

BRAIN TISSUE SEGMENTATION: A REVIEW

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Abstract: Segmentation of brain tissue is a prominent and most critical step of research areas in medical image processing. It is extensively used to measure and visualise the anatomical structures of the brain, to analyse brain changes, to delineate diseased regions, and to design surgical procedures and image-guided therapies. Researchers in the field of medical image processing have previously proposed many approaches with varying degrees of accuracy and complexity. In this review, we have studied the most relevant brain tissue segmentation method and their latest advancement in neuroscience research. The review also presents an effective comparison among the different brain tissue segmentation methods and their methodologies. Furthermore, a review of some of the validation measures used to compare different segmentation algorithms is presented.

I. INTRODUCTION

Medical picture segmentation is the task of segmenting objects in medical picture analysis. Image segmentation performs a central function in medicine, prognosis and Accurate treatment strategy. It is the method of partitioning the brain image into a collection of disjointed locations with comparable characteristics, like intensity, homogeneity, textures etc. in order to extract tissues from a brain image. For carrying out effective Quantitative brain analysis, methods of separating tissues like white matter (WM), Grey Matter (GM), and cerebrospinal fluid (CSF) is commonly employed. It aids in the differentiation of normal tissues from the abnormal ones to identify the disease like type of brain tumor, Parkinson's disease, multiple sclerosis, AD, Dementia, Schizophrenia and Alzheimer's disease [1]-[4]. There are numerous methods for segregating brain tissue have been proposed by researchers in the past and have been successfully utilised for illness Prognosis and therapy planning. Nevertheless, there are many challenges associated with these segmentation methods because medical photograph suffer from many imperfections, such as intensity homogeneity (IIH), noise and dysfunctional tissues with heterogenous signal intensity. Moreover, the effectiveness of brain tissue classification methods is influenced by a number of characteristics, including the tissue border, its size, shape, consistency, and its ambiguous placement, all of which are inherent in the image acquisition modalities [5]-[9].

The study's main contribution is a survey of the most recent brain tissue segmentation algorithms and their present state-of-the-art. The focus of this paper is on three essential features: latest developments in brain tissue algorithms segmentation, and the potential for existing methods to be improved more strong, as well as the unsolved issues. The

paper also looks at the difficulties that segmentation algorithm confronts as a result of inherent modality concerns. The benefits and drawbacks of the algorithm tested are summarized in a table to present a well-structured visions. In addition, we've presented and talked about how to quantify conventional validation measures the and the efficiency with which a segmentation approach works. Its usefulness in a variety of situation like their clinical use and hardware implementation is also discussed. The following is a breakdown of the paper's structure. The second section covers the various methods for segmenting brain tissue. The performance indices for computing the algorithm are described in Section III. The Remarks is presented in Section IV and Section V concludes with a conclusion..

II. METHODS FOR SEGMENTING THE BRAIN TISSUE

In this Paper we assess the most frequently used procedure of brain tissue segmentation as well as the current break throughs in these method. We have discussed several segmentation method using 2D and 3D MRI. These brain tissue segmentation method comprises of several standard image processing methodologies such as deformable models (DM), Fuzzy c-means (FCM), region growing, Gaussian mixture model (GMM), etc. and so on. Then, the merits and demerits of the strategies are outlined in table I.

Generally, there are five categories of brain tissue segmentation method which are grouped as follows:

1. Manual segmentation
2. Region-based segmentation
3. Clustering-based segmentation
4. Thresholding-based segmentation
5. Features extraction and classification-based

A. Manual Segmentation

Manual segmentation is a technique of manually separating pixels in the same intensity range by a human operator (e.g., an analyst or a surgeon). It involves a highly experienced medical professionals multidisciplinary board consisting of trained technologist, radiologist and pathologist. However, this approach has a number of drawbacks, including an blurry boundary, weak tissue contrast,

and shaky hand-eye coordination. With the recent improvement over the past few years, the manual segmentation has become a tedious and time-consuming. The

result of the segmentation method may vary with the expert. Hence this classical and traditional method of highlighting and classifying pixels in the same intensity range is also time taking and prone to errors. Furthermore, Manual segmentation also becomes a challenging task with these newly developed high dimensional and multifunctional imaging techniques. Many automatic approaches are given by the researchers to solve this problem.

One of the most often used methods for automatic brain tissue segmentation is Statistical Parametric mapping (SPM). It is a software packaged created by researchers at the university College London's Wellcome Department of Imaging Neuroscience [10], [11]. Many automatic segmentation methods have an extensive search approach and take a long time to compute. To deal with the problem of exhaustive research, segmentation methods use optimization tools such as the Genetic Algorithm (GA), Bacterial Foraging Optimization (BFO), Particle Swarm Optimization (PSO) and others. Furthermore, Evolutionary algorithm (EAs) can deal with a variety of ill-defined issues in brain tissue segmentation, such as multimodality, discontinuity and noise [11]-[13].

B. Region-based method

Region based segmentation methods rely on the image's intensity homogeneity to determine the object border. The following are the some most common tactics used in this method:

- 1) An approach based on contour and shapes
- 2) Region growing
- 3) Level setting mechanism based on region
- 4) Graph based method

T1-weighted MR images is used in contour and shape based technique and T2-weighted MR images are used in graph based methods.

1) *An approach based on contour and shapes:* An initial contour is supplied near to the intended border in the contour and shape-based technique. The approach then changes the contour to bring it closer to the goal border by minimising a predetermined criterion. The DM method is a prominent contour and shape-based strategy. Prior knowledge about the shape of the target object is used in a knowledge-based segmentation method. It all begins with a starting boundary shape that is arbitrary and in the form of a curve Active contours are DMs that deform and develop toward the target boundary. The first DM for recognizing item boundary from an image was proposed by Kass et al. [14]. The contour's deformation is governed by the minimization of an energy function. Internal and external energy terms make up the energy function. The smoothness of the shape is handled by internal energy. The external energy term in the image domain pushes the contour toward desirable qualities like gradient, texture, edge information, and so on. Traditional active contour algorithms rely on gradient data. In this method, The initial contour is drawn near to the object of

interest's boundary in this procedure. As a result, there is a lot of external energy, which makes it possible to do things bring the contour closer to the target object's edge. However, The approach is unable to handle the curve's topological alterations. In this case, level set approaches monitor contours and surfaces using parameterized curves [14]-[18]. Mesejo et al. [14] proposed a hybrid level set (HLS) segmentation approach for medical illustrations. The approach integrates prior shape knowledge with both region and edge-based information. In addition, GA calculates the level set's parameters. Furthermore, the shape prior is derived using scatter search.

There are two forms of active contours: parameterized active contours (PAC) and geometric/geodesic active contours (GAC). A parameterized curve in a Lagrangian formulation is described by PAC. The curve's explicit characterisation simplifies user interaction and the declaration of a priori shape limitations. GACs are primarily based on surface evolution theory and geometric flows in the light of the Euler formulation. The approach uses gradient information to define an edge and is able to handle these curves efficiently. First, It starts by creating an initial contour that is near to the intended boundary. Second, it minimizes a boundary-based energy function to construct the contour toward the strongest gradient. This model is implicitly described by a level set of 2-D functions, in which the number of iterations determines the halting criterion [14]- [18].

Furthermore, there are two types of DMs that are based on the feature of the item of interest: edge-feature (EF) and region feature (RF). EFs are the most commonly used approach for segmenting brain pictures into tissues such as WM, GM, and CSF for sickness Prognosis. Edge-detection methods produce arbitrary contour lines around the target object in EFs. Using various similarity measurements, the object of interest is retrieved by combining these contour lines. Edge detectors, on the other hand, rely on image gradient information. As a result, the detectors can only recognize objects in the image domain that are defined by a strong gradient function. The above approaches' performance is greatly dependent on the starting contour's location, edge opening, weak edges, inhomogeneity, and noise. In order to address the aforementioned issues, researchers have included the expectation maximization (EM) method, gradient vector flow, or self-affine mapping system in traditional models. To identify the region of interest, RFs rely on statistical and homogeneity properties (ROI). RFs, unlike EFs, construct the ROI curve using specified region statistics. They are, however, unable to locate object boundaries. Researchers recommended using a priori shape information or statistical information in the energy function to combat RF issues.

Many solutions, including region growth, region-based level set [15], [26]-[28], and graph-based methods [27], [28], rely on statistical estimation of regions or graph theory to overcome the limitations of prior methods.

2) *Growing Regions:* The mechanism for growing regions is determined by the homogeneity and connection conditions. A seed point (pixel) is chosen from each region in the classical approach of region expansion. The pixels in the

immediate vicinity are gathered based on their homogeneity requirements (e.g., intensity similarity). The seed point accumulation procedure continues until the termination condition is met. As a result, a network of interconnected regions emerges. In the segmentation of brain tissue, region growing is a typical approach. The regions of the object of interest are supposed to have the same or slightly varied intensity values to achieve homogeneity. As a result, segmentation performance may be influenced by seed selection and homogeneity requirements. For homogenous MR images, region expanding is usually sufficient. It's also well-suited to medical picture segmentation, as images are largely made up of object and backdrop. Combining the region-growing method with other technologies such as edge detection could be one solution to the problems. In addition, homogeneity criteria for numerous brain lesions have yet to be determined [19], [29]— [31].

3) *Region-Based Level Set Methods:* To evolve the contour, region-based level set methods rely on the level set. The energy function of the region-based level set approaches is developed using common clustering methods such as k-means, FCM, and GMM. Chan and Vese [15] proposed the CV model, which is a region-based level set technique. It is based on the concept of deforming the curve enclosing the target object by minimising an energy function. It is suitable for the piecewise constant situation [15] and is based on level set to develop the contour. In [15], the Mumford and Shah functions are derived using k-means in the piecewise (PC) level set approach to solve two homogeneous segments. The multiphase level set algorithm uses the same concept to solve multiple segments. This approach overcomes noise and blurred boundaries. Mandal et al. [13] proposed rewriting the CV model as an optimization problem. To decrease the fitting energy function, the authors employed PSO. Regardless of the starting contour choice, this improved technique can reach global minima [13], [25], [33], [34]. However, the efficacy of this technique degrades when medical images have a complicated intensity distribution. To overcome the estimate of phase value, [44] uses finite mixture models and GMM with the level set approach. The approach estimates the foreground homogeneous intensity distribution as well as the background complex intensity distribution at the same time.

Complex structures can be seen in a lot of medical photos. As a result, the assumption of homogenous intensity for the foreground is no longer valid. Statistical variational models such as shape and extra attributes are used to increase the accuracy of level set approaches. The size, shape, and intensity distribution of tissues and organs would varied greatly amongst patients. As a result, gathering training data with a wide range of variables becomes problematic. As a result, the segmentation accuracy of level set approaches including statistical prior models is limited [21], [36].

4) *Graph-Based Approaches:* Graph-based methods have recently gained popularity in the field of brain tissue segmentation. Unlike other region-based techniques, they use foreground and background seeds to locate the image's components. When combined with local pairwise pixel similarities, this additional information improves

segmentation accuracy when compared to previous approaches [3]. Graph-cut [27] and random walker (RW) [28] are some of the most often used graph-based approaches. Due to noise, complex intensity distribution, and uneven intensity of aberrant tissue, medical images typically have nonuniform foreground and background. The method's performance deteriorates in this case. To accomplish accurate segmentation, Li et al. [18] suggested a coupled statistical and graph (CSG) variational model. The multimodal intensity distribution of foreground and background is estimated using statistical functional analysis. A prior probability map is also used to distinguish pixels with tiny variations. The approach is used to segment tissues in computed tomography and magnetic resonance imaging, as well as to detect tumours. These seed points act as strong constraints for the optimal segmentation results, integrating global information with local pairwise pixel similarities.

C. Threshold-Based Methods

One of the most used segmentation methods is thresholding, in which the target objects are segregated by comparing their intensity values to one or more thresholds. Intensity thresholding is another term for it. Threshold values can be set globally or locally. Fixed thresholding and adaptive thresholding are two types of threshold-based approaches (see Fig. 2). In thresholding-based techniques, T2-weighted MR images are used. Pixels over the threshold level are assigned to a group, whereas pixels below the threshold are considered background in fixed thresholding. In MRI, however, the object of interest is marred by a slew of artefacts. As a result, fixed thresholding-based approaches use criteria including entropy, between-class variance, and others to detect the object of interest.

A single threshold value can be utilised to identify an item from the background when an image histogram is bimodal. It assigns a one to readings above the threshold and a zero to readings below the threshold. A global threshold T segments the image provided as $I(x, y)$ for an image $I(x, y)$.

$$I(x, y) = \begin{cases} 1, & I(x, y) > T \\ 0, & I(x, y) \leq T \end{cases} \quad (1)$$

where pixels with a value of 1 denote an object and pixels with a value of 0 denote a blank space. Such an approach's segmentation

accuracy is heavily dependent on statistical fluctuations. The choosing of thresholds becomes more difficult as the number of regions grows. It should be highlighted that brain tissue segmentation necessitates the segmentation of many tissues (i.e., WM, GM, and CSF).

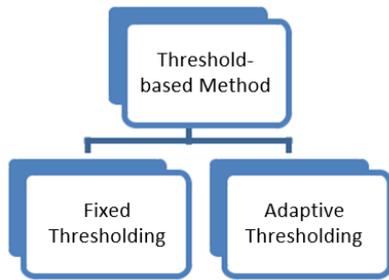


Fig. 1 Threshold-based Methods in brain tissue Segmentation

Adaptive thresholding is when fixed thresholding adaptively decides the threshold value for the object of interest. The threshold value is determined adaptively by a local neighbourhood surrounding a pixel in this method. The threshold values are frequently estimated using prior knowledge or local statistical features. To compute the threshold value from a T2-weighted MRI, Stadlbauer et al. [37] employed a Gaussian distribution of pixel intensity levels. The value defines a demarcated area that is used to identify diseased tissue. When imaging parameters use spatial information with a priori knowledge, however, they may not perform effectively. Many academics have proposed a thresholding strategy based on geographical information or the maximum entropy principle to reduce the impact of these issues.

Entropy-based, Otsu's approach, and evolutionary-based methods are some of the most common and effective thresholding-based methods for MRI brain tissue segmentation. To derive the appropriate threshold values from the histogram, Kapur et al. [22] proposed maximising of entropy. By maximising the between-class variance of grey levels, Otsu [23] introduced a nonparametric methodology called Otsu's method to identify optimal threshold automatically. With an increase in the number of thresholds, computational time increases in both methods due to the broad search strategy. There are many computational methods that are available in the literature to reduce the computational time [11], [12], [39]-[40].

EAs have recently been combined with thresholding to identify the best threshold values while minimising computational time. Multimodality, discontinuity, time-variance, unpredictability, and noise are examples of ill-defined problem domains that EAs can easily adapt to. Maitra and Chatterjee [35] used BFO in the histogram-based thresholding method to segment a variety of conventional brain MRIs. Manikandan et al. [24] found the optimal threshold values by maximising the entropy using real-coded GA (RGA) with simulated binary crossover (SBX) in multilevel thresholding for segmentation of T2-weighted MRI [11] using real-coded GA (RGA) with simulated binary crossover (SBX) in multilevel thresholding for segmentation of T2-weighted MRI [11].

D. Methods of Clustering

Clustering methods are statistical techniques based on pixels used in brain tissue segmentation. Some similarity measurements, such as distance, connection, and intensity, are used to partition the pixels into groups or clusters in this method. There are two sorts of clustering methods: 1) hard clustering and 2) soft clustering (see Fig. 3). T1-weighted MR images are used in the clustering algorithms.

The first method divides the pixels into clusters by using sharp border values. Hard clustering is exemplified by k-means. Soft clustering is divided into two types: FCM and mixture models. Pixels are gradually divided in this approach, with a membership function (based on FCM) or an underlying probability (based on mixture models) used to determine whether a pixel belongs to a cluster. The membership function in FCM-based approaches assigns a membership grade value to each pixel, indicating how much it belongs to a cluster. The underlying likelihood of the data clustering into separate groups is assumed to have some distributional form in the mixture models. [4], [70]-[75].

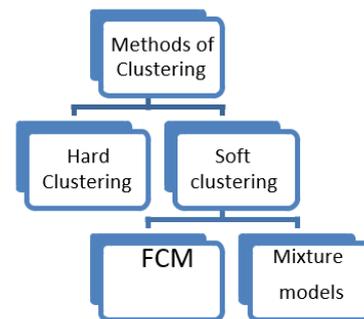


Fig.2 Method of Clustering in brain Tissue Segmentation

**TABLE 1
MERITS AND DEMERITS OF THE MOST COMMONLY USED BRAIN TISSUE SEGMENTATION METHODS**

Name of the Method	Merits	Demerits
Deformable Model	When the contour is initialised close to the intended Object boundary, the approach delivers good results. Minimizing an energy function controls the contour's Expansion or contraction over time.	The method's efficacy is entirely dependent on initial contour location. Sensitive to images with a blurry boundaries that are noisy.
Level set	Cavities, concavities, convolution, splitting and merging can all be controlled. Simple parameter tuning is required.	Noise, weak borders, low contrast between sections, misleading gradients.

PAC	PACs are efficient models that need basic computations.	PACs are efficient models that need basic computation
GAC	GACs have the ability to handle topological changes in the curve, making them useful for segmenting complex Curves. With the use of level set function, they can detect interior curves, cups and multijunction and other features.	Sensitive to the placement of the beginning of contour.
EF	Deform and move the curve in the direction of the target items limits, local edge information is used .	Weakly defined edges, noise, IIH, computing complexity are all major issues. To obtain hole -free art-facts, post processing is required.
RF	Capable of suppressing startup and noise issues in EFs.	In the presence of IIH, noise, and heterogeneous objects, performance suffers.
Region growing	The benefits of taking into account both visual and spatial information. It is impervious to changes in the inner workings, resulting in closed zones.	There are three major issues: 1) pixel processing order; 2) automatic selection; and 3) regions with holes and noise. Furthermore, region growth is ineffective when it comes to segmenting several items
CV model	It's a good way to get around the constraints of edge-based edge-based approaches. Interior contours can be detected, hence it could be utilised for medical imaging with weak With IIH, a piecewise smooth model could be useful for Medical pictures.	Images with a complicated background and erratic intensity limit you can do. Only images with homogenous regions operate with the piecewise constant case. Local minima are common during contour evolution due to the nonconvex and nonunique structure of the energy function. This type of

		convergence frequently results in unfavorable segmentation results
Graph based	For efficient segmentation, combine global information using local pairwise pixel similarities.	Using simply statistical classification, it is difficult to distinguish pixels with the same minimal changes between foreground or background
Fixed thresholding	For photos with homogenous intensity, high contrast, and discriminant grey levels between object and background, this method works well. Because of its ease of implementation and computing efficiency, it is employed in brain tissue segmentation.	The correlation of pixels is not taken into consideration in this method, which is a fundamental flaw. They also result in pixel misclassification due to noise, IIH, and tissue Overlapping. The histogram of the image is corrupted by these aberrations, making segmentation with global thresholding challenging.
Adaptive Thresholding	When a single threshold value is unable to segment or a threshold value cannot be obtained from an image's histogram, this approach is chosen. This is a quick and easy way to segment several items using an intensity histogram.	The grey scale distribution, noise, multichannel images, and images containing multimodal regions all affect the effectiveness of these approaches.
Hard clustering	Image with homogeneous regions is ideal. It's best for real-time image segmentation because it takes less time to compute.	Noise, IIH, and photos with diverse regions make it vulnerable.
Soft clustering	It does not use a sharp boundary to separate the pixels into groups, unlike hard clustering. To cluster the pixels, it defines a membership function.	Noise and IIH sensitivity. When grouping pixels in the image domain, no spatial information is taken into account. Further, because to bad initialization, it yields a local optimal solution.
Mixture model	Analyze an image statistically. By	Within a class, there is no spatial relationship

	modelling the intensity variation of each tissue type as a Gaussian distribution, they can handle bias field correction and spatial regularisation in the immediate region.	between nearby pixels. this leads to a local optimum.
DWT	Capable of analysing an image at different resolutions. Maintain the sharpness of the edge. Provide useful information about a signal's localised frequency, which is useful for classification.	Sensitive to time shifts, lack of directionality, and phase information. To increase performance its common to include a dimension reduction strategy. Complexity of computation is high.
Gabor filter	Local visual properties such as orientation, spatial Frequency (scale), and localisation can be captured.	The choice of scale and direction is made on trial-and-error basis. As a result, a high-dimensional feature vector is produced. It necessitates a big amount of memory. Complexity of computation is high.
Statistical features Extraction Method	Take a look at the pixels' interrelation. Capture local picture features that can be used to distinguish unusual formations from normal tissue such as brain tumour tissue. Computational complexity is reduced.	Sensitive to visuals with a wide range of intensity levels. The location, size, shape and texture of tissues, as well as the unclear tissue boundaries and noise inherent in MR images, all affect performance.
KNN	It's a classifier that's based on instances. In the training photos, it is capable of preserving information. Simple to implement.	The response time for large datasets is extremely long. Unwanted features are sensitive, as their contribution to similarity leads to misclassification.
ANN	The most widely used machine learning algorithm. The processing elements are organised in a way that resembles the human brain. Capable of performing effectively in non linear domains that are complex and	Computational complexity and response time are both high.

	multivariate. In contrast to statistical models, ANN does not require data allocation	
SVM	In high-dimensional feature space, this is the most common choice. High generalisation ability.	It necessitates a significant amount of training time. It necessitates a lot of storage space. Patient-specific education

SPM, a specific software for brain tissue segmentation based on mixture models, has been reported in the literature. It's capable of jobs like skull stripping, bias field correction and automatic segmentation. Brain tissue SPM segmentation can be done in three different ways:

- 1) segmentation by default;
- 2) SPM8-based segmentation;
- 3) a new design that incorporates a hidden Markov random field (HMRF)

The SPM programme has been widely used in the neuroimaging field to do automated functional and structural brain image analysis. However, there are few studies comparing the software's segmentation accuracy to other approaches for segmenting GM, WM, and CSF [10]. Furthermore, the involvement of a domain expert may be beneficial when developing any advanced programme for better brain tissue segmentation outcomes.

1) *FCM*: Out of all the soft clustering algorithms, FCM is the most common, as it assumes that image pixels (or voxels) belong to many clusters. A similarity criterion is used to divide pixels into clusters. As a result, it might not be suited for segmenting pictures that have been tainted by noise and artefacts, such as IIH or the shading effect in MRI. As a result, various modified FCM methodologies [50]–[52] have been proposed in the literature to aid in the preparation of FCM for better tissue segmentation.

Researchers also employed a multiplicative bias field (i.e., B-spline surface) to represent the intensity nonuniformity (INU) effect and a dissimilarity index for spatial voxel connection to suppress the INU effect. The approach efficiently segments noise and INU-affected brain MRI. Chuang et al. [52] presented a weighted membership function for spatial FCM (sFCM). The suppression of INU, the elimination of noisy areas, and the compression of spurious blobs are the key benefits of this technology. It effectively segments T1- and T2-weighted MRI images of the brain. Using wrapping-based curvelet mapping as a preprocessing step to eliminate noise in MRI is one technique to modify sFCM. Using the kernel technique for clustering, fast spatial constraint, fuzzy kernel FCM (FKFCM) maps input data (i.e., pixel intensities) to a higher dimensional space. The MRI segmentation performed

by FKFCM is satisfactory. The method's strength is demonstrated through studies with synthetic images, digital phantoms, and clinical images influenced by noise.

For robust brain tissue segmentation, many researchers have proposed generalised FCM by modifying its objective function. The effect of IIH caused by the bias field in the MRI is suppressed by bias-corrected FCM. The method alters the goal function and adds a regularisation, allowing for pixel labelling based on its surroundings. It works well for MR pictures with salt and pepper noise, but at the cost of a long computation time. FCM also incorporates a coherent local intensity clustering (CLIC) criterion for smoothness of bias field without any regularisation. This method assumes that local region intensity is coherent and incorporates a Gaussian kernel in the energy function to adjust for bias. The addition of regularisation improves the method's effectiveness even more. CLIC criteria were employed by some studies to convert a multiplicative bias field to an additive form, decreasing complexity at the expense of the partial volume effect (PVE). The nonlocal regularised FCM (NLRFCM) approach preserves fine brain structures by using nonlocal spatial regularisation [50], [52].

Adhikari et al. [4] recently introduced a conditional spatial FCM (csFCM) approach in MRI that is resilient even when there is IIH and noise. To change the membership function of standard FCM, the approach takes into account local intensity relationships between pixels. It also develops membership functions and other clusters using the conditioning variable associated with each pixel. Nonetheless, the existence of significant levels of noise and IIH may result in segmentation that is undesirable. Incorporating geographical information and IIH into the csFCM membership function could be a useful strategy for improving its performance.

To initialise cluster centres in the FCM, many researchers have used EAs like PSO, a probabilistic heuristic algorithm. Benaichouche et al. [53], for example, employed PSO to start cluster centres in FCM and found a global optimum solution. It also makes use of spatial information and Mahalanobis distance to make the method noisy and misclustering resistant. Based on PSO, Mekhmoukh and Mokrani suggested an improved kernel possibilistic c-means (IKPCM). For the initialization of cluster centres and the membership function, the author employed PSO. Different brain tissues are effectively segmented using this procedure.

2) *Mixture Models*: The intensity values of different substructures and tissues in brain MR images are relatively diverse. Statistical mixture models are used to characterise an image in this case. In this method, parametric models are used to estimate the probability distribution of intensity in a picture using the maximum-likelihood (ML) similarity criterion or the maximum a posteriori (MAP) criterion. GMM is a widely used statistical model in neuroscience. A Gaussian distribution is used to estimate the intensities of pixels (or voxels) in a region in this model. The GMM parameters are then estimated using the expectation maximisation (EM)

technique, which maximises the likelihood of the observed image.

Wells et al. [54] suggested an MRI algorithm based on EM-based adaptive segmentation (AS-EM). AS-EM assumed a Gaussian distribution for the bias field and used ML to model it. The model parameters are estimated using the EM algorithm. Guillemaud and Brady [55] proposed a more generalised strategy, taking into account the limitations of [54], such as the number of tissue classes to model, parameter definitions, and tissue spatial information. The approach effectively segments MR images of the brain and breast. The bias field is estimated using an automatic model based on the EM (AM-EM) approach in [56]. The approach divides tissues into WM, GM, and CSF using a digital MRI brain atlas. However, in both of the methodologies mentioned, the estimation of GMM

parameters using EM suffers from a lack of spatial information and segmentation ambiguity. Blekas et al. [58] used prior Gibbs distribution to add spatial information to GMM. They came to the conclusion that regularisation in the GMM might be introduced if the distance function became a discrete total variation. Their method produces a spatially limited GMM that is noise-resistant but lacks bias correction. Greenspan et al. [58] suggested a limited GMM that combines local spatial and global intensity modelling. Liu and Zhang [32] proposed a local GMM that took bias correction and spatial regularisation into account. A Gaussian kernel is used in the goal function for bias correction. Smooth segmentation is achieved by regularising an indicator function. However, their method did not preserve the entire brain structure. Dong and Peng [57] suggested a variational model that combined local GMM with nonlocal spatial regularisation. The authors employed a truncated kernel function in the GMM without any additional limitations to ensure bias field smoothness.

EAs have been employed by a number of academics in model-based methods such as EM-based ML estimation. The goal is to get over their inherent flaws, such as overfitting and the tendency to become stuck in local optima. For likelihood estimation, Tohka et al. [60] presented a GA-EM approach. Local convergence is also a problem with HMRF-EM-based approaches, as previously indicated. As a result, the EAs use the EM algorithm to estimate parameters instead of the traditional method. To estimate the parameters of HMRF, the evolutionary HMRF approach employs EAs such as the clonal selection algorithm (CSA). Both simulated and actual brain MR images can be segmented using this method. A new HMRF-CSA algorithm incorporates both CSA and MCMC to increase the HMRF technique's performance.

E. Classification-Based Methods and Feature Extraction

In brain tissue segmentation, feature extraction and classification approaches are critical. T2-weighted MR images are used. In this method, the main goal of this strategy is to compile a list of the most effective options and identifying characteristics in an MR brain picture. The classification is then based on the discriminating features. Many cutting-edge feature extraction techniques are available in the literature including DWT (Differential Wavelet

Transform) [43], Gabor filter, and several statistical approaches such as grey level co-occurrence matrices, grey level run length matrices, and so on [38]. However, due to abnormalities such as noise, IHH, and others, feature extraction from MR images remains a difficult task. Furthermore, with most feature extraction approaches, high dimensionality is an inherent difficulty. The dimensionality problem is partially solved by principal component analysis (PCA), linear discriminant analysis (LDA), and other techniques. For correct classification, they get a small number of significant features.

The examples of the State-of-the-art classification method are K-nearest neighbours (KNN), support vector machine (SVM), artificial neural network (ANN), self-organizing map. [45] provides a detailed description of their benefits and drawbacks.

The nature of the retrieved characteristics is unaffected by the training process of a classifier in most of the methods mentioned above. Furthermore, for accurate segmentation, most feature extraction approaches require spatial and intensity information. Convolutional neural networks (CNNs) and deep learning have recently gained popularity in the field of brain tissue segmentation [46]–[48]. They omit the explicit demand of spatial and intensity information, unlike traditional feature extraction and classification-based approaches. Convolutional neural networks (CNNs) learn from a series of convolutional kernels. The convolutional kernels are deliberately trained for the classification that is needed. Furthermore, CNNs optimize the kernels based on the training data input. Additionally, geographical and intensity data can be used to distinguish between classes. A CNN-based technique based on baby MRI is proposed in [49]. For segmentation of three tissues: WM, GM, and CSF, the authors used T1-weighted, T2-weighted, and fractional anisotropy images. As part of the medical imaging computing and computer-assisted intervention (MICCAI) competition on multiatlas labelling, In [48], the authors present a method for adult tissue segmentation using T1-weighted MRI. The approaches in

[48] and [49] make use of CNNs, although they don't have any intensity or spatial features. By approximating both spatial and intensity information, this learning approach allows for accurate segmentation of MRI into several tissue classes.

Table I shows the pros and cons of the most regularly used brain tissue segmentation methods.

III. MEASURES OF VALIDATION

We have included some of the most up-to-date validation measures for brain tissue segmentation in this study. Validation of a segmentation method is a required step in determining its effectiveness and limitations. It is also suggested before using a procedure in a clinical setting. Validation of a method, on the other hand, necessitates the collection of data in order to assess its effectiveness. The data used in brain tissue segmentation is a medical brain picture,

which might be synthetic or genuine. Here, we'll talk about the differences between synthetic and actual clinical photographs. We've also included a list of some of the most prominent publicly available databases that can be used to validate a segmentation approach.

A. Synthetic Image

Synthetic images are created on a computer rather than with a scanner. The advantage is that the user may set the parameters to create the image they want. For example, three types of MR images are obtained by defining different MR parameter values such as echo time (TE), repetition time (TR), resolution, sequence, noise, and IHH: T1-weighted (T1-w), T2-weighted (T2-w), and proton

density weighted. In addition, a ground truth image is available to compare the segmentation result's efficiency. An MRI simulator can create synthetic images with varying levels of complexity, ranging from piecewise constant to realistic. To test their segmentation method, some researchers employed synthetic brain MR images generated by a simulator.

Because of its simplicity, the most prevalent method of evaluation is synthetic images. Furthermore, the MR simulator's synthetic images may be a useful choice for comparing different approaches. The MR simulator, on the other hand, cannot produce excellent real-world images. Phantoms can be used to generate actual images, although dense ground truth for phantom images is difficult to come [42].

B. Clinical Photograph

Validating segmentation techniques with real-life medical illustration is an crucial element in determining their usefulness. When working with an actual medical record, we must consider the disease's diversity. As a result, data from a sufficient number of patients is collected. Another consideration is the lack of a ground truth picture. Though it is important to assess segmentation performance, it is not necessary to assess a method's reproducibility. The outcomes of fully automated segmentation method are frequently compared to segmentation via hand performed by a professional. Manual segmentation, however, is limited by a well-known mistake occurred due to variability between and within experts..

C. Databases

There are number of currently accessible standard databases like BrainWeb, IBSR, Harvard medical school website, Allen brain atlas etc. These have been used to assess brain tissue segmentation algorithms quantitatively. Figure 3 shows a simulated T1-w MR picture of a person obtained from BrainWeb. The picture is approximately 362 by 362 pixels [see Fig. 3(a)]. The database also includes WM's ground truth photographs of tissues [see Fig. 3(b)], GM [see Fig. 3(c)], and CSF [see Fig. 3(d)].

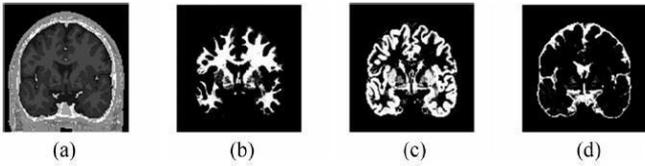


Fig. 3 Example Simulated T1-w MR image of a subject from Brainweb.

(a)Normal MRI. (b) Segmented WM. (c) Segmented GM (d)Segmented CSF

MR images are also available in the Allen brain database. Experts also used the aforementioned databases to acquire medical brain scans from institutions or by direct scanning. The effectiveness of the proposed segmentation approach for clinical usage is usually tested using real clinical images. Typically, techniques are tested first using simulated data and then with actual data.

D. Indicators of performance

A segmentation approach is validated using performance indices. Before a method may be used for clinical evaluation, it must first be validated. We've included a variety of performance indices for evaluating brain tissue segmentation methods in this part. The effectiveness of the segmentation algorithms is evaluated using no one metric. Different measures used for quantitative assessment of approaches in brain tissue segmentation are the following:

Dice index (DI): It is a quantifiable measure of crossover that is used to assess segmentation procedures. For each type of tissue, dataset, and procedure, DI is determined. It determines how much the segmented picture and the ground truth picture overlap. It is defined as [4]

$$= \frac{2 \times |S \cap G|}{|S| + |G|} \quad (2)$$

Partition coefficient (Vpc): Partition Coefficient is a useful metric for determining how fuzzy a partition is. It has a value between 0 and 1, with 1 being the best. The higher the value, the better the performance and the less fuzziness. It is written as

$$= \frac{1}{C} \sum_{k=1}^C \frac{M_k}{N} \quad (3)$$

where represents the weighted membership parameter, C represents the number of clusters, and N represents the number of data structures [4].

Partition entropy (Vpe): Another metric for indicating a fuzzy partition is partition entropy. Vpe's minimal value denotes the

best clustering. The best value for Vpe is zero. It is written as [1]

$$= - \sum_{i=1}^C \frac{M_i}{M} \log_2 \left(\frac{M_i}{M} \right) \quad (4)$$

Jaccard index (JI): JI is a criteria for determining how much the segmented picture and the ground picture overlap. A value of 0 signals no crossover with ground truth, whereas a value of 1 signals flawless segmentation.

$$JI = \frac{|S \cap G|}{|S \cup G|} \quad (5)$$

where S and G are two main parts yielded by the technique and ground truth [41].

Similarity index (ρ): To match the segmented image with reference image, the similarity index is applied. It's described as

$$= \frac{|S \cap G|}{|S| + |G| - |S \cap G|} \quad (6)$$

where Ai is the number of pixels from segmentation that correspond to cluster Ci, and Bi is the number of pixels in Ci according to ground truth. The range of is [0, 1], with = 1 being the best value [1].

Segmentation Accuracy (SA): Segmented Accuracy is calculated as the measure of correctly identified pixels divided by the total number of pixels in the clustered picture. It's written as

$$= \frac{\sum_{k=1}^M \min(M_k, N_k)}{\sum_{k=1}^M M_k} \quad (7)$$

where M is a cluster's total amount of pixels, is the amount of pixels in the kth cluster, as determined through segmentation, and is the amount of pixels in the kth cluster in ground picture. The SA's ideal value is 1 [1].

Tissue segmentation accuracy (TSA): It is described as

$$= \frac{\sum_k NCTK}{\sum_k NCITK} \quad (8)$$

where NCTK is the number of pixels accurately designated to tissue k by a particular technique (within the ground truth mask). NCITK is the total number of pixels assigned to tissue k (both in and out of the ground truth mask). The number of pixels in the discrete anatomical representation (the ground truth mask) that correspond to tissue k is NGTK. The recommended TSA value for ideal segmentation is 1 [1].

Uniformity measure (UM) : It is an empirical validation used to assess the effectiveness of methods of fragmentation. It's described as

$$UM = \frac{\sum_{j=1}^p \sum_{i=1}^N \epsilon_j}{\sum_{j=1}^p \sum_{i=1}^N \epsilon_j} \quad (9)$$

where p is the threshold's quantity, ϵ_j is the image's jth fragmented region, N is the image pixels,

μ_j is the pixels' average value in the ϵ_j region, fmax is the image's maximum grey level, and fmin is the image's minimum grey level.

UM has an ideal value of 1 [24].

False positive (FP) and false negative (FN): The level of misdiagnosis during fragmentation is represented by the false positive (FP) and false negative (FN) results. True positives (TPs) and true negatives (TNs) are also employed in addition to FPs and FNs. The right segmentation is represented by TPs and TNs. In binary fragmentation, sensitivity and specificity metrics are used to assess the impact of FPs and FNs on a method's effectiveness.

$$\text{Sensitivity} = \frac{TP}{TP + FN} \quad (10)$$

$$\text{Specificity} = \frac{TN}{TN + FP} \quad (11)$$

The best value for the two factors above is 1 [3].

IV. REMARKS

Due to IHH, noise, and other artefacts, segmenting cells of the brain including WM, GM, and CSF is a difficult activity. As stated in Section II, several approaches for fragmentation of brain tissues have been explored in the research. Because each method uses a distinct sources, picture type, segregating analysis, and confirmation metrics, comparing them is a challenging and time-consuming operation. MICCAI and the international symposium on bioimaging, for example, run a biomedical imaging competition as part of their symposia. They allow impartial testing of a large variety of techniques on the same dataset. MICCAI's MRBrains 2013, for example, is a current public competition with 37 works that have been ranked [119]. Researchers from all over the world took part in this challenge to evaluate their methods for segmenting cell of the brain (WM, GM, and CSF) using layer up procedures such inversion recovery, T1-w, T2-w and Fluid attenuated inversion recovery (FLAIR). On 15 test datasets, the determinants of performance such as DI, revised Hausdorff distance, and absolute volume difference are used to score all of the approaches. The 3-D deep learning strategy (voxnet1) surpassed all other solutions in terms of total fragmentation outcome and WM fragmentation in the MRBrains 2013 challenge. In terms of GM segmentation, the 3-D deep learning method (voxnet2) surpassed all other techniques. In CSF division, PyraMid-long short-term memory techniques were ranked first. In the case of WM and GM combined fragmentation, ISI-Neonatology produced better results. On cerebral cavity segregation, multilayer gated recurrent units showed remarkable results.

V. CONCLUSION

In recent years, brain tissue segmentation has become a research area. Brain tissue segmentation is important for scheduled medication and confirmation. Nevertheless, it is unlikely that subdivision algorithms will be able to substitute professionals in prognosis. They can be used to help professionals by reducing their workload or by providing a second perspective. The research lays out a framework for modern brain tissue segmentation algorithms. The readers may obtain knowledge on cutting-edge technology. The paper makes numerous contributions. Various validation measures are used in a quantitative analysis. This could provide researchers and physicians a better sense of which strategy is optimal for a particular application. To compare and assess the effectiveness of existing methods for fragmenting brain tissue, researchers conducted a study, we offered a comprehensive range of performance indexes as well as several public databases. Besides that, these analogies take each paradigm into account separately in order to determine the optimal strategy. Due to obvious problems in computed topography, the study focuses on the most recent issues in methods of fragmenting brain tissue. They are effective against bias-field and IHH. All available segmentation algorithms are discussed in terms of their benefits and drawbacks. Some of the unsolved issues are also discussed. This could point researchers in the right direction for improving subdivisions of brain tissue for more exact evaluation in the future.

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