A fuzzy clustering framework with neighbourhood constraints and quantitative analysis for segmentation of MRI images

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A Fuzzy Clustering Framework with Neighborhood Constraints and Quantitative Analysis for Segmentation of MRI Images

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in fulfillment of the requirement for the degree of
Doctor of Philosophy

2009

Statement of Originality

I hereby certify that the work embodied in this thesis is the result of original research done by me and has not been submitted for a higher degree to any other University or Institute.

**<A fuzzy clustering framework with neighborhood constraints and
quantitative analysis for segmentation of MRI >**

**Approved by
Supervising Committee:**

To my parents, who always give me love and support.

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Abstract

The development of computer-aided medical image processing over the past several decades has been truly revolutionary. The advantages of magnetic resonance imaging (MRI) over other diagnostic imaging modalities are its higher spatial resolution and its better discrimination of soft tissue. Automated recognition and diagnosis using MRI data require image enhancement, segmentation and quantification tools.

In the area of MR image segmentation, the well-known obstacles include noise, intensity inhomogeneity and partial volume effect. Noise can dramatically degrade the performance of image segmentation algorithms. In order to remove the noise from MR images, a fuzzy filter is used and a modified spatial fuzzy c-means algorithm is developed to overcome the intensity inhomogeneity in MR images. It is demonstrated through experiments that MR brain images can be segmented into three classes: gray matter, white matter, and cerebrospinal-fluid (CSF), while the intensity inhomogeneity is estimated and corrected. Comparisons with similar algorithms have been made. Experimental results show better achievement by the proposed method.

In order to overcome the partial volume effect a concept of mixture descriptor is proposed. The MR image voxels are modeled as mixture of more than one tissue. The partial volume labeling process is used to find the most-likely mixtures, which oversegment them to different tissue types. The partial volume labeling method can be implemented with the above noise filter and bias field estimator. Experiments on simulated images and real MR images have been conducted, and results show that the proposed framework works accurately and efficiently. Also comparison results with other methods show our algorithm has better performance.

Normally one complete MRI scans include PD, T1-weighted and T2-weighted data. The multispectral MRI images can provide more information of human tissues. In order to take the advantage of additional information to improve the segmentation, three approaches are proposed and their performances are compared. The first is directly segmenting the MRI images using three channel data at the same time by changing the parameters in the framework to the vectors. The second is segmenting the T1, T2, and PD data respectively and then combining their results. The third method takes advantage of different channel image's character. The results show that the third method is more efficient and achieves better results.

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Chapter 1

Introduction

There are many kinds of medical imaging techniques used as diagnostic imaging modalities, such as X-ray, computed tomography (CT), positron emission tomography (PET), single positron emission computer tomography (SPECT), magnetic resonance imaging (MRI), ultrasound and its fusion. These modalities combined with computer's processing power have helped humans to better understand the complex human anatomy and its behavior to a certain extent. MRI, since its first implementation by Lauterbur [4], has revolutionized diagnostic imaging in medical science, for its advantages of high spatial resolution and soft-tissue contrast. So MRI images are widely used not only for diagnosing brain tumor, heart disease and so on which are difficult to detect by using other images but also for examining anatomical state of tissues.

Increasingly, there is a need for quantitative analysis of MRI such as precise delineation of tumors and to extract the necessary boundaries, surfaces, and segmented volumes of these organs. For example, in the study of degenerative brain illnesses such as Alzheimer's disease, multiple sclerosis, and schizophrenia, it is necessary to measure precisely the amounts of gray matter, white matter, white matter lesions, cerebro-spinal fluid (CSF), as well as their spatial distribution (asymmetry in the case of schizophrenia) and temporal changes. This part of tumor and organ extraction is segmentation. Image segmentation is essentially a process of pixel classification, wherein the image pixels are segmented into subsets by assigning the individual pixels to classes. Segmentation of MRI images is also fundamental for registration across patient, time, or image modality.

However, a typical MRI analysis of a patient involves vast amounts of data, which makes manual segmentation too time consuming. For this reason, an automated algorithm for segmentation is inevitably required.

MRI image segmentation is a complex and challenging task due to the intrinsic nature of the images. In segmenting MRI image data, we have three mainly considerable difficulties: noise, partial volume effect (where more than one tissue is inside a pixel volume) and intensity inhomogeneity. Noise in MRI depends upon a number of factors including strength of the static magnetic field, type and characteristics of radio frequency coils, imaging parameters, and chosen pulse sequence [2]. Some of these are intrinsic and beyond our control. So MRI images always contain a significant amount of noise caused by above factors and patient performance. Noise can dramatically degrade the performance of many image segmentation techniques and must be concerned by all the studies.

Spatial intensity inhomogeneity or bias field induced by the radio-frequency inhomogeneity and magnetic field nonuniformity of the scanners in MRI is a major problem in the computer analysis of MRI data. Although MRI images may appear visually uniform, such inhomogeneities can cause serious misclassifications when intensity-based segmentation techniques are used. Ideally, for any given set of MR imaging parameters, the intensity values of the voxels of any given tissue class should be constant, or, in view of the partial volume effect, correspond to a Gaussian distribution with small standard deviation. Therefore the differentiation of white matter from gray matter in the brain should be easy since these tissue types exhibit distinct signal intensities. But in practice, spatial intensity inhomogeneities can be as much as 40% of image amplitudes and cause the distributions of image intensities associated with these tissue classes to overlap significantly. Therefore, the correction of spatial intensity inhomogeneity has been regarded as a necessary requirement for MRI segmentation.

Most of the segmentation techniques assign each voxel to a single specific tissue type. However, the limited spatial resolution of MRI and the complexity of tissue boundaries imply that a large part of the voxels in MRI images don't only contain a single tissue, but rather a mixture of two or more tissue types, which are called partial volume voxels. For improving the segmentation accuracy of MRI in this condition one voxel should be oversegmented into several tissue types. So the partial volume labeling is preferred in the segmentation of MRI images.

All of above facts motivate some researchers attempting to develop an accurate and efficient system to conquer the difficulties and classify the tissues of MRI images.

1.1 MOTIVATION

In the last ten years, thousands of methods have been proposed for the segmentation of MRI images. However, the accuracy and the efficiency of these algorithms are still not satisfactory for the applications of medical image analysis and diagnosis. An intelligent and robust system with more accuracy and efficiency is therefore required for automatic segmentation of MRI images.

1.2 OBJECTIVE

In the field of computer-aid MRI image analysis, many researchers want to develop a fully automated system that can accurately segment the MRI brain images, which have the most complexity of human bodies, into three parts: white matter (WM), gray matter (GM), and cerebrospinal-fluid (CSF). So this is our aim as well. The big obstacles facing current MRI images segmentation methods are noise, intensity inhomogeneity, and

partial volume effect. Most methods can deal with one or two of them but seldom can conquer all of them.

For MRI images segmentation clustering is the most popular method, with fuzzy c-means (FCM) clustering and expectation-maximization (EM) algorithms being the typical methods. EM algorithm depends mainly on the data satisfying the assumption of variant models. If the data do not comply to the model, the obtained result can be very misleading. But it is a tough task to find the well-fitting models because the human being's brain is so different and the situation could be worse considering the effect of noise, intensity inhomogeneity, and partial volume. Hence, at this stage finding models that can fit all of these is too difficult and the result will produce many errors. Thus EM algorithm isn't adopted in our work.

To the classification problem, FCM is a well established and developed algorithm. Because MRI images only provide one value (normally as grey scale) for each voxel, many algorithms for MRI segmentation including FCM are intensity based and therefore very sensitive to above three factors. This fact motivated us to improve the basic FCM to overcome the obstacles and found a way to the satisfactory classification of MRI.

1.3 CONTRIBUTIONS

The major contributions of this thesis can be summarized as follows,

- A modified fuzzy clustering algorithm is developed. There are three new aspects in the proposed algorithm.
 - The first one is a fuzzy filter used for the noise removal. The noise is the first obstacle involved in every method of MRI segmentation. Hence, a special fuzzy filter is used to deal with the noise in a pre-processing step.

This filter can amend the image from heavy noise and improve the segmentation precision greatly. It's the first time that the filter is used in the MRI segmentation.

- The second one is the modified generalized objective function developed for the FCM algorithm. In this objective function, MRI image model is considered and the true log-transformed intensities are used for the segmentation. Because the spatial constraint is considered in bias field domain, our objective function could be concise and easy to implement.
- The third new aspect is that a mean spread filter is used to smooth the bias field and avoid the misclassification. Misclassification could be produced at the iteration step of bias field estimation. The smoothness of the bias field is an important property and can be used to take the spatial constraint on estimation and correction of intensity inhomogeneity. So in our algorithm the most doubtful misclassified voxels are found in the bias field domain by gradient. Then the proposed filter is used to adjust the bias field to a smooth one and push the voxels to the correct cluster center. Our filter spreads wider when the bigger gradient is found. Therefore with this filter the bias field can be corrected and estimated while the voxels can be classified to the right tissue types.

Hence, by using the modified fuzzy clustering algorithm incorporated with the MRI image model, the effect of the noise can be reduced and the bias field can be corrected. This algorithm has been used in MRI image segmentation and classification.

- Accurate and fully automatic segmentation of MRI images is complicated by partial volume voxels that contain a mixture of two or more tissue types. In order to overcome the partial volume effect, a fuzzy clustering framework for

partial volume segmentation is developed. This framework encompasses and extends above modified spatial constraint FCM method. For describing the partial volume effect in MRI images a mixed tissue types model is introduced. This model is only applied to voxels labeled as mixture. It is demonstrated through the experiments in the thesis that the mixed model is more sophisticated and efficient to represent some MRI image voxels. Besides the mixed model two properties are assumed to differentiate the partial volume voxels from the single tissues. The first is that their gray scales have a distance from the mean value of pure tissues that form them. The second: CSF is sufficiently separated from WM so that their mixtures must be adjacent with the pure CSF and WM voxels. From the above assumptions a two step method is proposed to label the mixture voxels. This method includes the global strength of the whole image and the local strength of the neighborhood. With this labeling process those partial volume voxels could be oversegmented to different tissue types. Hence, the developed framework can improve the segmentation and classification of MRI images.

- Normally one complete MRI scans include PD, T1-weighted and T2-weighted data. Different tissues have different performances in these three channel images. The multispectral MRI images: PD, T1, and T2 can therefore provide additional information than one channel data. However due to three parallel image data, the additional information to improve the segmentation becomes a problem. In order to segment the multi-channel images three approaches are proposed and their performances are compared. These approaches are basically the extensions of above methods. The previous framework has overcome the noise, the intensity inhomogeneities, and the partial volume effect. The first is directly changing the parameters in the framework to the vectors and then segmentation in the iteration. The second is segmenting the T1, T2, and PD

data respectively and then combining their results. The third method uses the characters of different channel images. From the experiments the segmentation of T2 images has better performance on CSF. Thus a two steps method is proposed to segment the tissues. In the first step the algorithm is implemented on T2 data to segment the CSF with other tissues (WM+GM). In the second step the algorithm is implemented again on T1 data except the CSF voxels to segment WM and GM. It is demonstrated through the experiments that the third method provides better results.

By combining our proposed methods, an intelligent system is developed that can automatically segment the MRI images with more accuracy and efficiency.

1.4 ORGANIZATION OF THE THESIS

The thesis is organized as follows.

- A literature review is given in Chapter 2. The previous methods are reviewed and some of them are presented. The performances of these methods are discussed.
- The unsupervised fuzzy clustering algorithm used for MRI image segmentation and classification is described in Chapter 3. Three new aspects are emphasized here. The first one is the fuzzy filter used for the noise removal. The second one is the modified generalized objective function developed for the FCM algorithm. The last one is about the mean spread filter used to smooth the bias field and avoid the misclassification.
- In chapter 4, the fuzzy clustering framework for partial volume segmentation is presented. The mixed tissue model is proposed to describe the partial volume effect in MRI images. Two assumptions are presented to discriminate the

partial volume voxels from normal ones. A two-step method is proposed to label the mixture voxels depending on the assumptions.

- The segmentation for multi-channel MRI data is proposed in Chapter 5. Multispectral MRI images take additional information for tissues. Three approaches to segment the multi-channel data are presented and their performances are compared. The optimal strategy is demonstrated based on the experiments.
- Finally, in Chapter 6, conclusions and recommendation of future research are given.

Chapter 2

Literature Review

2.1 INTRODUCTION

A multitude of medical imaging modalities are used to probe into the structure, function, and pathology of the human body. MRI is the most popular one for its advantages of high spatial resolution and soft-tissue contrast. The abundant information provided by MRI has boosted the development of precise and quantitative image processing and analysis methods, aiming to provide valuable tools in diagnostic medical image understanding. To assist visual interpretation of MRI images, the international researchers have developed numerous techniques for processing and analyzing, including four fundamental classes of algorithms: enhancement, segmentation, quantification, and registration, which have their merits, limitations, and realm of application.

Enhancement algorithms are used to reduce image noise and increase the contrast of structures of interest. Segmentation is the stage where a significant commitment is made during automated analysis by delineating structures of interest and discriminating them from background tissue. Quantification algorithms are applied to segmented structures to extract the essential diagnostic information such as shape, size, texture, angle, and motion. Registration of two images of the same part of the body is essential

for many applications where the correspondence between the two images conveys the desired information. This thesis is mainly focused on MRI image segmentation and noise reduction.

MRI image segmentation has been a very active research area since the last decade, and a wide variety of segmentation techniques has been proposed. However, the three difficulties of MRI: noise, intensity inhomogeneities, and partial volume effect have retarded the applications so that no one standard segmentation technique can produce satisfactory results.

In this chapter, a survey of MRI image segmentation is given. Since the applications in this thesis are mainly on segmentation of MRI brain images, the head image segmentation and region of interest (ROI) extraction are firstly addressed in Section 2.2. Because this thesis is focused on overcoming the three obstacles of MRI image segmentation, the methods for noise depression, intensity inhomogeneities estimation and correction, and partial volume segmentation are then reviewed in Section 2.3, 2.4, 2.5. Finally, in Section 2.6, several popular MRI segmentation methods are reviewed and concluding remarks are made. Reviews and discussions on other aspects or problems in MRI image segmentation can be found in many publications, such as [1, 5, 68, 86].

2.2 MRI HEAD SEGMENTATION

MRI head images are often used in studies of brain tissue volume and diagnosis of brain pathology, where regions of interest (ROI) are examined in detail, for example in segmentation of brain [3] and pathology studies [6-11]. In tradition the ROI is manually outlined by skilled experts and this is ineffective in many computer-assisted applications. Fully automatic segmentation algorithms of ROI are therefore developed.

In the early days several thresholding algorithms have been developed. Some of them are based on the image histogram; others are based on local properties. Suzuki and Toriwaki use iterative thresholding to distinguish brain tissues from others [12]. Li et al. use knowledge-based thresholding to classify voxels into multiple intensity categories and then find the brain edge [13]. Brummer et al. use histogram analysis and morphology to generate a brain mask [14]. Aboutanos and Dawant [15] use histogram analysis to determine the threshold selection and generate a brain mask. A deformable model is then used to refine an initial mask. Region growing method extends thresholding by combining it with connectivity conditions or region homogeneity criteria [92, 93].

The deformable model that has attracted the most attention is popularly known as “Snakes” [16]. This active contour model algorithm is often used to approximate the locations and shapes of object boundaries in images based on the reasonable assumption that boundaries are piecewise continuous or smooth. Given an initial estimate of an object boundary, snake approaches the actual boundary by solving an energy minimization problem. This algorithm is used by Snell et al. [17] to attract the surface template to the intracranial boundary. Lobregt and Viergever [18] propose a different dynamic contour model based on deformation of a set of vertices connected by edges. The deformation is caused by internal (derived from the shape of the contour model) and external (derived from some image feature energy distribution) forces acting on the vertices. Thedens et al. [19] proposed another method to search for borders in MRI images, based on graph searching for minimum cost edge detection applied to a temporal or spatial sequence of images. Lundervold and Storvik [20] proposed a model-based segmentation method and also use a new Bayesian dynamic contour (BDC) model to detect the boundaries. The advantages of this approach over the snakes active contour is that the energy functions used to find the boundary can be more generally based on information about the whole region, rather than just the local boundary characteristics.

Based on the fact that the MRI signal forms a trough at the skull, Van den Elsen et al. [21] have developed an automatic skull boundary detection method for the purposes of automatic registration of MRI head images.

Atkins and Mackiewicz have developed a three-stage method to segment the brain [22]. First intensity histogram analysis has been used to remove background noise and provide a head mask defining the head. They showed that background noise in reconstructed MR volumes has a Rayleigh distribution:

$$p_{noise}(f) = \frac{f}{\sigma^2} \exp\left(-\frac{f^2}{2\sigma^2}\right) \quad (2.2.1)$$

where f is the noise intensity and σ is the standard deviation of the white noise. The subtraction of the best-fit Rayleigh curve, $r(f)$, from the volume histogram, $h(f)$, produces a bimodal distribution:

$$g(f) = h(f) - r(f) \quad (2.2.2)$$

Then standard morphological operations are used to remove misclassified regions within the head. Based on this mask, a nonlinear anisotropic diffusion filter combined with morphology is used to generate initial brain mask in second stage. The anisotropic diffusion filter is formulated as diffusion process that encourage intraregion smoothing while inhibiting interregion smoothing

$$\frac{\partial}{\partial t} I(\bar{x}, t) = \nabla \cdot (c(\bar{x}, t) \nabla I(\bar{x}, t)) \quad (2.2.3)$$

where $I(\bar{x}, t)$ is the MR image. $\bar{x}$ refers to the image axes and t refers to the iteration step. $c(\bar{x}, t)$ is called the diffusion function and is a monotonically decreasing function of the image gradient magnitude. The diffusion function used in their algorithm is following:

$$c(\bar{x}, t) = \exp\left(-\left(\frac{|\nabla I(\bar{x}, t)|}{\sqrt{2\kappa}}\right)^2\right) \quad (2.2.4)$$

where κ is referred to as the diffusion constant or the flow constant, which controls the behavior of the filter. The nonlinear anisotropic diffusion filter is used to attenuate the skull and some other nonbrain regions in MR images. At last stage an active contour model algorithm is used to locate the intracranial boundary with the initial brain mask as a seed. The algorithm deforms the contours defined by the perimeter of the initial brain mask to lock onto the edge of the brain. Each active contour is defined as an ordered collection of n points in the image plane

$$\begin{aligned} V &= \{v_1, \dots, v_n\} \\ v_i &= (x_i, y_i), \quad i = \{1, \dots, n\} \end{aligned} \quad (2.2.5)$$

The points in the contour iteratively approach the intracranial boundary through the solution of an energy minimization problem. For each point v_i , an energy matrix $E(v_i)$ is computed:

$$E(v_i) = \alpha E_{cont}(v_i) + \beta E_{bal}(v_i) + \gamma E_{int}(v_i) + \kappa E_{grad}(v_i) \quad (2.2.6)$$

where $E_{cont}(v_i)$ is a “continuity” energy function that influences the contour to take the shape of a circle, $E_{bal}(v_i)$ is an adaptive “balloon” force that pushes the contour outward until it reaches a strong gradient, $E_{int}(v_i)$ is an “intensity” energy function, computed from the MR image volume, that influences the contour to move toward low intensity regions, and $E_{grad}(v_i)$ is a “gradient” energy function, computed from the diffused MR image volume, that influences the contour to move toward regions of strong gradient. $\alpha, \beta, \gamma, \kappa$ are scalar constants providing relative weightings of the energy terms. Each v_i is then iteratively moved to the point of minimum energy in its neighborhood, which corresponds to the smallest element in $E(v_i)$.

Lemieux et al. have presented a seven step method for automatic segmentation of whole brain [23]. Their approach is based on automatic foreground thresholding, morphological operations, and connected component analysis. The result of each step of the algorithm is a binary brain mask. The segmentation steps include: calculation of the

foreground threshold level, initial brain disconnection, initial marrow/dura removal, secondary marrow/dura removal, removal of major venous sinuses, conditional gray-level dilation or erosion, and brainstem cutting.

Ardekani et al. adopt a fuzzy clustering technique to classify the regions that were obtained from intensity thresholding and morphological operations into brain and nonbrain [24]. They used the threshold to eliminate background noise and removed the speckles by morphological operations. The anisotropic diffusion filter is also used to reduce noise in the images. A combination of four features was selected for their fuzzy clustering algorithm. The features include mean, standard deviation, average energy of intensities, and the Euclidean distance between the region centroid to the centroid of the largest object.

Statistical techniques have been used in the MRI head segmentation from the early date. Bezdek et al. [5] reviewed many supervised and unsupervised statistical methods for MRI segmentation in general, and discussed their possibilities and limitations. As early as 1990, Cline et al. [25] have segmented the brain from MRI head images using statistical classification. Firstly, samples of brain voxels and nonbrain voxels are interactively identified. Then bivariate normal distributions are fitted to the sampled intensities and all the image voxels are classified according to where their intensities lie in the distributions. Finally, the results are smoothed to remove discontinuities in classified regions. Several texture analysis methods have been used to isolate brain tissues from MRI slices by Lachmann and Barillot [26]. They use texture information to create an initial voxel classification. Cluster analysis and Bayesian relaxation is then used to refine the classification. Another statistical relaxation method incorporated gradient magnitude as well as voxel intensities for brain segmentation was also developed by Stringham et al. [27].

Marroquin et al. use the affine and nonrigid transformation to map a mask that separates brain from nonbrain tissue as well as map the anatomical model to get an initial segmentation [28]. This is an atlas-based segmentation method, in which prior information about the approximate location of the different tissue classes is incorporated into the segmentation procedure [29, 30]. The standard anatomical model can be obtained from statistical studies [31], in which hand-segmented MRI images for a given population of subjects are brought to a standard pose, so that the frequencies with which each tissue class appears at each standard voxel location can be computed. Then the affine and nonrigid transformation is proposed to map the standard model into the specimen to be segmented. In the first step, an affine transformation is found, so that it minimizes the sum of square differences between the intensities derived from the transformed anatomical model and the specimen. For this, a multiscale Broyden-Fletcher-Goldfarb-Shanno (BFGS) minimization algorithm was used to find the optimal affine transformation parameters A^*, b^*

$$(A^*, b^*) = \arg \min_{A, b} \sum_{r \in L} (I_R(Ar + b) - I_S(r))^2 \quad (2.2.7)$$

Thus the affine-transformed reference image is:

$$\hat{I}_R(r) = I_R(A^*r + b^*) \quad (2.2.8)$$

In the second step, a level-set based partial differential equation (PDE) scheme was used to refine the above map. By setting the initial nonrigid deformation field $V^{(0)}(r) = r$, iterate until convergence

$$V(r) = V^{(t)}(r) + (I_S(r) - \hat{I}_R(V^{(t)}(r))) \frac{\nabla \hat{I}_R(V^{(t)}(r))}{|\nabla \hat{I}_R(V^{(t)}(r))|} \quad (2.2.9)$$

$$V^{(t+1)} = S(V) \quad (2.2.10)$$

where S is a smoothing operator. Let V^* be the fixed point of this iterative procedure, and let I be an image in the atlas space. The corresponding transformed image $\hat{I}$ in the specimen space is found as

$$\hat{I}(r) = I(V^*(r)) \quad (2.2.11)$$

with $I(r) = I(A^*r + b^*)$.

2.3 NOISE REMOVAL

Noise has been considered in most applications of image processing. The local filters, such as mean filter and median filter, have been used to suppress noise for many years. The frequency domain filters are also the fundamental techniques used on medical images. Random field methods are another popular technique for medical images whose central problem is the estimation of various statistical parameters from the knowledge of image signal and the background noise. In the applications of MRI image segmentation, all of the above techniques have been used to remove noise or reduce the misclassification produced by noise. Their effects are therefore depended on the following segmentation techniques.

Lundervold and Godtliebsen [32] have used the non-linear Gaussian window filter to perform noise reduction. Goshtasby and Turner [33] have used the Gaussian filter to reduce noise on cardiac MRI images.

Gerig et al. [34] propose the nonlinear anisotropic diffusion filter to reduce the noise of MRI data. The anisotropic diffusion filtering method developed by Perona and Malik [35] as a multiscale smoothing and edge detection scheme is mathematically formulated as a diffusion process, and encourages intraregion smoothing in preference to smoothing across the boundaries. In this method smoothing is considered as a diffusive process

which can be formulated mathematically as (2.2.3). In [34] two different diffusion functions have been proposed:

$$c_1(\bar{x}, t) = \exp \left(- \left(\frac{|\nabla I(\bar{x}, t)|}{\kappa} \right)^2 \right) \quad (2.3.1)$$

$$c_2(\bar{x}, t) = \frac{1}{1 + \left(\frac{|\nabla I(\bar{x}, t)|}{\kappa} \right)^{1+\alpha}}, \alpha > 0 \quad (2.3.2)$$

The parameter κ is chosen according to the noise level and the edge strength. The 2-D procedure is implemented as:

$$\begin{aligned} \frac{\partial}{\partial t} I(\bar{x}, t) &= \nabla^T [c(\bar{x}, t) * \nabla I(\bar{x}, t)] \\ &= \frac{\partial}{\partial x} \left[c(\bar{x}, t) * \frac{\partial}{\partial x} I(\bar{x}, t) \right] + \frac{\partial}{\partial y} \left[c(\bar{x}, t) * \frac{\partial}{\partial y} I(\bar{x}, t) \right] \\ &= \frac{1}{\Delta x^2} \left[c \left(x + \frac{\Delta x}{2}, y, t \right) * (I(x + \Delta x, y, t) - I(x, y, t)) - c \left(x - \frac{\Delta x}{2}, y, t \right) * (I(x, y, t) - I(x - \Delta x, y, t)) \right] \\ &\quad + \frac{1}{\Delta y^2} \left[c \left(x, y + \frac{\Delta y}{2}, t \right) * (I(x, y + \Delta y, t) - I(x, y, t)) - c \left(x, y - \frac{\Delta y}{2}, t \right) * (I(x, y, t) - I(x, y - \Delta y, t)) \right] \\ &= \Phi_{east} - \Phi_{west} + \Phi_{north} - \Phi_{south} \end{aligned} \quad (2.3.3)$$

where $\Phi(\nabla I)$ was defined as the product $c * \nabla I$, called flow. In implementation the pixel intensities are updated by the local sum of the flow contributions:

$$\begin{aligned} I(t + \Delta t) &\approx I(t) + \Delta t * \frac{\partial}{\partial t} I(t) \\ &= I(t) + \Delta t * (\Phi_e - \Phi_w + \Phi_n - \Phi_s) \end{aligned} \quad (2.3.4)$$

The resulting iterative method is easy to implement. Guillemaud and Brady [36] also use this filter to depress the noise in their EM algorithm. They suggest that the algorithm first estimate the bias field, followed by noise filtering, finally followed by segmentation.

As one of intensity-based algorithms FCM has the shortcoming of its sensitivity to noise. For accommodating noise in FCM algorithm many researchers have presented various extensions. An early approach known as NC presented by Dave [37] takes the idea of clustering the noise data into a separate cluster which is unique from signal clusters. Obviously it is not suitable for image segmentation in which all the pixels should be assigned to the most appropriate clusters.

Krishnapuram and Keller [38] developed another similar method called possibilistic c means (PCM) by modifying the objective function directly. In this approach clustering is interpreted as a possibilistic partition and a second term is included in the objective function to force the membership to be as high as possible without a maximum limit constraint of one.

The spatial continuity constraint also has a noise suppression capability due to the adaptive smoothing operation. Tiliias and Panas [39] present a method which enhances the results of FCM by imposing spatial constraints on membership function. In this method a rule-based neighborhood system is used as post-processing to smooth the effect of noise. Acton and Mukherjee [40] propose the area open-close (AOC) and area close-open (ACO) scale spaces classification method which incorporates multiscale information to enforce spatial constraints. For images the ordinary scale space operators tend to create the new edges and drift the old ones. The Gaussian scale space [41] has increased edge localization error with increased scale. Morphological scale spaces using standard open and close filters [42] produce edge movement due to the shape of the structuring element. Scale spaces based on anisotropic diffusion [43] can produce false edges at increased scales. Comparing with above methods the AOC and ACO scale spaces possess the strong causality property which guarantees the reasonable edges.

Pham in [44] reports a new adaptive fuzzy c-means algorithm. In his method a modified objective function was proposed for incorporating spatial context into FCM.

A parameter controls the tradeoff between the conventional FCM objective function and the smooth membership functions.

Zhang and Chen [45] present an improved version of FCM by modification of the objective function. They used a different penalty term containing spatial neighborhood information in the objective function, and simultaneously the similarity measurement in the FCM, was replaced by a kernel-induced distance.

Liew et al. [46] introduced an adaptive spatial fuzzy c-means clustering algorithm. The proposed algorithm takes into account the spatial continuity constraints by using a dissimilarity index that allows spatial interactions between image voxels. The local spatial continuity constraint reduces the noise effect. A steepness parameter controls the degree of influence of the neighboring voxels on the center voxel and tries to keep important image structures.

Shen et al. [47] present a neighborhood attraction method which is based on FCM to reduce the noise. In this method an attraction entitled neighborhood attraction is considered to exist between neighboring voxels. During clustering, each pixel attempts to attract its neighboring voxels toward its own cluster. The neighborhood attraction depends on two factors: the pixel intensities or feature attraction and the spatial position of the neighbors or distance attraction. This algorithm considers the neighborhood attraction in the measurement of similarity between x_j and v_i .

$$d^2(x_j, v_i) = \|x_j - v_i\|^2 (1 - \lambda H_{ij} - \xi F_{ij}) \quad (2.3.5)$$

where H_{ij} represents the feature attraction and F_{ij} represents the distance attraction. The two parameters λ and ξ are between 0 and 1, and are used to adjust the degree of the two neighborhood attractions.

$$H_{ij} = \frac{\sum_{k=1}^S u_{ik} g_{jk}}{\sum_{k=1}^S g_{jk}} \quad (2.3.6)$$

where g_{jk} is the intensity difference between the study pixel j and its neighbor pixel k , defined by

$$g_{jk} = |x_j - x_k| \quad (2.3.7)$$

u_{ik} is the membership of neighboring pixel k to the i th cluster, and S is the number of neighboring pixels

$$F_{ij} = \frac{\sum_{k=1}^S u_{ik}^2 q_{jk}^2}{\sum_{k=1}^S q_{jk}^2} \quad (2.3.8)$$

where q_{jk} is the relative location between pixel j and its neighborhood pixel k .

A neural-network model is proposed to optimize the two parameters λ and ξ which control the degree of attraction.

2.4 BIAS FIELD ESTIMATION AND CORRECTION

The estimation and correction of the spatial intensity inhomogeneity or bias field from MRI images is difficult because the inhomogeneities could change with different MRI acquisition parameters from patient to patient and from slice to slice. In the last decade, a number of algorithms have been proposed for the intensity inhomogeneity estimation and correction.

2.4.1 Early Approach

Early methods for intensity inhomogeneity estimation and correction used prior acquisition of a phantom image to empirically measure the bias field [48], [49]. Wicks et al. [50] proposed a method based on the signal produced by a uniform phantom to correct MRI images of any orientation. Furthermore, Tincher et al. [51] model the bias field function by a second-order polynomial and fitted it to a uniform phantom-scanned MRI image. They observed that an examination of the eigenvalues of the singular value decomposition (SVD) can reduce further the number of degree of freedom for the fit that need to be considered. However, all such approaches based on a prior phantom acquisition have the drawback that the geometry relationship of the coils and the image data is typically not available with the image data. They also require the same acquisition parameters for the phantom scan and the patient. In addition, these approaches assume that the intensity corruption effects are the same for different patients, which is not valid in general [52]. In a similar vein, bias correction methods have been proposed for surface coil MR imaging, using an analytic correction of the MR antenna reception profile [53], but these suffer from the same drawbacks as phantom-based methods.

While bias field correction is needed for good segmentation, many approaches have exploited the idea that a good segmentation helps to estimate the bias field. Meyer et al. [54] presented an edge-based segmentation scheme to find uniform regions in the image followed by a polynomial surface fit to those regions. The result of their correction is, however, very dependent on the quality of the segmentation step. They used Liou-Chiu-Jain (LCJ) segmentation algorithm [113,114] because it is assumed that the original image is piecewise-constant, and so they suppose that each region found by the LCJ algorithm corresponds to a constant value. That is, they assume that the LCJ algorithm

may over-segment a tissue class but that it will not group together voxels from two different tissue regions. Obviously this is a requirement too tough to meet.

Dawant et al. [55] developed a two-step approach for estimation of bias field: first, “reference points” are selected for at least one tissue class throughout the image, then a thin-plate spline is least-square fitted to the reference point data. They suggest that the coefficient of variations as a measure for the degree of restoration. The selection of reference points is either done manually, or by a tissue classification algorithm after a partial classification. They find that expert selection of reference points can give better results than automatic selection; but that it is prone to errors when points are mislabeled.

The homomorphic filtering approach to remove the multiplicative effect of the inhomogeneity has been commonly used due to its easy and efficient implementation [9]. However, high image contrasts that generate filtering artifacts and the overlapping of the patient data and the bias field frequency spectrums limit the efficiency and feasibility of this approach [51, 55]. Image blurring [48], smoothing [56], averaging [57], and Fourier domain filtering [58] were also considered, while the use of homomorphic unsharp masking, matching the local and global median or mean, was reviewed and optimized in [59].

Wang et al. [60] used the histogram matching method which is based on minimizing the windowed square residual difference to correct the interexamination variations. Brechbühler et al. [61] propose a parametric bias estimation method which fits polynomials to image data by using multiple-valley criterion functions instead of least squares.

Sled et al. [62] developed a nonparametric approach. Described as nonparametric nonuniform intensity normalization (N3), the method is independent of pulse sequence and insensitive to pathological data that might otherwise violate model assumptions. Their method also modeled the intensity inhomogeneity as a smooth multiplicative field

and change to an additive one by taking a logarithm. Making the approximation that the log-transformed real image intensity and bias field are independent or uncorrelated random variables, the distribution of their sum is found by convolution as follows:

$$P_y(y) = P_b(y) * P_x(y) = \int P_b(y-b)P_x(b)db \quad (2.4.1.1)$$

where P_y , P_x , and P_b be the probability densities of y , x , and b , respectively. From this equation, the inhomogeneity distribution can be viewed as blurring the real intensity distribution. After the computation of bias field estimate they take a B spline to smooth the field which can decrease the effect of unperfect model and noise.

Styner et al. [63] developed a parametric method to correct the bias field. The estimated bias field is modeled by products of Legendre polynomials and the tissue class in the image is modeled by a mean intensity and a variance. To get a more robust estimation which is less sensitive to outliers, a valley function is selected to substitute the least squares technique. Then the estimation of the parametric bias field is formulated as a nonlinear energy minimization problem using an evolution strategy.

2.4.2 Stochastic Approach

A different approach used to segment images with intensity inhomogeneities is to simultaneously compensate for the bias field while segmenting the image. This approach has the advantage of being able to use intermediate information from the segmentation while performing the correction. Geman and Geman [64] are the first to make an analogy between images and statistical mechanics systems. They apply a stochastic relaxation algorithm, Gibbs distributions, and the Bayesian restoration for image segmentation.

For the problem of intensity-based image classification one of the most popular methods is using the expectation-maximization (EM) algorithm [95]. This approach starts from a parametric statistical model for MR brain images, typically using Gaussian

intensity models for each of the tissue under consideration, and estimates the tissue classification and the model parameters simultaneously by interleaving between these two [96, 97, 98].

Wells et al. [65] developed a statistical approach based on the expectation-maximization (EM) algorithm to estimate the bias field and the tissue classification iteratively. The observed MRI signal is modeled as follows:

$$Y_i = X_i B_i + N_i \quad (2.4.2.1)$$

where Y_i is the given image intensity at voxel i ; X_i is the image intensity to be “restored” by the segmentation algorithm; B_i is the slowly varying bias field and N_i is the image noise. Ignoring the noise, they use the logarithm to convert the relationship of bias field and real tissue intensity from product by addition.

$$y_i = x_i + b_i \quad (2.4.2.2)$$

Then they model the distribution of observed intensities as a normal distribution (include an explicit bias field)

$$p(y_i | \Gamma_i, b_i) = G_{\psi_{\Gamma_i}}(y_i - \mu(\Gamma_i) - b_i) \quad (2.4.2.3)$$

where

$$G_{\psi_{\Gamma_i}}(x) \equiv (2\pi)^{-m/2} |\psi_{\Gamma_i}|^{-1/2} \exp\left(-\frac{1}{2} x^T \psi_{\Gamma_i}^{-1} x\right)$$

is the m -dimensional Gaussian distribution with variance ψ_{Γ_i} , and Γ_i is tissue class at the i th voxel; $\mu(x)$ is mean intensity for tissue class x ; ψ_x is covariance matrix for tissue class x ; and the bias field is modeled by a n -dimensional zero mean Gaussian prior probability density.

$$p(b) = G_{\psi_b}(b) \quad (2.4.2.4)$$

where

$$G_{\psi_b}(x) \equiv (2\pi)^{-n/2} |\psi_b|^{-1/2} \exp\left(-\frac{1}{2} x^T \psi_b^{-1} x\right)$$

Thus the whole MR intensity distribution can be modeled as a Gaussian mixture

$$p(y|b) = \prod_i p(y_i|b_i) \quad (2.4.2.5)$$

where

$$p(y_i|b_i) = \sum_{\Gamma_i} p(y_i, \Gamma_i|b_i) = \sum_{\Gamma_i} p(y_i|\Gamma_i, b_i)p(\Gamma_i)$$

and using Bayes' rule they obtain the posterior probability of the bias field by giving observed intensity data.

$$p(b|y) = \frac{p(y|b)p(b)}{p(y)} \quad (2.4.2.6)$$

Now the problem changes to given observed intensity data, estimate the value of bias field to get the largest posterior probability. A zero-gradient condition on the logarithm of the posterior probability is used to assess this maximum. Now EM algorithm can be used to obtain bias field estimation and tissue classification iteratively.

However, this method has a number of problems. First of all, like all optimization techniques, the EM algorithm sometimes converges to a local minimum value which is far from the desired result, as described in [36]. Second, all the classes have been modeled as the Gaussian distribution in this method, but this is not true and has produced misclassifications. Third, this method does not regard neighborhood dependencies for the tissue segmentation and hence the quality of this type of segmentation degrades rapidly if noise is present in the data. Fourth, this method has included too many parameters which need to be chosen manually or by use of estimation. All of the above restrict the use of this method. So some researchers begin to refine this method.

Guillemaud and Brady [36] firstly improved this approach by introducing an extra class "other" with a non-Gaussian probability distribution. This new extra class is intended to gather all the pixels which are far from the Gaussian distributions of the identified tissue classes. So the grey level probability density on the image becomes:

$$p(Y_i|\beta_i) = \sum_{\Gamma_j \text{ is Gaussian}} p(Y_i|\Gamma_j)p(\Gamma_j) + \lambda \cdot p(\Gamma_{other}) \quad (2.4.2.7)$$

where λ is a constant. With the new distribution they obtain two equations:

$$W_{ij} = \frac{p(Y_i | \Gamma_j, \beta_i) p(\Gamma_j)}{\sum_{\Gamma_j} p(Y_i | \Gamma_j, \beta_i) p(\Gamma_j)} \quad (2.4.2.8)$$

$$\beta = HR \quad (\text{styner} 2.4.2.9)$$

where

$$R_i = \sum_{\Gamma_j - \Gamma_{\text{other}}} W_{ij} \psi_j^{-1} (Y_i - \mu_j)$$

Equation (2.4.2.8) is the probability with a bias-corrected voxel i belonging to a particular tissue class j . In Equation (2.4.2.9), the bias field is derived by applying a linear operator H to the mean residual field which is estimated only with respect to the Gaussians classes.

$$H = [\psi^{-1} + \psi_{\beta}^{-1}]^{-1} \quad (2.4.2.10)$$

In their algorithm H is implemented as linear lowpass filter. In addition, they also explore the possibility of using the minimum entropy to automatically choose the number of tissue classes and the associated parameters. But this EM approach requires a good initial guess for either the bias field or the classification estimation. Otherwise it could be easily trapped in a local minimum, resulting in an unsatisfactory solution.

Some researchers use markov random field (MRF) as a convenient means for introducing context or neighborhood effect in the classification. Held et al. [66] continue to refine the adaptive segmentation algorithm described by Wells et al. [65]. They combine the following three characteristics in their method. First of all, tissue intensities are modeled as nonparametric distribution of Parzen-window statistics [67].

$$p(z | x, y) = \frac{1}{n_{x_i}} \sum_{k=1}^{n_{x_i}} \frac{1}{(2\pi)^{d/2} |\Sigma|^{1/2}} \exp\left(-\frac{1}{2} (y_i z_i - \bar{z}_{k, x_i})^T \Sigma^{-1} (y_i z_i - \bar{z}_{k, x_i})\right) \quad (2.4.2.11)$$

For every tissue class $\bar{x}$ a set of $n_{\bar{x}}$ training points $\bar{z}_{k,\bar{x}} (k = 1, \dots, n_{\bar{x}})$ is selected by a supervisor. Secondly, the spatial correlation within the segmented image is modeled as a markov random field to manage the noise data. The MRF is a statistical process that specifies the local characteristics of an image and is combined with the given data to reconstruct the true image. It is a conditional probability model, where the probability of a voxel depends on its neighborhood, and equivalent to a Gibbs joint probability distribution [64] determined by an energy function.

$$p(x) \propto e^{-E(x)} \quad (2.4.2.12)$$

with the Gibbs energy

$$E(x) = \sum_{\langle i, j \rangle} e_{x_i, y_j}$$

where $\langle i, j \rangle$ denotes the sum over all voxels i and their neighbors j . The local potential e_{x_i, y_j} is the most general potential between two voxels. It must be minimal for neighboring voxels of the same tissue ($x_i = x_j$) to prefer equal segmentation at neighboring voxels. Thirdly, signal inhomogeneities are also modeled by a priori MRF:

$$p(y) \propto e^{-U(y)} \quad (2.4.2.13)$$

with the Gibbs energy

$$U(y) = \alpha \sum_{\langle i, j \rangle} (y_i - y_j)^2 + \beta \sum_i y_i^2$$

For given MR intensities z , Bayes rule is used to calculate the posteriori probability of the segmentation x and the bias field y

$$p(x, y | z) \propto p(z | x, y) p(x) p(y) \quad (2.4.2.14)$$

They use the simulated annealing (SA) and iterated conditional modes (ICM) to estimate the maximum a posteriori (MAP) of the true image and the bias field. Their results are better than original one [65], but it still has some problems. Since the conditional probability of observing the intensity z for given segmentation x and bias field y is

modeled by a Parzen-window distribution. Their method needs a supervisor to select a set of training points for every tissue class, which may result in segmentations that are not fully objective and reproducible. Because they use MRF to model spatial correlation within bias field and the real image intensity, the exact computation of the optimal segmentation becomes too complicated or we can say intractable.

Rajapakse and Kruggel [69] also use the MRF to model the piecewise contiguous nature of the segmentation. In their method noise and bias field are explicitly incorporated in a measurement model.

$$y_i = (1 + \beta_i)\mu_{x_i} + \eta_i \quad (2.4.2.15)$$

where μ_{x_i} denotes the mean intensity of the tissue class, η_i denotes the random noise signal and β_i represents the variation of the gain of the intensity due to the intensity inhomogeneities at the site i . The tissue classes are modeled with Gaussian distributions and the prior model of the segmentation is considered to be a MRF which models the piecewise contiguous nature of the image elements considering that the adjacent voxels are more likely to have similar constituents and belong to the same tissue class.

$$p(x) = \frac{1}{Z} \exp \left\{ - \sum_{c \in C} V_c(x) \right\} \quad (2.4.2.16)$$

where Z is the normalizing constant and the summation is taken over the prior potentials $V_c(x)$ for the set of cliques C over the image. A clique is a set of voxels that are neighbors of one another. They assume that the noise is class-conditional and that the distribution for each class to be additive, random, white and Gaussian and consider the bias field to be multiplicative with the tissue intensities and depend on the location. Then a local minimum of the associated energy function in the posterior probability is sought as an approximation to the optimal segmentation using a greedy algorithm based on the iterative conditional modes (ICM) algorithm.

Leemput et al. [70, 71] develop a generalized EM algorithm (GEM) for bias field correction. Contrasting with Wells' method, they share the same idea to model each class by a normal distribution and use the mixture Gaussian distribution to express the image. But Wells used the constant parameters of mean and variance for each tissue class while Leemput uses the variable parameters which will change in the algorithm implementation. They derive the parameter estimators for normal distribution mean μ and variance σ^2 .

$$\mu_j = \frac{\sum_i y_i p(\Gamma_i = j | y_i, \theta)}{\sum_i p(\Gamma_i = j | y_i, \theta)} \quad (2.4.2.17)$$

$$\sigma_j^2 = \frac{\sum_i p(\Gamma_i = j | y_i, \theta) (y_i - \mu_j)^2}{\sum_i p(\Gamma_i = j | y_i, \theta)} \quad (2.4.2.18)$$

where $\Gamma_i \in \{j | j = 1 \dots K\}$ is the tissue class at position i and $\theta_j = \{\mu_j, \sigma_j\}$ is the distribution parameters for class j . These equations were used to update the parameters iteratively in the EM algorithm. Another difference between them is the model of bias field. Wells also used the Gaussian distribution while Leemput used a linear combination of smooth basis functions to model the inhomogeneity. So their approach includes three steps, iterating between tissue classification (step 1), class distribution parameter estimation (step 2), bias field estimation (step 3) and the likelihood increases iteratively. Considering the special image background they add an explicit model of logarithm Rayleigh distribution for the background noise. They also use a digital brain atlas to initialize a priori estimate of the class probabilities for each voxel and class.

Zhang et al. [72] extend the previous methods by using the hidden markov random field model, which is a stochastic process generated by a markov random field whose state sequence cannot be observed directly but which can be observed through a field of

observations. This spatial dependent model is used to substitute Wells' finite Gaussian mixture model in which the individual voxels are considered to be independent samples drawn from a population. Then MRF-MAP estimation is proposed to recover and classify the true image from the observed image. Obviously this type of MAP estimation presents a computationally infeasible problem and therefore the ICM algorithm is adopted to find an approximation solution. The EM algorithm is also used to do model fitting which is a procedure for estimating the unknown parameters of the statistical model. For the bias field correction, Guillemaud and Brady's algorithm is incorporated into the above framework.

Marroquin et al. [73] continue to develop a new Bayesian method for automatic segmentation of MRI brain images. The main features of their method are :

- 1) They use separate parametric, smooth models for the intensity of each class instead of a single multiplicative bias field that affects all tissue intensities. So this avoids the need for a logarithmic transformation and, hence, the related nonlinear distortions.
- 2) They also use the digital brain atlas, together with a robust registration procedure to find a nonrigid transformation that maps the standard brain to the specimen to be segmented. This transformation is then used to segment the brain from nonbrain tissue; compute prior probabilities for each class at each voxel location and find an appropriate automatic initialization.
- 3) They use a variant of the EM algorithm. The classical EM algorithm consists of an (E) step in which one first computes the expected value of vector of tissue classification given an estimate of the model parameters, and a (M) step in which one maximizes the posteriori probability by adjusting the model parameters, given the expected value of tissue classification. In the E step the expected value is equal to the given posterior marginal probabilities. They use a different approach to obtain the marginal probabilities by solving a set of decoupled, linear equations. Then in the M step, they

use a model to obtain the optimal parameters by solving a system of linear equations. So the whole procedure becomes computationally efficient.

2.4.3 Fuzzy Clustering Method

Another approach based on the fuzzy clustering technique [87] has been used for image segmentation in general [74, 75, 76] and also in segmenting MR images [77-81, 89]. Like any other intensity-based segmentation methods the fuzzy clustering approach is also sensitive to the intensity inhomogeneities of MR images which make many voxels misclassified.

A fuzzy rule-based system is proposed by Tolias and Panas [39] to impose spatial continuity on Fuzzy c-means. They also used a small positive constant to modify the membership of the center pixel in a 3×3 window in another paper [88].

Pham and Prince [82] extend the traditional fuzzy c-means (FCM) algorithm to deal with intensity inhomogeneities of MR images. They change the FCM objective function to model the variation in intensity values via a multiplicative bias field applied to the cluster centroids. In their objective function first- and second- order regularization terms are used to ensure that bias field is spatially smooth and slowly varying. The computation of the bias field is formulated as a variational problem and the bias field is estimated at every voxel using a multigrid algorithm. Their method, however, is computationally intensive.

To solve the problem of computational complexity of Pham and Prince, Ahmed et al. [83] consider another effective way to modify the objective function of FCM. They propose a modification of the objective function by introducing a term that allows the labeling of a voxel to be influenced by the labels in its immediate neighborhood. However their method has the problem that no constraint is put on bias field.

Pham [90] proposed another approach to penalize the FCM objective function to constrain the behavior of the membership functions, similar to methods used in the regularization and Markov random field theory.

Zhu and Jiang [84] present a multicontext fuzzy clustering method to eliminate the adverse impact of intensity inhomogeneities in MR images. In their method the input images are separated into nonoverlapping small parts so that the FCM algorithm could be performed in a local way. The information fusion is used to keep the classifications spatially continuous and statistically reliable.

Suckling et al. [91] propose a moving window method to deal with bias field. Weighted fuzzy-clustering algorithm is implemented in a moving window regime. Starting in the most superior planes, fuzzy clustering is invoked using data only within the window and the window is then moved from the upper to the lower part of the image by half the window width.

Liew and Yan [46] continue to extend the fuzzy c-means clustering algorithm by taking into account the spatial continuity constraints. They define a dissimilarity index to measure the dissimilarity between voxels and the cluster centroids. A weighting factor is used to control the degree of influence of the neighboring voxels in computing the dissimilarity index. For estimating the intensity inhomogeneities the log of multiplicative bias field is modeled by a stack of smoothing B-spline surfaces and calculated by a two-stage algorithm. The objective function is therefore modified to include the first regularizing term which minimizes the thin plate energy of each of the spline surfaces and the second regularizing term which forces smoothness between slices of spline surfaces. These two regularizing terms allow the spline surfaces to be estimated slice by slice, resulting in smoothness of each individual slice.

Zhang and Chen [85] propose a kernelized fuzzy c-means method to tackle the intensity inhomogeneities of MR images. They modified the objective function by

using the Gaussian radial basis function kernel. This kernel function map the original Euclidean distance to a higher dimensional kernel feature space with a non-linear transform. Neighborhood effect is also included in objective function to take the spatial constraints. One parameter is used to control the steepness of Gaussian mapping. Another parameter is used to control the neighborhood constraints. Their method is not including an explicit bias field model, but removing the bias field by kernelized non-linear transform and spatial constraints. Because the computation time for Gaussian radial basis function kernel is long, their method is time consuming.

Following their method, Liao and Lin [115] propose a Gibbs Random Field model to constraint the spatial continuity with the same kernel above in [85]. But the GRF model makes their method spending longer time.

Saha and Bandyopadhyay [116] propose a fuzzy symmetry based genetic clustering method to segment the MRI images. They use a new point symmetry distance to substitute the Euclidean distance. The new distance includes the neighborhood effect in its definition, which is also used to remove the bias field. Then they use the genetic method to calculate the cluster number which is constant in other algorithms.

Zhou and Bai [117] propose a combined method including atlas registration, fuzzy connectedness, and parametric bias field correction, to segment the MRI images. Their parametric bias field correction method is the same as Styner et al. [63].

2.5 PARTIAL VOLUME SEGMENTATION

So far all of the above reviewed methods assume that each voxel belongs to a signal specific tissue type. However, in MR images the complexity of tissue boundaries causes many voxels to contain mixtures of tissues. Niessen et al. [94] showed that consistently misplacing the tissue borders in a 1mm isotropic brain MR image with only a

single voxel in each slice resulted in volume errors of approximately 30%, 40%, and 60% for white matter, gray matter and CSF, respectively. The accuracy of classification methods is, therefore, deeply influenced by these “blurring” regions, especially when lower resolution images are used. This is so-called the partial volume effect problem.

Choi et al. [99] present a statistical mixture voxel model based on Markov random field and an algorithm for the classification of these mixtures. They model the mixture voxel as an n -dimensional random variable which sums up to 1 for its components. The MRF is used to express the idea that neighboring voxels are similar to one another and is formulated as Gibbs distribution. Then a variant of iterated conditional modes (ICM) is used to identify combinations of tissues for each voxel. But a single measurement taken within a voxel to represent its contents limits its accuracy.

Santago and Gage [100] address a statistical model of partial volume effect together with a finite mixture density description of the tissues. In their method each voxel can be written as the weighted sum of its mixture tissues plus the Gaussian noise and a finite mixture density (the sum of Gaussians) is used to model the histogram of the voxel values. Then the distance minimization method is used by fitting the mixture density model to the histogram of the brain data to get the optimal parameters for segmentation.

Laidlaw et al. [102] propose a Bayesian probability approach to estimate the highest-probability combination of mixture tissues within each voxel-sized region. This method also uses the histogram fitting, but information from neighboring voxels is incorporated into the classification process. They treat each voxel as a region and reconstruct a continuous function from the samples. The histograms over the voxels are also calculated from this function. They continue to derive basis functions that model histograms of voxels containing a pure tissue and of voxels containing a mixture of two tissues. Linear combinations of these histograms are fit to each voxel, and the most likely combination of tissues is chosen probabilistically.

Pham and Prince [103] deal with the partial volume effects of single-channel image data based on a statistical image model and maximum a posteriori estimation method. The original image is assumed to be blurred by the point spread function, point sampled, and additive noise in the image acquisition process. Then they define the tissue spread function to be the convolution of the characteristic function for one tissue and the point spread function. From this model the tissue class means and the tissue spread coefficients are estimated from MAP estimation.

A Markov random field method using partial volume modeling is presented to classify brain tissues of MR images by Ruan et al. [104]. In their algorithm the intensity value of a mixture voxel is represented by the weighted sum of pure tissues. The algorithm includes two steps: firstly it segments the brain into pure and mixclasses using the mixture model; then they reclassify the mixclasses into the pure classes using the knowledge obtained about pure classes. Both steps use MRF models and classifications are achieved by using MAP estimator.

Shattuck et al. [105] describe a sequence of low-level operations to classify MR brain tissues including the partial volume model. The measurement model uses mean tissue intensity and noise variance values. The Potts model, a Markov prior which specifically models local spatial interaction, is used to ensure the local continuity. From the Bayes's formula a MAP classifier is formulated and ICM algorithm is developed to find the optimal labeling.

Leemput et al. [106] propose a statistical framework for partial volume segmentation based on the expectation-maximization approach. An additional downsampling step which causes partial volume effects along the borders between tissues is introduced and the intensity distribution model for mixture voxels is given by the sum of the normal distributions of all nonpure mixtures. Then the MRF and EM algorithm is used to find

the parameters that maximize the likelihood of the data and estimate the tissue fractions in each voxel.

2.6 CONCLUDING REMARKS

While considerable progress has been made over the past few years, a significant number of challenging problems are still open. One of these issues is fully unsupervised automatic classification of MR images. In this chapter, a literature survey on these issues was presented. The survey focuses on the methods used to deal with the inherent obstacles from MR imaging. It is obvious that the statistical methods and fuzzy clustering methods play an important role in MR image segmentation. However the solutions for the noise removal, intensity inhomogeneities correction and partial volume labeling are still unsatisfactory. Author has developed a FCM based novel approach which successfully removes the noise, and corrects the bias field. The proposed modified FCM algorithm is described in the next chapter.

Chapter 3

The Fuzzy Clustering Algorithm

3.1 INTRODUCTION

MR image classification is an important pattern recognition problem since quite often human life is at stake. The major subjects in pattern recognition are about feature analysis, clustering, and classifier design. Clustering is one of most primitive mental activities of humans used to handle the huge amount of information that they receive every day. Humans tend to categorize entities into clusters. Each of them is then characterized by the common attributes of the entities it contains. In a word a cluster consists of a number of similar objects which are grouped together and clustering procedures yield a description of clouds of data in terms of clusters that possess strong internal similarities. Therefore, clustering approaches can be used to discover the similarities and differences among input data and then to derive useful conclusions about them. Clustering given input data consists of dividing the data into clusters and establishing the cluster centers and cluster boundaries. An a priori knowledge of the number of clusters and their approximate distributions definitely simplifies the task. Otherwise, the unsupervised clustering method is required to determine the number of clusters in the class.

In MR image classification the number of classes is generally taken as the *a priori* information. The tasks of MR image segmentation are therefore simplified to find the

different tissue features and label the voxels with different classes. One such algorithm is fuzzy c-means which uses a minimum-distance classifier to determine the cluster center and computes the voxel's similarities iteratively. Theoretically different tissues should be shown in different grey levels on MR images. But noise and intensity inhomogeneity often make their grey levels overlapping completely, even transforming to frequency domain is no help. Most of researchers use spatial constraints to solve this problem according to the assumption that bias field is smooth and slowly varying. Some of them assume that the overlapping grey levels are composed by several Gaussian distributions. Each distribution denotes one tissue. Sometimes bias field model is also included in algorithm explicitly. But the intensities of tissue are not always fitting Gaussian distribution. Using spatial information to distinguish different tissue voxels which have the same intensity has become overwhelming thought in researchers. All kinds of spatial continuity constraints are proposed in algorithms. In this chapter, a modified fuzzy c-means algorithm is proposed. It can overcome some shortcomings of the existing fuzzy clustering methods. There are three new aspects in the proposed algorithm. Using a fuzzy filter for the noise removal at a pre-processing step is the first. The noise is always annoying in classification algorithms. The heavy noise even destroys the spatial continuity and makes the spatial constraint models ineffective in MR image segmentation. Hence, before the segmentation a special fuzzy filter is used to remove the noise. This filter can restore the image from noise or at least downgrade it to harmless level and therefore improving the segmentation accuracy.

The second is the modified generalized objective function developed for the FCM algorithm. In this objective function, bias field is included in observed MRI image model explicitly. After logarithm transforming this model becomes the addition of the true log-transformed intensities and the log-transformed bias field. The MR image segmentation and the bias field estimation and correction could be implemented iteratively.

The third new aspect is that a mean spread filter is used to perform the spatial continuity constraint and therefore avoid the misclassification. Different with other FCM algorithms the bias field is expressed explicitly in our objective function so that the spatial constraint could be forced on it. The smoothness of the bias field is an important property and has been used for estimation and correction of intensity inhomogeneity by many approaches. In our proposed constraint method the misclassification voxels are inspected with doubtful bias values. These voxels are pushed to the correct cluster centers by smoothing the doubtful bias values to its neighborhood. With this filter the bias field could be corrected and estimated while the voxels could be classified to the right tissue types. Because our filter is only implemented on doubtful parts of the image, the computing time is reduced. Hence, by using the spatial continuity constraints incorporated with the MRI image model, our proposed algorithm could segment the MR images and estimate the bias field simultaneously.

The organization of this chapter is as follows. First of all, a literature review of fuzzy clustering algorithms is presented in Section 3.2. In Section 3.3, the preprocessing stages for head segmentation and noise filter are introduced. In Section 3.4, the MR image model is presented and the modified fuzzy c-means algorithm based on the generalized objective function is developed. Section 3.5 presents the mean spread filter for smoothing the bias field. Experimental results on synthetic images, synthetic phantoms and simulated 3-D brain images are presented in Section 3.6, 3.7, and 3.8 respectively. In Section 3.9, the proposed modified spatial fuzzy c-means algorithm is applied to the real MR images and the quantitative evaluations and comparisons are given. Finally, some concluding remarks are given in Section 3.10.

3.2 LITERATURE REVIEW – FUZZY CLUSTERING

The review of fuzzy clustering methods focuses on fuzzy c-means families.

3.2.1 Prototype-Based Clustering

In prototype-based clustering methods, the c-means (or k-means) families are the best known and most well developed families of batch clustering models probably because they are least squares models. The history of this methodology is long and important in applied mathematics because least-squares models have many favorable mathematical properties. In the c-mean families each class is represented by a proto-typical point, known as the prototype. Each data point, such as an input pattern, belongs to a class with a degree of likelihood as indicated by its membership in the interval $[0, 1]$. Distance between an input pattern and a prototype is usually used as an optimizing measure in the objective function. Optimization is often performed by minimization of such distances over all the data points and prototypes.

The aim of a c-means clustering algorithm given a set of data $X = x_1, \dots, x_n, x_i \in R^d$ is to divide it into c self-similar groups ($c \geq 2$). These groups form a c -partition of X . A real $(c \times n)$ matrix U can be used to succinctly represents the results of a cluster analysis of X by interpreting u_{ik} as the degree to which x_k belongs to cluster i . A family of c -partitions is derived from the interpretation of U : hard, fuzzy and possibilistic (we mainly discuss the fuzzy one here). There are three main advantages of this objective-function based fuzzy clustering. The first is that the data points can move from one cluster to another to minimize the objective function. The second is that the knowledge about the shape or size of the clusters can be incorporated by using an appropriate distance measure in the objective function. Here, the size of a cluster means the number of data points in the cluster. The third is that the overlapping of the clusters is taken into account and partial belongingness of the object to all the clusters is allowed.

The higher the degree of membership of an object to a cluster more similar is this object to the prototype of this cluster.

The fuzzy c-means families

Fuzzy c-means (FCM), proposed by J.C.Bezdek [107], is a simple and well-known fuzzy clustering algorithm. There are many variants of the FCM algorithm, which can be considered as parts of the FCM families. Basically, the FCM families share a fuzzy c-prototype form [108]. For a set of N input patterns, i.e. the data set $X = \{x_k \in \mathbb{R}^n, k = 1, 2, \dots, N\}$, and let c be the number of clusters, then

$$J_m^f(U, P; X) = \sum_{i=1}^c \sum_{k=1}^N (u_{ik})^m D(P_i, x_k) \quad (3.1)$$

where, $m \in [1, \infty)$ is a weighting exponent on the fuzzy membership function. It is used to control the influence of intermediate membership values in the objective function. $P = \{P_1, P_2, \dots, P_c\}$ are the clusters formed by the input pattern X . $D(P_i, x_k)$ is some measures of similarity (error, proximity, etc.) between the cluster P_i and x_k . $U = \{u_{ik}\}$ is a fuzzy c-partition of X , i.e. the fuzzy membership matrix. u_{ik} denotes the grade of membership of the input pattern x_k in the cluster P_i . It should satisfy the following conditions:

$$\begin{aligned} 0 &\leq u_{ik} \leq 1 \forall i, k, \\ \sum_{i=1}^c u_{ik} &= 1 \forall k, \\ 0 &< \sum_{k=1}^N u_{ik} < N \forall i. \end{aligned} \quad (3.2)$$

Normally $D(P_i, x_k)$ is a norm metric. So Equation (3.1) can be rewritten as follows,

$$\begin{aligned} J_{m,p}^f(U, V; X) &= \sum_{i=1}^c \sum_{k=1}^N (u_{ik})^m \left\{ \|x_k - V_i\|_p \right\}^p \\ &= \sum_{i=1}^c \sum_{k=1}^N (u_{ik})^m \left[\sum_{j=1}^n |x_{kj} - V_{ij}|^p \right] \end{aligned} \quad (3.3)$$

where, $p \geq 1$. $V = V_i \in \mathbb{R}^n, i=1,2,\dots,c$ are the prototypical points corresponding to the clusters $P = \{P_i, i=1,2,\dots,c\}$. If an input pattern x_k belongs to the cluster P_i , it means that the distance between x_k and V_i is the smallest. If the 2-norm distance ($p=2$) is used to measure the similarity, it is then the well-known FCM algorithm. The simplified standard FCM objective function is

$$J(U,V;X) = \sum_{i=1}^c \sum_{k=1}^n u_{ik}^m \|x_k - v_i\|^2 \quad (3.4)$$

where c is the number of cluster centers or data subsets; n is the number of data sets; m is the weighting exponent; u_{ik} is the fuzzy membership value of pattern k in cluster i ; x_k is the k th data; v_i is the cluster center for class i in feature space; U is the $c \times n$ fuzzy c -partition matrix, the element is u_{ik} ; V is the matrix of prototypes of the clusters; X is the input data set.

The above FCM algorithm uses iterative operation to get U , V and finally minimizes the objective function. The algorithm is described as following:

1. Fix the number of cluster c ;
2. Initialize the prototypes matrix of the clusters V ;
3. Calculate the fuzzy c -partition U with V ;

$$u_{ik} = \left(\sum_{j=1}^c \left(\frac{\|x_k - v_i\|}{\|x_k - v_j\|} \right)^{\frac{2}{m-1}} \right)^{-1}; \forall i, k \quad (3.5)$$

4. Update V ;

$$v_i = \frac{\sum_{k=1}^n u_{ik}^m x_k}{\sum_{k=1}^n u_{ik}^m}; \forall i \quad (3.6)$$

5. Repeat steps 3, 4 till termination. The termination criterion is as follows:

$$\|V_{new} - V_{old}\| < \varepsilon \quad (3.7)$$

where $\|\cdot\|$ is the Euclidean norm and ε is a small number that can be set before the computation.

3.2.2 Remarks on FCM

In the past several decades fuzzy clustering algorithm has been proved to be an excellent classification approach and solve many problems. Considering the noise, intensity inhomogeneities and partial volume effect it is hard to say which model the tissue class should fit in MR image segmentation. The least squares model used by fuzzy clustering is therefore a good measurement and easy implementation choice. The following discussions are about various aspects of the point prototype c-means models. The first is the choice of parameters. In MR image segmentation the number of classes c is generally taken as the *a priori* knowledge. The weighting exponent m controls the degree of fuzziness exhibited by the soft boundaries in the fuzzy c-partition U . Normally the weighting exponent m is chosen in the range $[1.1, 5]$, with $m = 2$ an overwhelming favorite.

The second is the choice of norms. In MR image segmentation the published results do not indicate a clear advantage for any distance. The images themselves take the final decision about which distance will provide the best results. Actually in most published methods Euclidean distance is the overwhelming favorite, probably because human beings can perceive it more comfortable.

Initialization is also important because many examples have illustrated that different starting points will produce different solutions in FCM. There is no general agreement about a good initialization in MR image segmentation. But initializing the cluster centers of different classes with the same value should be strictly prohibited since this algorithm cannot subsequently change them unless there is a roundoff error that upsets

equality. The normally used methods include the output of the other classification algorithm, the analysis of image histogram, the *a priori* knowledge about different tissues etc.

The termination of FCM algorithm is affected by both the measurement of $\|\cdot\|$ and ε in the termination criterion. The Euclidean norm is normally used by most researchers as the measurement of $\|\cdot\|$. The choice of ε controls the duration of iteration and relies on the proposed methods and input data sets. In addition to ε the maximum iteration is often used to stop the algorithm. The choices of initialization and termination with the prototypes matrix of the clusters V or the fuzzy c-partition U are both acceptable and the only difference is about storage and speed.

3.3 HEAD SEGMENTATION AND NOISE REMOVAL

3.3.1 Head Segmentation

MR images provide details of living tissues, and is used for both brain and body studies. The MRI regions of interest (ROI) are often examined in details. In the MRI head scans the ROI is the human brain. Segmenting the brain from the head scans is a special topic in MR image segmentation. Various methods have been proposed, but MRI head scans are so different that no one can fit them all. Comparison between these methods is also difficult because most of them use different data set. According the fitness, efficiency, and experience we use the combined method of Atkins' [22] and Ardekanis' [24] to discard other parts of the head and focus our work on ROI in this thesis.

In first stage, we remove background noise using a threshold which is estimated by locating the immediate local minimum after the first mode in the smoothed histogram of the MR volume. In MR T1 image with gray level from 0-255, the intensities below 30 will be removed. Then we use the standard erosion and dilation morphological operations

to remove the speckles outside the head region and within the head. In our application the square structure element with width 3 or 4 is used.

In the second stage, we use an anisotropic diffusion filter [34] to smooth the brain and attenuate narrow non-brain regions. Once each MRI slice has been diffused we choose a threshold determined by fitting a Gaussian curve to the histogram of the diffused volume to segment the brain region. Voxels with the intensity values of more than two standard deviations below the mean of the fitted Gaussian peak were assigned to zero. Then performing a dilation-erosion sequence on the inverted binary mask breaks the initial head mask into several disconnected regions. Finally the largest object is selected as the brain or ROI.

3.3.2 Noise Removal

As an intensity-based algorithm FCM has the shortcoming of over-sensitivity to noise. Since MR images always include considerable uncertainty and unknown noise, a noise filter is used to overcome the effects of noise.

Here we use a fuzzy filtering for mixed noise removal which is presented in [110]. The noise is assumed to be mixed Gaussian. This filter combines the weighted averaging method and median method. Even the heavy noise (9%) could be removed or downgraded to follow the spatial continuity constraint. Considering a neighborhood (a 3×3 window is used in our algorithm), the filtered center voxel $I_{m,n}$ is computed as follows:

$$I_{m,n} = \frac{\sum_{i=-1}^1 \sum_{j=-1}^1 \Pi(\Delta x'_{i,j}) x'_{i,j}}{\sum_{i=-1}^1 \sum_{j=-1}^1 \Pi(\Delta x'_{i,j})} \quad (3.8)$$

where the new window of voxels $x'_{i,j}$ is obtained by replacing the maximal and minimal gray level voxels in the original window with the median intensity x_{med}

$$\begin{aligned}\max x_{i,j} &= x_{med} \\ \min x_{i,j} &= x_{med}\end{aligned}$$

The $\Delta x'_{i,j} = x'_{m,n} - x'_{i,j}$. The Π - function is described mathematically as

$$\Pi(x) = \begin{cases} S(x; \gamma - \beta, \gamma - \beta/2, \gamma) & \text{for } x \leq \gamma \\ 1 - S(x; \gamma, \gamma + \beta/2, \gamma + \beta) & \text{for } x > \gamma \end{cases} \quad (3.9)$$

where $S(x; \alpha, \beta, \gamma)$ is the S-function which is expressed as the following:

$$S(x; \alpha, \beta, \gamma) = \begin{cases} 0 & \text{for } x \leq \alpha \\ 2\left(\frac{x - \alpha}{\gamma - \alpha}\right)^2 & \text{for } \alpha \leq x \leq \beta \\ 1 - 2\left(\frac{x - \gamma}{\gamma - \alpha}\right)^2 & \text{for } \beta \leq x \leq \gamma \\ 1 & \text{for } x \geq \gamma \end{cases} \quad (3.10)$$

The shape of the Π - function is shown in Fig. 3.1(a) [110]. It can be used to weigh the difference of the gray level of two voxels, which is shown in Fig. 3.1(b).

(a)

(b)

Fig 3.1: Π - type fuzzy set membership function.

In our application $\gamma = 0$ and $\alpha = \gamma - \beta$ which imply $\alpha < 0$ and $\beta > 0$. From Fig. 3.1 we can see when the distance is small the weight of voxel is big and decrease slowly. When the distance is bigger than half of β the weight of voxel is small and decrease quickly. So we need only one parameter α or β to control the filter. This will be discussed in this chapter. Actually we set β as 25 in light-noise (Fig. 3.1(b)) and 40 in heavy-noise for 0-255 intensity range.

3.4 THE MR IMAGE MODEL AND MODIFIED FCM

3.4.1 The MR Image Model

Inhomogeneity in the magnetic fields used during image acquisition and magnetic susceptibility variations in the scanned subjects causes intensity nonuniformities in MRI which produces heavy overlapping in tissue distributions. As a result, compensation for these nonuniformities is necessary in classification and quantitative studies of MRI. In our algorithm the nonuniform image gain is modeled as a spatially slowly varying multiplicative bias field.

The following model is used for MR images:

$$Y_k = X_k B_k + N_k \quad (3.11)$$

where Y_k is the observed image intensity at voxel k ; X_k is the real (ideally piecewise constant) image intensity to be "restored" by the segmentation algorithm; B_k is the slowly varying bias field and N_k is the image noise. After noise removal we can simply omit the noise in our algorithm. So after filtering and log-transform we can obtain a more meaningful equation.

$$y_k = x_k + b_k \quad (3.12)$$

where x_k and y_k are the true and observed log-transformed intensities at the k th voxel, respectively, and b_k is the log-transformed bias field at the k th voxel. Because this model includes the bias field explicitly and the relationship becomes addition the segmentation of images and the estimation of the bias field could be done iteratively. Many researchers ([65], [66], [83], etc.) have taken advantages of this model in various methods.

3.4.2 Modified FCM

The standard objective function of FCM is given in Equation (3.4). Considering the MR image model we can use $y_k - b_k$ to substitute x_k in the objective function. But this also introduces an unknown parameter b_k . The following section will describe how to use the modified FCM to estimate the bias field and tissue class iteratively.

Substituting Equation (3.12) into Equation (3.4), we obtain the new generalized objective function of FCM:

$$J_m = \sum_{i=1}^c \sum_{k=1}^n u_{ik}^m \|y_k - b_k - v_i\|^2 \quad (3.13)$$

The generalized objective function J_m can be minimized in a fashion similar to the standard FCM algorithm. Taking the first derivatives of J_m with respect to u_{ik}, v_i , and b_k and by setting them to zero results in three estimators of U , V , and B . With these estimators we can form an iterated algorithm to compute the tissue class and bias field.

A. Bias-Field Estimation

Taking the derivative of J_m with respect to b_k and setting the result to zero we have

$$\left[\sum_{i=1}^c \frac{\partial}{\partial b_k} \sum_{k=1}^n u_{ik}^m (y_k - b_k - v_i)^2 \right]_{b_k = b_k^*} = 0 \quad (3.14)$$

Since only the k th term in the second summation depends on b_k , we have

$$\left[\sum_{i=1}^c \frac{\partial}{\partial b_k} u_{ik}^m (y_k - b_k - v_i)^2 \right]_{b_k = b_k^*} = 0 \quad (3.15)$$

Differentiating the distance expression, we obtain

$$\left[y_k \sum_{i=1}^c u_{ik}^m - b_k \sum_{i=1}^c u_{ik}^m - \sum_{i=1}^c u_{ik}^m v_i \right]_{b_k=b_k} = 0 \quad (3.16)$$

Thus, the zero-gradient condition for the bias-field estimator is expressed as:

$$b_k = y_k - \frac{\sum_{i=1}^c u_{ik}^m v_i}{\sum_{i=1}^c u_{ik}^m} \quad (3.17)$$

B. Cluster Prototype Updating

Taking the derivative of J_m with respect to v_i and setting the result to zero, we have

$$\left[\sum_{k=1}^n u_{ik}^m (y_k - b_k - v_i) \right]_{v_i=v_i} = 0 \quad (3.18)$$

Solving for v_i , we have

$$v_i = \frac{\sum_{k=1}^n u_{ik}^m (y_k - b_k)}{\sum_{k=1}^n u_{ik}^m} \quad (3.19)$$

C. Membership Evaluation

We compute this using one Lagrange multiplier

$$F_m = \sum_{i=1}^c \sum_{k=1}^n u_{ik}^m \|y_k - b_k - v_i\|^2 + \lambda \left(1 - \sum_{i=1}^c u_{ik} \right) \quad (3.20)$$

Taking the derivative of F_m with respect to u_{ik} and setting the result to zero, we have

$$\left[\frac{\partial F_m}{\partial u_{ik}} = m u_{ik}^{m-1} \|y_k - b_k - v_i\|^2 - \lambda \right]_{u_{ik}=u_{ik}} = 0 \quad (3.21)$$

Solving for u_{ik} we have

$$u_{ik} = \left(\frac{\lambda}{m \|y_k - b_k - v_i\|^2} \right)^{1/(m-1)} \quad (3.22)$$

Since $\sum_{j=1}^c u_{jk} = 1$ for $\forall k$

$$\sum_{j=1}^c \left(\frac{\lambda}{m \|y_k - b_k - v_j\|^2} \right)^{1/(m-1)} = 1 \quad (3.23)$$

or

$$\lambda = \frac{m}{\left(\sum_{j=1}^c \left(\frac{1}{\|y_k - b_k - v_j\|^2} \right)^{1/(m-1)} \right)^{m-1}} \quad (3.24)$$

Substituting into (3.22), the zero-gradient condition for the membership estimator can be rewritten as:

$$u_{ik} = \left(\sum_{j=1}^c \left(\frac{\|y_k - b_k - v_i\|^2}{\|y_k - b_k - v_j\|^2} \right)^{\frac{1}{m-1}} \right)^{-1} \quad (3.25)$$

The modified iterated algorithm for estimating the bias field and segmenting the image into different clusters can be summarized as follows:

Step 1. Select initial class prototypes V using histogram and experience. Set $\{b_k\}_{k=1}^n$ to equal and very small values (0.0001 in our application).

Step 2. Compute the partition matrix using Equation (3.25).

Step 3. Update the prototypes of the clusters using Equation (3.19).

Step 4. Update the bias field using Equation (3.17).

Repeat steps 2-4 until termination. The termination criterion is as given in Equation (3.7): $\|V_{new} - V_{old}\| < \varepsilon$. Where $\|\cdot\|$ is the Euclidean norm and ε is a small number that can be set before computation (0.000001 in our application).

3.5 MEAN SPREAD FILTER

The above modified FCM algorithm doesn't consider the effect of neighborhood and the constraint of bias field. So the bias field estimator pushes the intensity of voxel to the most close cluster center and hence produces the misclassification. In order to correct the misclassification, we need to use the property of the bias field to push the voxels converging into the correct cluster center.

As we known, the bias field may be very large in some parts of MRI, but it must be smooth and slowly varying. This is the foundation that medical expert can accurately segment the image. They delineate the edges of white matter, gray matter and CSF. So we can assume the edges of three tissues are obvious in intensity. Now we consider the most prone to misclassification part. Assuming two voxels which are neighbors and belong to two classes are segmented to one tissue class (this is the most normal condition). This means $y_k - b_k \approx y_{k-1} - b_{k-1}$. If y_k and y_{k-1} are very different in intensity, b_k and b_{k-1} will also have a large gradient. So we can use a filter to avoid these conditions and hence avoid the misclassification. To get a smooth and slowly varying bias field, we use a mean spread method to filter it. This method is robust and can avoid the misclassification efficiently. Furthermore, this method has very large freedom hence can remove Gaussian noise effectively and need only one threshold value. The mean spread method is given below:

First, we will sweep the whole image except the border voxels. For each voxel under sweeping we consider its 4-neighborhood. We compare the center voxel with each one of 4 neighbors. If the difference of any two voxels are bigger than a threshold (set at the beginning), then we set the two voxels equal to their mean and spread the comparison along the line which the two voxels belong to until any two neighboring voxels have the gradient smaller than the threshold or reach the border. After this kind of smoothing on

4 directions we continue the filtering on next voxel until the completion of the sweeping. Then we can do the next sweeping and the number of sweeping is a pre-setting constant.

Mathematically, this algorithm can be described as following:

Set the MR image in 2-dimension and express it as a $(512 \times 512 \times 1mm)$ matrix $A(x, y)$, x and y are integers and $1 \leq x, y \leq 512$. And set the threshold as ε_1 .

Step 1: Omitting all $A(x, y), \forall x, y \in 1, 512$ we begin the sweeping from $A(2, 2)$.

Step 2: For each voxel our mean spread procedure is : Assume the central voxel is $A(i, j)$. Compare it with its 4 neighbors: $A(i-1, j)$, $A(i+1, j)$, $A(i, j-1)$, $A(i, j+1)$ in series.

Step 3: If $|A(i-1, j) - A(i, j)| \geq \varepsilon_1$, set $A(i-1, j)$ and $A(i, j)$ equal to $\frac{A(i-1, j) + A(i, j)}{2}$, then compare $A(i-1, j)$ and $A(i-2, j)$. If $|A(i-2, j) - A(i-1, j)| \geq \varepsilon_1$, set $A(i-2, j)$ and $A(i-1, j)$ equal to $\frac{A(i-2, j) + A(i-1, j)}{2}$. Continue this processing until $|A(i-k, j) - A(i-(k-1), j)| < \varepsilon_1$ or $i-k=1$. Do the same spread in another direction. That is compare $A(i, j)$ and $A(i+1, j)$, if $|A(i, j) - A(i+1, j)| \geq \varepsilon_1$, set $A(i, j)$ and $A(i+1, j)$ equal to $\frac{A(i, j) + A(i+1, j)}{2}$. Continue this processing until $|A(i+k, j) - A(i+k+1, j)| < \varepsilon_1$ or $i+k+1=512$.

Step 4: Sequentially repeat step 3 with $A(i+1, j)$, $A(i, j-1)$, $A(i, j+1)$.

Step 5: Repeat step 2, 3 from $A(2, 2)$ to $A(511, 511)$. This is a whole sweeping. Then on the bias field we do the next sweeping until no neighboring voxels' gradient is bigger than ε_1 or it reaches the iterated counts.

After 5 steps, the bias field becomes a smooth and slowly varying one. Especially, our filter begins spread procedure from the edges which have been misclassified. So the

edge voxels are firstly pushed to the right tissue class. This is very important in the segmentation of MRI. We have a parameter ε_1 in this filter. This is an important factor which decides the effect and efficiency of our method. It should be chosen to separate the different tissues but not affect the normal changes in one tissue class. We will discuss its choice later.

Now we can get the whole iterated algorithm for MRI segmentation based on our modified FCM approach.

Step 1: Discard the non-brain parts from the MR head scans and get the ROI, using the methods in Section 3.3.1.

Step 2: Use the proposed fuzzy filter (Section 3.3.2) to remove the noise in image.

Step 3: Select initial class prototypes V . To do this, we compute a smooth histogram of the data and take the maximum of the tissue intensity range. Set $\{b_k\}_{k=1}^n$ to equal and very small values (0.0001 in our application).

Step 4: Compute the partition matrix using Equation (3.25).

Step 5: Update the prototypes of the clusters using Equation (3.19).

Step 6: Update the bias field using Equation (3.17).

Step 7: Filter the bias field to a smooth one by using our proposed mean spread filter in Section 3.5.

Repeat steps 4-7 until termination. The termination criterion is the same as given in Equation (3.7): $\|V_{new} - V_{old}\| < 0.000001$ or when it reaches the maximum iteration times ITMAX=10 in our application.

Step 8: Perform a final hard classification by assigning the data to the cluster with the highest membership value.

The whole procedure of the proposed modified FCM algorithm is illustrated in Fig. 3.2.

Fig 3.2: The flowchart of the proposed modified FCM algorithm.

3.6 EXPERIMENTS USING SYNTHETIC IMAGES

In this section, we describe the results of our modified FCM algorithm on synthetic images corrupted with multiplicative bias field and Gaussian noise.

3.6.1 Segmentation Sequences of Modified FCM

We use the two intensity values of 80 and 120 to represent the two tissue classes. The image is corrupted with a multiplicative bias field that is sinusoidal ($B_k = (9 + \sin(2\pi \times (2)(k/k_{\max}))) / 10$) and the resulting original image is shown in Fig 3.3(a). The proposed algorithm is applied to the image. Fig 3.3(b)-(f) show the segmenting stages of this algorithm. Each figure is the segmentation result of iteration 3, 4, 5, 6, 7 respectively; Fig 3.3(g) shows the final segmented image and Fig 3.3(h) shows the estimated bias field. The bias field has been removed from original image and the segmentation is nearly perfect. We also find that our method corrects bias field on the thin strip more easily and quickly than the wide one. This is because our proposed mean spread filter corrects the bias field from the border of misclassified tissues. Hence, the correcting strength is proportional to the distance from the border.

Fig 3.3: **Segmentation sequences of proposed algorithm** (a) synthetic original image with intensity inhomogeneity; (b)-(f) segmentation results on iterative sequences; (g) final segmented image; (h) the estimated bias field.

3.6.2 Capability to Deal With Light Noise

The classical FCM algorithm has the shortcoming of sensitive to the noise. But the noise is inevitable in most of MR images. Thus the capability to deal with light noise is important to our algorithm. For experiments, we choose two more closely intensities 120, 150 to simulate grey and white tissues respectively. In addition to the same bias field as above we add a small Gaussian noise (3%) to the image. The resulting original image is shown in Fig 3.4(a). Fig 3.4(b) shows the segmentation result of this image. The segmentation result is fine. This demonstrates that our proposed algorithm can correct the bias field in a small noise environment without the fuzzy filter's preprocessing. This is a good property because no filter can completely remove the serious noise in an image. Therefore our proposed algorithm is more robust to the noise than traditional one.

Fig 3.4: **Segmenting the image in a small noise environment**; (a) synthetic image with bias field and small noise; (b) the segmented image.

3.6.3 Comparison with Other Method

Here we compare our proposed method with Ahmed et al. [83]'s modified FCM. They propose a modification to standard objective function of FCM by introducing a term that allows the labeling of a voxel to be influenced by the labels in its neighborhood. But

their method has the disadvantage of blurring the edge. We can see this from Fig. 3.4. Fig 3.5(a) is the synthetic image with the same bias field, 3% Gaussian noise and grey level 80, 120. Fig 3.5(c) is the segmentation result of Ahmeds' method (with $\alpha=0.85$). Obviously some voxels on edge have been misclassified. Fig 3.5(b) shows the segmentation result of our method and as it can be seen these problem have disappeared.

Fig 3.5 **Comparison with Ahmed et al.'s method**; (a) synthetic image with bias field and noise; (b) the segmentation result of our proposed method; (c) the segmentation result of Ahmed et al's method (with $\alpha=0.85$).

3.6.4 Selection of Threshold Value

In our proposed algorithm, the mean spread filter has a threshold value ε_1 to control the smoothness of bias field. This parameter influences the efficiency of the segmentation result. If the threshold is too big it can't correct the misclassified tissue voxels. But if

the threshold is too small the computation would be very time-consuming and the freedom of bias field would be reduced. Fig 3.6 shows that the parameter is able to vary in a range but the segmentation result is the same. This time we use three intensities 80, 120, 150 with the same bias field as above. Fig 3.6(a) is the synthetic image. Fig 3.6(b)-(d) show the segmentation results with threshold 0.0013, 0.002, and 0.003 respectively. All of them have been segmented correctly.

Fig 3.6 **Segment the image with different threshold**; (a) original image with intensity inhomogeneities; (b) image after segmentation with threshold 0.0013; (c) image after segmentation with threshold 0.002; (d) image after segmentation with threshold 0.003.

3.6.5 The Robustness of Initialization Cluster Centers

We have discussed the initialization problem in the Section 3.2. The initialization value of prototype matrix V or fuzzy c-partition matrix U can influence the segmentation result significantly. In MR image segmentation the initialization of V is normally done. Thus from the beginning of the algorithm we need to choose several cluster centers to represent the different tissue classes. For an algorithm, the larger range of usable initialization values means better robustness. We will compare the robustness of initialization V with Ahmed et al.'s method (with $\alpha=0.85$). Fig 3.7(a) is the synthetic image with the same bias field and two intensities 80, 120. Fig 3.7(b), (d), (f), (h) are the segmented images using Ahmed et al.'s method with initialization (60,130), (72,120), (75, 115), and (80,108) respectively. Fig 3.7(c), (e), (g), (i) are the segmented images using our proposed algorithm with the same initialization values as above. This experiment shows that we can choose the available initialization intensities in a large range. At the same time the threshold value influences Ahmed et al.'s method more than us. To get an accurate classification our method has a larger parameter range, therefore, it is more robust.

Fig 3.7 **Comparison of robustness for initialization**; (a) original image with intensity inhomogeneities; (b), (d), (f), (h) are the segmented images using Ahmed et al.'s method with initialization (60,130), (70,120), (75, 115), and (80, 108) respectively (with $\alpha=0.85$); (c), (e), (g), (i) are the segmented images using our proposed method with the same initialization.

3.7 EXPERIMENTS USING SYNTHETIC PHANTOMS

Here all of the simulated phantoms come from the Internet Brain Segmentation Repository (IBSR) [109], including the sphere software phantom and brain shaped software phantom. Each image slice is 256×256 by 16-bit.

3.7.1 The noise removal

We use a large noise image with large bias field to observe the effect of our fuzzy filter. From the experiments we observed that the fuzzy filter could be applied on images

several times to get better effects. The only parameter for controlling the filter α is set at a fixed value of 40 in the large noise environment. In Fig 3.8 we applied the fuzzy filter on one slice of sphere phantom 3 times, and the results on each filtering are shown below. Fig 3.8(a) is the original image, Fig 3.8(b)-(d) are the filtering results using fuzzy filter 1-3 times respectively.

Fig 3.8: **The noise removal**; (a) original image with large noise and large intensity inhomogeneities; (b) image after 1 time filtering; (c) image after 2 times filtering; (d) image after 3 times filtering.

3.7.2 Sphere1: phantom with noise, no gradient

This data set is an object that is a roughly spherical gray matter core surrounded by white matter. It includes 52 slices with noise and no bias field. Our algorithm is applied to

this data set with the initialization cluster center coming from histogram analysis and the same mean spread filter threshold $\varepsilon_1 = 0.005$. Fig 3.9(a)-(e) show the (10), (20), (30), (40), (48) original slices respectively. Fig 3.9(f)-(j) show their segmentation results. As it can be seen our algorithm provides good classification results.

Fig 3.9 **Segmentation of phantom with noise, no gradient**; (a)-(e) are the (10), (20), (30), (40), (48) original slices respectively; (f)-(j) are their segmentation results.

3.7.3 Sphere2: phantom with noise, small gradient

This data set is an object that is a roughly spherical gray matter core surrounded by white matter. It includes 52 slices with noise and small bias field, resulting in few overlapping intensities. Our algorithm is applied to this data set with the initialization cluster center coming from histogram analysis and other parameters as above. Fig 3.10(a)-(e) show the (10), (20), (30), (40), (48) original slices respectively. Fig 3.10(f)-(j) show their respective segmentation results. These figures demonstrate the noise and small gradient in the phantom can't affect our algorithm to segment the tissues.

3.7.4 Sphere3: phantom with noise, larger gradient

This data set is an object that is a roughly spherical gray matter core surrounded by white matter. It includes 52 slices with noise and larger bias field, resulting in intensities overlap by about half. Our algorithm is applied to this data set with the initialization cluster center coming from histogram analysis and other parameters as above. Fig 3.11(a)-(e) show the (10), (20), (30), (40), (48) original slices respectively. Fig 3.11(f)-(j) show their segmentation results. From the segmented images we can see that the different tissues have been separated.

Fig 3.10 **Segmentation of phantom with noise, small gradient**; (a)-(e) are the (10), (20), (30), (40), (48) original slices respectively; (f)-(j) are their segmentation results.

Fig 3.11 **Segmentation of phantom with noise, larger gradient**; (a)-(e) are the (10), (20), (30), (40), (48) original slices respectively; (f)-(j) are their segmentation results.

3.7.5 Sphere4: phantom with noise, large gradient

This data set is an object that is a roughly spherical gray matter core surrounded by white matter. It includes 52 slices with noise and large bias field, resulting in intensities overlap completely. Our algorithm is applied to this data set with the initialization cluster center coming from histogram analysis and other parameters as above. Fig 3.12(a)-(e) show the (10), (20), (30), (40), (48) original slices respectively. Fig 3.12(f)-(j) show their segmentation results. This figure illustrates the noise and large bias field could be corrected by our algorithm. As it can be seen the segmentation is almost perfect.

3.7.6 Synthetic brain phantoms

The synthetic brain phantoms also come from Internet Brain Segmentation Repository (IBSR) [109] and include two data sets. One has gradient and another has gradient and noise. Each set has 55 slices and each image slice is 256×256 by 16-bit. In these data sets, non-brain tissues are removed from all images prior to segmentation and our algorithm is implemented in Matlab 6.5. For these segmentation experiments, maximum number of iterations ITMAX=10. The algorithm usually converges in around 4-5 iterations. We also use the default parameters of mean spread filter (MSF): MSF_TH=0.005 and maximum number of iterations MSF_ITMAX=10.

First we compare our segmentation result with the Sled's N3 method [62]. They assume the ideal real data should be several constant intensities, each for one tissue class. From a signal processing perspective, the blurring of observed image data due to the bias field and noise, reduces the high frequency components of real data. The task of correcting the intensity inhomogeneity is that of restoring the frequency content of real data.

Fig 3.12 **Segmentation of phantom with noise, large gradient**; (a)-(e) are the (10), (20), (30), (40), (48) original slices respectively; (f)-(j) are their segmentation results.

So they use a method to propose a distribution for real data by sharpening the observed data, and then to estimate a corresponding smooth field which produces a distribution of real data close to our proposed method. In Fig. 3.13, (a) is a slice of synthetic brain from IBSR corrupted by bias field; (c) is its histogram; (b) is the segmentation result of slice (a); (d) is the corresponding histogram. We can see that the segmentation result of our algorithm is a piecewise smooth one. The voxel intensities of a tissue class are converged to its prototype or the whole set's data is converged to several cluster centers.

Fig 3.13: **The change of histogram in segmentation;** (a) original image with intensity inhomogeneities; (b) segmented image; (c) the histogram of original image (a); (d) the histogram of segmented image (b).

Then we use the same slice in the two data sets to illustrate our algorithm. Fig. 3.14(a) is the original image with gradient and (b) is its histogram; Fig. 3.14(c) is the segmentation result of image (a) and (d) is corresponding histogram; Fig. 3.14(e) is the original image with gradient and noise, (f) is corresponding histogram; Fig. 3.14(g) is the segmentation result of image (e) and (h) is corresponding histogram. We can see our algorithm works well under these two conditions.

Fig 3.14: **Segmentation on synthetic brain phantoms**; (a) original image with gradient; (c) segmentation result of (a); (e) original image with gradient and noise; (g) segmentation result of (e); (b), (d), (f), (h) are corresponding histogram of images (a), (c), (e), (g) respectively.

3.8 EXPERIMENTS USING SIMULATED BRAIN IMAGES

In this section, we describe the results of our modified spatial FCM algorithm on simulated 3-D MR brain images. These images are obtained from the BrainWeb Simulated Brain Database at the McConnell Brain Imaging Center of the Montreal Neurological Institute (MNI), McGill University [111]. In our experiments non-brain tissues are removed from all images prior to segmentation and the proposed algorithm is implemented in Matlab 6.5. For these segmentation experiments, maximum number of iterations $ITMAX=10$. The algorithm usually converges in around 5-6 iterations. We also use the default parameters of mean spread filter (MSF): $MSF_TH=0.005$ and maximum number of iterations $MSF_ITMAX=10$.

3.8.1 Noise removal

A. Visual Evaluation

Noise always affects the accuracy of intensity-based algorithms in image classification. In our algorithm heavy-noise will be removed before the segmentation, which makes segmentation results more meaningful.

This simulated brain data of varying noise and intensity inhomogeneity levels could be used to perform quantitative assessment of our algorithm since ground truths are known for them. In these data sets, the intensity inhomogeneity artifact was produced by multiplying the simulated MR image by a bias field recovered from an actual MR scan according to the image formation model of Equation (3.11). Figure 3.14 shows the segmentation on a slice of the simulated 3-D brain image, taken at $z=80$ with different noise levels.

The number of tissue classes in the segmentation is set to three, which corresponds to gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF). Background voxels are ignored in the computation. For these two data sets, maximum number of iterations ITMAX=10. The algorithm usually converges in around 5-6 iterations. We also use the default parameters of mean spread filter (MSF): MSF_TH=0.005 and MSF_ITMAX=10. For the simulated 3-D MRI brain image of dimension $217 \times 181 \times 181$ [row(x) $\times$ column(y) $\times$ depth(z)], the total computation time is around 4-6 min on a Pentium 4 2-GHz PC.

The brain image of Fig 3.15(f) is generated based on a discrete anatomical normal brain model, and serves as the true model. The image of Fig 3.15(a) and Fig 3.15(c) were simulated from the true model with the following settings: T1 modality, slice thickness of 1 mm (1 mm^3 voxels), 3% noise, 20% intensity inhomogeneity (INH) and 9% noise, 20% INH. Fig 3.15(b) and Fig 3.15(d) are corresponding segmentation results of Fig 3.15(a) and Fig 3.15(c) using our proposed algorithm. Fig 3.15(e) is the segmented image of pattern (c) using traditional FCM. The segmentation results by our method can be observed to correspond well to the true model of Fig 3.15(f). Although Fig 3.15(a) and Fig 3.15(c) are almost completely different images in sight their segmentation results fit well. Comparing with segmented image Fig 3.15(e) by FCM, our method provides better results.

Fig 3.15: **Segmentation with noise removal on a slice of the simulated 3-D brain image from MNI ($z=80$)**; (a) Image corrupted with 3% noise and bias field; (b) The segmentation result of (a) by proposed method; (c) Image corrupted with 9% noise and bias field; (d) The segmentation result of (c) by proposed method; (e) The segmentation result of (c) by FCM; (f) True model.

B. Variation of Parameter

We have shown that in our application the fuzzy noise filter is controlled by only one parameter: β . Now we look at the effect of different β on the segmentation results. Here we use the misclassification rate (MCR) to illustrate it. The MCR is defined as the number of pixels misclassified by the algorithm divided by the total number of pixels in the image. Table 3.1 shows the MCR after applying our proposed algorithm to the simulated data set (T1 weighted, 1 mm^3 voxels, 20% INH) with different noise (3%, 5%, 7%, 9%) when varying the parameter β .

TABLE 3.1
Misclassification Rate On Varying Fuzzy Filter Parameter Of Different Noise

β	3% Noise	5% Noise	7% Noise	9% Noise
20	0.0357	0.0487	0.0632	0.0751
23	0.0353	0.0475	0.0608	0.0698
24	0.0355	0.0472	0.0599	0.0685
25	0.0354	0.0471	0.0592	0.0676
26	0.0354	0.0471	0.0584	0.0658
27	0.0357	0.0470	0.0579	0.0650
30	0.0361	0.0465	0.0559	0.0615
40	0.0370	0.0467	0.0535	0.0561
50	0.0380	0.0471	0.0552	0.0538
60	0.0391	0.0487	0.0566	0.0543

As can be seen, when noise becomes heavier, the parameter β corresponding to the best MCR becomes bigger. This is reasonable considering the property of fuzzy filter. This can be explained that when noise becomes heavier we need wider intensity of neighborhood to compute the real value of centroid. So we set $\beta=25$ for the 3% noise data or less and set it bigger according to the noise level.

C. Quantitative Evaluation

For a quantitative evaluation of the performance of the noise filter, we calculate the MCR on the segmentation results of the simulated MRI data (T1 weighted, 1 mm³ voxels, 20% INH) with varying level of noise (1%, 3%, 5%, 7%, 9%). For comparison, we compute the MCR on segmentation results with/without noise filter and also apply it on M-FCM, (M-FCM denotes the Ahmed et al.’s modified FCM algorithm [83]). We try to implement the noise filter addition to M-FCM and list the results in Table 3.2.

TABLE 3.2
Misclassification Rate On With/Without Noise Removal For Different Segmentation Methods At Different Noise Level

	1% Noise	3% Noise	5% Noise	7% Noise	9% Noise
M-FCM	0.0354	0.0487	0.0817	0.1367	0.1846
M-FCM with N-filter	0.0342	0.0439	0.0550	0.0678	0.0824
Proposed	0.0291	0.0407	0.0742	0.1156	0.1544
Proposed with N-filter	0.0260	0.0336	0.0457	0.0532	0.0540

From Table 3.2, we can see that the MCR generally increases following the increase in noise level. Without noise filter the increase is prominent for both M-FCM algorithm and our proposed method. With N-filter the increase is suppressed for both algorithms. We can also observe that on heavy noise images algorithm with N-filter gets much better segmentation results. For all the data sets our algorithm performs better than M-FCM. Especially the MCR is only 0.0540 on 9% noise environment. All the above demonstrates that our proposed fuzzy filter is useful in the classification of noise data.

3.8.2 Performance Using Simulated Data

A. Visual Evaluation

These MRI images are obtained from MNI (T1 weighted, 1 mm^3 voxels, 40% INH, 3% noise). Fig 3.16 shows the models and the segmentation results for slices taken at $z=40$ (near the base of the brain) and $z=130$ (near the top of the skull). Although these kinds of border slices are more difficult to segment than center slices of the brain, we can also observe that the segmentations correspond well to the true models.

Fig 3.16: Segmentation results for two slices of 3% noise, 40% INH data; (a) True model ($z=40$). (b) Segmentation result. (c) True model ($z=130$). (d) Segmentation result.

B. Variation of Parameter

In this section we look at the influence of mean spread filter threshold (MSF_TH) ε_1 . This parameter is used to control the strength of spatial continuity. Table 3.3 lists the MCR after implementing our modified spatial FCM algorithm on the simulated data set (T1 weighted, 1 mm³ voxels, free noise) when varying the mean spread filter threshold ε_1 with different bias field. As can be seen, the algorithm is insensitive to this parameter in a fairly big range. Thus this parameter is robust enough to be fixed in most of our experiments. Therefore in the following experiments we use the constant $\varepsilon_1=0.005$ to implement the proposed algorithm.

TABLE 3.3
Misclassification Rate On Varying MSF_TH

ε_1	0% INH	20% INH	40% INH
0.003	0.0262	0.0255	0.0250
0.004	0.0264	0.0251	0.0248
0.005	0.0250	0.0246	0.0245
0.006	0.0254	0.0248	0.0244
0.007	0.0257	0.0250	0.0245

C. Quantitative Evaluation

We calculate the overlap metric and the misclassification rate (MCR) for quantitative evaluation. The overlap metric is defined as $2V_{ae}^k/(V_a^k + V_e^k)$, where V_{ae}^k denotes the number of voxels assigned to class k by both the ground truth and the algorithm, V_a^k and V_e^k denote the number of voxels assigned to class k by the algorithm and the ground truth, respectively, for the three tissue classes. The value of overlap metric is between 0 which means no overlap at all and 1 which means full overlap. The computation results on different noise level and INH images are presented in Table 3.4. WM, GM and CSF denote the different tissue classes and the corresponding rows are overlap metrics. The

last row is the corresponding MCR. Table 3.4 demonstrates that our method performs well on these image volumes in the presence of varying levels of noise and INH.

TABLE 3.4
Overlap Metrics And Misclassification Rate For Different Noise Level And INH Level

	1% Noise			3% Noise			5% Noise		
	0% INH	20% INH	40% INH	0% INH	20% INH	40% INH	0% INH	20% INH	40% INH
WM	0.9728	0.9780	0.9742	0.9680	0.9726	0.9685	0.9604	0.9622	0.9615
GM	0.9674	0.9753	0.9708	0.9654	0.9701	0.9673	0.9514	0.9558	0.9547
CSF	0.9679	0.9715	0.9665	0.9625	0.9628	0.9575	0.9438	0.9473	0.9443
MCR	0.0314	0.0260	0.0296	0.0354	0.0336	0.0376	0.0473	0.0457	0.0468

For comparison, we quote the MCR of the different INH estimation algorithms as reported in [46]. The results are presented in Table 3.5. FCM denotes the conventional FCM algorithm. FM-AFCM and TM-AFCM denote the full multigrid adaptive FCM algorithm and the truncated multigrid adaptive FCM algorithm, respectively [82]. EM1 and EM2 denote the unsupervised EM algorithm for finite Gaussian mixture models, where EM1 refers to the standard model and EM2 refers to the model where variances and mixture coefficients of the Gaussian components are assumed equal. AMRF denotes the adaptive Markov random field algorithm. MNI-FCM denotes the method where N3 inhomogeneity correction technique [62] from MNI is applied first,

followed by FCM segmentation. AS-FCM denotes the adaptive spatial FCM algorithm [46]. M-FCM denotes the modified FCM algorithm [83]. Last one is our proposed method. The experiments are conducted using the simulated MRI data (T1 weighted, 1 mm³ voxels, 3% noise).

TABLE 3.5
Misclassification Rate For Different INH Correction And Segmentation Methods At Different INH Level

Method	0% INH	20% INH	40% INH
FCM	0.0399	0.0545	0.0902
FM-AFCM	0.0417	0.0432	0.0506
TM-AFCM	0.0417	0.0432	0.0494
EM1	0.0634	0.0759	0.1377
EM2	0.0424	0.0564	0.0960
AMRF	0.0388	0.0479	0.0687
MNI-FCM	0.0498	0.0497	0.0562
AS-FCM	0.0372	0.0368	0.0383
M-FCM	0.0353	0.0439	0.0656
Proposed	0.0354	0.0336	0.0376

From Table 3.5, we can see our method has better performance than other methods and is robust on increased inhomogeneity. For the 0% INH level, M-FCM almost has the same performance with our method, but 40% INH level, our method shows an improvement of 43% over the M-FCM method. Comparing with AS-FCM method, our method has an improvement of 5%, 9%, 2% for 0% INH, 20% INH, 40% INH respectively.

3.9 EXPERIMENTS USING REAL MR IMAGES

These real MRI images come from Internet Brain Segmentation Repository (IBSR) [109]. We applied our method to the 20 complete head MR scans in IBSR, using the same parameter values: $\beta=25$ and $\varepsilon_1=0.005$. The dimensions of the image stacks were $256 \times 256 \times 64$ voxels, and the average total processing time was 3-4 min on a Pentium 4 2-GHz PC. IBSR provides the experts' manual segmentation of these 20 scans, which are taken as the ground truth.

A. Visual Evaluation

Fig 3.17 shows two slices of the segmentation results for real T1-weighted MR images using the proposed algorithm. Fig 3.17(a) and (b) are the original images. Fig 3.17(c) and (d) are corresponding proposed MSC-FCM segmentation results. Fig 3.17(e) and (f) are corresponding manual segmentation by experts. Visual inspection shows that our segmentation results are very close to the expert's manual segmentation.

B. Quantitative Evaluation

The 20 head scans from IBSR have been used in the published volumetric studies of many researchers because they have various levels of difficulty and the worst scans have low contrast and relatively large spatial inhomogeneities. For a quantitative evaluation of the performance of the algorithm, IBSR also contains performance indexes that measure the amount of overlap between the experts' manual segmentation and a collection of automatic methods. The index in this case is the Tanimoto coefficient [73], and is defined as $I(k) = \frac{V_{p \cap g}(k)}{V_{p \cup g}(k)}$, where $V_{p \cap g}(k)$ denotes the number of voxels classified as class k by both the proposed method and the expert, and $V_{p \cup g}(k)$ denotes the number of voxels classified as class k by either the proposed method or the expert. These images are therefore used as a standardized mechanism for testing the sensitivity of our proposed method to signal-to-noise ratio, contrast-to-noise ratio, shape complexity,

degree of partial volume effect, etc. For comparison, we implement our proposed method and M-FCM [83] method (the neighborhood effect $\alpha=0, 0.85$) on these images. When $\alpha=0$, their method has the same objective function as us. When $\alpha=0.85$, their method seems to give the best results [83]. The results are compared with the cited performance index $I(k)$ from IBSR and reported in [73], [117]. The comparison results are presented in Table 3.6.

Fig 3.17: **Segmentation of real MRI images;** (a), (d) Original images. (b), (e) Corresponding manual segmentation. (c), (f) Corresponding Proposed MS-FCM segmentation.

In Table 3.6 GM and WM express the average overlap (index I) of gray matter and white matter between manual segmentation and various methods for the 20 brain scans respectively. The results of Adaptive MAP, Biased MAP, FCM, MAP, Tree-structure k-means, Maximum-Likelihood, and Manual are cited from IBSR [109]. The results of MPM-MAP method are reported in [73]. The results of M-FCM method are calculated by us for comparison (with $\alpha=0, 0.85$) [83]. The results of ABFC method are quoted from [117]. Comparing with M-FCM method, their method has the same objective function as us when $\alpha=0$. But they have no constraints on bias field. In the segmenting procedure, misclassification will happen at the step of bias field estimation. In our method the mean spread filter is used to smooth the estimated bias field and therefore corrected misclassification. This improves the accuracy of 24% on GM and 17% on WM comparing with M-FCM ($\alpha=0$). When they take the neighborhood effect in the objective function ($\alpha=0.85$, which they suggest to give the best results), their method has no constraints on bias field yet. Their bias field estimator is the same as us with Equation (3.17). So taking the advantage of bias field constraints our method gives the better results of 16% on GM and 10% on WM than M-FCM ($\alpha=0.85$).

TABLE 3.6
Average Overlap Between Manual Segmentation And Various Methods For The 20 Brain Scans of The MGH Data Base

Method	GM	WM
Adaptive MAP	0.564	0.567
Biased MAP	0.558	0.562
FCM	0.473	0.567
MAP	0.550	0.554
Tree-structure k-means	0.477	0.571
Maximum-Likelihood	0.535	0.551
MPM-MAP	0.662	0.683
M-FCM ($\alpha=0$)	0.604	0.617
M-FCM ($\alpha=0.85$)	0.647	0.658

ABFC	0.770	0.658
Proposed	0.750	0.724
Manual (4 brain averaged over 2 experts)	0.876	0.832

For the bias-corrected segmentation methods MPM-MAP [73], our method shows an improvement of 13% on GM, 6% on WM respectively. The newest ABFC method has better performance on GM, but still worse on WM.

In Fig 3.18 we can see that most overlap ratios are above 0.7, indicating the validity of our method. We also notice that the segmentation results of 2_4, 5_8, 17_3 are relatively bad. Investigating these images we find they are corrupted with heavy noise and large partial volume effect, which is difficult to restore by our spatial continuity constraints.

Fig 3.18: Overlap ratios of the 20 brain scans from IBSR

3.10 CONCLUDING REMARKS

We have described a modified spatial FCM algorithm for automatic segmentation and intensity correction of MR brain images. The algorithm was formulated by modifying the objective function of the standard FCM algorithm to compensate for intensity inhomogeneity. In the iteration procedure we use a mean spread filter to smooth the bias field for obtaining the correct classification. We also use a fuzzy filter to make our algorithm robust.

Several data sets are used to evaluate the performance of the modified spatial FCM algorithm. Our algorithm requires only two parameters to be selected: threshold ε_1 controlling the smoothness of the estimated bias field and accuracy of the segmentation, initialization controlling the cluster center of the FCM and the convergence rate of FCM. It can be concluded from the experiments that segmentation using the proposed method is far less sensitive to initialization and more reliable than the compared methods. Moreover, we compared our algorithm with some other segmentation methods. Our approach outperformed other methods in many aspects, especially in the accuracy of segmentation, which is the most important in MR brain tissue classification.

So far we have presented the segmentation of MR images considering the noise and intensity inhomogeneity. Our proposed method to overcome the partial volume effect is described in the next chapter.

Chapter 4

Partial Volume Segmentation

4.1 INTRODUCTION

MR image classification is a big challenge because of partial volume effect incorporated with noise and intensity inhomogeneity. Although MRI images have the best resolution in all of the medical image modalities the mixture of two and more tissues inevitably occurs in scans. The expert can classify the tissues under this situation using their medical knowledge and experience. But it is difficult for computers to consider this high level information. In this thesis, a new strategy for MR image classification is proposed by taking the partial volume effect into account. The mixed image model is proposed to represent the voxels.

This framework is also based on the FCM algorithm incorporated with a partial volume labeling method. Considering the partial volume effect the single tissue model is not enough to represent the mixture voxels. Alternatively, a multiple tissue image model is proposed to represent image voxels.

The chapter is organized as follows. The concept of mixed image model is proposed in Section 4.2. In Section 4.3 the partial volume labeling method is presented. Experimental results using simulated 3-D brain images are presented in Section 4.4, as part of the algorithm evaluation. In Section 4.5 the partial volume labeling method is incorporated with modified spatial FCM to form a whole fuzzy clustering framework for MRI segmentation. In Sections 4.6 and 4.7 the proposed algorithm is applied to

simulated 3-D brain images and the real MR images respectively. The quantitative evaluation and comparison are also given. Finally, some concluding remarks are provided in Section 4.8.

4.2 MIXED IMAGE MODEL

4.2.1 Review of Image Model

The partial volume effect is present in nearly all medical imaging data. It occurs when more than one type of class or tissue occupies one voxel of an image and causes the blurring of boundaries between different tissues. To describe and compensate these phenomena in MR images several models have been proposed. The most widely used represents the intensity Y_m of a mixture voxel as follows [99]-[102]:

$$Y_m = \sum_{k=1}^N a_k I_k + \eta_m, \quad \forall k \in [1, N] \quad (4.1)$$

where η_m is white Gaussian noise with standard deviation σ . N represents the number of tissues. I_k is related to the intensity value of the tissue class k , and a_k its proportion, which is assumed to be a uniform random variable in the interval $[0,1]$.

In the case of mixture voxels of just two pure tissue classes, the probability density function of intensity Y_m is given by

$$p(Y_m) = \int_0^1 \frac{1}{\sqrt{2\pi}\sigma} \exp \frac{-[Y_m - ((1-a)I_1 + aI_2)]^2}{2\sigma^2} da \quad (4.2)$$

This voxel intensity model includes four influence factors in MR images: noise, intensity inhomogeneity, partial volume effects, and the intrinsic heterogeneity of the tissue types. For simplification most published classification algorithms have attempted to overcome one or two of above difficulties, assuming that the others play a minor role.

Pham and Prince [103] proposed their model to describe the observed image. They assume each tissue class possesses a distinct intensity c_k for $k = 1, \dots, K$, called the class mean. The true image $I(x)$ maps a spatial location $x \in \Omega_c$ to a class mean and can be written as

$$I(x) = \sum_{k=1}^K \chi_k(x) c_k, x \in \Omega_c \quad (4.3)$$

where $\chi_k(x)$ is the characteristic function of set k and Ω_c is a continuous spatial domain.

Then in the MR image acquisition process the original image is blurred by a linear shift invariant filter $h(x)$ (called the point spread function), point sampled, and corrupted by additive noise. Let $\Omega \subset \Omega_c$ be the set of the discrete samples in the observed image. The observed image can then be written as

$$Y_j = \sum_{k=1}^K (\chi_k * h)_j c_k + \eta_j, j \in \Omega \quad (4.4)$$

where “*” denotes a convolution, η_j is white Gaussian noise with variance σ^2 .

They substitute the convolution of the characteristic function for tissue k and the point spread function with the tissue spread function $s_k(x)$:

$$s_k(x) = (\chi_k * h)(x) \quad (4.5)$$

They continue to define the tissue spread coefficients s_{jk} to be samples of the tissue spread function at $j \in \Omega$:

$$s_{jk} = (\chi_k * h)_j \quad (4.6)$$

Finally they model the observed image as

$$Y_j = \sum_{k=1}^K s_{jk} c_k + \eta_j, j \in \Omega \quad (4.7)$$

with the following constraints:

$$\sum_{k=1}^K s_{jk} = 1, \text{ for all } j \in \Omega \quad (4.8)$$

$$s_{jk} \geq 0, \text{ for all } j \in \Omega, k = 1, \dots, K \quad (4.9)$$

Their Equation 4.7 has the same form with Equation 4.1.

Ruan et al. [104] present an improved model for the mixture voxel. The observed image is written as:

$$y_m = \sum_{k=1}^N a_k y_k^p, \quad \text{with } \sum_{k=1}^N a_k = 1, \quad \forall k \in [1, N] \quad (4.10)$$

where y_m denote the intensity of a mixture voxel and N the number of pure tissue classes present in an image. a_k is the contribution of pure class k to the observed intensity y_m . The random variable y_k^p refers to the pure class k whose probability density results from the distributions of acquisition parameters T_{1k}^p , T_{2k}^p , and ρ_k^p , and from instrumental noise.

The probability density function $p(y_k^p)$ may then be assumed to be asymptotically normal by application of the central limit theorem. In the case of mixture voxels including two pure tissue classes, the model takes the following expression:

$$y_m = a y_1^p + (1 - a) y_2^p, \quad 0 \leq a \leq 1 \quad (4.11)$$

where a is the relative quantity of the first class.

A downsampling process is used to describe the partial volume effect of MR images by Leemput et al. [106]. They show that the observed intensity y_i in a voxel with underlying set of labels is governed by a normal distribution that only depends on the voxel's mixing proportions. The intensity distribution model for partial volume voxels is given by the sum of the normal distributions of all nonpure mixtures.

4.2.2 Partial Volume Image Model

In last chapter we described the estimation of bias field. By considering the partial volume effect we assume that the intensity X_k at a particular voxel is a linear combination of the intensities of two or more pure types, with the exception of the MR bias field.

$$X_k = \sum_{m=1}^n a_m I_m, \text{ with } \sum_{m=1}^n a_m = 1, \forall m \in [1, n] \quad (4.12)$$

where I_m is related to the intensity value of the class k , and a_m its proportion, which is in the interval $[0,1]$. To restrict the numerical complexity, we only consider models that allow maximum two different tissue types in a voxel at the same time. So we can simplify Equation (4.12) to (4.13) as given below:

$$X_k = \alpha I_a + (1 - \alpha) I_b, \quad (I_a, I_b) \in \{(I_c, I_g), (I_g, I_w), (I_c, I_w)\} \quad (4.13)$$

where I_c, I_g, I_w are related to the intensity value of tissue CSF, GM, WM respectively.

Now we consider the intrinsic heterogeneity of the tissue types. In [47], the authors first find normal distributions of the pure classes using regions of interest enclosing pure tissues. This model is also used in many algorithms [41]-[45]. So we assume that in the MR image $X^{r \times c}$ the pure tissues CSF, GM, WM, because of the intrinsic heterogeneity, have the normal distributions, which mean:

$$P(I) = \frac{1}{\sqrt{2\pi}\sigma} \exp \frac{-(I - \mu)^2}{2\sigma^2}, \quad I \in I_c, I_g, I_w \quad (4.14)$$

where μ is mean value and σ is standard deviation. In our algorithm the μ is the cluster center v . One obvious way to find the standard deviation is to fit the histogram of image $X^{r \times c}$ with the normal distribution curve.

4.3 PROPOSED PARTIAL VOLUME LABELING METHOD

We assume that the partial volume voxels have two properties:

1. Its gray scale has a distance from the mean values of pure tissues that form it.
2. CSF is sufficiently separated from WM so that their mixtures must be adjacent with the pure CSF and WM voxel.

From the above assumptions we propose a two step method to label the mixture voxels. The first step is for the mixture of (CSF, GM) and (GM, WM) and the second is for the (CSF, WM).

First step: fit the histogram of image $X^{r \times c}$ with the normal distribution model (4.14) and obtain the distribution of CSF, GM, WM: $P_c(I_c; \mu_c, \sigma_c)$, $P_g(I_g; \mu_g, \sigma_g)$ and $P_w(I_w; \mu_w, \sigma_w)$.

Then calculate the intersection of the three distributions, obtain the intersection I_1 between CSF and GM, I_2 between GM and WM. Compute the cumulative probabilities of I_1, I_2 in the three distributions respectively, getting $P_c^c(I_1)$, $P_g^c(I_1)$ and $P_g^c(I_2)$, $P_w^c(I_2)$. We use the two pair of probabilities to form the intervals of probable mixture voxels $[I_3, I_4]$ for mixture of CSF and GM, $[I_5, I_6]$ for mixture of GM and WM. Where $P_c^c(I_3) = P_c^c(I_1) + P_g^c(I_1)$, $P_g^c(I_4) = P_c^c(I_1) + P_g^c(I_1)$ and $P_g^c(I_5) = P_g^c(I_2) + P_w^c(I_2)$, $P_w^c(I_6) = P_g^c(I_2) + P_w^c(I_2)$.

This step is based on the global consideration. $P_c^c(I_3)$ is the cumulative probability of I_3 belonging to CSF and $P_g^c(I_4)$ is the cumulative probability of I_4 belonging to GM. They are both decided by $P_c^c(I_1)$ and $P_g^c(I_1)$. The value of $P_c^c(I_1)$ and $P_g^c(I_1)$ demonstrate the mixture proportion of these two tissues. The bigger means the heavier mixture so that the mixture voxels have bigger probabilities to pure ones. So in this step we choose all voxels between $[I_3, I_4]$ and $[I_5, I_6]$ as the partial volume candidates. For every candidate with its neighborhood, such as 5×5 , we choose the highest probability

voxels of mixture tissues respectively. If the probability is bigger than 0.8 we consider them as the pure ones and take their values as I_a and I_b in Equation (4.13). If not we take mean values of these pure tissues as I_a and I_b . Then we can calculate the α for the candidate. If α is bigger than 0.2 or smaller than 0.8 we label the voxel as a mixture and take it out of the image.

Second step: this is used to label the CSF and WM mixtures. We assume that the thickness of CSF and WM mixture won't exceed one voxel even in the 1mm MR scans. This is reasonable for MR brain images. So we first choose the voxels which they have the highest membership for GM and in their 4 neighborhood there are high probabilities for CSF and WM as the candidates. This means for the neighborhood voxels: V_1, V_2, V_3, V_4 we can find $P_c(I; I \in V_1, V_2, V_3, V_4) > 0.8$ and $P_w(I; I \in V_1, V_2, V_3, V_4) > 0.8$. Then we check 8 neighborhood candidate: V1 to V8 for the highest membership. If none of them belongs to GM we label candidate as mixture. If more than two of them belong to GM then do not label it. If only one or two of them belong to GM we continue to check 3 more voxels along the direction. As shown in Figure 4.1, in the V0's 8 neighbors, if V1 and V3 belong to GM we continue to check with V9-V11 along V1's direction and V12-V14 along V3's direction. In V9-V11 if two or three of them belong to GM we end the check without label. If none of them belongs to GM we end the check on this direction, but continue on V12-V14. If one of them (such as V10) belongs to GM then continue to check with V15-V17 along the direction of V10. We only extend the search for 3 steps from V0. Thus V15-V17 is the last part. If 2 or 3 of them belong to GM, do not label; otherwise we take V0 as a possible mixture and continue to check on another direction. In V12 -V14 we use the same strategy. If only one of them (such as V14) belongs to GM we check with V18-V20. If none or one of them belong to GM we label the V0 as a mixture, otherwise do not label it. Final for mixtures we take the two adjacent voxels as the pure ones to compute α and take it out of the image.

Fig 4.1: Labeling of the CSF and WM mixtures

Now we can form the partial volume labeling algorithm based on fuzzy c-means method.

Step 1: Initialize the vector of cluster centers V using the image histogram.

Step 2: Calculate the fuzzy c-partition U with Equation (3.19).

Step 3: Update V using Equation (3.17).

Step 4: Repeat steps 3, 4 till termination. The termination criterion is $\|V_{new} - V_{old}\| < 0.000001$.

Step 5: Label the mixture voxels in the image. If the number of labeled mixture voxels is greater than ε_2 (50 in our experiments), go back to step 2.

4.4 EXPERIMENTS FOR PV LABELING METHOD

In this section, we describe the results of partial volume labeling method on simulated 3-D MR brain images. The simulated 3-D MR images are obtained from the BrainWeb Simulated Brain Database at the McConnell Brain Imaging Center of the Montreal

Neurological Institute (MNI), McGill University [52]. In these data sets, non-brain tissues are removed from all images prior to segmentation and our algorithm is implemented in Matlab 6.5. For all the segmentation experiments, maximum number of iterations ITMAX=10. The algorithm usually converges in around 7-8 iterations.

We can see, the segmentation result of our algorithm includes 6 classes (CSF, GM, WM, CSF_GM, GM_WM, CSF_WM). For the comparison with other methods we reassigned each mixture voxel by setting its label to the pure tissue having the greatest proportion.

Now we take a look at the partial volume segmentation results of high-resolution T1-weighted images with 1% noise and zero bias field. Fig 4.2 shows a slice of the segmentation results for T1-weighted MR images using the proposed approach. Fig 4.2(a) is the original image. Fig 4.2(b) is the true model. Fig 4.2(c)-(e) are segmentation results for CSF, GM and WM respectively. Fig 4.2(f) is the labeled mixtures for CSF and GM. Fig 4.2(g) is the labeled mixtures for CSF and WM. Fig 4.2(h) is the labeled mixtures for GM and WM. The segmentation results seem satisfactory under this condition.

Fig 4.2: **Partial volume segmentation of a slice ($z=55$) of T1 simulated MRI image;** (a) Original image; (b) Image model; (c) CSF; (d) GM; (e) WM; (f) CSF and GM mixtures; (g) CSF and WM mixtures; (h) GM and WM mixtures.

4.5 THE COMPLETE CLUSTERING FRAMEWORK

In this section we combine the noise filter, mean spread filter and partial volume labeling method to overcome the obstacles in MR images. When heavy noise appears in image

the noise filter is used to remove it. The mean spread filter is used to estimate and correct the bias field. And the mixture voxels are also labeled in the segmentation.

Now incorporating the proposed modified spatial FCM algorithm we can obtain the whole fuzzy clustering framework for MRI segmentation.

Step 1: Discard the non-brain parts from the MR head scans and obtain the ROI, using the methods in Section 3.3.1.

Step 2: Use the fuzzy filter in Section 3.3.2 to remove the noise in image.

Step 3: Select initial class prototypes V . To do this, we compute a smooth histogram of the data and choose the maximum of the tissue intensity range. Set $\{b_k\}_{k=1}^n$ to equal and very small values (0.0001).

Step 4: Compute the partition matrix using Equation (3.25).

Step 5: Update the prototypes of the clusters using Equation (3.19).

Step 6: Update the bias field using Equation (3.17).

Step 7: Filter the bias field to a smooth one by our proposed mean spread filter (Sec. 3.5).

Repeat steps 4-7 until termination. The termination criterion is $\|V_{new} - V_{old}\| < 0.000001$ or when it reaches the maximum iteration times ITMAX=10 in our application.

Step 8: Label the mixture voxels in the image. If the number of labeled mixture voxels is greater than ε_2 (50 in our experiments), go back to step 4.

Step 9: Perform a final hard classification by assigning the data to the cluster with the highest membership value for residual voxels.

The whole procedure of the proposed framework is illustrated in Figure 4.3.

Fig 4.3: The flowchart of the proposed fuzzy clustering framework.

4.6 EXPERIMENTS USING SIMULATED MR IMAGES

Our fuzzy clustering framework presented in this chapter tackles the problem of partial volume segmentation of MR brain images from a different angle. In the traditional FCM algorithm, widely used to classify MR brain images into pure tissue types, an additional partial volume labeling step is introduced in the segmentation. The resulting framework is a natural extension of the usual FCM method, estimating the relative amounts of the various tissue types in voxels that have low probability to be pure ones. Now we look at the performance of our proposed algorithm on high-resolution T1-weighted images.

First we use the simulated 3-D MR images obtained from the BrainWeb [111]. This time the images are corrupted with 3% noise and 40% bias field. Fig 4.4 shows a slice of the segmentation results for T1-weighted MR images using the fuzzy clustering framework. Fig 4.4(a) is the original image. Fig 4.4(b) is the true model. Fig 4.4(c)-(e) are segmentation results for CSF, GM and WM respectively. Fig 4.4(f) is the labeled mixtures for CSF and GM. Fig 4.4(g) is the labeled mixtures for CSF and WM. Fig 4.4(h) is the labeled mixtures for GM and WM. Visual inspection shows that our segmentation results for mixtures are almost on the borders of different tissues. The mixtures for CSF and GM are along the borders between CSF and GM tissues. They are not continuous because we take limitation on mixture proportions and original intensities. The mixture voxels for CSF and WM are only a few because normally they separate far from each other and we take strictly constraint on their labels. The mixtures for GM and WM have some chunks because those parts have obvious different gray level from GM and WM. So we take all of them as mixtures.

Fig 4.4: **Partial volume segmentation of a slice ($z=80$) of T1 simulated MRI image**; (a) Original image; (b) Image model; (c) CSF; (d) GM; (e) WM; (f) CSF and GM mixtures; (g) CSF and WM mixtures; (h) GM and WM mixtures.

For quantitative evaluation and comparison with the previous pure tissue method we compute the overlap metric and misclassification rate (MCR) for different noise level and INH. In calculation we reassign each labeled mixture voxel with pure tissue label having the largest fraction. These results are shown in Table 4.1. WM, GM and CSF denote the different tissue classes and the corresponding rows are overlap metrics. The last row is the corresponding MCR. Comparing with the segmentation results of modified FCM algorithm in table 3.4, the partial volume method improves overlap metrics and reduces the MCR for these images, indicating the effectivity of our method.

TABLE 4.1
Overlap Metrics And Misclassification Rate For Different Noise Level And INH
Level

	1% Noise			3% Noise			5% Noise		
	0% INH	20% INH	40% INH	0% INH	20% INH	40% INH	0% INH	20% INH	40% INH
WM	0.9731	0.9781	0.9735	0.9688	0.9724	0.9687	0.9612	0.9635	0.9618
GM	0.9684	0.9752	0.9706	0.9684	0.9704	0.9691	0.9534	0.9579	0.9562
CSF	0.9729	0.9775	0.9715	0.9692	0.9698	0.9657	0.9527	0.9532	0.9531
MCR	0.0311	0.0258	0.0297	0.0341	0.0329	0.0342	0.0469	0.0445	0.0458

4.7 EXPERIMENTS USING REAL MR IMAGES

These real MRI images come from Internet Brain Segmentation Repository (IBSR) [109]. We applied our partial volume framework to the 20 complete head MR scans in IBSR. The dimensions of the image stacks were $256 \times 256 \times 64$ voxels, and the average total

processing time was 4-5 min on a Pentium 4 2-GHz PC. IBSR provides the experts' manual segmentation of these 20 scans, which are taken as the ground truth. The segmentation results obtained from five automatic methods are also been cited for comparison.

A. Visual Evaluation

Fig 4.5 shows two slices from 20 normal MR brain scans in IBSR. We reassigned the mixtures to the pure tissues according to the greatest fraction. Although they have heavy noise and intensity inhomogeneity which are hard to segment even for expert, we can see that our segmentation results are very close to the expert's manual segmentations.

Fig 4.5 **The segmentation results on real MR images:** (a), (b) Original images; (c), (d) segmentation results of our proposed method; (e), (f) corresponding manual segmentation.

B. Quantitative Evaluation

For quantitative evaluation and comparison with other methods, our proposed framework is implemented on the 20 head scans and the Tanimoto coefficient [109] is calculated. The index is defined as $I(k) = \frac{V_{p \cap g}(k)}{V_{p \cup g}(k)}$, where $V_{p \cap g}(k)$ denotes the number of voxels classified as class k by both the proposed method and the expert, and $V_{p \cup g}(k)$ denotes the number of voxels classified as class k by either the proposed method or the expert. For comparison, we quote the performance index I(k) in Table 3.6. The results are presented in Table 4.2 and Figure 4.6.

In Table 4.2 GM and WM express the average overlap (index I) of gray matter and white matter between manual segmentation and various methods for the 20 brain scans respectively. In this table MPM-MAP, M-FCM, and ABFC are the same with Table 3.6. Proposed modified spatial constraint fuzzy c-means (MSC-FCM) algorithm is the one we proposed in Chapter 3. From Table 4.2 we can see that our method has a better performance of 16% (MPM-MAP), 19% (M-FCM), 2% (MSC-FCM) on GM and 10% (MPM-MAP), 14% (M-FCM), 4% (MSC-FCM) on WM than these bias-corrected methods. ABFC algorithm has a little improvement on GM, but 14% less on WM than our method.

TABLE 4.2
Average Overlap Between Manual Segmentation And Various Methods For The 20
Brain Scans of The MGH Data Base

Method	GM	WM
Adaptive MAP	0.564	0.567
Biased MAP	0.558	0.562
FCM	0.473	0.567
MAP	0.550	0.554
Tree-structure k-means	0.477	0.571
Maximum-Likelihood	0.535	0.551
MPM-MAP	0.662	0.683
M-FCM ($\alpha=0.85$)	0.647	0.658
ABFC	0.770	0.658
Proposed MSC-FCM	0.750	0.724
Partial Volume Framework	0.768	0.754
Manual (4 brain averaged over 2 experts)	0.876	0.832

Fig. 4.6 shows the overlap ratios of 20 head scans one by one on GM and WM. We can see that most of the overlap ratios have some improvement comparing with Fig. 3.18. To the images of 2_4 and 5_8, the partial volume method improves 11% and 9% on GM, 12% and 8% on WM respectively than MSC-FCM method, indicating the validity of partial volume labeling method.

Fig 4.6: Overlap ratios using partial volume framework.

4.8 CONCLUDING REMARKS

In this chapter, some mixture tissue models are introduced. For partial volume segmentation one model is proposed to represent the mixture voxels. A partial volume labeling method is proposed to separate the mixture voxels and pure tissues. Finally we have demonstrated fuzzy clustering framework for partial volume segmentation of MR brain images. The framework is based on the FCM algorithm and partial volume image model. In the iteration procedure we use a partial volume labeling step to find the mixture voxels and put them out of the algorithm which makes the segmentation more accurate. Our approach does not need prior knowledge of the data and can be applied at the first stage of automatic classification system.

Experiments with simulated MR volumes and real MR images show that our approach accurately segments the different tissue classes under serious intensity inhomogeneity and noise environment. We compared our results with some other methods. It demonstrated that our approach outperformed several published methods.

So far we have only done the segmentation on one-channel MR data. Since each of the channels of multi-spectral MR images provides additional information, we can extend our algorithm to multi-channel data in order to improve the classification. Normally one complete MRI scans include PD, T1-weighted and T2-weighted data. In next chapter we extend our algorithm to these multi-channel data.

Chapter 5

Multi-channel MRI segmentation

5.1 INTRODUCTION

MR images are generated by the resonating nuclei, which, for each spatial location, encode three physical properties. The first is the proton density, while the second and third are two relaxation times denoted T1 and T2. The proton density variations among soft tissues are typically within a few percent, whereas T1 and T2 relaxation times in different tissues vary by more than 100%. It is this large degree of variation in relaxation times that creates the greatest contrast in MRI. Table 5.1 exhibits the difference [2].

Table 5.1
Approximate Values of Relaxation Times at 1.5 Tesla

Tissue	T1(ms)	T2(ms)
Gray matter	920	101
White matter	790	92
Cerebrospinal fluid (CSF)	2650	280
Kidney	650	58
Liver	490	43
Skeletal muscle	870	47

Because the combinations of the relaxation times T_1 , T_2 and the proton density contribute to the image contrast, by varying the time of application of the RF pulses and gradients, the contributions of these parameters can be varied to produce an image that is said to be T_1 -weighted, T_2 -weighted, or proton-density weighted. Although it is possible to separate the three components of the MR signal, by collecting data under three different setups, in practice MR images represent all three properties with weights. A particular value of pulse sequence parameters will provide the best contrast between different tissue types and a series of these images can be combined to provide a multi-spectral data set. Therefore, a normal MRI scan includes three channels data: T_1 -weighted, T_2 -weighted, and proton density weighted. For example, when imaging the head of a patient, a set of images corresponding to slices through the head is collected. Each brain slice consists of three images: T_1 , T_2 and PD. In the different channels the same tissue appears with different intensities and the contrast between tissues is also different. Table 5.2 exhibits a brief synopsis of T_1 , T_2 , and PD effects on the MRI [112].

The multi-channel MRI scans give us more information about tissues. In order to improve the accuracy and efficiency of MR image segmentation, a multi-channel segmentation method is proposed in this chapter to take advantage of the information. The organization of this chapter is as follows. In Section 5.2, the properties and intensity distributions of three channel images are demonstrated. The performance of proposed fuzzy clustering framework on all three channel images is presented in Section 5.3. The algorithm for multi-channel segmentation is presented in Section 5.4. In Section 5.5, some segmentation strategies for multi-channel MR image segmentation are proposed and the performance of these approaches on simulated images is demonstrated and discussed. Finally, in Section 5.6, some concluding remarks are given.

Table 5.2
PD, T1 and T2 effects on MRI

Pulse Sequence	Tissues	Effect (Signal intensity)
PD	Fat, Fluids	High proton density (Bright)
	Calcium, Air, Fibrous Tissue, Cortical, Bone	Low proton density (Dark)
T1	Fat, Lipid-Containing Molecules, Proteinaceous, Fluid, Paramagnetic Substances (Gadolinium)	Short T1 relaxation (Bright)
	Neoplasm, Edema, CSF, Pure Fluid, Inflammation	Long T1 relaxation (Dark)
T2	Iron Containing Substances (Blood-breakdownproducts)	Short T2 relaxation (Dark)
	Neoplasm, Edema, CSF, Pure Fluid, Inflammation	Long T2 relaxation (Bright)

5.2 PROPERTIES OF T1, T2, AND PD DATA

We have known that the same tissue has the different intensities in different channels. Now we look at their difference on histogram distribution. Figure 5.1 shows a slice ($z=80$) in the multi-channel scans corrupted with 3% noise and 40% bias field and its corresponding histogram.

Fig 5.1: Intensity distribution of one slice ($z=80$) in T1, T2, and PD data; (a), (b) are T1 image and its histogram; (c), (d) are T2 image and its histogram; (e), (f) are PD image and its histogram.

In Figure 5.1, CSF is dark in T1 image but bright in T2 and PD images. Gray matter is darker than white matter in T1 image, whereas it's brighter in T2 and PD images. From the histogram of T1 image (Fig. 5.1(b)), we can see that it has three tops corresponding to three tissues and overlap only a little. From the histogram of T2 image (Fig 5.1(d)), we find that there are only two obvious tops representing gray matter and white matter. Their distributions are heavily overlapped. CSF has very wide range of intensities in T2. From the histogram of PD image (Fig 5.1(f)), we can see that the distributions of three tissues are totally overlapped and only one top can be observed.

Another slice ($z=50$) of multi-channel data is shown in Figure 5.2. This slice includes a large amount of gray matter. From the histogram of T1 image (Fig 5.2(b)), we can see that distribution of intensities appears three tops and the top in the middle is much higher than other two, which means the gray matter voxels in the image occupy larger percentage. In spite of the difference in quantities the three tissues are still separated wide enough. From the histogram of T2 image (Fig 5.2(d)), we can observe that only one top appears in the image this time. The bright CSF has the same distribution as the above, but the quantitative difference of gray matter and white matter makes them mixed together. From the histogram of PD image (Fig 5.2(f)), we can see that the intensities of three tissues are mixed together and form a "hill" with one top.

It is demonstrated from above two examples that T1-weighted images provide the best contrast for three tissues: CSF, gray matter, and white matter. T2-weighted images provide the widest intensity range for CSF, but the difference between gray matter and white matter is not as obvious as T1. In PD images the distributions of three tissues are combined together and therefore are the most difficulty to segmentation.

Our proposed fuzzy clustering framework has been implemented on T1-weighted images in last chapter. In next section we will exhibit its performance on T2 and PD images.

Fig 5.2: **Intensity distribution of one slice ($z=50$) in T1, T2, and PD data;** (a), (b) are T1 image and its histogram; (c), (d) are T2 image and its histogram; (e), (f) are PD image and its histogram.

5.3 EXPERIMENTS USING SINGLE-CHANNEL DATA

Normally one complete MRI scans include T1-weighted, T2-weighted and PD data. It can be deduced from above discussion that segmentation on T1 images is easier than T2

and PD images. In the last chapter we have demonstrated the segmentation results of our proposed fuzzy clustering framework on T1-weighted images. In this chapter we describe the implementation of our algorithm on T2-weighted images and PD images.

The simulated multi-channel MR images are obtained from the BrainWeb Simulated Brain Database at the McConnell Brain Imaging Center of the Montreal Neurological Institute (MNI), McGill University [46]. In T2 and PD images segmentation we initialize the cluster center by using the results of traditional FCM. Thus we need to execute FCM first and utilize the final cluster center of FCM as the initial cluster center of our algorithm.

A. Visual Evaluation

Fig 5.3 shows the segmentation results of our proposed algorithm on T1-weighted, T2-weighted and PD individually. The experimental MR brain images are corrupted with 3% noise and 40% bias field. In all of our experiments, non-brain tissues are removed from all images prior to segmentation and our algorithm is implemented in Matlab 6.5. Although T2 and PD images are harder to segment than T1 it is easy to observe from Fig 5.3 that the segmentation results of three channel data are all close to the true models.

B. Quantitative Evaluation

For comparison and later use we calculated both the misclassification rate (MCR) and the overlap metric. The overlap metric is defined as $2V_{ae}^k / (V_a^k + V_e^k)$, where V_{ae}^k denotes the number of voxels assigned to class k by both the ground truth and the algorithm, V_a^k and V_e^k denote the number of voxels assigned to class k by the algorithm and the ground truth, respectively, for the three tissue classes. The value of overlap metric is between 0 which means no overlap at all and 1 which means full overlap.

Fig 5.3: Segmentation results for slice of 3% noise, 40% INH on 3 channel data: T1, T2 and PD; (a), (d), (g) are original images of T1, T2 and PD ($z=60$); (b), (e), (h) are corresponding segmentation results of T1, T2 and PD; (c), (f), (i) are corresponding true models.

The overlap metric used for comparing image similarity is also called the Dice coefficient. In previous chapters we have used the Tanimoto coefficient to compare the segmentation results on IBSR [109] data. Now we illustrate the relationship between them. The Dice coefficient is defined as:

$$\kappa(S_1, S_2) = \frac{2|S_1 \cap S_2|}{|S_1| + |S_2|} \quad (5.1)$$

The Tanimoto coefficient can be expressed as:

$$J(S_1, S_2) = \frac{|S_1 \cap S_2|}{|S_1 \cup S_2|} \quad (5.2)$$

S_1 denotes the phantoms assigned to set one and S_2 denotes the phantoms assigned to set two. The range for this index is from 0 for sets that have no common elements to 1 for sets that are identical. We can rewrite the Tanimoto coefficient as:

$$\begin{aligned} J(S_1, S_2) &= \frac{|S_1 \cap S_2|}{|S_1 \cup S_2|} \\ &= \frac{2|S_1 \cap S_2|}{2|S_1 \cup S_2|} \\ &= \frac{2|S_1 \cap S_2|}{|S_1| + |S_2| - |S_1 \cap S_2| + |S_1 \cup S_2|} \\ &\leq \frac{2|S_1 \cap S_2|}{|S_1| + |S_2|} \\ &< \frac{2|S_1 \cap S_2|}{|S_1| + |S_2|} \quad \text{when } |S_1 \cap S_2| \neq 0 \text{ and } |S_1| \neq |S_2| \\ &< \kappa(S_1, S_2) \end{aligned} \quad (5.3)$$

The Equation (5.3) shows that the Tanimoto coefficient is always smaller than the Dice coefficient, except at 0 where S_1 and S_2 are completely dissimilar and 1 where S_1 and S_2 are equal.

We also want to find the function between two coefficients.

$$\begin{aligned} J(S_1, S_2) &= \frac{|S_1 \cap S_2|}{|S_1 \cup S_2|} \\ &= \frac{2|S_1 \cap S_2|}{2|S_1 \cup S_2|} \\ &= \frac{2|S_1 \cap S_2|}{\frac{|S_1| + |S_2|}{2\|S_1 \cup S_2\|}} \\ &= \frac{\kappa}{\frac{2(|S_1| + |S_2| - |S_1 \cap S_2|)}{|S_1| + |S_2|}} \\ &= \frac{\kappa}{2 - \kappa} \end{aligned} \tag{5.4}$$

Thus the Tanimoto coefficient is related to the Dice coefficient by function (5.4)

$J = \frac{\kappa}{2 - \kappa}$. Figure 5.4 shows a plot of this relationship.

Fig 5.4: Comparison of the Tanimoto coefficient and the Dice coefficient.

In Figure 5.4 both coefficients agree that 0 means the two sets are totally different and 1 means the two sets are identical. The metrics are consistent for the purpose of comparison, as an increase in the dice coefficient also means an increase in the Tanimoto coefficient. For reference, a Dice score of 0.9000 corresponds to a Tanimoto score of 0.8182, while a Dice score of 0.8000 corresponds to a Tanimoto score of 0.6667. These coefficients have been used for assessment of MR image segmentation in many publications. They are also calculated to assess our algorithm’s performance.

Table 5.3 shows the Dice coefficient for different tissue class WM, GM and CSF between T1, T2, and PD with different intensity inhomogeneity (INH) (all with 3% noise). The last row shows the corresponding MCR. We can see that segmentation results of T1 images have the less MCR than T2 and T2 have the less MCR than PD, which mean that our algorithm has better segmenting accuracy on T1 images than T2 images and PD images. At the same time MCRs change slightly with different INH for T1, T2 and PD. This also proves that our algorithm can deal with INH very well.

TABLE 5.3
Comparison Segmentation Results Between T1, T2 and PD: In Terms Of Dice Coefficient For Different Tissue Class, And The MCR, For Different INH Level.

	0% INH			20% INH			40% INH		
	T1	T2	PD	T1	T2	PD	T1	T2	PD
WM	0.9680	0.9584	0.9485	0.9726	0.9579	0.9462	0.9685	0.9575	0.9459
GM	0.9654	0.9567	0.9497	0.9701	0.9545	0.9472	0.9673	0.9531	0.9467
CSF	0.9625	0.9831	0.9368	0.9628	0.9821	0.9367	0.9575	0.9792	0.9361
MCR	0.0354	0.0413	0.0532	0.0336	0.0439	0.0530	0.0376	0.0458	0.0547

5.4 MULTI-CHANNEL SEGMENTATION METHOD

We extend our algorithm to fit the multi-channel images. We rewrite the modified objective function here:

$$J_m = \sum_{i=1}^c \sum_{k=1}^n u_{ik}^m \|y_k - b_k - v_i\|^2 \quad (5.5)$$

In this function c is also the number of classes. n is the number of data sets. y_k is the 3×1 vector of the observed log-transformed intensities at the k th voxel of multi-channel data. b_k is the 3×1 vector of the log-transformed bias field at the k th voxel of multi-channel data. v_i is the 3×1 vector of the log-transformed cluster center for class i of multi-channel data. u_{ik} is also the partition of voxel k in class i . For a 3×1 vector $[\sigma_1, \sigma_2, \sigma_3]^T$, the measurement of $\|\cdot\|$ is defined as :

$$\|[\sigma_1, \sigma_2, \sigma_3]^T\| = \sqrt{\sigma_1^2 + \sigma_2^2 + \sigma_3^2} \quad (5.6)$$

Thus in the multi-channel condition the observed intensity of image Y and corresponding bias field B are both $3 \times n$ matrixes. The cluster center V is a $3 \times c$ matrix. The partition matrix U is still a $c \times n$ matrix.

Now we can minimize the objective function J_m iteratively using three estimators of U , V , and B .

A. Bias-Field Estimation

Taking the derivative of J_m with respect to b_k and setting the result to zero we have

$$\left[\sum_{i=1}^c \frac{\partial}{\partial b_k} \sum_{k=1}^n u_{ik}^m \|y_k - b_k - v_i\|^2 \right]_{b_k = b_k^*} = 0 \quad (5.7)$$

Since only the k th term in the second summation depends on b_k , we have

$$\left[\sum_{i=1}^c \frac{\partial}{\partial b_k} u_{ik}^m \|y_k - b_k - v_i\|^2 \right]_{b_k=b_k^*} = 0 \quad (5.8)$$

Differentiating the distance expression, we obtain

$$\left[y_k \sum_{i=1}^c u_{ik}^m - b_k \sum_{i=1}^c u_{ik}^m - \sum_{i=1}^c u_{ik}^m v_i \right]_{b_k=b_k^*} = 0 \quad (5.9)$$

Thus, the zero-gradient condition for the bias-field estimator is expressed as

$$b_k^* = y_k - \frac{\sum_{i=1}^c u_{ik}^m v_i}{\sum_{i=1}^c u_{ik}^m} \quad (5.10)$$

B. Cluster Prototype Updating

Taking the derivative of J_m with respect to v_i and setting the result to zero, we have

$$\left[\sum_{k=1}^n u_{ik}^m (y_k - b_k - v_i) \right]_{v_i=v_i^*} = 0 \quad (5.11)$$

Solving for v_i , we have

$$v_i^* = \frac{\sum_{k=1}^n u_{ik}^m (y_k - b_k)}{\sum_{k=1}^n u_{ik}^m} \quad (5.12)$$

C. Membership Evaluation

We compute this using one Lagrange multiplier

$$F_m = \sum_{i=1}^c \sum_{k=1}^n u_{ik}^m \|y_k - b_k - v_i\|^2 + \lambda \left(1 - \sum_{i=1}^c u_{ik} \right) \quad (5.13)$$

Taking the derivative of F_m with respect to u_{ik} and setting the result to zero, we have

$$\left[\frac{\partial F_m}{\partial u_{ik}} = m u_{ik}^{m-1} \|y_k - b_k - v_i\|^2 - \lambda \right]_{u_k = u_k^*} = 0 \quad (5.14)$$

Solving for u_{ik}^* we have

$$u_{ik}^* = \left(\frac{\lambda}{m \|y_k - b_k - v_i\|^2} \right)^{1/(m-1)} \quad (5.15)$$

Since $\sum_{j=1}^c u_{jk} = 1$ for $\forall k$

$$\sum_{j=1}^c \left(\frac{\lambda}{m \|y_k - b_k - v_j\|^2} \right)^{1/(m-1)} = 1 \quad (5.16)$$

or

$$\lambda = \frac{m}{\left(\sum_{j=1}^c \left(\frac{1}{\|y_k - b_k - v_j\|^2} \right)^{1/(m-1)} \right)^{m-1}} \quad (5.17)$$

Substituting into (5.15), the zero-gradient condition for the membership estimator can be rewritten as

$$u_{ik}^* = \left(\sum_{j=1}^c \left(\frac{\|y_k - b_k - v_i\|^2}{\|y_k - b_k - v_j\|^2} \right)^{\frac{1}{m-1}} \right)^{-1} \quad (5.18)$$

Now we can use the three function (5.10), (5.12), (5.18) to update B , V , and U respectively.

In the estimation and correction of bias field, the intensity inhomogeneity is assumed to be smooth and slowly varying in each channel of data, but is independent for each

other. Thus the huge difference of bias field in a voxel between channels is allowed. For the mean spread filter, the spread control function becomes

$$\|b_i - b_j\| \geq \varepsilon_3 \quad (5.19)$$

where b_i and b_j are adjacent bias field. Using Equation (5.19) all difference bigger than ε_3 in bias field of each channel would be found. Therefore we can use the mean spread filter to obtain the smooth bias field. When the distance between b_i and b_j is bigger than the threshold ε_3 the following smooth procedure is performed:

$$b_i^* = b_j^* = [b_i, b_j] \begin{bmatrix} 0.5 \\ 0.5 \end{bmatrix} \quad (5.20)$$

The procedure continues along each of four directions until the distance of adjacent bias field is smaller than ε_3 or reaches the edge.

Now we can obtain the extended modified spatial FCM algorithm for multi-channel MR image segmentation.

Step 1: Discard the non-brain parts from the MR head scans and obtain the ROI, using the methods in Section 3.3.1.

Step 2: Use the fuzzy filter in Section 3.3.2 to remove the noise in image.

Step 3: Select initial class prototypes V . To do this, we execute traditional FCM completely for T2 and PD images. Set $\{b_k\}_{k=1}^n$ to equal and very small values (0.0001).

Step 4: Compute the partition matrix using Equation (5.18).

Step 5: Update the prototypes of the clusters using Equation (5.12).

Step 6: Update the bias field using Equation (5.10).

Step 7: Filter the bias field to a smooth one by the proposed new version of mean spread filter using Equation (5.20).

Repeat steps 4-7 until termination. The termination criterion is $\|V_{new} - V_{old}\| < 0.000001$ or when it reaches the maximum iteration times ITMAX=10.

This algorithm is implemented on simulated multi-channel MR images. The results are shown in Figure 5.5.

Fig 5.5: Segmentation results for slice of 3% noise, 40% INH on multi-channel data: T1, T2 and PD; (a), (c), (e) are original images of T1, T2 and PD ($z=50$); (b), (d), (f) are corresponding segmentation results of T1, T2 and PD.

5.5 PERFORMANCE OF MULTI-CHANNEL METHOD

For comparison purpose two other strategies are proposed to segment the multi-channel data. One is combination segmentation of three partition matrixes. Here we segment the T1, T2 and PD data respectively and obtain three partition matrixes U_{T1} , U_{T2} and U_{PD} . Then we compute the new partition matrix:

$$U = U_{T1} + U_{T2} + U_{PD} \tag{5.21}$$

Finally we segment using $\text{MAX}(U)$ to obtain the classification results.

Another approach uses the characters of different channel images. From the Section 5.2 and Table 5.3 we perceive that segmentation of T2 images has better performance on CSF, while the segmentation on PD images provides the worst result, therefore we use two steps to segment the tissues. In first step we implement our algorithm on T2 data only and segment the CSF with other tissues (WM+GM). In the second step we implement our algorithm again on T1 data except the CSF voxels to segment WM and GM. This method makes use of only two channel images: T1 and T2.

The segmentation results of the three methods are shown in Fig. 5.6 on T1 images.

Fig 5.6: **Comparison of Three multi-channel segmentation strategies;** (a) is original image ($z=45$); (b), (c), (d) are segmentation results of M1, M2, M3.

The quantitative evaluations of above three strategies are illustrated in following table. In Table 5.4, M1, M2, M3 mean the three multi-channel segmentation methods proposed above. We implement these methods on 3% noise with different bias field data (0, 20%, 40%). The Dice coefficient for different tissues: WM, GM and CSF are shown in the table for comparison. The last is the overall segmentation accuracy: MCR. As we have seen from the table, the first and the second methods have almost the same Dice index and the same MCR. Furthermore, they are also almost the same with the single channel method. However the third method has better performance and also better results than others. This is because it takes advantage of multi-channel data. Although the contrasts of gray matter and white matter in T2 and PD are worse than T1, the contrasts of CSF in T2 images are better than T1. Thus the performance of M3 on CSF shows some improvement. Another good character of the third method is that it requires less time, compared with other two methods.

TABLE 5.4
The Comparison of Segmentation Results with Three Methods: In Terms Of Dice Coefficient For Different Tissue Class, and The MCR, For Different INH Level.

	3% N, 0% INH			3% N, 20% INH			3% N, 40% INH		
	M1	M2	M3	M1	M2	M3	M1	M2	M3
WM	0.9668	0.9683	0.9683	0.9724	0.9720	0.9726	0.9681	0.9678	0.9684
GM	0.9664	0.9647	0.9678	0.9717	0.9718	0.9722	0.9670	0.9668	0.9671
CSF	0.9652	0.9645	0.9832	0.9632	0.9635	0.9821	0.9578	0.9578	0.9792
MCR	0.0352	0.0354	0.0334	0.0332	0.0332	0.0318	0.0375	0.0374	0.0348

5.6 CONCLUDING REMARKS

In this chapter, the characters of three channels MR brain images: T1-weighted, T2-weighted, and PD are illustrated. The disadvantages of heavy overlapping in intensity distribution and lower contrasts on gray matter and white matter make the segmentation on PD and T2 images more difficult. The segmentation results of our proposed fuzzy clustering algorithm on these three channel images indicate that our method can also deal with PD and T2 images.

We also proposed the extended multi-channel MR image segmentation algorithm. The three channel data are included and processed in this method simultaneously. A new mean spread filter is proposed to smooth the bias field of multi-channel data. For the best use of multi-spectral information of MR images several segmentation strategies are presented and compared. The additions of T2 and PD information in the first and

second strategies can't obviously improve the segmentation performance. The third method takes the advantage of better contrast of CSF on T2 images and therefore gets the best results.

Chapter 6

Conclusions and Future Research Suggestions

6.1 CONCLUSIONS

In current computer-aid MRI image understanding, automatic segmentation of different tissues is the critical problem. The goal of this thesis is to develop an intelligent system to accurately segment the MRI brain images into three meaningful parts: white matter, gray matter, and cerebrospinal-fluid. The major factors that influence automatic segmentation include noise, partial volume effect, and random field nonuniformity. It is demonstrated that a successful automatic segmentation algorithm must consider these difficulties and overcome all of them.

MODIFIED SPATIAL FUZZY CLUSTERING

After addressing the obstacles in the MRI image segmentation, a mixed method is described to preprocess MRI head scans and obtain the brain: (the regions of interest (ROI)). The modified spatial fuzzy clustering algorithm is proposed to segment the MRI images and simultaneously estimating and correcting the intensity inhomogeneities as well. There are three new aspects in our algorithm. The first one is a fuzzy filter used for the noise removal. The noise is the primary obstacle involved in every intensity-based method of image processing. Hence, a special fuzzy filter is used to deal

with the noise in a pre-processing step. This filter can remove the noise and avoid the blurring of edges. As a result, it decreases effect of noise on our algorithm and improves the segmentation precision greatly.

The second one is the modified generalized objective function developed for the proposed algorithm. In this objective function, MRI image model is considered and the true log-transformed intensities are used for the segmentation. Because the true log-transformed intensities are calculated from the observed images and the log-transformed bias field, the segmentation accuracy can be improved while the bias field can be estimated simultaneously.

The third new aspect is that a mean spread filter is used to smooth the bias field to avoid misclassification. The smoothness of the bias field is an important property and has been used for estimation and correction of intensity inhomogeneity in many approaches. Therefore in our algorithm this filter is proposed and used to adjust the bias field to a smooth level and push the voxels to the correct cluster center. This filter makes use of the neighborhood constraints and allows the largest freedom. Therefore with this filter the bias field can be corrected and estimated while the voxels can be classified to the right tissue types.

Altogether, our algorithm is formulated by modifying the objective function of the standard FCM algorithm to compensate for intensity inhomogeneity. In the iteration procedure we use a mean spread filter to smooth the bias field for obtaining the correct classification. We also use a fuzzy filter to make our algorithm robust in the noisy environment. In particular, this method does not require a model of the tissue intensities in terms of discrete tissue classes, nor does it rely on the complicated initialization. Our algorithm requires only two parameters to be selected: parameter α controlling the efficiency of noise removal, threshold ε_1 controlling the smoothness of the estimated bias field and accuracy of the segmentation. The experiments show that both of these

parameters are robust in the different conditions of noise and bias field. This is a considerable advantage in automated data analysis as the method can be applied at the first stage of automatic classification system, without prior knowledge of the data.

PARTIAL VOLUME LABELING

After conquering the noise and intensity inhomogeneity, partial volume effect is another obstacle in the MRI image segmentation. Accurate and fully automatic segmentation of MRI images is complicated by partial volume voxels that contain a mixture of two or more tissue types. In order to overcome the partial volume effect, a fuzzy clustering framework for partial volume segmentation is developed in this thesis.

This framework encompasses and extends above method. For describing the partial volume effect in MRI images a mixed tissue types model is introduced. This model is only applied to voxels labeled as mixture. It is demonstrated through the experiments in the thesis that the mixed model is more sophisticated and efficient to represent some MRI image voxels. Besides the mixed model two properties are assumed to differentiate the partial volume voxels from the single tissues. The first is that their gray scales have a distance from the mean value of pure tissues that form them. The second: CSF is sufficiently separated from WM so that their mixtures must be adjacent with the pure CSF and WM voxels. From the above assumptions a two-step method is proposed to label the mixture voxels. This method includes the global strength of the whole image and the local strength of the neighborhood. The Gaussian distribution of the ideal tissue class is used to estimate the possibilities of mixture voxels. The neighborhood searching method is presented to label the CSF and WM mixtures. With this labeling process those partial volume voxels could be oversegmented to different tissue types. The results are quantified both on simulated and real MR images to demonstrate the robustness and the stability of the algorithm.

MULTI-CHANNEL MRI SEGMENTATION

Normally one complete MRI scans include PD, T1-weighted and T2-weighted data. Different tissues have different performances in these three channel images. The experimental results show that our proposed algorithm performs very well on all of three channel images. The multispectral MRI images: PD, T1, and T2 can therefore provide additional information than one channel data. Now due to the three parallel image data, how to use the additional information to improve the segmentation is a problem. In order to segment the multi-channel images three approaches are proposed and their performances are compared. These approaches are basically the extensions of above method. The previous framework has overcome the noise, the intensity inhomogeneities, and the partial volume effect. The first is directly changing the parameters in the framework to the vectors and then performing the segmentation. The second is segmenting the T1, T2, and PD data respectively and then combining their results. The third method uses the characters of different channel images. From the experiments the segmentation of T2 image has better performance. Therefore a two steps method is proposed to segment the tissues. In the first step the algorithm is implemented on T2 data only to segment the CSF with other tissues (WM+GM). In the second step the algorithm is implemented again on T1 data except the CSF voxels to segment WM and GM. It is demonstrated through the experiments that the third method provides better results.

6.2 FUTURE RESEARCH SUGGESTIONS

There are a lot of research directions that can be pursued as there are many unsolved problems in MR image classification. Some suggestions of the future work based on the work carried out in the thesis are given as follows.

The work in the thesis focuses on segmentation of MR normal images. The automated algorithm for segmentation of abnormal MR images, (for example, multiple sclerosis lesions, brain tumors, Alzheimer's disease, cerebrovascular disease etc.), can also be explored.

Functional MRI (fMRI) has been developed as a tool that makes it possible to observe the brain as it performs various tasks. In functional brain imaging the observations might be statistical parametric maps (SPMs) which are typically the result of a temporal linear model of the four-dimensional functional brain imaging data. Thus the task to classify areas in the brain as either activating, deactivating, or not activating is important and should be studied.

Cardiac MR imaging is also an area of active and continuous development which provides all kind of challenging. Computer-aid methods can help to answer the questions such as if coronary arteries are patent, if the cardiac muscle is adequately perfused, and if the tissue contracts properly in order to supply the needed amount of blood.

With the development of MR imaging techniques, such as real-time imaging, more sophisticated methods can be explored to help the clinical analysis.

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