they repeat the task three times at 1 month intervals [Mazzara et al., 2004]. Lowest variability was found for physicians who spent most time in producing the contours of brain tumours [Mazzara et al., 2004].

Furthermore, clinical practitioners benefit from automatic MR image tumour segmentation as it assists them in applying the latest treatment technologies such as computer-assisted surgery and radiation therapy. In addition to information collected through manual segmentation, automatic segmentation results provide objective information which allows more efficient and appropriate treatment options in comparison with previously available treatment methods. In this context, automatic MR image tumour segmentation is clearly valuable in clinical and scientific applications.

2.3.1. Challenges in Automatic Brain MR Image Tumour Segmentation

The background of MRI introduced in Section 2.1 suggests that this imaging technique is useful in differentiating brain anatomical structures. However, automatic brain MR image tumour segmentation methods that achieve accuracy comparable to that of human experts are still out of reach. The significant computational difficulty of this task is mainly caused by the overlapping uncertainties and artefacts from both general and tumour-affected brain MR images. This section first presents some of the major challenging problems in
general MR image segmentation, and then focuses on discussing important issues in brain MR image tumour segmentation.

In addition to the challenges related with MRI physics in general MR image segmentation, automated brain MR image tumor segmentation tasks often associate themselves with a number of other areas such as clinical pathology. One of the most prominent issues in brain tumour segmentation is that tumour pixels could have similar or identical signal intensity in comparison to normal pixels even within the same image [Just and Thelen, 1988]. Overlapping intensity distributions of healthy tissue, tumour, and surrounding oedema further degrade segmentation results [Prastawa et al., 2003]. An additional challenge is that tumour areas often have heterogeneous intensities, thereby complicating automated segmentation methods using MRI intensities in detecting precise boundaries of the tumour [Prastawa et al., 2004]. Furthermore, the large variation of properties amongst different tumour types [Louis et al., 2007] makes the task of distinguishing tumour from normal brain tissues more complex. For instance, brain tumours may be of any size, have a variety of shapes, appear at any location, and appear differently in image contrasts. Some tumours also deform other normal structures and appear together with oedema that alters intensity properties of the nearby region [Prastawa et al., 2004]. [Prastawa et al., 2005] further summarised some specific problems as follows:

1. The deformation of non-tumour structures due to tumour mass effect.

2. Infiltration of brain tissue by tumour and oedema. Oedema appears around the tumour mainly in white matter (WM) regions.
3. There is a gradual transition from tumour to oedema, making it difficult to detect the boundary between the two structures.

After the injection of a contrast agent, some tumours respond well and appear clearly enhanced, or may show an enhanced boundary. However, a significant number of tumour types always resist imaging enhancement through contrast agent. It is estimated that approximately 10% of all brain tumours do not brighten in MR images after a contrast agent is injected [Fletcher-Heath et al., 2001]. Furthermore, when using T1-weighted with contrast enhancement (typically using gadolinium) MR images to detect tumour, blood vessels and cortical CSF tend to be brightened along with tumour. However parts of tumour that are of necrotic tissues do not appear enhanced at all [Fletcher-Heath et al., 2001]. [Prastawa et al., 2005] reported that, generally, it is impossible to segment tumours in the CE-T1-weighted MR images by the simple thresholding approach. Imaging enhancement achieved through injection of contrast agent is helpful in indicating the existence of tumours, but the large variety of brain tumour types leads to significant variations in their appearance, and therefore makes segmentation challenging.

A further challenge arises from similarities observed in the appearance of both oedema and CSF in T2-weighted images as hyper-intense areas [Fletcher-Heath et al., 2001]. So distinguishing oedema from CSF in T2-weighthed MR images is another challenging problem for automated segmentation methods. It can be seen that brain tumour affected MR images include a large number of properties that make MRI intensity values not strongly correlated with their
respective anatomical meaning. This fact impairs the accuracy of results obtained through automatic tumour segmentation. Therefore, simple intensity-based methods of image segmentation are insufficient for accurate automatic tumour segmentation in MR images.

2.3.2. Related Works

Similar to the existing methods on general medical image segmentation (see Section 2.2), approaches to brain MR image tumour segmentation can also be categorised as unsupervised and supervised, with the employment of more specific analyses and processes to address the challenges in brain MR image tumour segmentation.

[Gibbs et al., 1996] presented an unsupervised approach for the tumour segmentation in T1-weighted MR images. In order to separate tumour pixels from other pixels, this approach uses a region growing algorithm to expand the thresholded region up to the edges defined by a Sobel edge detection filter [Gonzalez and Woods, 2002]. Focusing on the problem of the badly defined region within medical images, a similar tumour segmentation approach through enhancing boundary was proposed by [Zhu and Yan, 1997]. [Ho et al., 2002] presented a fully unsupervised approach for tumour segmentation. This approach also focuses on segmenting tumours with an enhanced border. The main disadvantage of using edge based methods is due to the fact that these methods are by nature designed for single image, therefore the rich information provided by multi-spectral MR images is not fully utilised.
In order to further improve segmentation results for brain tumour segmentation, an FCM clustering algorithm has been applied along with a linear sequence of human-engineered knowledge-based rules and operations [Clark et al., 1998]. In this approach, the clustering algorithm divides the pixels into groups with similar intensities, while the set of knowledge-based (intensity- and anatomy-based) rules and low-level image processing operations are designed to select and adjust the results used for the final segmentation results.

[Shen et al., 2003] proposed a system that applies a novel intensity standardisation method in a pre-processing step followed by a modified FCM algorithm that incorporates dependencies between neighbouring pixels. This work addresses the challenging issues in brain MR image segmentation in the pre-processing component and is capable of handling multi-spectral MR images by improving unsupervised pattern recognition method. However, some of the other challenging issues in brain tumour segmentation (e.g., the weak correlation between MRI intensity and anatomical meaning) are yet to be addressed.

The supervised $k$-NN algorithm has been employed rather effectively by undertaking several pre-processing steps prior to classification by [Vinitski et al., 1997]. This work addressed several issues previously ignored by most automatic systems for tumour segmentation, and demonstrated fair improvements in segmentation results.

An approach that combined both supervised classification and template registration for the segmentation of brain tumours from T1-weighted images has also been developed by [Kaus et al., 2001]. This method uses a $k$-NN classifier
with patient-specific training and a label-based registration algorithm. After pre-processing, a ‘distance transform’ is computed based on the distance of each pixel to the template labels and is used to improve the \(k\)-NN classifications. The idea of using registration to remove normal structures that may have similar intensities to tumour pixels was an important component used by this method. However this approach is not particularly reliable due to the fact that tumour-intensities often vary substantially between different tumour types.

In the study conducted by [Mazzara et al., 2004] on assessing the effectiveness of MR image tumour segmentation with knowledge-based and the \(k\)-NN methods, it can be seen that the knowledge-based and the \(k\)-NN classification methods have quantitatively similar performance, however the \(k\)-NN method was able to segment all cases, whereas the knowledge-based method was limited to enhancing tumours with clear enhancing edges.

The support vector machines (SVM) method, which has seen much popularity in recent years [Zhang et al., 2004; Ruan et al., 2007], is based on separating the tumour and non-tumour classes for each pixel through constructing a hyper-plane in the input data. The brain MR image segmentation method designed by [Ruan et al., 2007] used multi-spectral MR image pixel intensities as input features and produced fair results. With the use and modification of the above mentioned supervised pattern recognition algorithm, the inclusion of patient specific training further improves brain tumour segmentation performance. However, the input features in these existing systems are limited to the MRI intensities which may not correctly denote their anatomical meaning.
In order to address the most challenging issue of the weak correlation between MRI intensities and anatomical meaning, [Iftekharuddin et al., 2008] recently proposed an enhanced segmentation system. Rather than just working on implementing and improving supervised segmentation methods, this approach extracts texture feature calculated by using fractal dimension (FD) [Mandelbroth, 1983; Zook and Iftekharuddin, 2005] and applies the feature for brain tumour segmentation. With the findings that the texture represented by FD values of brain tumour is different from that of other structures, FD values describing texture and multi-spectral brain MRI intensities are combined as input feature set for the following multi-layer feed-forward neural network (MLFF-NN) classifier; tumour regions are then separated from non-tumour regions. Featuring with several up-to-date image processing and pattern recognition methods in sequence, this work could be viewed as the state of the art approach in the brain MR image tumour segmentation.

From the above discussion on existing methods for medical image segmentation (see Section 2.2) and the more complicated applications of brain MR image tumour segmentation, it can be seen that the main difference between the up-to-date approaches and their prior counterparts lies in that the newer methods incorporate more features from the images in order to process and analyse as much information associated with the images as possible. The difference is particularly obvious when one compares some of the earlier methods that rely only on intensity feature from a single image, with the more up-to-date approaches that not only utilise input data from the multi-spectral MR
images but also retrieve and employ information such as texture as additional feature. This is consistent with recent findings in granular computing that emphasise the merits of pre-processing (granulation) of data as a means of enhancing information content of a data set [Bargiela and Pedrycz, 2002; Bargiela and Pedrycz, 2008]. As a result, pattern recognition methods have become the standard of the field of multi-spectral MR medical image segmentation in recent years, mainly due to their capacity to handle multi-dimensional input data. In addition to working on intensity in multi-spectral MR images, the newer approaches try to incorporate features with more anatomical meaning within their algorithms.

Both supervised and unsupervised pattern recognition based segmentation methods are now widely used due to the fact that multi-spectral dataset of the same anatomical location can be used as input data [Clarke et al., 1995]. Meanwhile, pattern recognition algorithms have also been modified consistently to be more suitable for specific segmentation tasks. In order to deal with the challenging issues within both general and tumour-affected MR images, more advanced pre-processing methods have also been employed. Furthermore, the frontiers of brain MR image tumour segmentation are being pushed forward at present by employing techniques such as registration methods and deformable model [Pham et al., 2000] in order to enhance the efficiency of the segmentation methods.
2.4. Summary

This chapter provides background knowledge on medical imaging and MRI and offers an introduction to medical image segmentation. After the literature review on medical image segmentation and the discussion of common segmentation system structure, general functions of its inclusive components of pre-processing, feature extraction, segmentation and classification are explained. In the discussion of the feature extraction component, the significance of extracting relevant features is emphasised. Discussion on challenges in brain MR image tumour segmentation and related works identifies several important issues. It can be summarised that for MR images, the most important factor that defies accurate tumour segmentation is the weak correlation between MRI intensity and its respective anatomical meaning. This issue leads to the motivation of the approach proposed in this research.
CHAPTER 3: USING LATERAL VENTRICULAR DEFORMATION FOR BRAIN TUMOUR SEGMENTATION

What the mind of man can conceive and believe, it can achieve.

--- Napoleon Hill

Digital image segmentation is to label pixels according to their similarity of characteristics and properties measured from feature data [Clarke et al., 1995; Shapiro and Stockman, 2001; Gonzalez and Woods, 2002]. In common medical magnetic resonance (MR) image segmentation systems, one important step is the extraction of more relevant features for segmentation [Schad et al., 1993; Clarke et al., 1995].

To establish the idea that the high level feature derived from brain lateral ventricular deformation could be used to increase tumour segmentation, this chapter firstly introduces brain lateral ventricles from both anatomical and magnetic resonance imaging (MRI)-related aspects in Section 3.1. Based on observations of lateral ventricular shape variation in MR images, correlation between lateral ventricular deformation and compression caused by brain tumours is examined in Section 3.2. The idea of using lateral ventricular deformation for brain tumour segmentation is introduced in Section 3.3. In
Section 3.4, this idea is then expanded by the considering the main tasks in lateral ventricular deformation feature extraction. This chapter is summarised in Section 3.5.

3.1. Properties of Lateral Ventrices

As illustrated in Figure 3.1 and Figure 3.2, a ventricle is an internal cavity of brain. A normal brain contains a connecting system of ventricles, commonly referred to as the ventricular system, which is filled with cerebrospinal fluid (CSF) [Bear et al., 1996; Gunderman, 1998; Goetz and Pappert, 1999].

Figure 3.1: Drawing showing brain ventricular system in sagittal view, image adapted from [Gray’s Anatomy, Online].
CSF is produced mainly by a structure called choroid plexus in the brain ventricular system [Bhatnagar, 2007]. It first flows through the ventricular system, and then circulates into the sub-arachnoid space [Bear et al., 1996; Goetz and Pappert, 1999; Fix, 2001].

Development of the brain ventricular system can be traced back to the cavity of the neural tube [Swiss Embryology, Online] within the human embryo [Fix, 2001]. The two lateral ventricles, along with the third and fourth ventricles, make up the ventricular system within the brain. Classified as part of the telecephalon [Fix, 2001], they are the largest of the ventricles [Fix, 2001; Gaser et al., 2001].

The lateral ventricles are two horseshoe-shaped cavities conforming to the general shape of left and right cerebral hemispheres, and are separated by the septum pellucidum, i.e., they do not communicate directly with each other [Goetz
and Pappert, 1999; Fix, 2001]. Each of the lateral ventricles has four parts: anterior horn, body, posterior horn and inferior horn which are present in the frontal lobe, the parietal lobe, the occipital lobe and the temporal lobe respectively [Fix, 2001; Cherian et al., 2008].

Figure 3.3: Sequences of healthy T1- (first row) and T2-weighted (second row) brain MR image slices in axial view showing the lateral ventricles, images adapted from [The Whole Brain Atlas, Online].

Figure 3.3 illustrates some scans from sequences of T1- and T2-weighted MR images in axial view where lateral ventricles are located in the brain centre. Figure 3.3 (c) and (g) show that, even though lateral ventricles do not contain all of the CSF inside the brain, they are the biggest structures that mainly contain CSF in the axial view of the brain centre [Brown and Semeka, 2003]. As mentioned in Chapter 2, CSF appears dark in T1-weighted MR images and bright in T2-weighted MR images [Brown and Semeka, 2003; Westbrook et al., 2005]. Therefore, lateral ventricles accordingly appear dark and bright in T1- and T2-weighted MR images, respectively.
3.2. Lateral Ventricular Shape Variation

In a healthy brain, the two lateral ventricles (left and right) are roughly symmetrical to each other\(^4\). Pathological studies have shown that certain diseases and/or abnormalities associated with the brain ventricular system may alter the shape of the lateral ventricles. Swellings or shrinkages of structures within ventricular system may be caused by congenital defect, trauma, or tumour [Bear et al., 1996; Goetz and Pappert, 1999; Graham et al., 2006]. If there is a blockage of the ventricular system that interrupts the flow of CSF, e.g., due to a blockage within the cerebral aqueduct, the normal flow of fluid between the lateral ventricles and the third ventricle would be disrupted, and the lateral ventricles and third ventricle would swell with CSF [Graham et al., 2006].

This swelling or enlargement is also termed as hydrocephalus [Goetz and Pappert, 1999]. Hydrocephalus may also be the result of the formation of CSF that exceeds the amount that can flow through the ventricular system or from a downstream-diminished capacity to absorb CSF [Graham et al., 2006]. The swellings or shrinkages of lateral ventricles are clinically utilised in the disease diagnosis process [Goetz and Pappert, 1999; Graham et al., 2006]. These cases suggest that the shapes of lateral ventricles are highly susceptible to deformation in the presence of abnormalities or diseases.

As can be seen clearly from Figure 3.4, in cases where brain tumours exist, one or two of the lateral ventricles are compressed; whereas for a healthy brain the two lateral ventricles are nearly symmetrical to each other (see Figure 3.3).

\(^4\) Volume of the lateral ventricles is known to increase with age [Chung et al., 2006].
Figure 3.5 illustrates the direction of compression from brain tumour and the deformed lateral ventricle. It can be seen that one lateral ventricle is compressed in the opposite direction of the location of the brain tumour. With the segmentation results retrieved from a \( k \)-means clustering [Gerig et al., 1992] method, [Clarke et al., 1995] reconstructed brain image in 3-dimensional view to show that the tumour pushes the right ventricle downwards.

Figure 3.4: Nine axial view MR image slices from different patients showing brain tumour and lateral ventricles (Images courtesy of University Malaya Medical Centre).
However, due to the fact that brain tumours vary substantially in their location and size, and have diverse effects on lateral ventricles, it is not always the case that brain tumour and deformed lateral ventricles appear in the same image plane. Figure 3.6 illustrates how this correlation becomes clear when seen from different planes. The positions of the deformed parts of the lateral ventricle in Figure 3.6 (c) and (d) are basically the same as that of the brain tumour shown in Figure 3.6 (b). Figure 3.6 (a) illustrates the compression caused by a brain tumour on one lateral ventricle (coronal view). It can be seen that correlations between lateral ventricular deformation and the brain tumour still exist, even though it may not be observable in the same plane or view of MR images.
3.3. Lateral Ventricular Deformation and Brain Tumour Segmentation

Anatomical properties of lateral ventricles have substantial advantages for their shape retrieval, which is one key step in the process of feature extraction. The fact that lateral ventricles constitute one of the major structures in the brain allows for their boundaries to be easily delineated from their associated MR images [Gaser et al., 2001]. This is especially true for the case with axial view where lateral ventricles show large size [Gaser et al., 2001]. In addition, lateral ventricles normally exhibit simple geometry even after deformation caused by
pathological reasons. This makes the feature extraction process based on deformation of this structure relatively more reliable. Therefore, this research focuses only on lateral ventricular deformation, even though a number of other soft tissue structures in the brain such as grey matter (GM) and white matter (WM) are also found deformed due to the existence of tumours.

As a result, lateral ventricular deformation caused by the presence of brain tumours provides an intuition that one could exploit the information derived from the correlations between them to assist brain tumour segmentation.

3.4. Considerations of Lateral Ventricular Deformation Feature Extraction

Having established the idea that relevant features extracted from deformed lateral ventricles could possibly improve brain MR image tumour segmentation results, the feature extraction component in the common MR image segmentation system discussed in Chapter 2 can then be refined by incorporating the new features. The high level features (i.e. computed lateral ventricular deformation features) can be combined with existing low level features (i.e. MRI intensity features).

In the brain tumour segmentation system proposed by [Iftekharuddin et al., 2008], extracted texture features by using fractal dimension (FD) [Mandelbroth, 1983; Zook and Iftekharuddin, 2005] are applied to brain tumour segmentation. In this work, MRI intensity features are combined in the feature extraction component, followed by a multi-layer feed-forward neural network (MLFF-NN) classification [Clarke, 1991; Hall et al., 1992; Duda et al., 2001]. Although texture
feature is not suitable for MR image segmentation based on pixels [Clarke et al., 1995] and the large number of brain tumour types [Louis et al., 2007] makes texture not a robust feature for brain tumour segmentation, it provide further information which are relevant to brain tumour. This work suggests that two key processes are needed in utilising high level features extracted from low level features for segmentation systems:

1. Relevant methods for transforming low level features into high level features in the feature extraction process [Bargiela and Pedrycz, 2002].

2. Combination of the computed high level features with other features which can be employed as multi-dimensional input feature set for suitable segmentation methods.

In this research, only MRI intensities are used as low level features. High level features are calculated using intensity values of all pixels in the image. Considering that lateral ventricular deformation is a geometrical variation, the process of feature extraction needs to address the following tasks:

1. Retrieval of lateral ventricular shape;

2. Transforming lateral ventricular deformation into feature data (applicable for brain tumour segmentation) based on measurement of the geometrical variation.

Characteristics of lateral ventricles offer substantial advantages in shape retrieval due to their relatively large volume and sharp boundaries as can be visualised in the MR images of axial view [Gaser et al., 2001]. However, accurate
retrieval of lateral ventricular shape is a challenging task when lateral ventricles are deformed by the compression from brain tumours.

As can be seen from Figure 3.4(b) and Figure 3.4(d) to Figure 3.4(i) (see Section 3.3), brain tumours in several cases are joined with lateral ventricles in Figure 3.4 (d) to Figure 3.4(g) and Figure 3.4(i); lateral ventricles are shown in a fractured manner in Figure 3.4(h) and Figure 3.4(i); large volume of oedema exists in Figure 3.4(b), Figure 3.4(h) and Figure 3.4(i), and brain tumours are similar in intensity as that of lateral ventricles in Figure 3.4(b) and Figure 3.4(g)\(^5\). It can be seen that developing robust methods for accurate retrieval of lateral ventricular shapes in all situations is a difficult task.

The process of extracting lateral ventricular deformation feature can be decomposed to two parts: estimating lateral ventricular deformation and transforming the estimated data to feature. The step of estimating lateral ventricular deformation is to associate template and deformed lateral ventricles, and to model, calculate and quantify shape variation between their normal and deformed forms. Hence, both healthy and deformed lateral ventricles must be available for shape comparison. However, the previous discussions on lateral ventricles suggest that lateral ventricles of one person are subject to shape variation with age, even with the absence of pathology or abnormality [Chung et al., 2006]. Furthermore, because of the varieties of size, location and type of brain tumours [Prastawa et al., 2004; Prastawa et al., 2005; Louis et al., 2007], their compression effects on lateral ventricles are significantly diverse [Prastawa

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\(^5\) Evaluations of lateral ventricles and tumours are from are from Tan Jui Kok, Manager of Radiology Department in Penang Adventist Hospital, George Town, Penang, Malaysia.
et al., 2005]. There is no lateral ventricular shape that can be used as a general template (of a pair of healthy lateral ventricles) to perfectly associate the shape of the deformed lateral ventricles in all situations. Therefore, an additional step of adjusting feature data is necessary in the lateral ventricular deformation feature extraction component.

It can be summarised from the above discussions that, the following four factors must be considered in the lateral ventricular deformation feature extraction component in order to obtain desirable results:

1. Adequate methods for retrieving lateral ventricular shape must be selected or designed.
2. A relevant method suitable for measuring lateral ventricular deformation must be selected.
3. Template and deformed lateral ventricles should be correctly associated to allow the deformation measurement to be accurately performed.
4. Relevant feature data adjustment process is required due to the difficulty in associating template and deformed lateral ventricles.

3.5. Summary
This chapter firstly provides the background knowledge on lateral ventricles from their anatomical properties and visualisations in MR images. This is followed by the discussion of lateral ventricular deformation due to compression from brain tumours. With this background information, the idea that brain tumour segmentation accuracy can be improved by using lateral ventricular deformation
as features is proposed. After discussing several key factors and their related challenges in the process of transforming lateral ventricular deformation into feature, this chapter outlines essential factors for building the lateral ventricular deformation feature extraction component.

This chapter also provides rationale for the proposed approach, and leads naturally to the design of the lateral ventricular deformation feature extraction component in the next chapter.
There is a single light of science, and to brighten it anywhere is to brighten it everywhere.

--- Isaac Asimov

Chapter 3 establishes that important tasks of lateral ventricular deformation feature extraction should include retrieval of lateral ventricular shape, and transformation of lateral ventricular deformation into feature. To achieve the latter, one process to model and estimate the deformation of the retrieved lateral ventricular shape must be applied. Therefore the design of lateral ventricular deformation feature extraction component actually consists of the three streamlined processes as illustrated in Figure 4.1. Within these processes, the important factors of lateral ventricular shape retrieval, lateral ventricles association, deformation measurement and deformation adjustment discussed in Chapter 3 can be accordingly taken into account.
Following the flow of the processes in the feature extraction component, the rest of the chapter is organised as follows. The processes of retrieving lateral ventricular shape, estimating lateral ventricular deformation and transforming lateral ventricular deformation to feature are described in Section 4.1, Section 4.2 and Section 4.3, respectively. Section 4.4 demonstrates the overall design of the feature extraction component. Section 4.5 summarises the chapter.

4.1. Retrieving Lateral Ventricular Shape

Some of the properties associated with lateral ventricles, such as their relative prominence and sharp boundaries, facilitate the task of obtaining accurate shape retrieval results. However in cases where lateral ventricles are deformed, for example, lateral ventricles are in a fractured manner or merged with brain tumour or oedema, the segmentation becomes more challenging. Due to the fact that the

Figure 4.1: Overview of the lateral ventricular deformation feature extraction component.
primary objective of this research is to utilise lateral ventricular deformation for brain tumour segmentation, the majority of MR image cases studied do not have healthy lateral ventricles, but those deformed by the compression from brain tumours. This issue requires carefully designed schemes and methods in order to achieve satisfactory results.

Among existing works on brain lateral ventricular shape retrieval and brain magnetic resonance (MR) image lateral ventricles segmentation, a method proposed by [Worth et al., 1998] addressed the task of segmenting brain ventricles through choosing intensity thresholds by making use of anatomical information and location of ventricular pixels in the histograms of MR images. However, the thresholding method employed is limited to handle only single MR images. [Wu et al., 2003] used a combination of the segmentation expectation maximisation-field approximation-local prior algorithm (EM-MF-LP) together with intensity-based statistical segmentation and topologic constraints, to segment all compartments of the ventricular system. But the use of spatial probability of tissue classes in the brain makes segmentation results of deformed lateral ventricles unstable. The disadvantage of this approach can be easily seen from the fact that, when brain tumours exist, parts of the lateral ventricles are often pushed into locations within the intracranial region that ventricular system does not normally occupy, making results obtained through the use of topological constraints unreliable.

Although applications vary in the above mentioned works, it can be seen that the two schemes are both based on the approach of discriminating ventricle
tissues through the analysis on its intensity and geometric location. Since the lateral ventricles are located at the brain centre and substantially filled with cerebrospinal fluid (CSF) [Bhatnagar, 2007], the process of lateral ventricular shape retrieval can be viewed as a brain tissue segmentation step which focuses on differentiating CSF, followed by extraction of the specific lateral ventricular region from the identified CSF tissue area. Therefore, the lateral ventricular shape retrieval process is designed with the three steps of brain tissue segmentation, CSF identification and lateral ventricles extraction.

In the brain tissue segmentation process, the rich information available in multi-spectral MR images, for example, both T1- and T2-weighted MR images need to be exploited and combined as multi-dimensional input data for segmentation. Therefore, segmentation methods which support multi-dimensional dataset should be selected. As discussed in Chapter 2, the most common approach for multi-spectral MR image segmentation is the family of pattern recognition methods [Clarke et al., 1995] due to their capacity of handling multi-dimensional dataset. Analogously, this research employs pattern recognition methods for brain MR image tissue segmentation.

The general types of the pattern recognition methods include both supervised and unsupervised techniques. The most fundamental aspect that differentiates supervised methods from unsupervised methods is the use of training data to automatically learn a model for segmentation.

Supervised methods use operator input for segmentation, they normally train the core algorithms or functions [Duda et al., 2001]. In image segmentation, it is
normally done by first selecting training pixels or training regions on the images [Clarke et al., 1995].

Unsupervised methods partition data into subsets without employing an explicit training process [Duda et al., 2001]. Clustering methods are commonly viewed as the instances of unsupervised learning where no training data is required. The objective is to partition a collection of data points into a number of subgroups or clusters, where objects within a cluster demonstrate a certain degree of closeness or similarity based on one or more empirical criteria. In another word, methods using this approach divide scattered data into several groups so as to ease the task of further analysis [Duda et al., 2001]. The final grouping of pattern is achieved by defining and quantifying similarities between individual data points or patterns and assigning patterns that are most similar to the same cluster [Duda et al., 2001]. Despite the differences, there is an intuitive similarity between clustering and segmentation: both processes share the common goal of finding accurate separation of the input objects [Clarke et al., 1995; Duda et al., 2001].

CSF tissue usually has a large volume and distinctive range of intensity value compared to other tissue types [Gaser et al., 2001] in both healthy and tumour-affected brain MR images. These characteristics circumvent the requirement for the process of patient-specific training in the CSF tissue segmentation. To reduce human involvement in the segmentation process to the minimum level, it is desirable to employ segmentation methods which do not require the tedious process of collecting training data. Therefore, in this work,
unsupervised pattern recognition methods are employed for the task of brain MR image tissue segmentation.

Unsupervised segmentation methods only separate brain tissues without labelling them. Therefore, to automatically select the CSF tissue, an identification step is necessary for automatically separating the CSF from other types of brain tissue.

[Gunderman, 1998] suggested that CSF appears dark on T1-weighted MR images and bright on T2-weighted MR images, more specifically, the intensity values of CSF are high in T2-weighted magnetic resonance imaging (MRI) while low in T1-weighted MRI. This particular characteristic of the multi-spectral MRI can be utilised to differentiate CSF from other tissue types.

Although lateral ventricular compartment is one of the most clearly distinguishable regions within the segmented CSF tissue, the fact that CSF exists in several other regions outside of ventricular system of the brain [Gunderman, 1998] requires additional operations to be performed in order to extricate the precise CSF region constituting the lateral ventricles. An important step in this process therefore involves removing non-ventricular CSF regions.

As mentioned in Chapter 3, the volume of lateral ventricles is known to increase with age [Chung et al., 2006]. Although lateral ventricles are deformed by pathologies, the images used in this research show that they are still generally located in the brain centre. Therefore, normally lateral ventricles can be extracted by selecting the particular CSF region in the brain centre.
Figure 4.2: Structure of the process of retrieving lateral ventricular shape.

4.2. Estimating Lateral Ventricular Deformation

The objective of lateral ventricular deformation estimation is to measure positional differences between every pixel of a target image with that of the image representing template lateral ventricles. As suggested in Chapter 3, for effectively estimating lateral ventricular deformation, the factors of associating lateral ventricles and measuring deformation must be addressed. The purpose of lateral ventricular deformation measurement is to analyse positional differences between every pixel of a target image with that of the image representing template lateral ventricles. This step is partially dependent on the associated or
aligned points which are correspondingly selected from both template and target lateral ventricular boundaries. Therefore, the process of estimating lateral ventricular deformation can be designed with two major steps of lateral ventricles alignment and lateral ventricular deformation measurement.

Appropriate alignment of lateral ventricular boundary is an important step for the effectiveness of deformation estimation. The alignment of lateral ventricles can be achieved by coupling corresponding landmark points on both template and target lateral ventricles. These landmark points can be sampled from the aligned template and target lateral ventricular boundaries.

In the lateral ventricles alignment step, it is important to find an approach that can be used to correlate points on lateral ventricular boundaries with regards to their anatomical meanings. A key observation that is helpful for performing the alignment of lateral ventricles can be drawn from the work presented in [Gaser et al., 2001]. It is reported that lateral ventricular deformation tends to have the most prominent effects on the anterior horn region [Fix, 2001]. The location of the anterior and posterior horns at the tips of the lateral ventricles [Fix, 2001; Cherian et al., 2008] suggests that these regions are easily deformed as a result of compression caused by the presence of brain tumours [Gaser et al., 2001]. Therefore, the tips of anterior and posterior horns in the pair of lateral ventricles can be used as the key points for accurately aligning target and template lateral ventricles, thereby taking the maximum possible shape variation caused by compression into account. After the four pairs of key points are selected, a
number of additional point pairs can be subsequently selected to complete the alignment.

Lateral ventricular deformation measurement is the core step in the process of estimating lateral ventricular deformation. Due to the fact that deformation can be described by mathematical functions that map points in one form to another [Zelditch et al., 2004], positional differences of all image points can be obtained by using modelling deformation functions which map all points between template and deformed images, followed by calculating displacements of all points in both images.

Generally, in order to model deformation, both linear and non-linear functions can be used. However, with regards to brain MR images, linear transformation functions, such as affine transform, cause the images to be globally smoothed, thereby accommodating only very small and simple deformations [Tittgemeyer et al., 2002] and making the process of employing them for modelling deformations of complex brain structures undesirable. With theses considerations, nonlinear deformation modelling function is employed.

By using the nonlinear functions to map each point of the image into a new position and calculating the displacement of each point in the image [Sanchez-Ortiz et al., 1996], the lateral ventricular deformation data can be measured.
Summarising the discussions above, Figure 4.3 illustrates the structured process of estimating lateral ventricular deformation. The two major steps of lateral ventricles alignment and lateral ventricular deformation measurement are included in this process.

4.3. Transforming Lateral Ventricular Deformation to Features

After lateral ventricular deformation information is quantified by the approach discussed in the previous section, it can then be transformed to feature which is relevant to brain tumour.

As discussed in Chapter 3, many factors in actual clinical cases contribute to shape variation of lateral ventricles [Prastawa et al., 2004; Prastawa et al., 2005; Chung et al., 2006; Louis et al., 2007]. It is rather difficult to retrieve an ideal template which can perfectly map the target lateral ventricles for all cases. This challenge directly affects the accuracy of the deformation estimation.
To alleviate this problem, one estimated lateral ventricular deformation data adjustment step is added in the component. In this step, the direction of the displacement vector is taken into account so as to adjust the deformation estimation. The lateral ventricular deformation estimation step allows users to select one point as an offset reference, thus reducing the effects from misalignment between template and target lateral ventricles.

After the lateral ventricular deformation data is retrieved in the lateral ventricular deformation estimation step, it is necessary to convert it to feature data to be included in feature set for brain tumour segmentation.

In this research, the feature set for brain magnetic resonance (MR) image tumour segmentation include both low level features of MRI intensities and high level computed lateral ventricular deformation features. The high level features are obtained by normalising and converting the estimated deformation data to image greyscale values [Iftekharuddin et al., 2008].

Figure 4.4 summarises the above mentioned steps in the process of transforming lateral ventricular deformation to feature. The process is achieved by the two steps of estimated lateral ventricular deformation data adjustment and estimated deformation data to feature conversion.
4.4. Architecture of Lateral Ventricular Deformation Feature Extraction Component

The structure of the lateral ventricular deformation feature extraction component is composed of the three continuous processes of retrieving lateral ventricular shape, estimating lateral ventricular deformation and transforming lateral ventricular deformation to feature. Each of these processes is further composed of several more specific consistent steps. The structure of the component is illustrated in Figure 4.4.

Within the component, the input is brain MR image data after pre-processing, and output is the extracted lateral ventricular feature data. The output is then combined with other low level features to be used for brain tumour segmentation (see Chapter 6).
The steps in the component as shown in the architecture diagram in Figure 4.5 are performed in a sequential manner. The accuracy of the final output of the extracted lateral ventricular deformation feature is dependent on each inclusive step. Therefore, all employed methods and algorithms must be validated. Details of employed methods and their respective experimental results and evaluations are presented in Chapter 5.
4.5. Summary

This chapter extends the idea of using lateral ventricular deformation for brain tumour segmentation to the component design of lateral ventricular deformation feature extraction. Based on the key factors and major tasks identified in Chapter 3, the design of the three processes of retrieving lateral ventricular shape, estimating lateral ventricular deformation and transforming lateral ventricular deformation to features are presented.

In the process of retrieving lateral ventricular shape, methods employed for brain MR image tissue segmentation are overviewed. With the study of the related work and analysis of the nature of this application, unsupervised pattern recognition techniques are selected for the segmentation task.

This chapter also introduces the scheme selected for the process of estimating lateral ventricular deformation. In this process, lateral ventricles alignment serves as the prerequisite for carrying out the estimation. Based on the study of structure of lateral ventricles, an approach of selecting lateral ventricles landmark points is introduced. With the aligned lateral ventricles, the quantified lateral ventricular deformation data can be obtained at the end of lateral ventricular deformation measurement step.

In the process where lateral ventricular deformation is transformed to feature, the problem from the misaligned lateral ventricles is discussed, which leads to the idea of incorporating a deformation adjustment step, followed by the normalisation of deformation data to image greyscale as an additional feature for segmentation.
By integrating the above mentioned processes, the architecture of the component for lateral ventricular deformation feature extraction is derived. The detailed methods and algorithms used in each constituent are to be explained in details in Chapter 5.
CHAPTER 5: IMPLEMENTATION OF FEATURE EXTRACTION COMPONENT

The three great essentials to achieve anything worthwhile are, first, hard work; second, stick-to-itiveness; third, common sense.

--- Thomas Alva Edison

The brain magnetic resonance (MR) image lateral ventricular deformation feature extraction component consists of three streamlined processes of retrieving lateral ventricular shape, estimating lateral ventricular deformation, and transforming lateral ventricular deformation to feature. These processes are used to obtain the lateral ventricular boundary by extracting lateral ventricles, estimate deformation by measuring the geometrical variation between aligned template and target lateral ventricles, and convert the estimated lateral ventricular deformation data into feature for segmentation. Following the component architecture, the implementation details of these processes are presented in this chapter, in particular, methods and algorithms for each of the processes are explained. To validate the applicability of the proposed methods, extensive experiments are performed and the results are evaluated and discussed.
The rest of the chapter is organised as follows. Section 5.1 elaborates implementation of the lateral ventricular shape retrieval process. Taking the limitations of the conventional fuzzy c-means (FCM) algorithm into consideration, a brain tissue segmentation scheme combining the enhanced FCM method with Gaussian smoothing is proposed. It is designed to resolve some of the problems associated with the conventional FCM algorithm when employed for MR image segmentation, such as sensitivity to noise and incapability of adjusting feature weights. After brain tissue segmentation step, additional methods and techniques for extracting lateral ventricles are also presented to complete the lateral ventricular shape retrieval process. Section 5.2 demonstrates the proposed scheme for estimating brain lateral ventricular deformation, which is achieved by the two steps of lateral ventricles alignment and lateral ventricular deformation measurement. The process of transforming brain lateral ventricular deformation information to features is explained in Section 5.3. In this section, with the consideration of the challenge posed by imperfect template lateral ventricles, estimated data of lateral ventricular deformation is adjusted by using the information implied by the position of tumour. The adjusted lateral ventricular deformation information is then converted to feature for brain tumour segmentation. Section 5.4 summarises the chapter and discusses some of the issues on using the extracted brain lateral ventricular deformation feature to enhance brain tumour segmentation.
5.1. Lateral Ventricular Shape Retrieval

Methods for accurate retrieval of lateral ventricular shape are indispensable for extracting lateral ventricular deformation feature. The importance of this process can be seen from the subsequent process of estimating lateral ventricular deformation which uses the retrieved lateral ventricular shape as input data. For example, in the lateral ventricles alignment step of the component, key points for aligning lateral ventricles in the template and target MR images are sampled from the boundaries of the lateral ventricles, which are essentially determined by the lateral ventricular shape.

As discussed in Chapter 4, the lateral ventricular shape retrieval can be achieved through three steps: brain MR image tissue segmentation for separating cerebrospinal fluid (CSF) tissue from other tissues, CSF identification for locating the image pixels/regions of which lateral ventricles are composed and lateral ventricles extraction for removing CSF pixels outside the lateral ventricular regions.

Brain tissue segmentation aims to separate CSF from several different types of tissues in the brain MR image. It is the most important step in this process because it directly affects the accuracy of lateral ventricular shape retrieval.

As an unsupervised pattern recognition (clustering) method, fuzzy c-means (FCM) [Dunn, 1973; Bezdek, 1980; Gerig et al., 1992] has been widely used in literatures for MR image segmentation tasks. Satisfying results have been reported with the use of conventional or modified FCM methods [Philips et al.,
FCM algorithm is able to retain more information from original images [Pham and Prince, 1999], compared to crisp or hard clustering methods such as \(k\)-means [Duda et al., 2001] clustering for instance. However, conventional FCM algorithm exhibits some limitations that make it difficult to obtain sufficiently accurate brain tissue segmentation results, especially on the deformed lateral ventricles used in the experiments of this research. Therefore, the conventional FCM method needs to be enhanced in order to give more desirable brain tissue segmentation results.

In this section, the conventional FCM algorithm and its limitations in MR image segmentation applications are discussed first. Based on the discussion, an enhanced FCM segmentation scheme is proposed. Experiments using the methods are performed and the results are evaluated to validate the proposed methods.

5.1.1. FCM Method

FCM clustering method is suitable for the task of brain tissue segmentation because it supports multi-dimensional feature data, therefore, the rich information contained in multi-spectral MR images can be well utilised. However this method has some disadvantages when employed for brain MR image tissue segmentation, such as sensitivity to noise and incapability to vary relative importance (adjustable weights) of different features [Pedrycz and Waletzky,
5.1.1. Conventional FCM Algorithm

FCM is a widely used clustering method that groups data elements to two or more clusters, associating with each element a set of membership levels. These membership levels indicate the strength of association between that data element and a particular cluster. Fuzzy clustering is a process of assigning these membership levels, and then using them to assign data elements to desired clusters [Bezdek, 1980].

Let an image be represented as \( X(x_1, x_2, x_3, \ldots, x_N) \), where \( x \) represents individual pixel within multi-dimensional (multiple features\(^6\)) data and \( N \) denotes the number of pixels. The algorithm works through an iterative optimisation procedure to minimise the cost function which is defined as follows:

\[
J = \sum_{j=1}^{N} \sum_{i=1}^{c} u_{ij}^m \| x_j - v_i \|^2 , \quad 1 \leq m < \infty
\]

(5.1)

where \( u_{ij} \) represents the degree of membership of data elements \( x_j \) in the \( i^{th} \) cluster, \( v_i \) is the centroid of the \( i^{th} \) cluster, \( c \) is the number of clusters to be partitioned, \( \| \cdot \| \) is a norm (Euclidean distance measures are commonly applied) representing the distance which expresses the similarity between measured

\(^6\) In pattern recognition methods, multiple feature data is created using multi-dimensional datasets [Clarke et al., 1995].
multi-feature data and the cluster centroid, and $m$ is a real constant greater than 1 which controls the fuzziness of the resulting partition [Bezdek et al., 1993].

Through updating cluster centroids iteratively, the cost function can be minimised as the summation of distances between image pixels to the centroid of clusters decreases. By indicating the closeness between pixels and cluster centroids, the membership function represents the probability that a pixel belongs to a specific cluster. A high membership value with a cluster suggests that a pixel is near to the centroid of this cluster, and low membership value means this pixel is far from the centroid of this particular cluster. In the FCM algorithm, the probability is dependent solely on the distance between each point and individual cluster centroid in the feature domain [Bezdek et al., 1993]. The membership function and cluster centroids are iteratively updated based on Equations 5.2 and Equation 5.3 as shown below:

$$ u_{ij} = \frac{1}{\sum_{k=1}^{c} \left( \frac{\|x_j - v_i\|}{\|x_j - v_k\|} \right)^{\frac{1}{m-1}}} $$

$$ v_i = \frac{\sum_{j=1}^{N} u_{ij}^m x_j}{\sum_{j=1}^{N} u_{ij}^m} $$

The iteration will stop when $\max \{ J_{p+1} - J_p \} < \sigma$, where $\sigma$ is the termination criterion between 0 and 1, and $p$ is the iteration step.
5.1.1.2. Disadvantages of Conventional FCM Method for Brain MR Image Tissue Segmentation

Compared to other clustering methods such as $k$-means [Duda et al., 2001], FCM method is able to retain more information from original images [Pham and Prince, 1999], leading to better segmentation results. By using membership function in FCM algorithm, fuzziness is introduced for the belongingness of each image pixels to deal with uncertainty [Bezdek et al., 1993; Pham and Prince, 1999; Cai et al., 2007].

However, conventional FCM method has limitations that make it difficult to derive desirable tissue segmentation results from certain brain MR image cases. These limitations can be summarised as follows:

1. The pixels on an MR image are normally highly correlated, i.e., pixels in the immediate neighbourhood possess nearly the same data in most cases. Exploiting the spatial relationship between neighbouring pixels could therefore potentially improve the accuracy of segmentation process [Pedrycz and Waletzky, 1997; Chuang et al., 2006]. While the spatial information in MR images is not fully utilised by the conventional FCM algorithm [Pedrycz and Waletzky, 1997; Bargiela et al. 2004; Chuang et al., 2006].

2. Conventional FCM algorithm is very sensitive to noise [Chuang et al., 2006].

3. The conventional FCM algorithm supports input dataset with multiple features, and is suitable for multi-spectral MR image segmentation. It
applies standard Euclidean distance function, making the weights for different input features fixed and identical to each other. As a result, conventional FCM is likely to ignore useful details and to retain noises and artefacts [Yeung and Wang, 2002; Hung et al. 2008].

It is more difficult to generate desirable tissue segmentation results from tumour-affected brain MR image than from healthy ones. Therefore, to obtain more accurate segmentation result, the conventional FCM method needs to be improved.

5.1.1.3. Related Works on Improving FCM Method

A number of methods have been developed recently to deal with the limitations of conventional FCM algorithm which does not take into account spatial information from image data. For instance, the idea presented by [Pedrycz and Waletzky, 1997] incorporates classification information obtained from supervised learning as a part of an objective function. In a similar work, [Dulyakarn and Rangsanseri, 2001] proposed an approach that modifies the conventional FCM algorithm to be semi-supervised, thus allowing the clustering process to employ conventional FCM with spatial information. The modified methods, however, have an obvious drawback: being semi-supervised, they cannot completely eliminate the requirement for using training data, therefore restraining them from being applied in some segmentation tasks.

[Ahmed et al., 2002] modified the objective function of conventional FCM algorithm to allow pixels in the immediate neighbourhood of a pixel to contribute
to its labelling. The work notably improves the results of conventional FCM methods, especially when applied to noisy images. However, the way in which this method incorporates the neighbouring information limits its application to 1-dimensional input feature set. [Chuang et al., 2006] proposed an approach of incorporating spatial information into the membership function for clustering by summing the membership function in the neighbourhood of each pixel under consideration. However the simple summation of neighbouring pixels used in this approach tends to substantially ignore details in the MR images. In a more recent work, [Cai et al., 2007] proposed an approach which incorporates both local and spatial information. The similarity of local and spatial information is then evaluated and applied in the FCM algorithm, thus creating a trade-off factor between insensitivity to noise and preservation of details. This approach is fairly effective for single image clustering. However, similar to some of the above mentioned works, it does not take multi-spectral MR images into account.

An approach that addresses some of the impairing effects arising from noise and inhomogeneous intensity is proposed by [Xiao et al., 2007a]. In this work, Gaussian smoothed image data is included as an additional feature into FCM input data. The procedure combines the details of the original image with those of the same image that has undergone a process of Gaussian smoothing. The experimental results achieve the expected improvements, showing that the addition of Gaussian smoothing enables conventional FCM to create more accurate and homogeneous clustering results. The segmentation performance
improvement of this approach is caused by eliminating superfluous detail from image data while preserving the essence.

There are also some other approaches in improving the conventional FCM algorithm. For instance, FCM has been applied along with a sequence of human-engineered knowledge-based rules and operations to produce desirable results [Clark et al., 1998]. In this work, the clustering algorithm divides the pixels with similar multi-spectral MRI intensities into groups, and the set of knowledge-based (intensity along with anatomy) rules and image processing operations are designed to select and adjust the final segmentation results. The incorporation of knowledge-based rules makes FCM algorithm insensitive to noise. More effective systems based on the use of FCM and knowledge-based rules have since been developed. Instances of these include systems that focus on the segmentation of tumours which cannot be enhanced by contrast agent through previous methods [Fletcher-Heath et al., 2001], and that apply a modified FCM algorithm that incorporates dependencies between neighbouring pixels [Shen et al., 2003].

However, none of the above approaches deals with the key issue of finding appropriate trade-offs among the various inputs for multiple features. To deal with this problem, [Xiao et al., 2007b] proposed a scheme to incorporate factors for assigning adjustable weights on specific features for different applications. Experimental results demonstrate that FCM clustering is particularly sensitive to the selection of feature weights, and that optimal feature weighting factors lead to more accurate clustering results [Yeung and Wang, 2002; Wang et al., 2004; Xiao et al., 2007b]. Previous works on selecting optimal feature weights include a
learning method proposed by [Wang et al. 2004] based on a defined similarity measure which was firstly suggested by [Yeung and Wang, 2002].

More recently, [Hung et al., 2008] proposed an FCM feature weights selection method based on measuring statistical variations within dimensions of the input data by using a bootstrapping [Efron, 1979] approach, and applied the method in colour image segmentation. This approach relies on the clear intensity value relationship among the three primary colour components, red, green and blue, available within colour images. A drawback with this approach arises from the fact that it was designed primarily to deal with the specifics of colour images. However, in the case of MR images, T1- and T2-weighted MR images do not demonstrate such clear relationships and are rather different from each other. As an example relevant to brain MR image tissue segmentation, CSF tissues in T1-weighted MR images appear dark (implying low MRI intensity values), while they appear bright in T2-weighted MR images (implying high MRI intensity values). Therefore it is not suitable to be used for conducting automatic FCM feature weights selection for MR image segmentation.

To make clustering results more insensitive to noise, and to include adjustable feature weights into conventional FCM algorithms with the emphasis of distinguishing CSF from other tissue types in MR images, a new weighted FCM clustering scheme is proposed. The scheme consists of applying Gaussian smoothed image data as an additional feature into FCM clustering, and using iterative searching of validity function values to select optimal feature weights. In addition to the experimental results on brain MR image tissue segmentation, the
clustering results are also validated by comparing the performance of the proposed FCM scheme with that of the conventional FCM method through a number of criteria, for instance, clustering validity functions and change of centroid values caused by the added noise [Xiao et al., 2008a].

5.1.2. Feature Weights Adjustable FCM Method with Gaussian Smoothing

With regards to the previous discussions about disadvantages and related works on improving conventional FCM for MR image segmentation, this section proposes an enhanced FCM method termed “feature weights adjustable FCM (fwaFCM)” with Gaussian smoothing. Techniques of incorporating Gaussian smoothing, the fwaFCM method and automatic feature weight selection for fwaFCM are introduced. These techniques attempt to reduce errors caused by noise, enable feature weights to be adjustable, and select optimised feature weights.

5.1.2.1. Incorporating Gaussian Smoothing to Conventional FCM Method

As discussed in Chapter 2, noise is one of the primary factors that affect MR image segmentation results. To address this challenge, Gaussian 2-dimensional convolution operator can be used to smooth image data for removing noise [Davies, 1990; Shapiro and Stockman, 2001; Gonzalez and Woods, 2002]. A 2-dimensional circularly symmetric Gaussian smoothing function has the form:

\[
G(x, y) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2 + y^2}{2\sigma^2}}
\]  

(5.4)
where $x$ is the distance in the horizontal axis, $y$ is the distance in the vertical axis, and $\sigma$ is the standard deviation of the Gaussian distribution.

The Gaussian smoothing function provides gentler smoothing and preserves edges better than a similarly sized mean filter because the Gaussian function outputs a “weighted average” of each pixel neighbourhood [Shapiro and Stockman, 2001; Spatial Filters, Online]. With the fact that the conventional FCM algorithm supports multiple feature inputs, the original and its Gaussian smoothed MRI intensity data can be treated as two features and combined in the input feature set as a multi-dimensional dataset [Xiao et al., 2007a]. As a result of combining the two features, clustering results can be affected by both the original image and the smoothed image data, i.e., the details in the original image and the smoothed image data (in which noise is reduced) are incorporated for clustering.

5.1.2.2. Algorithm of Feature Weights Adjustable FCM Method

As discussed earlier in this section, another problem in the conventional FCM is that, conventional FCM algorithm employs the standard Euclidean distance function, hence assigns the same and non-adjustable weight to all features, although it supports multi-dimensional feature set.

By expressing $\|x_j - y_i\|$ with Euclidean distance function $D_{ij}$, as in the standard FCM, Equation 5.1 can be expressed as:

$$J = \sum_{j=1}^{N} \sum_{i=1}^{c} u_{ij}^m D_{ij}^2$$  \hspace{1cm} (5.5)
where \( N \) is the number of data points, \( D_{ij} \) is the distance of data \( x_{jk} \) (in Equation 5.6) to the centroid of \( i^{th} \) cluster and takes the following form:

\[
D_{ij} = \sqrt{\sum_{k=1}^{M} (x_{jk} - v_{ik})^2}
\]

(5.6)

where \( M \) is the number of features, or the dimension of the input data.

In the measurement of input feature set using standard Euclidean distance function, weights of all features in the input feature set are exactly the same. As a result, the conventional FCM algorithm is not able to provide fine-tuning of the clustering results by changing feature weights. This becomes problematic when one or more input features need to be emphasised and other features to be de-emphasised.

To adjust the weights of each input feature, Equation 5.6 can be modified by adding factors \( \alpha_k \), hence it becomes:

\[
D_{ij} = \sqrt{\sum_{k=1}^{M} (\alpha_k x_{jk} - v_{ik})^2}
\]

(5.7)

where \( \alpha_k \) is the weighting factor for the \( k \)-th feature.

Introducing \( \alpha_k \) makes weight of each input feature adjustable. The algorithm of fwaFCM [Xiao et al., 2007b] is described as in Algorithm 5.1.
Algorithm Name: fwaFCM Clustering

Input:
- array of image data;
- array of feature weighting factors $\alpha$;
- number of clusters $c$;
- number of maximum iterations $max$.

Output: Set of clustered regions presented in the membership function $u$.

1: Set the initial membership value, $u_{ij}$

2: for $p=1$ to $max$ do

3: Update the new centroids of clusters: $v_j = \frac{\sum_{j=1}^{N} u_{ij}^m x_j}{\sum_{j=1}^{N} u_{ij}^m}$

4: Estimate the distances between all pixels to cluster centroids:
   $D_{ij} = \sqrt{\sum_{k=1}^{M} (\alpha_k x_{jk} - v_{jk})^2}$

5: Calculate the cost function: $J_p = \sum_{j=1}^{N} \sum_{i=1}^{c} u_{ij}^m D_{ij}^2$

6: Update the new membership function: $u_{ij} = \frac{1}{\sum_{k=1}^{c} \left( \frac{D_{ij}}{D_{kj}} \right)^{2-1}}$

7: if $\| J_{p+1} - J_p \| < \sigma$ {Convergence condition}

8: break

9: end for

Algorithm 5.1: fwaFCM clustering.

Based on the conventional FCM algorithm, according to Equation 5.7, the fwaFCM clustering algorithm adds the weighting factors into standard Euclidean distance function in line 4. As a result, the modified fwaFCM allows the feature
weights to be tuned in the clustering according to specific application requirements.

5.1.2.3. Adding Gaussian Smoothing to Feature Weights Adjustable FCM Method

In cases where there is only one input feature available (e.g., only T1- or T2-weighted MR image is available), for better clustering results, the original and its Gaussian smoothed image data can be combined to create input feature set. Therefore, fine tuning of the weights of each feature can still be achieved. This approach offers a means of adjusting effects between the Gaussian smoothed and original image data.

In the implementation of this method, input feature set can be created by combining the original image data and the Gaussian smoothed image data. The combination of the features is presented as below:

\[
Data = [Data_1 \ Data_2]
\]  

(5.8)

where \( Data_1 \) and \( Data_2 \) represent an original MR and its Gaussian smoothed image data respectively. Algorithm 5.2 outlines the process of combining the input data.
Algorithm Name: **CombineData**

**Input:**
- Image $I$;
- Set of number of clusters, $c$; number of maximum iterations, $max$;
- Size of Gaussian filter, size and value of Gaussian standard deviation, $sigma$.

**Output:** Combined data.

1: Convert image data $I$ to an array of original feature data, $Data_1$

2: Create 2-D Gaussian low pass filter $PSF$ by Gaussian kernel function $F_{Gau}$ with size and standard deviation, $sigma$: $PSF = F_{Gau}(\text{size,}\sigma)$

3: Convolve $Data_1$ by the filter $PSF$ to create Gaussian smoothed $Data_2$: $Data_2 = G(Data_1, PSF)$

4: Create an input feature set array $Data$ by combining $Data_1$ and Gaussian smoothed $Data_2$: $Data = [Data_1 Data_2]$

Algorithm 5.2: Combining Gaussian smoothed and original images.

Multi-dimensional input feature set also can use more information from multi-spectral MR images, e.g., four features in the input data are T1-, T2-weighted, Gaussian smoothed T1- and T2-weighted MR images. The input data then becomes:

$$Data = [Data_1 Data_2 Data_3 Data_4] \quad (5.9)$$

where $Data_1$ to $Data_4$ represent T1-, T2-, Gaussian smoothed T1- and T2-weighted MR images respectively. Each of them represents one dimension in the multi-dimensional data of feature set.
5.1.2.4. Selecting Optimal Feature Weights Using Clustering Validity Functions

Validity functions are widely used to evaluate performance of clustering algorithms. Two common classes of validity functions are based on fuzzy partition and feature structure [Bezdek, 1974; Bezdek, 1975; Fukuyama and Sugeno, 1989; Xie and Beni, 1991; Wang et al., 2004; Chuang et al., 2006].

The representative functions based on fuzzy partition are partition coefficient \( V_{pc} \) [Bezdek, 1974] and partition entropy \( V_{pe} \) [Bezdek, 1975]. They are defined respectively as follows:

\[
V_{pc} = \frac{\sum_{i=1}^{N} \sum_{j=1}^{c} u_{ij}^2}{N} \tag{5.10}
\]

\[
V_{pe} = \frac{-\sum_{j=1}^{N} \sum_{i=1}^{c} [u_{ij} \log u_{ij}]}{N} \tag{5.11}
\]

These two validity functions are based on the idea that the partition with less fuzziness signifies better performance [Bezdek, 1974; Bezdek, 1975]. In both Equation 5.10 and Equation 5.11, \( u_{ij} \) (\( i=1,2,\ldots,c; j=1,2,\ldots,N \)) is the membership of data point \( j \) in cluster \( i \). The closer this value approaches to unity, i.e., value of 1, the better the data is classified. As a result, the best clustering is achieved if \( V_{pe} \) is minimal and \( V_{pc} \) is maximal [Bezdek, 1974; Bezdek, 1975; Wang et al., 2004; Chuang et al., 2006].

Another class of clustering validity functions based on geometric sample data structure has also been widely used. The idea of these validity functions is
that, in a good clustering, samples within one partition should be closely united, and samples between different clusters should be separated far from each other. To quantify the ratio of total variation within clusters and the separation level of clusters, [Fukuyama and Sugeno, 1989] proposed Fukuyama-Sugeno validity function \( V_{fs} \), [Xie and Beni, 1991] proposed Xie-Benie validity function \( V_{xb} \).

\( V_{fs} \) is defined as follows:

\[
V_{fs} = \sum_{j=1}^{N} \sum_{i=1}^{c} (u_{ij})^2 \left( \| x_j - v_i \|^2 - \| v_i - \bar{v} \|^2 \right)
\]  

(5.12)

where \( \bar{v} \) is the average value of all cluster centroids.

\( V_{xb} \) is defined as:

\[
V_{xb} = \frac{\sum_{j=1}^{N} \sum_{i=1}^{c} (u_{ij})^2 \| x_j - v_i \|^2}{N \cdot \min_{i,k} \{ \| v_i - v_k \|^2 \}}
\]  

(5.13)

In \( V_{fs} \) and \( V_{xb} \), optimal clustering generates samples near their assigned cluster centroid and far from other cluster centroids. Minimised \( V_{fs} \) or \( V_{xb} \) is expected to lead to a good partition [Fukuyama and Sugeno, 1989; Xie and Beni, 1991; Wang et al., 2004].

Computation of partition coefficient and partition entropy is only based on the membership function [Fukuyama and Sugeno, 1989; Xie and Beni, 1991]. Their main disadvantage is that the geometrical properties of the data are not included, and they depend monotonically on the number of clusters; while \( V_{fs} \) and \( V_{xb} \)
quantify the performance of the clustering by taking into account the total variation within each clusters and the separation between clusters [Fukuyama and Sugeno, 1989; Xie and Beni, 1991; Wang et al., 2004].

Due to the fact that the values of clustering validity functions can be used as indicators for FCM clustering performance, this research not only employs them to evaluate clustering performance, but also utilises them for selecting optimal feature weights. By iteratively changing weighting factors of the fwaFCM algorithm and evaluating the validity function values, better weighting factors can be selected by choosing the validity function value which indicates the best clustering performance\(^7\). Algorithm 5.3 illustrates the process of selecting optimal feature weights by using validity functions.

In Algorithm 5.3, through the running fwaFCM clustering iteratively (as shown from line 2 to line 7), line 5 and line 6 perform the task of finding the best \(\alpha\) value by evaluating clustering performance according to the selected validity function.

\(^7\)This selection is based on the rules that minimal \(V_{pe}, V_{fs}\) or \(V_{xb}\) and maximal \(V_{pc}\) indicate best clustering performance [Bezdek, 1974; Bezdek, 1975; Fukuyama and Sugeno, 1989; Xie and Beni, 1991].
Algorithm Name: **SelectOptimalFeatureWeights**

**Input:**
- feature set of combined \( k \) features;
- set of number of clusters, \( c \); number of iteration number, \( l \);
- choose one validity function from \( V_{pc} \), \( V_{pe} \), \( V_{fs} \) or \( V_{xb} \) to evaluate clustering performance.

**Output:** best clustering result and feature weighting factors.

1: set initial values of feature weighting factors \( \alpha_1 \) to \( \alpha_k \).

2: for \( l = 1 \) to \( n \) do

3: update the feature weighting factors, \( \alpha_1 \) to \( \alpha_k \), according to \( l \).

4: run fwaFCM clustering method as in Algorithm 5.1

5: evaluate clustering performance using one chosen validity function

\[
V_{pc}^l = \frac{\sum_{j=1}^{N} \sum_{i=1}^{c} u_{ij}^2}{N}, \quad V_{pe}^l = \frac{-\sum_{j=1}^{N} \sum_{i=1}^{c} u_{ij} \log u_{ij}}{N},
\]

\[
V_{fs}^l = \sum_{j=1}^{N} \sum_{i=1}^{c} (u_{ij})^2 \left( \|v_j - v_i\|^2 - \|v_j - \bar{v}\|^2 \right) \quad \text{or} \quad V_{xb}^l = \frac{\sum_{j=1}^{N} \sum_{i=1}^{c} \left( u_{ij} \right)^2 \|v_j - v_i\|^2}{N \times \min_{i,k} \left( \|v_k - v_i\|^2 \right)}
\]

6: mark \( \alpha_1 \) to \( \alpha_k \) as the best feature weighting factors if the maximised \( V_{pc} \), minimised \( V_{pe} \), \( V_{fs} \) or \( V_{xb} \) is derived.

7: end for

8: return best clustering result and corresponding \( \alpha_1 \) to \( \alpha_k \)

**Algorithm 5.3:** Automatic fwaFCM clustering with Gaussian smoothing in finding the best feature weights.

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**5.1.3. Segmentation Experiments Using Feature Weights Adjustable FCM Method with Gaussian Smoothing**

By employing the proposed fwaFCM algorithm with Gaussian smoothing, experiments have been conducted on brain MR image tissue segmentation. In

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8 The pattern for updating weighting factors can be determined according to specific applications.
particular, synthetic image, healthy and tumour-affected MR images have been used in the experiments for validation purposes. In order to investigate the effectiveness of the proposed fwaFCM algorithm with Gaussian smoothing for noise reduction, artificial noise has also been added into some of the input image data. The experimental results are then validated by standard evaluation methods.

5.1.3.1. Parameter Settings

In this research, a value of \( m=2 \) as suggested by [Chuang et al., 2006; Hung et al., 2008] for Equation 5.5 applied in all cases to standardise clustering fuzziness. An important parameter when using the FCM algorithms is the number of clusters or prototypes. This number can be determined by an assessment of the different objective tissue types to be separated [Kannan, 2005]. In this thesis, unless otherwise specified, the parameters for fwaFCM algorithm are set as follows. In Equation 5.2 and Equation 5.5, cluster number \( c=5 \) is selected for healthy brain images, the clusters are used to separate MR image pixels that fall in background, CSF, cerebral white matter (WM), grey matter (GM) and other tissues. 6 clusters are chosen for tumour-affected cases, where an extra cluster is added for tumours. The best weighting factor \( \alpha \) for the fwaFCM algorithm is automatically retrieved as illustrated in Algorithm 5.3. In addition, the kernel size \((x, y)\) and sigma \((\sigma)\) in the Gaussian smoothing function illustrated in Equation 5.4 are respectively set to 3x3 and 1 [IVEPI, Online], because they give the best clustering performance compared to that from other parameters (with the rule of “the best clustering performance can be achieved when \( V_{pe} \) and \( V_{xe} \) validity
functions are minimal and $V_{pc}$ is maximal” [Bezdek, 1974; Bezdek, 1975; Fukuyama and Sugeno, 1989; Xie and Beni, 1991; Wang et al., 2004], the table of experimental clustering results in Appendix 7 shows the greatest $V_{pc}$ and smallest $V_{pe}$ values in the all the noise-added and noise-free cases where filter kernel size = 3x3 and sigma=1 are applied).

To examine the noise insensitivity of the proposed clustering scheme, noise is added in MR images in the experiments. Due to the fact that the estimation of local noise strength can be represented by its signal to noise ratio (SNR) [Sled et al., 1999; Worth et al., 1998], Gaussian white noise of various SNR values of 10, 20 and 50 are applied to represent strong, medium and weak strengths of added noise, respectively.

5.1.3.2. Experiments Using Synthetic Images

Before experimenting on the MR images, one synthetic image is used for evaluating the clustering performance of fwaFCM incorporated with Gaussian smoothing.

Figure 5.1 (a) and Figure 5.1 (b) show the original and Gaussian white noise corrupted four-level simulated greyscale images, respectively. Figure 5.1 (c) and Figure 5.1 (d) illustrate the clustering results obtained from fwaFCM methods and conventional FCM. After the clustering process, all pixels within one cluster are assigned with a distinguishing greyscale value to visualise the clustering results.

As can be seen from Figure 5.1 (c) and Figure 5.1 (d), spots generated from the clustering error of the conventional FCM are significantly reduced by the
proposed fwaFCM algorithm with Gaussian smoothing. Different from the conventional FCM which only utilises the original image data, the fwaFCM algorithm uses weighted input feature set that consist of both original and Gaussian smoothed image data for clustering. Therefore information from both the original and Gaussian smoothed image data can be exploited. The feature weighting factors in fwaFCM algorithm act as the tuning parameters for adjusting the effects between noise insensitivity obtained by Gaussian smoothing and the details from the original image data.

In Figure 5.1 (d), it is counted that the number of wrongly clustered pixels represented by the small spots is 7432. The wrongly clustered pixels mainly exist in one cluster. While in Figure 5.1 (c) it is reduced to 427. The results signify that the proposed clustering scheme of fwaFCM method with Gaussian smoothing is much more insensitive to noise than the conventional FCM method.
5.1.3.3. Experiments Using Healthy Brain MR Images

To test the performance of the fwaFCM algorithm for brain MR image tissue segmentation, a pair of healthy brain T1- and T2-weighted MR image data of axial view illustrated in Figure 3.3 (c) and Figure 3.3 (g)\(^9\) (see Chapter 3) have been used as the two features in the input feature set. The two images are obtained from the same patient and the same scan slice, and the most noticeable lateral ventricular compartments in the sequence of images are displayed.

\(^9\) T1- and T2-weighted MR images of axial view in the same slice show the biggest volume of lateral ventricles in an MRI sequence.
Firstly, the effect of noise insensitivity of FCM clustering by incorporating Gaussian smoothing has been examined. Noisy image data shown in Figure 5.2 (c), Figure 5.2 (d), Figure 5.2 (e), Figure 5.2 (f), Figure 5.2 (g) and Figure 5.2 (h) for testing has been created by adding Gaussian white noise with different SNR values of to the original images of Figure 5.2 (a) and Figure 5.2 (b), respectively. These different SNR values on MR images are used for representing the noise of various strengths from different sources [Worth et al., 1998; Sled et al., 1999].

From the clustering results shown in Figure 5.3 and Figure 5.4, it can be seen that by using the combined features of T1- and T2-weighted MR images (Figure 5.3 (a) and Figure 5.3 (b)) as input feature set, conventional FCM algorithm is able to segment brain tissues in MR images. However, the left and right lateral ventricles as shown in Figure 5.4 (a) and Figure 5.4 (c) are joined together.
These results are not desirable since in a healthy brain, left and right lateral ventricles are actually separated [Goetz and Pappert, 1999; Fix, 2001]. By combining the original image and the Gaussian smoothed image data as two features, the clustering results as shown in Figure 5.4 (b) and Figure 5.4 (d) demonstrate that the left and right lateral ventricles have been fully separated. It can be seen that, adding Gaussian smoothed image data as an additional feature into the feature set for FCM reduces the number of spurious blobs, and creates more homogeneous clustering results.

Figure 5.3: Visualised clustering results of MR images using FCM with features of (a) T1- and T2-weighted MR images at 4 clusters; (b) T1- and T2-weighted MR images at 5 clusters; (c) T1-weighted and its Gaussian smoothed MR images at 4 clusters; (d) T2-weighted and its Gaussian smoothed MR images at 5 clusters.

Figure 5.4: Visualised CSF regions in the brain centre after FCM clustering with features of (a) T1- and T2-weighted MR images; (b) T1- and its Gaussian smoothed MR images; (c) T1- and T2-weighted MR images; (d) T2- and its Gaussian smoothed MR images.
Figure 5.5 shows the clustering result after applying conventional FCM and fwaFCM with Gaussian smoothing by using the feature weighting factors of $\alpha_1=0.5/\alpha_2=0.5$ to noise-contained MR images, with the cluster number of 4$^{10}$. It can be seen that the conventional FCM misclassifies location of many pixels inside lateral ventricular compartments when noisy pixels are present. On the contrary, fwaFCM with Gaussian smoothing creates more homogeneous clustering result due to the incorporation of Gaussian smoothed image data, especially those wrongly clustered in the area outside skull are all cleared. In this case, because of identical feature weighting factors are applied in fwaFCM, it has the same clustering performance as conventional FCM$^{11}$. However, the incorporated Gaussian smoothing causes the clustering to be more insensitive to noise.

Figure 5.5: Visualised clustering results on noisy T1- and T2-weighted MR images of SNR=10 as feature set under 4 clusters by: (a) conventional FCM; (b) fwaFCM with Gaussian smoothing.

---

$^{10}$ Clustering number 4 is applied here with the primary objective of separating tissue types of CSF, WM, GM and skull.

$^{11}$ Standard Euclidean distance formula can be treated as a special case as shown in Equation 5.7, where all weighting factors $\alpha$ are same.
Figure 5.6: Visualised clustering results on one noisy T1-weighted MR image and one original T2-weighted MR image as input feature set under 4 clusters by: (a) conventional FCM on a noisy image of SNR=20; (b) fwaFCM of feature weighting factors of $\alpha_1=0.1/\alpha_2=0.9$ on a noisy image of SNR=20; (c) conventional FCM on a noisy image of SNR=50; (d) fwaFCM of feature weighting factors of $\alpha_1=0.1/\alpha_2=0.9$ on a noisy image of SNR=50.

Figure 5.6 shows that further enhancement is gained by adjusting feature weights in the fwaFCM. In this experiment, one highly noisy image and one noise-free image data are used as the two features in the feature set. The higher weighting factor value is applied on the feature of noise-free MR image data, and lower value is applied on the feature of noisy image data. As can be seen from Figure 5.6 (b), inside the lateral ventricles region, the wrongly clustered pixels of the lateral ventricles as shown in Figure 5.6 (a) caused by the interference from the added noise are substantially reduced. Figure 5.6 (c) and Figure 5.6 (d) show
the nearly separated lateral ventricles, compared to the well connected lateral ventricles in Figure 5.6 (a) and Figure 5.6 (b).

5.1.3.4. Experiments Using Tumour-Affected Brain MR Images

After experimenting with the fwaFCM with Gaussian smoothing on synthetic and healthy brain images, further experiments have been conducted on tumour-affected brain MR images. The objective of these experiments is to examine the viability of the proposed brain tissue segmentation method on the tumour-affected MR images.

Figure 5.7: Results of brain tissue segmentation using fwaFCM on tumour-affected MR images: (a) Input tumour-affected T1-weighted MR image data; (b) Input tumour-affected T2-weighted MR image data; (c) Visualised clustering results using fwaFCM with Gaussian smoothing.

As can be seen from the segmentation result shown in Figure 5.7, the majority of pixels located in the lateral ventricles are precisely included into one cluster. Although the compression from brain tumour causes the left and right lateral ventricles join together, pixels in the regions of deformed lateral ventricles are well grouped and differentiated from the other clusters.
Figure 5.8 illustrates more brain tissue segmentation experimental results. These results are validated by medical experts focusing on separating CSF tissue. It is summarised that the segmentation results are generally accurate with minor errors caused by interferences from brain tumour and oedema.

As can be seen in the above shown cases in Figure 5.8, the CSF cluster may wrongly include other tissue types. This is mainly because that being different from classification algorithms, clustering methods like FCM have no training data. The clustering is based on measuring the similarity of input feature,

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Segmentation results validation are arranged by Tan Jui Kok, Manager of Radiology Department in Penang Adventist Hospital, George Town, Penang, Malaysia.
and a cluster is not a well defined concept [Everitt, 1972]. As a result, some MR image pixels within different structures may not be correctly separated. Nevertheless, the experimental results show that the proposed clustering scheme of fwaFCM method with Gaussian smoothing enhances the brain tissue segmentation performance.

5.1.4. Results Evaluation for Brain MR Image Tissue Segmentation

By focusing on the evaluation of noise insensitivity and clustering performance, brain MR image tissue segmentation results are evaluated and discussed in the remainder of this section based on standard evaluation methods.

5.1.4.1. Evaluation Methods

Gaussian white noise with different strength (measured by SNR) is added into the MR images. The experiments are then carried out using different parameter settings, e.g., different values for the number of clusters and weighting factors in the fwaFCM algorithm. Validity functions [Bezdek, 1974; Bezdek, 1975; Fukuyama and Sugeno, 1989; Xie and Beni, 1991] using different weighting factors for the fwaFCM algorithm are used to quantitatively evaluate the clustering performance.

The added noise affects the location of cluster centroids [Chuang et al., 2006], and a clustering method which results in less displacement of centroids is considered as less sensitive to noise. Therefore, measurement of cluster centroid displacement can also be used for comparing and evaluating noise sensitivity of
the conventional FCM method and the proposed fwaFCM method with Gaussian smoothing.

5.1.4.2. Evaluation Using Clustering Validity Functions

The performance of the proposed fwaFCM algorithm has been evaluated by medical experts using T1- and T2-weighted MR images as illustrated in Figure 5.2 (a) and Figure 5.2 (b) with noise of SNR=10, respectively. The image data is served as the two features in the input feature set.

Table 5.1 presents the values of the different validity functions\(^{13}\) [Bezdek, 1974; Bezdek, 1975; Xie and Beni, 1991] for evaluating the performance of fwaFCM clustering using different cluster number and feature weights (details of the various validity functions can be found in Sub-section 5.1.2). When high feature weighting factor of \(\alpha_1\) and low feature weighting factor of \(\alpha_2\) are applied, it can be seen from the results that in all cases, \(V_{pc}\) values increase while \(V_{pe}\) and \(V_{xb}\) decrease.

Figure 5.9 (a) and (b) compare the results of validity functions for evaluating the performance of FCM and fwaFCM clustering methods. Healthy T1- and T1-weighted images with noise of different SNR are applied as the two features of the input data. When Gaussian smoothing filter and the feature weighting factors of \(\alpha_1=0.1/\alpha_2=0.9\) (lower weights assigned on noisy image data and higher

---

\(^{13}\) The validity function and centroid values may be slightly varied when running FCM at different times due to the fact that the initial centroid values are randomly selected in the algorithm. Therefore mean of the results from running each FCM clustering for 3 times is practiced in this thesis. Furthermore, with an assumption of error rate of 1%, all results are rounded to retain 3 significant figures (subject to the condition of keeping at least 1 digit after decimal point) [Classical Mechanics, Online]. This rule of retaining significant figure number has also been applied for presenting the specificity and sensitivity values in Chapter 6.
weights on noise-free image data) are applied in fwaFCM, all validity function values of \( V_{pe} \) and \( V_{xb} \) obtained from fwaFCM are lower than those from conventional FCM method, and values of \( V_{pc} \) from fwaFCM are higher than those from conventional FCM method. It also can be seen from the Figure 5.9 that, the validity function values change more in the cases where strong noise of SNR=20 is added, compared to the relatively less changes in the cases where weak noise of SNR=50 or no noise is added.

<table>
<thead>
<tr>
<th>Clustering Number(^{14})</th>
<th>Weighting Factors</th>
<th>( V_{pc} )</th>
<th>( V_{pe} )</th>
<th>( V_{xb} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>( \alpha_1=0.9/\alpha_2=0.1 )</td>
<td>0.819</td>
<td>0.146</td>
<td>5.40</td>
</tr>
<tr>
<td></td>
<td>( \alpha_1=0.5/\alpha_2=0.5 )</td>
<td>0.779</td>
<td>0.177</td>
<td>6.46</td>
</tr>
<tr>
<td></td>
<td>( \alpha_1=0.1/\alpha_2=0.9 )</td>
<td>0.795</td>
<td>0.165</td>
<td>5.53</td>
</tr>
<tr>
<td>4</td>
<td>( \alpha_1=0.9/\alpha_2=0.1 )</td>
<td>0.764</td>
<td>0.196</td>
<td>4.62</td>
</tr>
<tr>
<td></td>
<td>( \alpha_1=0.5/\alpha_2=0.5 )</td>
<td>0.694</td>
<td>0.255</td>
<td>6.80</td>
</tr>
<tr>
<td></td>
<td>( \alpha_1=0.1/\alpha_2=0.9 )</td>
<td>0.738</td>
<td>0.221</td>
<td>6.86</td>
</tr>
<tr>
<td>5</td>
<td>( \alpha_1=0.9/\alpha_2=0.1 )</td>
<td>0.734</td>
<td>0.228</td>
<td>5.02</td>
</tr>
<tr>
<td></td>
<td>( \alpha_1=0.5/\alpha_2=0.5 )</td>
<td>0.656</td>
<td>0.296</td>
<td>6.65</td>
</tr>
<tr>
<td></td>
<td>( \alpha_1=0.1/\alpha_2=0.9 )</td>
<td>0.683</td>
<td>0.271</td>
<td>6.27</td>
</tr>
<tr>
<td>6</td>
<td>( \alpha_1=0.9/\alpha_2=0.1 )</td>
<td>0.707</td>
<td>0.259</td>
<td>5.60</td>
</tr>
<tr>
<td></td>
<td>( \alpha_1=0.5/\alpha_2=0.5 )</td>
<td>0.626</td>
<td>0.333</td>
<td>5.88</td>
</tr>
<tr>
<td></td>
<td>( \alpha_1=0.1/\alpha_2=0.9 )</td>
<td>0.656</td>
<td>0.304</td>
<td>5.67</td>
</tr>
</tbody>
</table>

Table 5.1: Validity function results of using fwaFCM with different feature weighting factors and clustering number with input data of features of original T1- and T2-weighted MR images with noise of SNR=10.

\(^{14}\) For testing the clustering performance of fwaFCM method under various circumstances, multiple cluster number values are selected.
Figure 5.9: Comparison of the validity function results of (a) $V_{pc}$ and $V_{pe}$ (b) $V_{xb}$ for clustering results of MR images using FCM and fwaFCM.

By using the previously discussed evaluation rules of validity functions that “the best clustering performance can be achieved when $V_{pe}$ and $V_{xb}$ are minimal and $V_{pc}$ is maximal” [Bezdek, 1974; Bezdek, 1975; Fukuyama and Sugeno, 1989; Xie and Beni, 1991; Wang et al., 2004], it can be seen that by incorporating
Gaussian smoothing and finding the optimal feature weighting factors, the clustering performance of fwaFCM is better than the conventional FCM method with features from T1 and T2 images.

The clustering validity functions can also be employed as useful tools to automatically select appropriate feature weighting factors. By comparing and selecting validity function values from a sequence of fwaFCM clustering using different feature weighting factors, performance of the fwaFCM clustering can be automatically optimised.

5.1.4.3. Evaluation Using Measurement of Cluster Centroid Displacement Caused by Noise

Centroids of FCM clustering are displaced after noise is added [Chuang et al., 2006]. The sensitivity to noise of FCM and fwaFCM can then be compared by measuring displacement of cluster centroids. Table 5.2 tabulates the values of all cluster centroids. It is calculated that, with the added strong noise of SNR=10 on one feature, the average displacement in conventional FCM and fwaFCM with Gaussian smoothing are 30.1 and 18.6, respectively. By using the fwaFCM clustering method, the noise on the MR image creates less centroid displacement. Therefore it is suggested that fwaFCM exhibits higher insensitivity to noise than conventional FCM.
From the above results and discussions, it is shown that, by incorporating Gaussian smoothing with fwaFCM algorithm, the proposed brain MR image tissue segmentation scheme tends to be more insensitive to noise, and creates more homogeneous clustering results, as compared to conventional FCM method. By using fwaFCM method together with optimised feature weighting factor selection through validity functions, more accurate brain tissue segmentation results can be obtained.

### 5.1.5. Methods for CSF Identification and Lateral Ventricles Extraction

Following brain tissue segmentation, two further steps of CSF identification and lateral ventricles extraction are needed to complete the lateral ventricular shape retrieval process. The objective of CSF identification is to select the particular cluster which accommodates CSF tissue from all the clusters obtained from the precedent clustering process. Lateral ventricles extraction aims to remove the CSF pixels outside of the lateral ventricular compartments.

<table>
<thead>
<tr>
<th></th>
<th>Conventional FCM on Original T1- and T2-weighted MR Images</th>
<th>Conventional FCM on MR Images with Added Noise on T2-weighted image</th>
<th>fwaFCM on MR Images with Added Noise on T2-weighted image</th>
</tr>
</thead>
<tbody>
<tr>
<td>Feature 1 Feature 2</td>
<td>Feature 1 Feature 2</td>
<td>Feature 1 Feature 2</td>
<td>Feature 1 Feature 2</td>
</tr>
<tr>
<td>Centroid Values</td>
<td>1.12 1.18</td>
<td>1.29 8.71</td>
<td>1.16 10.3</td>
</tr>
<tr>
<td>Centroid Values</td>
<td>62.3 173.0</td>
<td>69.3 49.0</td>
<td>64.8 48.1</td>
</tr>
<tr>
<td>Centroid Values</td>
<td>83.7 42.5</td>
<td>85.2 80.6</td>
<td>83.6 84.0</td>
</tr>
<tr>
<td>Centroid Values</td>
<td>139.7 107.9</td>
<td>147.1 111.3</td>
<td>138.8 109.4</td>
</tr>
<tr>
<td>Centroid Values</td>
<td>197.8 83.5</td>
<td>197.6 170.3</td>
<td>196.9 173.7</td>
</tr>
</tbody>
</table>

Table 5.2: Centroids values retrieved in FCM and fwaFCM on original or noise added MR images.
5.1.5.1. CSF Identification

After brain tissue segmentation, CSF extraction can be conducted by selecting the cluster labelled as CSF from the multiple clusters created by the fwaFCM method. Based on the study of brain tissue properties in multi-spectral MR images by [Gunderman, 1998], it can be easily seen that within several major tissue types, CSF is the only one that appears bright in T1-weighted and dark in T2-weighted MR images. As a result, intensity values of CSF in T2-weighted MRI are high while those in T1-weighted MRI are low. Therefore, the particular cluster accommodating CSF tissue can be selected from these clusters (5 tissue clusters for healthy brain MR images, and 6 tissue clusters for tumour-affected brain MR images) by finding the cluster with the greatest difference of average pixel greyscale values between the T2- and T1-weight MR image data.

In implementing the fwaFCM method, the two features in the input feature set are both directly extracted from multi-spectral MR images, (input features of $Data_1$ and $Data_2$ in Equation 5.8 represent T1- and T2-weighted image data, respectively). After brain MR image tissue segmentation by fwaFCM method, centroids of all clusters are obtained. As discussed previously, at the end of the FCM clustering iteration, the summation of distances between image pixels to the cluster centroids is decreased. It can be seen that the cluster centroid is a value that is near to all data elements in that cluster. Therefore, to reduce computational complexity, the process of identifying the cluster of CSF can be achieved by a step of selecting the cluster whose centroid value has the maximum difference between $Data_2$ and $Data_1$ features. This selection process
can be expressed as: \( \max_i \left\{ v_{T2,i} - v_{T1,i} \right\} \), where \( i \) is the cluster number, \( v_{T2} \) and \( v_{T1} \) represent the centroid values in the T2- and T1-weighted features respectively in the input feature set of the fwaFCM clustering.

5.1.5.2. Brain Lateral Ventricles Extraction

Although from brain MR images of axial view, lateral ventricles are of large volume, CSF can still fall outside of the ventricular system [Gunderman, 1998] (examples can be found in Figure 3.3 (c) and Figure 3.3 (g) (see Chapter 3)). Furthermore, the proposed brain tissue segmentation step may wrongly assign non-CSF pixels to the cluster of CSF. Therefore, pixels located in the lateral ventricles need to be retained while others need to be removed.

To remove undesired pixels, this research uses a global mask to remove pixels outside the area where pixels of lateral ventricles normally reside. Due to the fact that lateral ventricles volume will increase with age [Chung et al., 2006], brain MR images of an 81 year-old woman15 of good health condition [The Whole Brain Atlas, Online] are utilised to create the global mask. This global mask is slightly enlarged on the extracted lateral ventricles to allow lateral ventricles in all experimental cases to be included. It separates CSF regions from the area where lateral ventricles may exist, thereby leaves the regions as the extracted lateral ventricles.

Although lateral ventricles in the axial view mainly lie in the brain centre, a fully automatic lateral ventricles extraction method for all cases is extremely

15 Healthy brain MR images of the oldest person adapted from [The Whole Brain Atlas, Online].
difficult due to the fact that lateral ventricles may be deformed by brain tumour in any direction. Therefore, in the current research, a semi-automatic method has been employed. This method automatically selects the regions that are overlapping with the global mask, and manually removes some pixels identified as CSF but outside of the lateral ventricles.

5.1.6. Experiments and Discussions of CSF Selection and Lateral Ventricles Extraction

Experiments have been conducted to select CSF cluster and extract brain lateral ventricles using the proposed methods. Evaluation of the results is performed by medical experts based on visualisation.

5.1.6.1. CSF Identification

Figure 5.10 illustrates the CSF segmentation and identification results with one healthy and one tumour-affected brain MR images. Figure 5.10 (c) shows the visualised brain tissue clustering results from health input T1- and T2-weighted MR images (shown in Figure 5.10 (a) and Figure 5.10 (b), respectively). Figure 5.10 (g) is the visualised clustering results from tumour affected input T1- and T2-weighted MR images (shown in Figure 5.10 (e) and Figure 5.10 (f), respectively). In these clusters, CSF is identified and visualised in Figure 5.10 (d) and Figure 5.10 (h), respectively. From these results, it can be seen that the CSF tissue pixels are generally included. The experimental results suggest that the proposed method is viable for automatically identifying CSF without the need of human intervention. It also can be seen that lateral ventricles are included in the
centre of the selected CSF cluster. Therefore, lateral ventricles can be extracted by selecting region of the brain centre.

Figure 5.10: CSF segmentation of one healthy and one tumour-affected brain MR image: (a) input healthy T1-weighted MR image data; (b) input healthy T2-weighted MR image data; (c) visualised brain tissue segmentation result from (a) and (b); (d) selected CSF cluster of (c); (e) input tumour-affected T1-weighted MR image data; (f) input tumour-affected T2-weighted MR image data; (g) visualised brain tissue segmentation result from (e) and (f); (h) selected CSF cluster of (g).

5.1.6.2. Lateral Ventricles Extraction

Figure 5.11 shows the original healthy MR images and their corresponding extracted lateral ventricles as general masks for extracting lateral ventricles in tumour-affected MR images. After the lateral ventricles are extracted, they are slightly enlarged to the extent which allows lateral ventricles used in this research to be covered.
Figure 5.11: Original MR images and extracted lateral ventricles as the general mask: (a) a T1-; (b) a T2-weighted MR images from an 81 year old woman in excellent health (images adapted from [The Whole Brain Atlas, Online]); (c) segmented and enlarged lateral ventricles.

By using the global mask as shown in Figure 5.11 (c) (enlarged lateral ventricles segmented from the T1- and T2-weighted MR images illustrated respectively in Figure 5.11 (a) and Figure 5.11 (b)), lateral ventricles in both healthy and tumour-affected brain MR images can be obtained. Figure 5.12 demonstrates the lateral ventricles extraction results by applying this approach: Figure 5.12 (a) and Figure 5.12 (c) are the two selected CSF cluster cases; Figure 5.12 (b) and Figure 5.12 (d) show their corresponding extracted lateral ventricles.

More experiments have been conducted on tumour-affected brain MR images, and results are visualised in Appendix 6 (separated and broken lateral ventricles are linked by using the method to be discussed in Section 5.2).
There are several factors that make human intervention necessary in the process of lateral ventricles extraction. One of these factors can be generalised as the result of the wrongly clustered CSF tissue pixels which is caused by the employed brain tissue segmentation method. This is primarily due to the fact that the proposed brain tissue segmentation step using clustering method may wrongly include image pixels which are difficult to be distinguished from other tissue types (see discussions in Section 5.1). Another factor is that the MR image used in this research are associated with some of the extremely complicated cases, for example, lateral ventricles may be compressed into any shape and even broken into several parts. Despite the above mentioned issues, the
experimental results obtained have been validated by medical experts, and reveal that the proposed methods are viable with minimal human interference.

5.2. Estimating Lateral Ventricular Deformation

As discussed in Chapter 4, the process of estimating lateral ventricular deformation can be decomposed into two steps: lateral ventricles alignment and lateral ventricular deformation measurement. Lateral ventricles alignment is achieved by two sub-steps of lateral ventricles linking and landmark points selecting. The lateral ventricular deformation measurement step is also achieved by two sub-steps of modelling lateral ventricular deformation and calculating estimated deformation. In this section, firstly the related work on selecting deformation modelling function is introduced. Misalignment caused by the imperfect template lateral ventricles is then discussed, which initiates the need for lateral ventricular deformation adjustment which is discussed in Section 5.3.

5.2.1. Lateral Ventricles Alignment

In MR images, left and right lateral ventricles are actually separated [Goetz and Pappert, 1999; Fix, 2001]. Furthermore, because of the compression from brain tumours, left or right lateral ventricles may be broken, as shown in Figure 3.4 (h) and Figure 3.4 (i) (see Chapter 3). To effectively estimate deformation using modelling functions, left and right lateral ventricles are treated as one single object. Therefore left and right ventricles and the disjointed parts of lateral ventricles need to be linked together.
Based on the study of anatomical properties of brain lateral ventricles, anterior and posterior horns are employed as the key landmark points. The process of lateral ventricles alignment is completed by selecting intermediate landmark points based on these key landmark points.

5.2.1.1. Methods for Linking Lateral Ventricles

The linking of the left and right lateral ventricles and disjointed lateral ventricular parts are automatically conducted by selecting sample points on the border of each object which has the shortest distance to all other objects. The lateral ventricles are then linked by connecting these selected sample points with straight lines. This connecting approach of using shortest distances makes sure all objects are connected without redundancy, due to the fact that there is only one shortest distance connecting line between any two objects.

Take one sampled point on the boarder of an object A as an example, the distance between this point and a sampled point on the border of another object B can be calculated using the Euclidean distance function. By iterating the calculation and comparison of distance between the point on object A to all other sampled points on the border of object B, the shortest distance between this point and object B can be obtained. By extending to all points on the border of object A using the same approach to find the distance to object B, one point on object A and one point on object B that have the shortest distance between each other can therefore be selected.
In cases that lateral ventricles are separated to multiple (more than two) objects, this approach of linking objects can also be applied to merge all disjoint parts into one single object.

5.2.1.2. Methods for Landmark Point Selection

The alignment of lateral ventricles starts with finding corresponding landmark points from lateral ventricular boundaries and image borders in template and target images [Pelc et al., 1992; Venugopal et al., 2005]. These landmark points are then used to represent the variations of the lateral ventricular shape [Pelc et al., 1992]. [Gaser et al., 2001] summarised that deformation tends to affect significantly on anterior horns. In addition, due to the fact that both anterior and posterior horns are located at the end of the lateral ventricular compartments [Fix, 2001; Cherian et al., 2008], they are more susceptible to deformation caused by compressions from brain tumours. Therefore, the anterior and posterior horns are used as key landmark points for aligning healthy and target lateral ventricles in this research.

Figure 5.13 illustrates one healthy and two deformed lateral ventricles. The tips of the anterior and posterior horns are labelled by a cross covered by a circle. If a bounding box of quadrilateral polygon is used to cover the lateral ventricular region as shown in Figure 5.14 (a) and Figure 5.14 (b), it can be seen that the posterior horn tips are located near the four corners of the bounding box. This research takes advantage of this observation to locate the posterior and anterior horns, by employing a bounding box of quadrilateral polygon shape which covers the linked lateral ventricular region.
Figure 5.13: Labelled anterior and posterior horns on lateral ventricles from: (a) a healthy brain; (b) a brain with existing tumour; (c) a brain with existing tumour.

The quadrilateral polygon bounding box with minimum area can be treated as a special case of convex hull [Brown, 1979], where the number of its sides is fixed at 4. Therefore, the linked lateral ventricles can then be covered by a quadrilateral bounding box with minimum area [D'Errico, Online]. The tips of posterior and frontier horns of the lateral ventricles can be found near the four corners of the bounding box. The four key landmark points are selected by finding the four points on the lateral ventricular boundary which are nearest to the four corners of the quadrilateral polygon. Figure 5.14 illustrates bounding boxes obtained on both template and target lateral ventricles. The adjacent tips of both anterior and posterior horns of the lateral ventricles are located near the corners of the quadrilateral polygon.
Once both the template and target images are associated by the four pairs of landmark points, some intermediate landmark points between adjacent key landmark points are selected to align the two images. These intermediate landmark points are used to facilitate the deformation modelling functions to be applied.

In the implementation, 14 pairs of equally spaced landmark points are automatically sampled between two neighbouring key landmark points. The two neighbouring key landmark points are selected from one side of the quadrilateral polygon bounding box in each pair of template and target images. Furthermore, 60 additional landmark points are selected from both template and target image boundaries to be used to confine the scale of the aligned lateral ventricles. Altogether, the template and target lateral ventricles are aligned by the coordinates of 120 pairs of landmark points.
**Input:** Retrieved template and target lateral ventricular shapes  
**Output:** Selected landmark points on template and target lateral ventricles

**Step 1:** Determine the four corners of a quadrilateral polygon bounding box that covers the linked lateral ventricles

**Step 2:** Find all the boundary points

\[ p_{num\_total} = Number(Boundary) \]  
(Get the total number of boundary points for template and target images\(^ {16} \))

**Step 3:** From the boundary points, find 4 points on the lateral ventricular boundary as key landmark points that are nearest to the 4 corners of the quadrilateral polygon bounding box using Euclidean distance function

\[
K_{V_{adv1}} = \min\left(\sqrt{(V_{Boundary_{adv2}}^2 - Corner_{adv1}^2)}\right)
\]

**Step 4:** Starting from one of the 4 points on the lateral ventricles boundary corners defined by the quadrilateral polygon bounding box, trace 14 equally spaced intermediate landmark points towards the next point until a total of 60 landmark points are sampled.

\[
P_{adv4} = V_{Boundary_{Boundary_{index}}} + ceil(p_{num_{idx3}} / 16)
\]

(Sample other 56 pairs of points on the template boundary as intermediate landmarks points, \(P_{Template}\) and corresponding target boundary, \(P_{Target}\))

Algorithm 5.4: Selecting landmark points between lateral ventricles on template and target images.

---

\(^{16}\) Number of boundary points in template and target images may be different.
The algorithm of lateral ventricular boundary alignment is illustrated in Algorithm 5.4. In the algorithm, by using a quadrilateral polygon bounding box, Step 1 finds the four points which can be used to determine the four key landmark points. Step 2 samples all the points on the lateral ventricular boundary. The key landmark points are then determined in Step 3 through finding the points on the lateral ventricular boundary that has the shortest distance to the four points retrieved in Step 1. Step 4 determines all the intermediate landmark points.

5.2.1.3. Experiments and Discussions on Lateral Ventricles Linking
The proposed method for lateral ventricles linking has been applied on both healthy and tumour affected lateral ventricles\textsuperscript{17}. Figure 5.15 demonstrates a sample resultant image after the separated lateral ventricles are linked together through a connecting line with the shortest distance. Further results obtained from lateral ventricles linking step are shown in Appendix 6. From the experimental results, it can be seen that not only left and right lateral ventricles are connected, but all the broken lateral ventricular parts are also well linked.

\textsuperscript{17} Some segmented left and right lateral ventricles are already connected to each other, e.g., segmentation results illustrated in Figure 5.12 (b) and Figure 5.12 (d). In these case, lateral ventricles linking step is not necessary.
Figure 5.15: Lateral ventricles linking result: (a) separated left and right lateral ventricles; (b) linked left and right lateral ventricles through a line with the shortest distance.

5.2.1.4. Experiments and Discussions on Landmark Point Selection

Figure 5.16 illustrates a completed alignment example of a template and target lateral ventricles by using the selected landmark points. Figure 5.16 (a) and Figure 5.16 (b) show the extracted template and target lateral ventricles, respectively. Figure 5.16 (c) displays the selected landmark points overlapped in one image, where all corresponding landmark points in template and target lateral ventricles are coupled, although some misalignment can be clearly seen.

By applying the above mentioned approach of selecting landmark points as references on both segmented template (healthy) and corresponding target (deformed) lateral ventricles, two lateral ventricles are approximately aligned by the landmark point pairs.
From the experiments, it can be summarised that, the proposed method is able to take advantage of the anatomical properties of lateral ventricles and generally creates reasonably correct alignment results (these results are evaluated by medical experts). However, as can be seen in Figure 5.16 that, lateral ventricles in the template image can not be perfectly matched with that of the target image, which is caused by the fact that the template and target images...
are retrieved from different persons. As discussed in Chapter 3, lateral ventricles are highly susceptible to shape variation caused by diseases or even age. The complexity of the shape of lateral ventricles makes it extremely difficult to be applied in all situations, especially when lateral ventricles are deformed by brain tumour or other pathologies [Prastawa et al., 2005]. For example, in Figure 5.16, the left lateral ventricle is compressed by the brain tumour, and the posterior horn of the right lateral ventricle is enlarged. The challenging issue is further discussed in details in the next section.

5.2.2. Lateral Ventricular Deformation Measurement

The estimation of lateral ventricular deformation to feature is achieved by two procedures of modelling lateral ventricular deformation and calculating estimated deformation. The discussion of methods starts with the study of the background of deformation and related work of selecting deformation modelling functions. The experimental result obtained from an artificial image has been discussed for validating the employed methods. Further discussions on the experimental result obtained from the brain MR image case raise the issue of misalignment due to the imperfect template which is to be addressed in the next section.

5.2.2.1. Related Work on Deformation and Modelling Deformation

Deformation is a change in the shape or size of an object due to an applied force. Following the work on Cartesian transformations [Thompson, 1945], in which linear deformation function was introduced, researchers have developed more
sophisticated methods for solving more complex problems in many areas, e.g., biostatistics.

The study of variation and change in the physical form of organism is often referred to as morphometrics [Grenander and Miller, 1994; Zelditch et al., 2004]. A sub-branch of morphometrics is deformation-based morphometry (DBM) [Grenander and Miller, 1994; Davatzikos et al., 1996; Christensen et al., 1997; Haller et al., 1997; Iosifescu et al., 1997; Thirion et al., 2000; Gaser et al., 2001; Ferrant et al., 2002; Zelditch et al., 2004; Rohlfing et al., 2006], where deformation is usually modelled and represented as a transformation function [Zelditch et al., 2004].

DBM is a useful technique to detect morphological variations for neuroimaging since it analyses positional change of every pixel in an image [Gaser et al., 2001]. In the analytical work on brain MR image presented by [Gaser et al., 2001], consistency between results obtained from DBM analysis and visual tracing was demonstrated, suggesting that there is a strong relevancy between deformation of brain structures and the transformation function used to represent it.

A number of related works on DBM have been developed in the past. For example, algorithm for automatically hypothesising the number, location, orientation and shape of mitochondria and membranes constructed by [Grenander and Miller, 1994]; deformation function for measuring the enlargements and shrinkages associated with the elastic deformation of corpus callosum (the longitudinal fissure that connects the left and right cerebral
hemispheres) proposed by [Davatzikos et al., 1996]; the use of higher dimensional transformations to find diffeomorphic correspondence between brain anatomies [Christensen et al., 1997]; technique for elastically deforming the brain-atlas segmentation, and matching the WM and sub-cortical GM surfaces by [Iosifescu et al., 1997]; an approach of nonlinear image registration in detecting structural changes in whole brain MR images by [Gaser et al., 1999]; a general method of computing significance maps in studying the 3-dimensional dissymmetry of brain structures [Thirion et al., 2000]; deformable surface-matching algorithm to capture the deformation of boundaries of key structures (cortical surface, ventricles and tumour) throughout the neurosurgical procedure, by using a linear finite elastic model to infer a volumetric deformation [Ferrant et al., 2002], and analyses on the effects of alcoholism on brain structure for application of image-guided surgery systems [Rohlfing et al., 2006], which are justified by the invariance of relevant statistics under changes of the spatial and temporal reference coordinate system on the two acquired structural MR brain images. These existing works suggest the practicability of modelling deformation through the approach of applying DBM.

As a nonlinear deformation modelling function, thin plate splines (TPS) [Bookstein, 1989] have been applied in medical image registration and deformation analysis, after the work of [Bookstein, 1989] which used TPS for modelling deformation. The TPS function has since become a widely used method for applications in deformation-describing, non-linear smoothing and interpolating. TPS is ideal for modelling functions with local distortions which are
too complex to fit with polynomials [Meyer et al., 1997; Gobbi and Peters, 2003].

The prominence of applying TPS in deformation estimation and medical image registration comes from a major advantage in that there is a physical explanation for its energy function [Meyer et al., 1997]. Moreover, the model has no free parameter that needs manual tuning [Zheng et al., 2006]. The TPS function is regarded as a type of radial basis function (RBF). In the survey conducted by [Mardia et al., 2006], it was found that the TPS function provides nearly optimal soft tissue deformation modelling results among the wide class of radial type deformation functions.

TPS has also been widely employed within soft tissue DBM or deformation estimation. [Gaser et al., 2001] used TPS on MR images to match the diagnosis to the template images; [Lin and Lin, 2004] developed a 3-dimensional image deformation technique to integrate multi-spectral medical images by combining the 3-dimensional optical flow estimation and TPS transformation; [Ross et al., 2005] applied TPS and developed an average deformation model for applications in the area of fingerprint matching; [Mardia et al., 2006] addressed the problem of the distortion or deformation effects produced by different types of non-linear deformation strategies on textured images. Extensive analysis on a deterministic deformations and a landmark based deformation including TPS were also performed in their study. There are some other applications of using TPS in medical images [Pelc et al., 1991; Sanchez-Ortiz et al., 1996; DeQuardo et al., 1996; Meyer et al., 1997] that have demonstrated the viability of using TPS for soft tissue deformation estimation. In a study on evaluating the effectiveness of
using TPS for prostate deformation [Venugopal et al., 2005], it was found that
TPS algorithm attains an accuracy of 97% when compared to prostate volumes
defined by a professional radiation-oncologist [Venugopal et al., 2005]. These
applications suggest the relevancy of applying TPS for modelling deformation of
soft tissues, for example, lateral ventricles in this research.

5.2.2.2. Methods
In this research, TPS function is employed to perform the nonlinear mapping
between template and target lateral ventricular boundary image data set
[Bookstein, 1989]. A TPS \( f(x, y) \) is a smoothing function which interpolates a
surface that is fixed at landmark points \( P_i \) at a specific height. TPS can be
treated as a process of finding a function \( z(x, y) \) which minimises the bending
energy [Bookstein, 1989; Hajnal et al., 2001].

In the application for 2-dimensional images, instead of assuming that
\( f \) corresponds to a displacement orthogonal to the image plane at the landmark
points, one can treat it as a displacement in the image plane [Hajnal et al., 2001].
By using two separate TPS functions \( f_x \) and \( f_y \) which model the displacement
of the selected landmark points in the \( x \) and \( y \) direction, a vector-valued function
\( \mathbf{F} \) which maps each point of the image into a new point in the image plane can be
represented using Equation 5.14:

\[
(x', y') \rightarrow \left( f_x(x, y), f_y(x, y) \right)
\]

(5.14)
where $f_x$ and $f_y$ are the functions causing displacement on $x$ and $y$ coordinates respectively.

Once the vector-valued function $F$ is defined via the selected landmark points with TPS functions, it is then applied to the original coordinates of all pixels in the target image to retrieve new coordinates for all pixels. If one treats some selected horizontal and vertical lines of equal spaces in the original image as a mesh, then a corresponding distorted mesh can be used to describe the displacement of each node of the mesh. This effect is illustrated in Figure 5.17 by visualising the original and its corresponding deformed meshes after TPS function is applied to all pixels in the image.

![Figure 5.17: Example of landmark points with original and deformed TPS meshes formed by $x$ and $y$ coordinates: (a) original; (b) deformed.](image)

The effect of the deformation on the lateral ventricles can then be represented by finding out the coordinate displacement value of each pixel in the image. In the deformed image, each pixel is displaced from its original coordinate
at specific direction and distance. Therefore, vector\(^{18}\) which has magnitude and
direction can be used for representing the estimated deformation of each point.
Figure 5.18 illustrates an example on a segment of an image using magnitude
and direction of vectors to represent the deformation measurement.

![Illustration of the effect of deformation on four selected pixels in a zoomed view before and after deformation, solid and dashed lines are segments of the meshes from the original and deformed image, respectively; grey arrows indicate the vector of the displacement due to deformation.](image)

5.2.2.3. Experiments and Discussions
An experiment is performed by using an original image (as the template image)
and its manually deformed image (as the corresponding target image), as shown
respectively in Figure 5.19 (a) and Figure 5.19 (b). Figure 5.19 (c) illustrates the
result of deformation estimation and feature conversion. The arrows show the
direction of the displacement vector. White dots and grey crosses are the
landmark points selected from the original and deformed image boundary,

\(^{18}\) Also known as Euclidean vector, it is sometimes called geometrical or spatial vector.
respectively. The cross covered by a circle denotes the position where the maximum estimated deformation value exists. It can be seen that this point is located exactly at the concave of the deformed image, and all arrows point to the source of the concave where the square is deformed. The result shows that the method is effective for estimating lateral ventricular deformation and converting estimated deformation data to feature.

Figure 5.19: Estimating and converting deformation to feature data on a square: (a) original image; (b) deformed image; (c) estimated deformation after being converted to feature data.
In many clinical cases, lateral ventricles can be deformed into any geometry and at any direction; moreover shapes of lateral ventricles within different healthy brains are also different. Therefore, an ideal alignment which perfectly matches template and target lateral ventricles is extremely difficult, if not impossible to be obtained. Figure 5.20 illustrates the original MR image and measured deformation results by visualising vectors as image greyscale using Equation 5.15. It can be seen from Figure 5.20 (b) that the maximum measured deformation value is not in the area where tumour resides, and the direction of vector denoting the highest displacement value is irrelevant to that of the compression from the brain tumour. As discussed previously, this is mainly caused by the misalignment between the template and target MR images. This problem can be alleviated by adding one step of adjustment of lateral ventricular deformation data to be discussed in the next section.

Figure 5.20: Deformation measurement: (a) original image; (b) visualised deformation estimation, where magnitude of displacement vector is normalised and visualised as image greyscale value, arrows are showing the directions of displacement vectors, and a cross covered by a circle indicates the maximum displacement vector magnitude.
5.3. Transforming Lateral Ventricular Deformation to Features

The proposed approach quantifies the lateral ventricular shape variation caused by the compression from brain tumour. As discussed in the design of lateral ventricular deformation feature extraction component in Chapter 4, the process of transforming lateral ventricular deformation to features can be decomposed to two indispensable steps: lateral ventricular deformation data adjustment and estimated deformation data to feature conversion. In the implementation, estimated lateral ventricular deformation adjustment for alleviating the problem of misalignment caused by imperfect template of lateral ventricles is necessary, however to facilitate the understanding of the method, the step for converting estimated lateral ventricular deformation data to feature is discussed prior to the discussion of deformation data adjustment.

5.3.1. Methods for Converting Estimated Deformation Data to Feature

The estimated deformation data is normalised to the format of image greyscale value of 8 bits, which can be represented as Equation 5.15.

\begin{equation}
I_k = \frac{D_k}{\max[D]} \times 255
\end{equation}

where \( I \) is the normalised intensity value, \( k \) is the index of pixel in the image and 255 is the maximum 8 bits greyscale value of MR image pixels, and \( D \) is the magnitude of displacement vector which can be calculated by using the Euclidean distance as in Equation 5.16.

\begin{equation}
D = \sqrt{(P_{o,x} - P_{t,x})^2 + (P_{o,y} - P_{t,y})^2}
\end{equation}
where $P_{o-x}$ and $P_{o-y}$ are the original data point $x$ and $y$ coordinate values, while $P_{t-x}$ and $P_{t-y}$ are the obtained data point $x$ and $y$ coordinate values, respectively.

5.3.2. Methods for Adjusting Estimated Lateral Ventricular Deformation Data

Although the employed method for lateral ventricular deformation measurement has been validated to be effective, the estimated lateral ventricular deformation data may be irrelevant to the position of brain tumour. This is mainly because of the misalignment between the template and target lateral ventricles caused by using the imperfect lateral ventricles template.

To address this problem, a method for adjusting the estimated deformation data is proposed in this section. The method allows user to select one point in the brain tumour. As shown in Figure 5.21, a line can be drawn from the point to the centre of the image, at the direction from the border to the centre of the image. Through calculating the angle between this line and direction of displacement vectors, magnitude of the displacement vectors at opposite or nearly-opposite direction to brain tumour substantially decreases, thereby the deformation estimation values can be adjusted by Equation 5.17:

$$D' = D \left| \cos \left( \frac{\theta}{2} \right) \right|$$

(5.17)

where $D$ and $D'$ are the magnitudes of the original and adjusted displacement vector representing the estimated deformation, respectively. $\theta$ is the angle between the connecting line and the displacement vector.
It can be seen that when $\theta = \pi$ (the connecting line and the displacement vector are in the opposite directions), the adjusted displacement vector magnitude is reduced to 0. And when $\theta = 0$ (the connecting line and the displacement vector are in the same direction), magnitude of the adjusted displacement vector is 1, which means the estimated data is kept without any change.

Algorithm 5.5 illustrates the process of transforming lateral ventricular deformation to feature. By manually selecting a point in the brain tumour, the problem of wrongly estimated deformation data caused by imperfect template lateral ventricles can be alleviated by applying the method for adjusting deformation.
Algorithm Name: **TransformDeformation**

**Input:**
- Selected landmarks on template and target lateral ventricular boundaries, user input of tumour centre coordinates;

**Output:** Adjusted and normalised deformation data.

---

**Step 1: Creating deformation modelling function**

Input $LP^{\text{template}}$ as the source or initial position of landmarks

Input $LP^{\text{target}}$ as the target or final position of landmarks

Using TPS function to obtain deformation modelling functions: $(x', y') \to \left(f_x(x, y), f_y(x, y)\right)$ to be applied on coordinates of each pixel of target image, which maps the displacement of each pixel.

**Step 2: Deformation calculation**

Calculating displacement between original coordinates of points, $P_0$ and coordinates of the corresponding displaced points $P_i$ by

$$D = \sqrt{(P_{0_{-x}} - P_{i_{-x}})^2 + (P_{0_{-y}} - P_{i_{-y}})^2}$$

**Step 3: Calculate the angle $\theta$ between the user input tumour centre and displacement vectors**

**Step 4: Adjust deformation data by**

$$D' = D \left| \frac{\cos \left(\frac{\theta}{2}\right)}{} \right|$$

**Step 5: Normalise deformation estimation values as image greyscale value**

$$I_k = 255 \frac{D'_k}{\max[D']}$$

Algorithm 5.5: lateral ventricular deformation transformation.

In Algorithm 5.5, Step 1 and Step 2 carry out the lateral ventricular deformation process; Step 3 and Step 4 adjust the estimated deformation data; Step 5 normalises the estimated deformation data to image greyscale values to create the extracted feature.
5.3.3. Experiments and Discussions

Figure 5.22 (a) depicts a tumour-affected brain MR image, and Figure 5.22 (b) visualises the estimated deformation data by normalising it into greyscale values. It can be seen that the area where tumour resides demonstrates the highest estimated deformation value.

Figure 5.22: Adjusted deformation estimation by combining displacement magnitude and direction information: (a) original image; (b) visualised deformation estimation, where adjusted displacement vector magnitudes are visualised as image greyscale value, and a cross covered by a circle indicates the maximum adjusted displacement vector magnitude.

The transformed feature data of lateral ventricular deformation is illustrated in Figure 5.23. (See Appendix 1 for more feature extraction results). It can be seen that, although not perfect, the bright area which indicates the high deformation values is approximately in the same location as brain tumour in the original image.
The lateral ventricular deformation and brain tumour are then approximately associated through the estimated deformation data for further brain tumour segmentation. The normalised deformation estimation values can then be used as an additional feature in the feature set the brain MR image tumour segmentation methods that support input data of multiple features. Due to the fact that some other high-level features such as textures are not suitable for segmentation based on differentiating pixels [Clarke et al., 1995], it is hoped that the deformation feature provide each image pixel additional information which is more relevant to brain tumour and has more positive effect on brain tumour segmentation accuracy.

5.4. Summary and Discussion

The lateral ventricular deformation feature extraction is in fact a procedure of transforming deformation of lateral ventricles into data that can be used by methods for brain tumour segmentation. Within the procedure, the three
continuous processes of retrieving lateral ventricular shape, aligning lateral ventricles and transforming deformation to feature are used to retrieve, process and measure the lateral ventricular deformation caused by compression from brain tumours.

In the process of retrieving lateral ventricular shape, a new brain tissue segmentation scheme is proposed. To address the problems of conventional FCM algorithm, this segmentation scheme employs the fwaFCM algorithm with Gaussian smoothing so as to allow the input feature weights to be adjustable and hence reduce noise sensitivity of the clustering process. With this scheme, CSF tissue can be separated and grouped into one cluster. This cluster of CSF tissue is then selected by the step of CSF identification based on the properties of CSF. The lateral ventricles are then extracted by using a global mask along with human intervention to remove CSF pixels that are wrongly classified or reside outside of the lateral ventricular region.

In the process of estimating lateral ventricular deformation, alignment of lateral ventricles is achieved by automatically linking the disjointed lateral ventricles, followed by the process of selecting landmark points to associate the template and target lateral ventricles. These pairs of points are selected based on using tips of lateral ventricular anterior and posterior horns as key landmark points, along with some intermediate landmark points.

With the aligned lateral ventricles, the selected deformation modelling function can be used for lateral ventricular deformation measurement. The obtained deformation data can be then converted to image greyscale values.
which in turn can be used for brain tumour segmentation. The problem of misalignment due to imperfect template image is alleviated by the step of adjustment of the estimated lateral ventricular deformation data.

In this chapter, details of methods and algorithms employed in each step have been elaborated. By discussing and evaluating experimental results of these steps, applicability of the proposed approach for transforming lateral ventricular deformation into feature is validated.

It can be seen from the results that, the extracted lateral ventricular deformation feature generally coincides with the existence of brain tumour. This suggests the strong correlation between the extracted lateral ventricular deformation feature and brain tumour. It is hoped that by adding the extracted lateral ventricular deformation feature, brain tumour segmentation accuracy can be enhanced. The process of brain tumour segmentation with the extracted feature of lateral ventricular deformation is elaborated in the next chapter.
CHAPTER 6: BRAIN TUMOUR SEGMENTATION SYSTEM

Let me tell you the secret that has led me to my goal: my
strength lies solely in my tenacity.

--- Louis Pasteur

The results obtained in the proposed lateral ventricular deformation feature extraction component suggest that the correlation between brain tumour and lateral ventricular deformation is quantifiable, and the extracted feature is relevant to the position of brain tumour. In this chapter, the extracted feature is used to evaluate its effect on brain tumour segmentation. The common magnetic resonance (MR) image segmentation system is used in this work. By implementing the system on MR image cases, brain tumour segmentation results are evaluated by analysing the change in segmentation accuracy when the extracted lateral ventricular deformation feature is included in the input data.

The rest of the chapter is organised as follows. Overview structure and implementation details of the brain tumour segmentation system are firstly presented in Section 6.1. In Section 6.2, by setting up and performing experiments using eight multi-spectral MR image cases, evaluation is conducted
by analysing the segmentation results with the inclusion of the lateral ventricular deformation feature. This chapter is completed by a summary in Section 6.3.

6.1. System Implementation

Structure of the brain tumour segmentation system in this research follows the common MR image segmentation system shown in Figure 2.5 (see Chapter 2 for detail). To investigate the effect of brain tumour segmentation caused by the feature of lateral ventricular deformation, special considerations have to be given to the inclusive components of pre-processing, feature extraction and brain tumour segmentation.

6.1.1. Image Pre-processing

The artefacts presented in MR images of this research include noise, magnetic resonance imaging (MRI) intensity non-standardisation [Clarke et al., 1995; Worth et al., 1998; Sled et al., 1999; Nyul and Udupa, 1999] (Chapter 2 has discussed some other artefacts in MR images, however they are not noticeable in the image cases used in this research). In addition to these common artefacts in MR images, some other issues that affect the results of lateral ventricular deformation feature extraction need to be addressed.

As can be seen from Chapter 5, the measurement of lateral ventricular deformation in the feature extraction component is based on the aligned template and target lateral ventricles. Because the lateral ventricles alignment is conducted by associating geometrical boundaries of both template and target lateral ventricles, it is important for all brains in template and target MR images to
be geometrically comparable. However in the real MR image cases, brains have various sizes among different people and are unlikely located precisely in the centre of the image. This issue of geometrical non-uniformity will seriously affect the accuracy of the deformation measurement. In order to allow all brains to be resized to the same dimension and relocated to the centre of the image, a geometrical standardisation process performed on the input MR images is necessary.

Because this research focuses on the MR image pixels within the intracranial structures, pixels in the background and skull are treated as redundant data and should be removed because they are not going to be processed or analysed. Therefore processes for skull and background removal are required in the pre-processing component in order to reduce computation complexity in the whole system.

As the proposed feature weight adjustable fuzzy c-means (fwaFCM) algorithm has been modified to handle the issues of noise and creating homogeneous clustering results (see Chapter 5 for detail), the pre-processing component in this brain tumour segmentation system will only need to address the remaining issues of intensity non-standardisation, geometrical non-uniformity and redundant data in the image background and skull. These issues are respectively addressed by the four streamlined processes of intensity standardisation, geometrical standardisation, background and skull removal processes, as illustrated in Figure 6.1. The rest of this sub-section describes the implementation detail of these processes.
6.1.1.1. Intensity Standardisation

The purpose of the intensity standardisation step is to make images from different sources comparable in their intensity values. In this research the intensity standardisation approach proposed by [Shen et al., 2003] is employed. This method thresholds background pixels, and uses the mean and variance of foreground pixels to standardise both T1- and T2-weighted MRI intensities. With the assumption that the foreground MRI intensities follow a normal distribution, it utilises an approach of histogram matching to normalise the intensities within different MR images [Siegel and Morgan, 1996]. Compared to some of the earlier methods such as template-based intensity standardisation [Zijdenbos et al., 1998], the method proposed by [Shen et al., 2003] is computationally more efficient in the implementation stage. The obtained intensity standardisation results are demonstrated in Appendix 3.
6.1.1.2. Background Removal

The background removal process reduces redundant information outside the skull. With computational efficiency in mind and following the ideas in the related works of [Bomans et al., 1990; Sandor and Leahy, 1997; Shattuck et al., 2001], this research treats the region outside the skull as background, and skull together with the cerebral region as foreground\textsuperscript{19}. The background removal process can be further broken into three sequential steps of transforming MR images to binary images, reducing noise in binary images, and lastly removing background.

Transformation to binary images is performed by using Otsu’s method [Otsu, 1979] for thresholding, in other words, degrading the greyscale image to binary. This method assumes that image histogram is bimodal and finds the optimal threshold to separate the two classes of foreground and background.

After an MR image is transformed into a binary image, the next step involves the reduction/removal of background noise. It is achieved by using the ‘fill’ and ‘clean’ [MATLAB, Online] de-noising morphological operations [Gonzalez and Woods, 2002] that remove isolated pixels in the background.

Once the noise-reduced binary image is retrieved, the convex hull algorithm developed by [Brown, 1979] can then be used to remove image background. This algorithm is applied here to find the locations of outermost pixels in the binary image foreground region and join them up in order to create a mask covering all the pixels enclosed by the skull for the purpose of background removal.

\textsuperscript{19} Observations conducted on both T1- and T2-weighted MR images suggest that, the skull visualised in brain MR images is normally much brighter than that of the region outside of skull.
removal. Afterwards this mask is applied to extract the region inside the skull. Appendix 4 shows the image data flow in the background removal step.

6.1.1.3. Geometrical Standardisation
To allow the geometrical standardisation step to be performed accurately, a standard for specifying all images in a comparable dimension is necessary. This standard can be formulated based on the skull which does not contain soft tissue and therefore normally does not suffer from deformation.

The previously created mask for extracting the background region is utilised in this step again. According to the dimension of this mask which encloses all pixels inside the skull, the image can be resized and translated [Gonzalez and Woods, 2002] to the image centre by the processes of brain resizing and centring, respectively.

6.1.1.4. Skull Removal
The pre-processing component is completed by a skull removal process to allow further processing that is focused on the intracranial region. In the present research, skull removal is achieved by employing the erosion morphological operations [Gonzalez and Woods, 2002] iteratively.

6.1.2. Feature Extraction
By employing the approach for combining features as illustrated in Equation 5.8 and Equation 5.9 (see Chapter 5), the three features shown in Figure 6.2 (a), Figure 6.2 (b) and Figure 6.2 (c) are combined as the feature set as visualised in
Figure 6.2 (d) (see Appendix 1 for more extracted lateral ventricular deformation feature results). The combined feature set can then be used as input for segmentation methods which support multi-dimensional data.

Figure 6.2: Features to be used in the multi-dimensional feature set: (a) T1-weighted MRI intensity; (b) T2-weighted MRI intensity; (c) extracted lateral ventricular deformation; (d) combined features as input feature set.

6.1.3. Brain Tumour Segmentation

The brain tumour segmentation method performs the task of partitioning MR images into multiple segments. Selected supervised and unsupervised segmentation methods are used to evaluate the effect of lateral ventricular deformation feature on brain tumour segmentation. In order to achieve that, this research uses two feature sets, one includes the extracted lateral ventricular deformation feature, and the other does not. By comparing the segmentation
results using the same segmentation method, i.e., supervised or unsupervised, effectiveness of the feature of brain lateral ventricular deformation can be examined.

6.1.3.1. Selection of Supervised Segmentation Method

Two widely used supervised pattern recognition methods in MR image segmentation are supervised artificial neural network (ANN) [Clarke, 1991; Hall et al., 1992; Ozkan et al., 1993; Sammouda et al., 1996; Zhu and Yan, 1997; Iftekharuddin et al., 2008; Iscan et al., 2009] and $k$-nearest neighbours ($k$-NN) [Cover and Hart, 1967; Bezdek et al., 1993; Clarke et al., 1993; Mitchell et al., 1994; Clarke et al., 1995; Vinitoki et al., 1997; Mazzara et al., 2004; Duda et al., 2001].

An ANN, usually called neural network (NN), is a mathematical model or computational model that can be used to model complex relationships between inputs and outputs or to find patterns in data [Duda et al., 2001]. The family of ANNs not only has both the unsupervised and supervised learning paradigms [Duda et al., 2001] but also can be modelled as multiple types with different structures and mechanisms. For example, the simplest single-layer feed-forward neural network (SLFF-NN) used by [Clarke, 1991] and [Hall et al., 1992], multi-layer feed-forward neural network (MLFF-NN) applied by [Ozkan et al., 1993] and [Iftekharuddin et al., 2008]. [Sammouda et al., 1996] conducted a study of using hopfield neural network (HNN) and Boltzmann machine neural network (BMNN) on brain MR image segmentation. [Zhu and Yan, 1997] also conducted an MR image tumour boundary detection using HNN. [Iscan et al., 2009] recently
conducted a brain tumour segmentation by using a novel incremental supervised neural network (ISNN) classifier. Any one type of ANN can not be treated as a representative for the whole ANN family and therefore not selected for the supervised brain tumour segmentation testing in this research.

Compared to ANN, the \( k \)-NN method belongs to the single classification paradigm which follows \( k \)-NN rule [Cover and Hart, 1967]. Despite its simplicity, the \( k \)-NN method has been widely used in MR image segmentation for its effectiveness. Also because the \( k \)-NN algorithm does not require any knowledge or assumption about statistical properties of the data, it is often called a nonparametric method in the pattern recognition community [Clarke et al., 1993; Duda et al., 2001] and is more suitable for multi-spectral MR image segmentation (see Chapter 2 for detail). Compared to parametric methods, it gives superior results in practice in terms of both accuracy and reproducibility [Clarke et al., 1993]. Within the three widely used supervised classification methods of maximum likelihood (ML) method, \( k \)-NN, and a back-propagation ANN, it is found that \( k \)-NN provides the best results for multi-spectral MR image segmentation [Clarke et al., 1993].

The \( k \)-NN classifier relies on finding the closest training examples in multi-dimensional feature space to classify objects [Duda et al., 2001]. In this classification paradigm, distances between testing data to \( k \) nearest neighbours of a training sample are computed firstly. The similarities of one sample from testing data to the \( k \) nearest neighbours are then aggregated according to the class of the neighbours [Hu, Online]. The testing sample is assigned to the most
similar class. Equation and algorithm of $k$-NN classification can be found in Appendix 5.

6.1.3.2. Selection of Unsupervised Segmentation Method
Fuzzy c-means (FCM) is a widely used unsupervised pattern recognition method for brain MR image segmentation [Philips et al., 1995; Clark et al., 1998; Shen et al., 2003]. In the proposed system, the brain tumour segmentation component is mainly designed for evaluating the effect of using lateral ventricular deformation feature. Therefore, the conventional FCM method is selected, due to the fact that a more common method is preferable in this research.

6.2. Experimentation and Evaluation
This section presents the brain tumour segmentation experiments on the MR image cases and evaluation of the experimental results. Based on the experiment settings, the results of brain tumour segmentation using both supervised and unsupervised methods are obtained accordingly. By comparing between segmentation results using input feature sets with and without the extracted lateral ventricular deformation feature, brain tumour segmentation accuracy increase caused by this additional feature is analysed.

6.2.1. Input MR Images
In the experiments, eight tumour-affected multi-spectral MR image cases from the University Malaya Medical Centre are used. Retrieved from one 1.5-Tesla Siemens MRI scanner, all of these image cases contain both T1- and T2-
weighted modalities. In each of these cases, the image slice in the brain centre which shows the largest lateral ventricular compartments is selected\textsuperscript{20}.

To create the general mask for extracting deformed lateral ventricles (see Chapter 5 for details), one image case from a healthy old woman adapted from [The Whole Brain Atlas, Online] is employed.

6.2.2. System Environment

The system for experiments is coded in Mathworks Matlab 7.0 (R14) [MATLAB, Online] and all experiments are run on a personal computer with Pentium Dual CPU of 2.0GHZ and 2GB RAM running Microsoft Windows XP Professional version 2002 with service pack 2.

6.2.3. Experiments

Both supervised and unsupervised methods are applied on two feature sets (one with lateral ventricular deformation feature and another without).

To use the supervised \textit{k}-NN algorithm on brain tumour segmentation, manual tumour segmentation results from medical experts\textsuperscript{21} are used as training samples in which tumour areas are marked. Therefore all pixels in the images can be labelled as tumour or non-tumour. After the \textit{k}-NN classification, each testing image pixel is categorised as tumour or non-tumour.

\textsuperscript{20} In the experiments using \textit{k}NN classification method, images are resized to 128x128 to reduce computation time.

\textsuperscript{21} Manual tumour segmentation results are from Tan Jui Kok, Manager of Radiology Department in Penang Adventist Hospital, George Town, Penang, Malaysia.
In the brain tumour segmentation experiments using unsupervised FCM algorithm, the number of clusters is set to 6 for accommodating pixels into six clusters of white matter (WM), grey matter (GM), cerebrospinal fluid (CSF), brain tumour, background and other tissues. The cluster of tumour will be identified manually after the clustering process due to the fact that there is no training data for the FCM method. Segmentation results by medical experts only serve as the ground truth for evaluating segmentation accuracy.

### 6.2.4. Evaluation Methods

With the experiments by using input feature set with or without the extracted lateral ventricular deformation feature, pixels segmented as tumour which are in the same class as the corresponding pixels in the segmentation by medical expert are defined as correctly segmented tumour pixels; those segmented as tumour but labelled as non-tumour in the segmentation by medical expert are treated as wrongly segmented tumour pixels.

Statistical measures of sensitivity and specificity [Altman and Bland, 1994; Hayes, 1973] are applied for evaluating the segmentation results. By treating correctly segmented tumour, wrongly segmented tumour, correctly segmented non-tumour and wrongly segmented non-tumour pixel number as true positive, false positive, true negative and false negative number respectively, sensitivity and specificity values can be obtained according to Equation 6.1 and Equation 6.2 [Hayes, 1973], respectively:

\[
Sensitivity = \frac{true^+}{true^+ + false^-} \tag{6.1}
\]
\[
\text{Specificity} = \frac{\text{true}^-}{\text{true}^- + \text{false}^+}
\]  

(6.2)

where \text{true}^+ , \text{false}^+ , \text{true}^- and \text{false}^- denote true positive, false positive, true negative and false negative values, respectively. A sensitivity of 100% means that the test recognizes all actual positives, i.e., all brain tumour pixels are segmented as tumour. And a specificity of 100% means that the test recognizes all actual negatives, i.e., all non-tumour pixels are segmented as non-tumour [Altman and Bland, 1994]. Therefore in this research, higher sensitivity and specificity suggest better tumour segmentation and non-tumour identification results, respectively.

6.2.5. Evaluation of Results Using Supervised Method

The \(k\)-NN classification result of tumour case number 1 is illustrated in Figure 6.3 (c-f) with the training data in Figure 6.3 (b). This training data is created from the manual segmentation by medical expert as illustrated in Figure 6.3 (a). It can be seen from Figure 6.3 (f) that, the classification result obtained from the feature set with lateral ventricular deformation feature is closer to the segmentation result from medical expert than the result shown in Figure 6.4 (e), which is created from the feature set without lateral ventricular deformation feature. Segmentation results of tumour cases number 2 to 8 are visualised in Figure 6.4. The results of the eight cases are counted and demonstrated in Table 6.1. The wrongly classified tumour pixels are mainly caused by the weak correlation or irrelevancy between input features and anatomical meaning, as stated in [Mitchell, 1997].
Figure 6.3: Training data and tumour segmentation results using $k$-NN classifier of tumour case number 1: (a) labelled tumour segmentation by medical expert; (b) training data for classification converted from (a); (c) classification result without deformation feature; (d) classification result with deformation feature; (e) visualised tumour segmentation result without deformation feature; (f) visualised tumour segmentation result with deformation feature.
Figure 6.4: Training data and tumour segmentation results using k-NN classifier for tumour cases number 2 to 8: each row represents one tumour case. In each row, the first image is the segmentation result by medical expert used as training data; the second image is the classification result from k-NN classification without deformation feature; the third image is the result from k-NN classification with deformation feature.
Table 6.1: Results counts of tumour segmentation using $k$-NN classifier.

<table>
<thead>
<tr>
<th>Tumour case number</th>
<th>Tumour pixel number from medical expert</th>
<th>$K$-NN Classification results without estimated deformation data</th>
<th>$K$-NN Classification results with estimated deformation data</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Correctly classified Non-Tumour Tumour</td>
<td>Wrongly classified pixels</td>
<td>Correctly classified Non-Tumour Tumour</td>
</tr>
<tr>
<td>1</td>
<td>864</td>
<td>15469 841 23 51</td>
<td>15476 851 13 44</td>
</tr>
<tr>
<td>2</td>
<td>170</td>
<td>16199 150 20 15</td>
<td>16211 152 18 3</td>
</tr>
<tr>
<td>3</td>
<td>301</td>
<td>16069 275 26 14</td>
<td>16086 278 23 17</td>
</tr>
<tr>
<td>4</td>
<td>423</td>
<td>15892 271 152 69</td>
<td>15916 317 106 45</td>
</tr>
<tr>
<td>5</td>
<td>226</td>
<td>16100 93 133 56</td>
<td>16124 195 70 34</td>
</tr>
<tr>
<td>6</td>
<td>217</td>
<td>16155 179 38 12</td>
<td>16159 195 22 8</td>
</tr>
<tr>
<td>7</td>
<td>1207</td>
<td>15019 1086 121 158</td>
<td>15134 1183 24 43</td>
</tr>
<tr>
<td>8</td>
<td>313</td>
<td>16043 283 30 28</td>
<td>16056 290 23 15</td>
</tr>
</tbody>
</table>

As can be seen in Table 6.1, after the extracted lateral ventricular deformation feature is included into feature set for the classification, the correctly classified tumour pixels number increases for all eight cases. Except for a slight increase of wrongly classified non-tumour pixels in case number 3, 7 out of 8 cases show decreased number of wrongly classified tumour and increased number of correctly classified non-tumour pixels. Enhancement of classification accuracy demonstrates the correlation between the deformed lateral ventricles and the brain tumour.

Sensitivity and specificity values tabulated in Table 6.2 provide further evidence of the positive effect from the additional feature. It can be seen that, with the inclusion of the extracted lateral ventricular deformation feature, specificity values increase for all eight cases. Except for the decrease in case number 3, sensitivity values increase in 7 out of 8 cases. The increase of both sensitivity and specificity values demonstrate the positive effect of the extracted lateral ventricular deformation on supervised brain tumour segmentation. It also can be seen that the sensitivity value will generally increase more, especially in...
the cases if the value is low when only the MRI intensity features are employed. This can be found from the increase of 20.5% in case 5 from 61.6% to 82.1% where no lateral ventricular deformation feature is added, increase of 7.9% in case 4 from 79.7% to 87.6%, increase of 7.2% in case 2 from 90.9% to 98.1% and increase of 9.2% in case 7 from 87.3% to 96.5%, comparing with increase of 0.8% in case 1 from 94.3% to 95.1%, increase of 2.4% in case 6 from 93.7% to 96.1% and a decrease of -0.9% in case 3 from 95.3% to 94.2%. This suggests that if multi-spectral MRI intensity features are insufficient for classifier to distinguish tumour and non-tumour tissues, the added feature of lateral ventricular deformation will be more effective for the classification. The decreased sensitivity value in case 3 is an example that the low level features are sufficient enough for classifier to generate accurate results. In this case, the extracted lateral ventricular feature has little positive or even negative effect on the classification accuracy.

<table>
<thead>
<tr>
<th>Case</th>
<th>Specificity</th>
<th>Sensitivity</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Feature set without the extracted deformation feature</td>
<td>Feature set with the extracted deformation feature</td>
</tr>
<tr>
<td>Case 1</td>
<td>99.9%</td>
<td>100.0%</td>
</tr>
<tr>
<td>Case 2</td>
<td>99.9%</td>
<td>99.9%</td>
</tr>
<tr>
<td>Case 3</td>
<td>99.8%</td>
<td>99.9%</td>
</tr>
<tr>
<td>Case 4</td>
<td>99.1%</td>
<td>99.2%</td>
</tr>
<tr>
<td>Case 5</td>
<td>99.2%</td>
<td>99.6%</td>
</tr>
<tr>
<td>Case 6</td>
<td>99.8%</td>
<td>99.9%</td>
</tr>
<tr>
<td>Case 7</td>
<td>99.2%</td>
<td>99.8%</td>
</tr>
<tr>
<td>Case 8</td>
<td>99.8%</td>
<td>99.9%</td>
</tr>
</tbody>
</table>

Table 6.2: Specificity and sensitivity values of brain tumour segmentation using k-NN classifier with or without extracted deformation feature.
6.2.6. Evaluation of Results Using Unsupervised Method

The FCM tumour clustering result of tumour case 1 is visualised in Figure 6.5 (c-f) with the training data as shown in Figure 6.5 (b), which was also retrieved from segmentation conducted by medical experts as illustrated in Figure 6.5 (a). The clustering result with the added lateral ventricular deformation feature can be seen in Figure 6.5 (f).

![Figure 6.5: Tumour segmentation results using FCM clustering method from tumour case number 1: (a) labelled tumour segmentation by medical expert; (b) tumour segmented by medical expert visualised as mask; (c) tumour clustering result without deformation feature; (d) tumour clustering result with deformation feature; (e) visualised tumour segmentation result without deformation feature; (f) visualised tumour segmentation result with deformation feature.](image)

Figure 6.5 (c) and Figure 6.5 (d) visualise the tumour clusters without and with extracted lateral ventricular deformation, respectively. By comparing them, it
can be seen that the latter has less wrongly clustered tumour pixels (see Table 6.4). The segmentation process creates a tumour cluster which is more similar to the segmentation result by medical experts than the one shown in Figure 6.6 (e) where lateral ventricular deformation feature is not added.

After the extracted lateral ventricular deformation feature is added to the FCM clustering input feature set, as shown in Table 6.4, all correctly clustered tumour pixels number increases. This increase shows that the extracted lateral ventricular deformation feature also improves brain tumour segmentation using unsupervised method. However, from case number 4 to case number 8, the number of wrongly clustered tumour pixels also increases.

Table 6.3: Tumour segmentation results using FCM clustering method.

<table>
<thead>
<tr>
<th>Tumour case number</th>
<th>Tumour pixel number from medical expert</th>
<th>FCM clustering results without estimated deformation data</th>
<th>FCM clustering results with estimated deformation data</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Correctly clustered pixels</td>
<td>Wrongly clustered pixels</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Non-Tumour</td>
<td>Tumour</td>
</tr>
<tr>
<td>1</td>
<td>3456</td>
<td>6125</td>
<td>3438</td>
</tr>
<tr>
<td>2</td>
<td>678</td>
<td>5419</td>
<td>250</td>
</tr>
<tr>
<td>3</td>
<td>1203</td>
<td>60459</td>
<td>1118</td>
</tr>
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<td>855</td>
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<td>7</td>
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<td>3501</td>
</tr>
<tr>
<td>8</td>
<td>1249</td>
<td>63012</td>
<td>1232</td>
</tr>
</tbody>
</table>

Table 6.4 tabulates the sensitivity and specificity values in the segmentation using unsupervised FCM method. It can be seen that, with the inclusion of the extracted lateral ventricular deformation feature, specificity values increase for all eight cases. However, sensitivity values decrease in 4 out of 8 cases. This is mainly because clustering methods like FCM have no training data and the clustering is based on measuring the similarity of input feature, i.e., there is no
specific rule created for distinguishing between tumour and non-tumour pixels. In short, the clusters of tumour or non-tumour are not well defined concepts [Everitt, 1972]. Therefore, adjusted measurement of similarity caused by the additional lateral ventricular deformation feature may not only make more tumour pixels to be correctly assigned in one cluster, it also mistakenly accommodates more non-tumour pixels in that cluster.

<table>
<thead>
<tr>
<th>Case</th>
<th>Specificity</th>
<th>Sensitivity</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Feature set without extracted deformation feature</td>
<td>Feature set with extracted deformation feature</td>
</tr>
<tr>
<td>Case 1</td>
<td>100.0%</td>
<td>100.0%</td>
</tr>
<tr>
<td>Case 2</td>
<td>99.2%</td>
<td>99.8%</td>
</tr>
<tr>
<td>Case 3</td>
<td>99.9%</td>
<td>99.9%</td>
</tr>
<tr>
<td>Case 4</td>
<td>98.2%</td>
<td>99.8%</td>
</tr>
<tr>
<td>Case 5</td>
<td>99.9%</td>
<td>99.9%</td>
</tr>
<tr>
<td>Case 6</td>
<td>99.2%</td>
<td>99.3%</td>
</tr>
<tr>
<td>Case 7</td>
<td>97.8%</td>
<td>99.4%</td>
</tr>
<tr>
<td>Case 8</td>
<td>100.0%</td>
<td>100.0%</td>
</tr>
</tbody>
</table>

Table 6.4: Specificity and sensitivity values of brain tumour segmentation using conventional FCM clustering method with or without extracted deformation feature.

One of the challenges associated with using MRI intensity values for brain tumour segmentation is that tumour areas often have heterogeneous intensities [Prastawa et al., 2004]. Therefore, when only MRI intensity values are used as input features, a desirable tumour segmentation result is not always obtainable. As a result, tumour pixels may be incorrectly clustered into other clusters. The low sensitivity values in the case 2, case 3, case 4, case 5, case 6 and case 8 (less than 50% in these cases) suggest poor non-tumour segmentation results in the unsupervised segmentation. This can be explained by the discussions in
Chapter 2 that the use of unsupervised method is not suitable for accurate pathology segmentation.

6.3. Summary and Discussion

By constructing a brain tumour segmentation system and using supervised and unsupervised pattern recognition methods, e.g., $k$-NN and FCM algorithms, experiments have been performed to evaluate brain MR image tumour segmentation accuracy change with the incorporation of the extracted lateral ventricular deformation feature.

With the use of manual segmentation from medical experts as the ground truth, increased rate of correctly segmented tumour pixels can be obtained using both $k$-NN classification and FCM clustering methods when the extracted lateral ventricular deformation feature is added. The wrongly segmented brain tumour pixels are also reduced in the case of using the $k$-NN tumour classification. Both the specificity and sensitivity values increase with the additional extracted lateral ventricular deformation feature.

The results show that the extracted lateral ventricular deformation feature is relevant to the position of brain tumour. By incorporating the relevant lateral ventricular deformation feature in the feature set for pattern recognition segmentation methods, brain tumour segmentation accuracy increases.
CHAPTER 7: CONCLUSIONS AND FUTURE WORK

What appears to be the end may really be a new beginning.

---Anonymous

This chapter concludes the thesis with a review of the work presented in the previous chapters and highlights the research contributions. Furthermore, it discusses and suggests directions and some of the challenging issues for future research.

7.1. Conclusions
One of the most challenging issues in accurate tumour segmentation is the weak correlation between magnet resonance imaging (MRI) intensity and its actual anatomical meaning, which give rise to the motivation of extracting other high level features for the task. In line with recent studies, where additional features such as texture, neighbouring pixels and image moment are used, this thesis brings forward the idea of possible correlation between ventricular deformation and position of brain tumour, and proposes to quantify the deformation information with a design and implementation of a feature extraction component. The brain tumour segmentation experiments demonstrate the improvement of
segmentation accuracy as a result of the addition of the lateral ventricular deformation feature.

To have an accurate measurement of ventricular deformation, lateral ventricular shape must be retrieved accurately from the brain tissue segmentation results. The feature weight adjustable fuzzy c-means (fwaFCM) method with Gaussian smoothing is proposed for this purpose. Experiments have been conducted using both the artificially synthesized and clinical MR images. By employing multiple validation methods such as validity functions and centroid displacement measurement, the clustering results are compared to those generated by using conventional FCM algorithm and also to those evaluated by medical experts. One reason for the superior performance of this method is that it combines the strategy of eliminating superfluous information, while at the same time preserving the essence in the processed image (through the use of both the Gaussian smoothed and the original image). In addition, the degree of importance for each of the mentioned factors can be automatically balanced (through the automatic adjustment of input feature weights of the fwaFCM method). This general principle can in fact be applied for improving performance of general segmentation methods.

After brain tissue segmentation, lateral ventricles are extracted for the purpose of their deformation estimation. By aligning a pair of lateral ventricles from template and diagnostic MR images, non-linear deformation modelling functions are applied to measure the displacement which gives an indication of the direction and strength of compression acting on each sampled image point.
Due to the fact that a perfect lateral ventricular template is very difficult to come by, the displacement values adjusted relative to the position of brain is used instead. The experimental results from the visualised deformation data reveal that the resultant deformation data generally coincides with the direction and position of brain tumour. The compression on lateral ventricles from brain tumour can therefore be viewed as information which indicates the position of brain tumour and is potentially useful for its segmentation. Furthermore, this observation implies that the interaction between abnormal and normal structures can be effectively quantified by measuring the pathological shape change. This quantified data provides an additional tool for analysing abnormalities in a more objective manner.

In order to evaluate the proposed approach of brain MR image tumour segmentation with the extracted lateral ventricular deformation feature, eight tumour-affected brain MR image cases from real patients are used. In the final results, segmentation accuracy in terms of specificity and sensitivity values increases with the additional deformation feature using both supervised and unsupervised pattern recognition methods. It can also be seen from the results that lower the MR image quality is, the more improvement will be obtained from the deformation feature. From a biomechanical point of view, the principle of measuring and utilising lateral ventricular deformation could also be applied in quantitative study of the correlations between normal structures and pathology in other parts of biological bodies. This suggests an interesting and meaningful
future research topic which utilises the measured deformation of the normal structure to assist analysis of the structure of pathology.

This study also demonstrates the importance of system design in segmentation tasks. Although this study focuses on extracting more relevant features, appropriate pre-processing and segmentation methods are also crucial for obtaining desirable results. It is suggested that, in general information processing systems, with the tactically designed pre-processing and more relevant information obtained from feature extraction, suitable information processing methods can be effectively applied to produce desirable results.

7.2. Contributions

The research objectives specified in Chapter 1 have been fulfilled by the following major contributions.

1. **Investigation of the Use of Lateral Ventricular Deformation for Brain MR Image Tumour Segmentation**: with the objective of finding more relevant features for brain MR image tumour segmentation, the effect of deformation on the lateral ventricles caused by the compression from brain tumour is studied. The viability and rationale of using lateral ventricular deformation information for enhancing brain tumour segmentation performance are examined in detail.

2. **Lateral Ventricular Deformation Feature Extraction Component**: in order to incorporate lateral ventricular deformation into segmentation, the important tasks of feature extraction are turned into the processes of
retrieving lateral ventricular shape, estimating lateral ventricular deformation and transforming lateral ventricular deformation to feature. With the discussion of the approach of transforming lateral ventricular deformation into a feature for segmentation, these processes are then designed in the feature extraction component in a streamlined manner.

3. Developing a New Clustering Scheme Which Integrates the Modified fwaFCM with Gaussian Smoothing: there are some limitations in the conventional FCM algorithm for MR image segmentation. To address these issues, the fwaFCM algorithm is proposed in order to allow feature weights to be adjustable and automatically optimised. In addition, Gaussian smoothing is incorporated to address the issue of noise sensitivity in the conventional FCM method.

4. Methods for Estimating Lateral Ventricular Deformation: with the alignment between the template and target objects, the shape variation is modelled by the use of non-linear functions and vector displacement measurement. Lateral ventricular deformation can therefore be quantified. Experimental results demonstrate that this approach creates estimated data relevant to the deformation.

5. Adjustment of Estimated Deformation Results: in order to alleviate the problem caused by imperfect template, angles between the directions of displacement vectors and a manually selected reference point are utilised as offset. Empirical results show that after this adjustment
process, estimated deformation data becomes more relevant to the position of brain tumour.

6. **Brain Tumour Segmentation with Lateral Ventricular Deformation Feature**: with the proposed lateral ventricular deformation feature extraction component, the effects of incorporating lateral ventricular deformation in common MR image segmentation systems are evaluated through experiments on several tumour-affected brain MR images. The results obtained from the experiments using both unsupervised and supervised methods demonstrate that, with this additional feature in the input feature set, brain tumour segmentation accuracy increases. Compared to other high-level features such as textures, the extracted lateral ventricular deformation feature is suitable for assisting image pixel classification and is also stable within different brain tumour types.

**7.3. Future Work**

Further development of the approach of utilising information from deformation of normal structures to assist tumour segmentation can be explored. When considering the big picture of the MR image segmentation system, the most significant enhancement that could be made is to extend the application from 2 dimensions to 3 dimensions which provides a more comprehensive tumour visualisation for medical practitioners. To achieve accurate 3-dimensional segmentation of brain tumours, some processes presented in the current 2-dimensional deformation feature extraction component needs to be amended.
accordingly in order to make it suitable to be applied in a 3-dimensional MR image segmentation system.

An inherent limitation of the present approach is that the deformation feature extraction is based only on lateral ventricles. Some properties of lateral ventricles, such as sharp boundary and simple shape, clearly make the task of segmentation and deformation feature extraction with regards to lateral ventricles relatively less challenging compared to other structures within the human brain. However, lateral ventricles lie approximately in the centre of the brain, thus making the extracted deformation feature less useful for segmentation of tumours that are not located in the vicinity of the central region of the brain.

The work presented in this thesis has provided sufficient evidence that by exploiting the deformation of soft tissues, accuracy of the brain tumour segmentation can be increased. Since the lateral ventricular deformation has been utilised in the current research, a future work could be the estimation of deformation of other major intracranial structures, in particular cerebral white matter (WM) and grey matter (GM) which are not only located in the brain centre. Therefore, 3-dimensional brain tumour segmentation with the assistance from the deformation feature of these structures can potentially help to achieve more desirable results.

An important factor that needs to be considered when dealing with cerebral WM and GM segmentation for retrieving their shapes is the extra effort that is needed in selecting and/or designing suitable segmentation methods. This is primarily due to the fact that these structures, unlike the brain lateral ventricles,
do not normally possess sharp boundaries. This suggests that the use of the proposed fwaFCM method with Gaussian smoothing for brain tissue segmentation may require further enhancement to tackle different issues.

Another challenge regarding the deformation estimation of GM and WM is the association or alignment between the template and the target structures. The alignment method proposed in this thesis may not be applicable for aligning GM and WM because of their complex shapes. Therefore future research work may involve the use of deformable image registration methods which provide more sophisticated means for aligning objects (see [Montagnat et al., 2001] and [Mohamed et al., 2006]). For example, [Mohamed et al., 2006] proposed an approach which integrates the components of the deformable registration of 3-dimensional brain tumour images into a normal brain atlas. This approach significantly reduces registration error compared to the direct use of deformable image registration.

An additional direction that could be pursued would be the application of deformation modelling function for 3-dimensional deformation estimation, including those studied in this work as others such as the finite element model (FEM) [Ferrant et al., 2001]. Further analyses and experiments are needed regarding the feasibility of employing the nonlinear deformation modelling function used in this thesis for estimating deformation of complex structures, such as WM and GM.

A limitation associated with the use of fwaFCM method with Gaussian smoothing for brain tissue segmentation is the computational complexity. Since
clustering performance assessments through validity functions can be performed only after the fwaFCM iterative computations are completed, the process of finding the optimal feature weights for the fwaFCM algorithm is rather slow. A recent research work [Xiao et al., 2010] which utilises a bootstrapping method to calculate feature weighting factors attempted to address this issue. However, variation amongst different modalities of multi-spectral MR images still needs to be evaluated to obtain more suitable feature weighting factors automatically. Therefore, future research should also take a look at this aspect in order to optimise feature weights in fwaFCM algorithm for multi-spectral MR images without using the iterative clustering processes.

7.4. Epilogue

The work described in this thesis focuses on one of the most challenging issues in MR image tumour segmentation tasks: the weak correlation between brain MRI intensity and its anatomical meaning. The proposed method for lateral ventricular deformation feature extraction is devised in order to retrieve an additional feature to increase brain tumour segmentation accuracy. Empirical results show that the proposed method provides clear benefits to the research of brain tumour segmentation by increasing the segmentation accuracy. In addition, a number of open issues related to future research in this direction, such as using deformation of cerebral soft tissues to assist 3-dimensional brain tumour segmentation, have also been discussed. This thesis provides motivations for further research towards more accurate brain tumour segmentation, and is beneficial to medical practitioners in the process of practical diagnosis.
APPENDIX 1: LATERAL VENTRICULAR DEFORMATION FEATURE EXTRACTION RESULTS

First and third columns: Input T1-weighted MR image data; second and fourth columns: lateral ventricular deformation estimation results of input MR image data in the respective left cell (as an example, (b) includes visualised lateral ventricles alignment results and denotes the maximum estimated deformation value).
APPENDIX 2: IMAGE DATA OUTPUT FLOW WITHIN STEPS OF PRE-PROCESSING COMPONENT

(a) original MR image; (b) after intensity standardisation; (c) after background removal; (d) after geometrical processing; (e) after skull removal.
APPENDIX 3: MRI INTENSITY STANDARDISATION RESULTS

First row: T1-weighted original images; Second row: T1-weighted images in first row after intensity standardisation; Third row: T2-weighted original images; Fourth row: T2-weighted images in third row after intensity standardisation.
APPENDIX 4: IMAGE DATA OUTPUT FLOW WITHIN STEPS OF BACKGROUND REMOVAL

(a) input image; (b) after transforming (a) to binary image; (c) after de-noise operation on (b); (d) mask retrieved by convex hull from (c); (e) removal of background using (d) as a mask.
APPENDIX 5: K-NEAREST NEIGHBOURS FUNCTION AND ALGORITHM

Based on the $k$-NN rule [Cover and Hart, 1967], $k$-NN function can be abstracted as below:

$$F(x_q) = \arg \max_{v \in V} \sum_{i=1}^{k} \delta(v, f(x_i))$$

where $\delta$ denotes the classes of $k$ nearest neighbours between a query object $x_q$ to each vector $v$ in the training data set $V$.

The algorithm of $k$-NN classification:

| Input: number of nearest neighbours: $k$, training sample and testing data |
| Output: classified testing data |
| Step 1: Calculate the distance between the testing data and all the training samples. |
| Step 2: Sort the distance and determine the nearest neighbours based on the $k^{th}$ minimum distance. |
| Step 3: Gather the class of the nearest neighbours. |
| Step 4: Use the majority of the class of nearest neighbours as the prediction value of the query instance. |
APPENDIX 6: RETRIEVED LATERAL VENTRICLES AFTER LINKING

Input T1-weighted image data (first and fourth columns), input T2-weighted image data (second and fifth columns), and retrieved lateral ventricles (third and sixth columns)
APPENDIX 7: EXPERIMENTAL RESULTS ON SELECTING GAUSSIAN SMOOTHING FILTER PARAMETERS FOR FCM CLUSTERING

<table>
<thead>
<tr>
<th>Feature set composed of 4 features of T1-, T2-, Gaussian smoothed T1- and Gaussian smoothed T2-weighted MR image data</th>
<th>Feature set composed of 2 features of T1- and Gaussian smoothed T1-weighted MR image data</th>
<th>Feature set composed of 2 features of T2- and Gaussian smoothed T2-weighted MR image data</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cluster Number= 3</td>
<td>Cluster Number= 4</td>
<td>Cluster Number= 5</td>
</tr>
<tr>
<td>Sigma=1 and filter size = 3x3</td>
<td>Sigma=2 and filter size = 5x5</td>
<td>Sigma=3 and filter size = 7x7</td>
</tr>
<tr>
<td>$V_{pc}$</td>
<td>$V_{pe}$</td>
<td>$V_{pc}$</td>
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<tr>
<td>0.838</td>
<td>0.600</td>
<td>0.791</td>
</tr>
<tr>
<td>0.125</td>
<td>0.165</td>
<td>0.184</td>
</tr>
<tr>
<td>0.832</td>
<td>0.791</td>
<td>0.877</td>
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<td>0.130</td>
<td>0.171</td>
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<td>0.766</td>
<td>0.765</td>
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<td>0.135</td>
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<td>0.819</td>
<td>0.762</td>
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<tr>
<td>0.140</td>
<td>0.180</td>
<td>0.214</td>
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<tr>
<td>0.812</td>
<td>0.777</td>
<td>0.745</td>
</tr>
<tr>
<td>0.145</td>
<td>0.185</td>
<td>0.221</td>
</tr>
</tbody>
</table>

Table 1: Validity function values on using original T1- and T2-weighted images.
Feature set composed of 4 features of T1-, T2-, Gaussian smoothed T1- and Gaussian smoothed T2-weighted MR image data

<table>
<thead>
<tr>
<th>Cluster Number=3</th>
<th>Cluster Number=4</th>
<th>Cluster Number=5</th>
</tr>
</thead>
<tbody>
<tr>
<td>$V_{pc}$</td>
<td>0.791</td>
<td>0.722</td>
</tr>
<tr>
<td>$V_{pe}$</td>
<td>0.168</td>
<td>0.235</td>
</tr>
</tbody>
</table>

Feature set composed of 2 features of T1- and Gaussian smoothed T1-weighted MR image data

<table>
<thead>
<tr>
<th>Cluster Number=3</th>
<th>Cluster Number=4</th>
<th>Cluster Number=5</th>
</tr>
</thead>
<tbody>
<tr>
<td>$V_{pc}$</td>
<td>0.840</td>
<td>0.778</td>
</tr>
<tr>
<td>$V_{pe}$</td>
<td>0.131</td>
<td>0.186</td>
</tr>
</tbody>
</table>

Feature set composed of 2 features of T2- and Gaussian smoothed T2-weighted MR image data

<table>
<thead>
<tr>
<th>Cluster Number=3</th>
<th>Cluster Number=4</th>
<th>Cluster Number=5</th>
</tr>
</thead>
<tbody>
<tr>
<td>$V_{pc}$</td>
<td>0.846</td>
<td>0.812</td>
</tr>
<tr>
<td>$V_{pe}$</td>
<td>0.126</td>
<td>0.160</td>
</tr>
</tbody>
</table>

Sigma=1 and filter size = 3x3

| Sigma=2 and filter size = 5x5 |
|-------------------------------|------------------|------------------|------------------|
| Cluster Number=3 | Cluster Number=4 | Cluster Number=5 |
| $V_{pc}$ | 0.786 | 0.711 | 0.623 |
| $V_{pe}$ | 0.171 | 0.243 | 0.318 |

Sigma=3 and filter size = 7x7

| Sigma=4 and filter size = 9x9 |
|-------------------------------|------------------|------------------|------------------|
| Cluster Number=3 | Cluster Number=4 | Cluster Number=5 |
| $V_{pc}$ | 0.784 | 0.759 | 0.704 |
| $V_{pe}$ | 0.142 | 0.201 | 0.250 |

Sigma=5 and filter size = 11x11

| Sigma=6 and filter size = 13x11 |
|-------------------------------|------------------|------------------|------------------|
| Cluster Number=3 | Cluster Number=4 | Cluster Number=5 |
| $V_{pc}$ | 0.782 | 0.753 | 0.696 |
| $V_{pe}$ | 0.147 | 0.206 | 0.256 |

Table 2: Validity function values on using T1- and T2-weighted images with added noise of SNR=10.

Feature set composed of 4 features of T1-, T2-, Gaussian smoothed T1- and Gaussian smoothed T2-weighted MR image data

<table>
<thead>
<tr>
<th>Cluster Number=3</th>
<th>Cluster Number=4</th>
<th>Cluster Number=5</th>
</tr>
</thead>
<tbody>
<tr>
<td>$V_{pc}$</td>
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<td>0.790</td>
</tr>
<tr>
<td>$V_{pe}$</td>
<td>0.131</td>
<td>0.176</td>
</tr>
</tbody>
</table>

Feature set composed of 2 features of T1- and Gaussian smoothed T1-weighted MR image data

<table>
<thead>
<tr>
<th>Cluster Number=3</th>
<th>Cluster Number=4</th>
<th>Cluster Number=5</th>
</tr>
</thead>
<tbody>
<tr>
<td>$V_{pc}$</td>
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<td>0.862</td>
</tr>
<tr>
<td>$V_{pe}$</td>
<td>0.094</td>
<td>0.119</td>
</tr>
</tbody>
</table>

Feature set composed of 2 features of T2- and Gaussian smoothed T2-weighted MR image data

<table>
<thead>
<tr>
<th>Cluster Number=3</th>
<th>Cluster Number=4</th>
<th>Cluster Number=5</th>
</tr>
</thead>
<tbody>
<tr>
<td>$V_{pc}$</td>
<td>0.891</td>
<td>0.875</td>
</tr>
<tr>
<td>$V_{pe}$</td>
<td>0.089</td>
<td>0.106</td>
</tr>
</tbody>
</table>

Sigma=1 and filter size = 3x3

| Sigma=2 and filter size = 5x5 |
|-------------------------------|------------------|------------------|------------------|
| Cluster Number=3 | Cluster Number=4 | Cluster Number=5 |
| $V_{pc}$ | 0.827 | 0.781 | 0.761 |
| $V_{pe}$ | 0.135 | 0.183 | 0.213 |

Sigma=3 and filter size = 7x7

| Sigma=4 and filter size = 9x9 |
|-------------------------------|------------------|------------------|------------------|
| Cluster Number=3 | Cluster Number=4 | Cluster Number=5 |
| $V_{pc}$ | 0.821 | 0.846 | 0.814 |
| $V_{pe}$ | 0.109 | 0.141 | 0.174 |

Sigma=5 and filter size = 11x11

| Sigma=6 and filter size = 13x11 |
|-------------------------------|------------------|------------------|------------------|
| Cluster Number=3 | Cluster Number=4 | Cluster Number=5 |
| $V_{pc}$ | 0.814 | 0.824 | 0.793 |
| $V_{pe}$ | 0.115 | 0.149 | 0.181 |

Table 3: Validity function values on using T1- and T2-weighted images with added noise of SNR=20.
REFERENCE LIST


[IBSR, Online] IBSR (Online). Internet Brain Segmentation Repository provided by MGH CMA. http://www.cma.mgh.harvard.edu/ibsr/.


Zhang, J., Ma, K., Er, M., Chong, V. (2004). Tumor segmentation from magnetic resonance imaging by learning via one-class support vector machine. In: International Workshop on Advanced Image Technology, Pages:207-211.

