

REVIEW ON BRAIN TUMOUR ANALYSIS

Sayantan Chakraborty*, Suprovat Das, Arpan Singha, Debjit Chakraborty and Sudipta Das

Ramakrishna Mission Vivekananda Centenary College, Rahara.

*Corresponding Author: Sayantan Chakraborty

Ramakrishna Mission Vivekananda Centenary College, Rahara.

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ABSTRACT

The principal aim of brain MRI analysis is to extract clinical information that would improve diagnosis and treatment of disease. Obtaining clinical information requires detection and segmentation of normal and abnormal tissues. CAD systems can enhance diagnostic capabilities of physicians and reduce the time required for accurate diagnosis. The objective of this chapter is to review the published segmentation techniques and their state-of-the-art for the human brain MRI. The review of the literature reveals the CAD systems of human brain MRI images with their existing problems.

KEYWORDS: Brain Tumor, MRI Images, Fuzzy Transform, Morphological operation.

INTRODUCTION

Computer aided detection of brain tumors, stroke lesions, hemorrhage lesions, and multiple sclerosis lesions are the most difficult issues in the field of abnormal tissues segmentations because of many challenges.^[1-5] The brain injuries are of varied shapes and also distort other normal and healthy tissues structures. The intensity distribution of normal tissues is very complicated, and there exist some overlaps between different types of tissues. All the brain disorder segmentation methods use the dogma of the difference of the abnormal brain MRI from its normal counterpart.^[6-8] Over the last decade, various approaches have been proposed for the same. Some regarded the segmentation task a tissue recognition problem, which meant using a well-trained model that can determine whether a pixel belongs to a normal or abnormal tissue based on machine learning approach. Brain tumors are one of the most common brain diseases, so detection and segmentation of brain tumors in MRI are important in medical diagnosis.^[9-11] Existing methods leave significant room for increased automation, applicability and accuracy. In this chapter study of different existing methods for detection and segmentation of brain abnormalities (mostly tumors) in MR images.

Review Works**Threshold Based**

The threshold is one of the old procedures for image segmentation. These threshold techniques are very much useful for image binarization which is an essential task for any segmentation.^[12] There are several threshold segmentation methods exist, among them here some well-known and well-established thresholding techniques such as Otsu method, Bernsen method, Sauvola method,

Niblack method, Kapur method, and Th-mean method has been described below.

Otsu Method

Otsu^[13] is a global thresholding method where threshold operation has been calculated by partitioning of the pixels of an image into two classes objects and background at gray level. The threshold of an image has been computed by within-class variance and between-class variance then total variance. This algorithm does not work properly for all type MRI of the brain image, and this is because of large intensity variation of the foreground and background image intensity. Many researchers^[14, 15] use Otsu method in brain MRI by adding extra thresholding because only using Otsu threshold whole brain region appears as white. Otsu method is not suitable for brain abnormality segmentation because it suffers from over segmentation and spurious lesions generations.

Bernsen Method

Bernsen's method^[16] that classifies an image of poor quality accurately, with the inhomogeneous paper background, is suitable for text shadow boundaries removal. This method calculates the local threshold value based on the mean value of the minimum and maximum intensities of pixels within a window. This threshold works properly only when the contrast is large. Bernsen method generates a high threshold for brain MRI and produces better results than Otsu. But due to high threshold intensity, it suffers from under segmentation and generates normal tissues as abnormal tissues.

Niblack Method

Niblack^[17] proposed an algorithm that computes a pixel-wise thresholding by shifting a rectangular window across the image. This method varies the threshold over the image, based on the local mean and local standard deviation. It does not produce a good result for this type of image because of local threshold technique. This method is not a suitable for MRI of brain abnormalities segmentation because it suffers on the boundary region of the brain with a black background and abnormal tissues with normal tissues.

Sauvola Method

Sauvola and Pietikainen^[18] method solves Niblack's^[17] problem by hypothesizing on the gray values on an object and background pixels, resulting in the following formula for the threshold. The local mean and the standard deviation values of the local area denote the dynamics of the standard deviation fixed to 128. But Sauvola^[18] is not suitable for MRI of brain image binarization. These methods produce poor results for MRI of brain image because of local thresholding selection on normal tissues. This method is not a suitable method for MRI of brain abnormalities segmentation

Kapur Method

Kapur's algorithm^[19] is an extension of Otsu's method by two probability distributions (e.g. object distributions and background distributions) from the original gray level distributions of the image. Kapur method is one of the best methods which produce a very good result of all type of MRI of brain image and MRI of brain abnormalities images. This method is very effective for MRI of brain till it suffers from under segmentation and spurious lesions generation.

Th-Mean Method

Th-mean algorithms^[20] approach is the determining of thresholding of small region of the image, and the actual selection of threshold had done by mean of the all the thresholds. This method not a suitable for MRI of brain tumor segmentation because of low threshold generation and it produces unnecessary noise within the brain during segmentation.

Other Recent Methods

Some new thresholding based abnormalities techniques try to improve the lesion detection, but still, it fails due to diverse structural characteristics of brain MRI. A mean with standard deviation based method was proposed^[21], but it suffers from incorrect segmentation. A modification of Otsu method was proposed^[22] as initial states, but results of the method depend on the extra manual threshold intensity. Many MRI of brain suffers under and over estimation of abnormality from threshold based techniques.

Region Growing

Region growing method requires a seed point that is manually selected by the user and removes all pixels

connected to the preliminary seed based on some predefined conditions. These conditions can be based on intensity information or boundaries in the image.^[23] The possible criterion might be to grow the region until a boundary in the image is met. Region increasing is seldom used alone but usually within a set of image processing operations, mostly for the description of small, simple structures such as tumors or abnormalities and lesions.^[24] The manual dealings to obtain the seed point is the significant disadvantage for this region growing. Thus, for each region that needs to be extracted, a seed must be planted but split-and-merge is an algorithm related to region growing, but it does not require a seed point.^[25] Region growing has also been the restriction to susceptible to noise i.e. very much sensitive to noise; causing extracted regions to have holes or even become disjointed. These problems may overcome by using a chemotropic region growing algorithm. The region growing method is a well-developed technique for image segmentation. The technique is not entirely automatic^[26], i.e. it requires user interaction for the selection of a seed and secondly the method fails in producing acceptable results in homogeneous areas. Since this technique is noise sensitive, therefore, the extracted regions might have holes or even some discontinuities.

K-Nearest Neighbours

K-nearest Neighbours (KNN) classifier is considered a non-parametric classifier since it makes no underlying assumption about the statistical structure of the data.^[27] K-NN only requires an integer k, set of training data and a metric to measure closeness by Euclidean distance. K-NN is easy to implement and debug, in situations where details of the output of the classifier are functional, it can be very effective if some noise reduction techniques have been used to the classifier. k-NN can have poor run-time performance if the training set is large because all the work is done at run-time, k-NN is very sensitive to irrelevant or redundant features because all features contribute to the similarity and thus to the classification and this can be ameliorated by careful feature selection or feature weighting.^[28] This method did not include any spatial regularization, so it is very sensitive to noise and inhomogeneity of tumors. The KNN classification of anatomical brain atlas is then iterated to improve the result of classification.^[29] KNN fails in cases where the intensity distribution in the tumor is highly inhomogeneous and shows large spectral overlap with brain tissues. Other disadvantages of this KNN algorithm include the dependence on the parameter K, large storage requirements (for training points), sensitivity to noise (in the training data), and the undesirable behavior that can occur in cases where a class is under-represented in the training data, which make it unsuitable for brain tumor segmentation in MRI.

Bayesian Approach

This is a supervised and parametric approach, where the data are assumed to follow a multivariate normal

distribution, where mean and covariance are estimated from the training dataset.^[30] This method combines a graph-based algorithm and Bayesian model and segments the edema besides. Also, it can be extended to vectorial variables to operate on multi-modality images. A Bayesian network is a model of the compound probability distribution function of a set of the variable like directed acyclic graph with a probability table for each node. The nodes in a Bayesian network depends upon different variables in a domain, and the arcs between nodes represent the dependency relationships among the variables with probability.^[31]

The prior probabilities for the normal tissue classes white matter, gray matter and other are defined by the registered spatial atlas to the patient images, and the tumor spatial prior is calculated from the difference image are converted to probability values through histogram analysis. This method segments only the full enhanced tumors and in the case of the presence a significant deformation in the brain it fails. Also, the probability distribution of tumor and edema has been assumed to be a normal distribution, and it is not correct in all cases.^[32] The computationally efficient method runs orders of magnitude faster than current state-of-the-art techniques giving comparable or improved results. In most cases show a single, indicative slice from the volume, all processing is in three dimensions, and the results indicate good segmentation and classification on a comparatively large dataset with good accuracy.

Markov Random Field Models

Markov random field (MRFs) theory holds the promise of providing a systematic approach to the analysis of images in the framework of Bayesian probability theory. MRFs allow a host of statistical tools and methodologies to be turned to solving so-called ill-posed problems in which the measured data does not specify a unique solution.^[33] In medical imaging, they are typically used to take into account the fact that most pixels belong to the same class as their neighboring pixels^[34] and can be used within segmentation methods.^[35] This is only applicable to abnormalities (mostly tumors) that are homogeneous enough to be segmented into a single normal tissue class; therefore it is not applicable to heterogeneous tumors.

Supports Vector Machine

Supports Vector Machines (SVMs)^[36] are popular tools for classification by maximizing the margin between classes of data that is independent and identically distributed. An SVM classification to classify the brain into the abnormal and normal classes using T1- weighted and contrast enhanced T1- weighted images. Some morphological operations have been used to eliminate the classification inaccuracy. This system used patient-specific training and compared two different types of SVM, the standard 2-class method and the more recent 1-class method.^[37, 38] The SVM method has the advantage of generalization and working in high-

dimensional feature space, and it assumes that data are independently and identically distributed. Segmenting medical images with inhomogeneity and noise are creating problems of such classifiers. Also, the problem of patient-specific learning and storage must be added to the disadvantage of SVM-based methods.

Fuzzy C-Means

The partition of Fuzzy C-Means(FCM) have two properties one of them is the homogeneity inside clusters data, which belongs to one cluster, and another one is heterogeneity between the cluster's data, which belongs to different clusters.^[39] The traditional FCM clustering algorithm for MR images segmentation, which may perform very fast and simple, but this algorithm does not guarantee the high accuracy, especially for noisy or abnormal images. Unfortunately,^[40] MR images always contain a significant amount of noise caused by the operator, equipment, and the environment, which lead to serious inaccuracies in the segmentation.^[41] The membership functions to classes have a counter-intuitive shape, which limits their use, FCM is a traditional method for medical image segmentation, but it only considers image intensity is thereby producing unsatisfactory results in noisy images. A bunch of algorithms is proposed to make FCM robust against noise and inhomogeneity, but it's still not perfect. To solve this problem intensity standardization (using the pixel histograms) as a preprocessing step^[42] was used. This method is more robust to noise and provides a better segmentation quality in comparison with the other FCM based approaches.

K-Means Clustering

K-means image segmentation is impressive^[43], and the number of partitions used in the segmentation has a very large effect on the output.^[44] The algorithm also runs quickly enough that real-time image segmentation could be done with the K-Means algorithm. The k-means clustering algorithm^[45] clusters data by iteratively computing a mean intensity for each class. Segmenting the image by classifying each pixel in the class with the closest mean consists of unsupervised classification of patterns into clusters. The clustering algorithms essentially work such as classification methods without the use of training data set.

Atlas-Guided

Atlas captures spatial, intensity and shape distributions of the anatomical structures of interest.^[46] This atlas is then used as a reference frame for segmenting new images. Atlas-guided approaches have been applied mainly in MR brain imaging. An advantage of atlas-guided approaches is that labels are transferred as well as the segmentation. Even with non-linear registration methods, however, accurate segmentations of complex structures is difficult due to anatomical variability. The atlas-based segmentation has an ability to segment the image with no well-defined relation between regions and pixels' intensities.^[47] This can be due to lack of the

border or excessive noise or in the case when the objects of the same texture need to be segmented. If the information about the difference between these regions is incorporated in the spatial relationship between them, other regions, or within their morphometric characteristics, the atlas-based segmentation is expected to work well. Another important advantage of atlases is in their use in clinical practice, for computer aided diagnosis whereas they are often used to measure the shape of an object or detect morphological differences between patient groups.

On the other hand, the disadvantage of an atlas-based can be in the time necessary for atlas construction wherever iterative procedure is incorporated in it, or a complex nonrigid registration. Since the atlas-based segmentation is usually used when the information from the gray level intensities are not sufficient, it is difficult to produce objective validation. This atlas is created by manual segmentation or by other semi-automatic segmentation methods.^[48] Atlas can capture spatial, intensity and shape distributions of the anatomical structures of interest. This atlas is then used as a reference frame for segmenting new images. A global transformation or registration technique is used to align the Atlas to the new image that will be segmented and then the atlas information will be applied to refine the segmentation or to detect abnormalities in the image.^[49] Therefore these types of segmentation deal also with registration problems and the quality of segmentation depends on the registration method. The standard atlas-guided approach treats segmentation as a registration problem. It first finds a one-to-one transformation that maps a pre-segmented atlas image to the target image that requires segmenting.

Textures-Based

Texture analysis is a good task in image processing for classification, identification, and segmentation of images. Textures are the reproduction, symmetries, and amalgamation of a large number of basic patterns with some random changes. The goal is to assign an unknown sample image to one of a set of known texture classes texture segmentation consist of two phases they are learning phase and recognition phase.^[50] In the learning phase, the target is to build a model or pattern for each the texture content. The texture content of the training images is captured with the selected texture analysis techniques, which yields a set of textual description for each image. In the recognition phase, the texture content of the unknown sample is first described with the same texture analysis method. Then the textural features of the sample are compared to those of the training images with a classification algorithm, and the sample is assigned to the category with the best match. Four statistical texture analysis methods were used^[51] these are the histogram, co-occurrence matrix, gradient matrix and run-length matrix. The results show that there is a relatively good discrimination between the tumor and its surrounding edema, but no discrimination was made between a solid part and cystic or necrotic parts. Another texture-based

method was used^[52] to segment a specific type of non-enhanced homogeneous tumor in MRI and MRS images. This method used five texture extraction methods to compute features. Finally, a fact based post processing using morphological operations was used to eliminate the misclassified pixels and to refine the result. The use of multiple classifiers certified an extra robust classification than the individual classifiers. Second order textures provided the worst classification performance among the five texture extraction methods. Texture-based methods need a culture procedure and can segment particular types of tumor. Generalization of these methods to different more types of tumors is too much difficult. Also, it seems that these methods cannot segment all components of the tumor and are sensitive to noise and inhomogeneity.

Artificial Neural Networks

Artificial neural network (ANN) is one of the powerful artificial intelligence techniques that have the capability to learn from a set of data and construct weight matrices to represent the learning patterns. ANNs are massively parallel networks of processing elements or nodes that simulate biological learning. Each node in an ANNs is capable of performing elementary computations.^[53] The motivation for the development of neural network technology stemmed from the desire to develop an artificial system that could perform intelligent tasks similar to those performed by the human brain. The true power and advantage of neural networks lie in their ability to represent both linear and nonlinear relationships and in their ability to learn these relationships directly from the data being modeled. Traditional linear models are simply inadequate when it comes to modeling data that contains nonlinear characteristics.^[54] Because of the many interconnections used in a neural network, spatial information can be easily incorporated into its classification procedures.

Neural networks execute very well on complicated, difficult, multivariate non-linear domains, such as a tumor, stroke, and hemorrhage segmentation where it becomes harder to use decision trees or rule-based systems. They also perform better on noisy fields, and there is no need to assume a fundamental data allocation such as usually done in statistical modelling.^[55] But there are several disadvantages in using neural networks for tumor segmentation. Usually, they need a patient-specific learning which a very time-consuming process is. Another disadvantage is that neural networks do not give explicit knowledge representation in the form of rules, or some other easily interpretable form. The model is implicit, hidden in the network structure and optimized weights, between the nodes.

Fusions-Based

Fusion techniques are based on various theories such as probabilistic and Bayesian fusion, fuzzy set theory, possibility and belief functions theory. Since an abnormality (e.g., tumor) consists of different biological

tissues, one type of MRI cannot give complete information about abnormal tissues. Therefore, different MRI modalities information of a patient is combined to take a decision on the location, extension, prognosis and diagnosis of the abnormality (e.g., tumor).^[56] Another fusion^[57] using operators such as t-norm or an average operator was performed to fuse the membership functions. Finally, a fuzzy region growing is used to refine the final result. This method uses the fused information of several MRI types to segment the tumor automatically and is very fast to detect and segment the tumors.

Level Set

Level set methods use nonparametric deformable models with active contour energy minimization techniques which solve computation of geodesics or minimal distance curves. Level set methods are governed by curvature defining speeds of moving curves or fronts. There are large numbers of level set methods developed for segmentation of medical images and all most all these methods follow some common generic steps.^[58] The placement of the initial contour is still a key challenge in some level set segmentation methods. The contour can move inward or outward, and its initial placement determines the segmentation target.^[59] Different level set methods differ either regarding their initial contour or the energy functional to be minimized or some combination of both. There are still key challenges in this area, and there is no general level set method that works for all applications. Level sets methods to rely on two central embeddings; first, the inserting the interface as the zero level set of a higher dimensional function, and secondly the interface's velocity to this higher dimensional level set function. The development of the contour or surface is managed by a level set method. Level set segmentation is not suitable for the segmentation of complex medical images, and they must be combined with powerful initialization techniques to produce successful segmentation.

A possible method to fix this problem is to use the background estimation method based on motion detection techniques using only two images; that is, two images at different times with the pot, pot holder and conveyor mechanism appearing relatively on the same position on the images.^[60] Once the background is learned by this method, the background image (with all non-objects image) is subtracted from the original image and non-objects image. Level set methods present a commanding approach for the medical image segmentation because it can handle any of the cavities, concavities, convolutions, splitting, or merging. However, this method needs identifying initial curves and can only provide superior results if these curves are placed near symmetrically on the object boundary.

Combination of Watershed and Level Set

This approach combines the advantages of both methods: the watershed transform pre-segmentation is rough but

quick, and the level set needs only a few iterations to produce the final, fast, highly accurate, and smooth segmentation. The choice of watershed segmentation as the initialization of the level set method is made for two reasons.^[61] The first reason is that because of watershed transform blindness of segmentation is reduced, and the accuracy of segmentation is improved. The second reason is to do with improving the computation speed. After the initial segmentation based on watershed transform, the final segmentation is accomplished based on level set method.^[62] By combining watershed transform and level sets, this method can produce highly accurate segmentations of topologically and geometrically complex structures in much less time than where level sets alone.

Self-Organizing Maps

Self-Organizing Maps (SOMs) consists of two layers: first is the input layer, and the number of neurons in this layer is equal to the dimension of input and second is the competitive layer and each neuron in this layer correspond to one class or pattern. The number of neurons in this layer depends on the number of clusters and is arranged in a regular geometric mesh structure. Each connection from the input layer to a neuron in a competitive layer is assigned with a weight vector. The SOM functions in two steps^[63], firstly finding the winning neuron i.e. the most similar neuron to input by a similarity factor like Euclidean distance, and secondly, updating the weight of winning neuron and its neighbor pixels based on input.

SOMs is an unsupervised clustering network that maps inputs which can be high dimensional to one or two-dimensional discrete lattices of neuron units. The input data is organized into several patterns according to a similarity factor like Euclidean distance, and each pattern assigns to a neuron. Each neuron has a weight that depends on the pattern assigned to that neuron. Input data is classified according to their grouping in input space and neighboring neuron and moreover learns distribution and topology of input data.^[64, 65] For calculating that black and white similarity map, the more neighbors it uses to calculate the distance the better similarity map, we will get, but the number of distances the algorithm needs to compute increases exponentially.

Hybrid Self-Organizing Maps

Hybrid Self-Organizing Maps (HSOM) combines self-organization and topographic mapping technique. HSOM combines the idea of regarding the image segmentation process as one of data abstraction where the segmented image is the final domain independent abstraction of the input image.^[66] HSOM is organized in a pyramidal mannered structure consisting of multiple layers where each layer resembles the single layer SOM. The learning process has sequential corrections of the vectors representing neurons. On every step of the learning process a random vector is chosen from the initial data set, and then the best-matching neuron coefficient vector

is identified.^[67] The vector most similar to the inputs is selected as a winner.

Graph Cut

Numerous graph techniques exist which are exploited in image segmentation such as minimum spanning trees, shortest path, graph-cuts, etc. Among these entire typical graphs partitioning methods graph-cuts are comparatively new and the most powerful for image segmentation.^[68] A cut in the graph isolates the source from the sink points connected to the sink are labeled as tumor and points connected to the source as a brain. The problem of image segmentation is considered as a graph partitioning problem, and global criterion that measures both total dissimilarities among the different groups and the overall similarity inside then is used. An efficient method based on generalized Eigen value treatment is used to optimize the criterion to segment image.^[69]

Fractal-Based

A fractal is an irregular geometric object with an infinite nesting of structures at all scales. Some of the most important properties of fractals are self-similarity, chaos, and non-integer fractal dimension (FD).^[70] Mathematically, a fractal structure is defined as a set that has a fractal dimension exceeding its topological one. FD serves as an index of the morph metric complexity and variability of the object being studied. The disadvantage is that the size of sub-images is a problem because different sub-image sizes result in different FD. The second issue is the selection of reference images because the MR images have different sizes and different parameters^[71] and for abnormalities (eg.tumor, stroke, etc.) detection it is required to have a reference image similar to the patient image.

Parametric Deformable Models (Snakes)

Parametric models explicitly move predefined snake points based on an energy minimization scheme.^[72] The following section reviews available segmentation algorithms on parametric methods. The deformation process has played a critical role in shape representation. The first class of deformable model is parametric deformable curves model, also known as snakes. Since then, there has been an extensive burst of publications in the area of parametric deformable models and their improvements, such as balloon force, topology snake, and distance snake. Berger^[73] has proposed the first and primary uses of parametric models in medical image analysis to segment objects in 2D images. However, this classic snake model provides an accurate location of the edges only if the initial contour is given sufficiently near the edges because they make use of only the local information along the contour. This limitation indicates that basic snake model alone cannot serve the purpose of accurate segmentation and does not work image with weak edges. A gradient vector^[74] flow as an external force (region-based features) was used increases the capture range. In this method, they replaced the potential force in the traditional equation with a novel external

force field called Gradient Vector Flow (GVF). Parametric contour-based methods detect tumor boundaries better than region based methods, but they have two main limitations. First, when the initial model and the desired object boundary differ mostly in size and shape, the model must be re-parameterized to recover the object boundary fully. The second limitation with the parametric approach is that it has difficulty dealing with topological adaptation such as splitting or merging model parts.

Hidden Markov Model

Hidden Markov Model (HMM) is used to produce the ever finer resolution in spectral, spatial and temporal data, Non-brain structures removed and it estimates the tissue intensity variation. Regularity dimension and semi-variogram were used to extract structural features of the brains, and vector quantization method was applied to convert extracted feature vectors to prototype vectors.^[75, 76] The output then utilized to estimate parameters for HMM. The HMM topology finds right as well as its model parameters. This method can determine the optimal states in all cases. The HMM can be trained by genetic algorithms or more optimized methods.

Genetic Algorithms

Genetic algorithms (GAs) are the population based process to find an exact or approximate solution to optimization the search problem is inspired by the generic process of biological organism used in computing. GA mainly considers genotype, initial population, fitness function, operators on genotypes, stopping criterion. Individual description of the class of each pixel of the image segmentation results is called genotype, and an initial population is the set of people' characterization by their genotypes. A fitness function is a particular type of function that is used to summarize and enables us to quantify the fitness of an individual to the environment by considering its genotype.^[77] This criterion allows stopping the evolution of the population. It can examine the stability of the standard deviation of the assessment criteria of the population or set the maximal number of iterations. Basically this following five information^[78, 79] execute the genetic algorithm which is carried out in four steps: (1) definition of the initial population (segmentation results) and computation of the fitness function (evaluation criterion) of each individual, (2) mutation and crossing-over of individuals, (3) selection of individuals, (4) evaluation of individuals in the population, (5) back to Step 2 if the stopping criterion is not satisfied.

GA creates a sequence of populations for each successive generation by using a selection mechanism and uses operators such as crossover and mutation as key search mechanisms - the aim of the algorithm being to optimize a given objective or fitness function. A prominent feature of MRI brain images is the fact that the texture patterns of the various tissues are fixed. Texture descriptors can be used to capture the salient

features of the texture pattern to distinguish one type of tissue from another. Thus it can help refine the tumorous region already outlined by the existing process. GA is applied to enhance the detected border. The figure of merit is calculated to identify whether the detected border is exact or not. One of the disadvantages of the genetic algorithms is that it truly depends upon the fitness function.

CONCLUSIONS

A large number of approaches have been proposed by various researchers to deal with MRI images. The development of automatic and accurate CAD in characterizing brain lesions are essential and it remains an open problem. Lesion detection, segmentation or separation of a particular region of interest is an important process for diagnosis. Computer aided surgery also requires previous analysis of lesion area inside the brain. This process is a challenging process due to the complexity and large variations in the anatomical structures of human brain tissues, the variety of the possible shapes, locations and intensities of various types of lesions. Many methods need some preprocessing technique for improvement of accurate identification of brain abnormalities. In the threshold intensity based binarized segmentation; Kapur method can provide better results than other for brain abnormalities segmentation. But Kapur thresholding suffers from under segmentation and spurious lesion generations for many brain images. Most of the binarized fail due to large intensity difference of foreground and background i.e. the black background of MRI image. In region growing methodologies are not standard methods for validating segmentation; the main problem is the quality of segmentation in the border of the tumor. These methods are suitable for the homogeneous tumor but not for heterogeneous tumor. Classification based segmentation can segment tumor accurately and produce good results for large data set, but undesirable behaviors can occur in a case where a class is under-represented in training data. Clustered based segmentation performs very simple, fast and produces good results for the non-noise image but for noise images, it leads to serious inaccuracy in the segmentation. In a neural network-based segmentation perform little better on noise field and no need of assumption of any original data allocation, but the learning process is one of the great disadvantages of it. In spite of several difficulties, an atomization of brain tumor segmentation using a combination of a threshold based, preprocessing and the level set can overcome the problems and gives efficient and accurate results for brain abnormality detection. Accurate detection is the basis for calculating important features of brain lesion such as size, classification, heterogeneity, and volume of the lesions.

The following existing problems are selected from the literature study.

i) The problems for small abnormality detection, under Segmentation, over-segmentation, spurious lesion

generation, segmentation two or more abnormality in a brain, false identification, and segmenting abnormality with inhomogeneity during abnormality segmentation.

ii) The subcortical gray matter is underestimated, a cortical gray matter is overestimated, over and under-segmentation of normal brain tissue and non-brain part are performed by the existing tissues segmentation methodology.

ii) Increased number of structures in the segmentation problem also increases the problem's mathematical complexity and a likelihood of misclassified pixels during abnormal and normal tissues segmentation.

To accurate detection, solve and reduce the existing problems of abnormalities identification from MRI of a brain, there are several steps that need to be done. Thus proposed framework decomposed into several sub work to correctly identification of abnormality and normal tissues of the brain. From the mentioned problem statements discussed in summary of this chapter, the specific objectives of this research are as follows: i) Preprocessing stage: Artifacts removal and skull elimination are used to reduce the spurious lesion generation and false detection problem. ii) Binarization stage: Binarization can be used as an intermediate/preprocessing step of small, multiple, and low intense (or similar intensity with normal tissues) abnormalities detection (e.g., small tumor, multiple sclerosis). iii) Tissue detection and segmentation: Quantification of normal brain tissues and presence abnormality (disease like a tumor, stroke, hemorrhage, and MS) are identified (if any). A brain MRI is normal or abnormal that can be identified during this stage. This stage reduces over-segmentation, under-segmentation, false detection and misclassification problem of white matter, gray matter, Cerebrospinal fluid, marrow, and muscle skull. iv) Abnormality detection and segmentation: This stage used to accurate detection and quantification, overcome over and under-segmentation problem, reduce spurious lesion generation, reduce misclassified pixels during abnormal and normal tissues segmentation of brain abnormalities. v) Classification of brain tumor: This stage used to classify the five major brain tumors from brain MRI. The preprocessing steps are used to reduce noise and improve the classification accuracy.

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