IDENTIFYING BRAIN TUMOUR FROM MRI IMAGE USING MODIFIED FCM AND SUPPORT VECTOR MACHINE

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ABSTRACT

Brain tumor detection in magnetic resonance images (MRI) is essential in medical diagnosis because it provides information associated to anatomical structures as well as potential abnormal tissues necessary to treatment planning and patient follow-up. This paper proposes an intelligent segmentation technique to identify normal and abnormal slices of brain MRI data. It consists of four steps which includes i) Preprocessing ii) segmentation using Modified fuzzy C-means algorithm iii) Feature extraction of the region like mean, standard deviation, range and pixel orientation and iv) Final classification using the support vector machine. The performance of the proposed technique is systematically evaluated using the MRI brain images received from the public sources. For validating the effectiveness of the modified fuzzy c-means, we have considered the quantity rate parameter. For the evaluation of the proposed technique of tumor detection, we make use of sensitivity, specificity and accuracy values which we compute from finding out false positive, false negative, true positive and true negative. Comparative analyses were done by the normal and modified FCM using both the Neural Network (FFNN) and SVM. From the results obtained, we could see that the proposed technique achieved the accuracy of 93% for the testing dataset, which clearly demonstrated the effectiveness of the modified FCM when compared to the normal technique.

Keywords: MRI image, Skull stripping, Image enhancement, segmentation, Feature Extraction, support vector machine, Tumor detection
1. INTRODUCTION

Brain MRI image segmentation: Medical imaging is a vital component of a large number of applications. The imaging modalities can be divided into two global categories: anatomical and functional. Anatomical modalities, employed can be divided into two global categories: anatomical and functional. Anatomical modalities, depicting primarily morphology, include X-ray, CT (Computed Tomography), MRI (Magnetic Resonance Imaging), US (ultrasound), portal images, and (video) sequences [1]. MRI is the state-of-the-art medical imaging technology, which allows cross sectional view of the body with unprecedented tissue contrast [2]. MRI plays an important role in assessing pathological conditions of the ankle, foot and brain. MRI is a noninvasive procedure that has proven to be an effective tool in the study of the human brain. The information that MRI provides has greatly increased knowledge of normal and diseased anatomy for medical research, and is a critical component in diagnosis and treatment planning [3]. An equally impressive technology, MRI, has greatly improved the sensitivity and specificity (accuracy) of diagnostic imaging, particularly in structures such as the liver, brain, spinal cord, and joint spaces.

Image segmentation, play a role in biomedical imaging applications such as the quantification of tissue volumes diagnosis, localization of pathology study of anatomical structure, treatment planning, partial volume correction of functional imaging data, and computer integrated surgery [4]. It includes a wide range of applications such as therapy evaluation, image guided surgery and neuro-imaging studies [5]. A major goal of image segmentation is to identify structures in the image that are likely to correspond to scene objects. The task of image segmentation is to partition an image into non-overlapping regions based on intensity or textural information. The challenge in brain MRI segmentation is due to issues such as noise, intensity non-uniformity (INU), partial volume effect, shape complexity and natural tissue intensity variations. Under such conditions, incorporation of a priori medical knowledge, commonly represented in anatomical brain atlases by state-of-the-art studies is essential for robust and accurate automatic segmentation [6]. Quantitative analysis of MR images of the brain is of interest in order to study the aging brain in epidemiological studies, to better understand how diseases affect the brain and to support diagnosis in clinical practice. Manual quantitative analysis of brain imaging data is a tedious and time-consuming procedure, prone to observer variability. Therefore, there is a large interest in automatic analysis of MR brain imaging data, especially segmentation of cerebrospinal fluid (CSF), gray matter (GM) and white matter (WM) [7].

MRI Image segmentation refers to a process of assigning labels to set of pixels or multiple regions [8]. It plays a major role in the field of biomedical applications as it is widely used by the radiologists to segment the medical images input into meaningful regions. Thus, various segmentation techniques in medical imaging depending on the region of interest had been proposed [9]. Medical image segmentation problems has been approached with several solution methods by different range of applicability such as Particle Swarm Optimization [10], Genetic Algorithm [8], Adaptive Network-based Fuzzy Inference System (ANFIS) [11], Region Growing [12], Self Organizing Map (SOM) [13] and Fuzzy c-Means (FCM) [14]. However, segmentation of medical imagery remains as a challenging problem due to the complexity of the images. Brain tissue is a particularly complex structure and its segmentation is an important step for studies in temporal change detection of morphology [15]. Success of MRI in the detection of brain pathologies is very encouraging. However,
diagnosis and locations of abnormality are made manually by radiologists. It consumes valuable human resources, error sensitive [16] and making it prone to error [17].

Tumor detection in Brain MRI image: With the increasing size and number of medical images, the use of computers in facilitating their processing and analysis has become necessary. Segmentation becomes more important while typically dealing with medical images where pre-surgery and post surgery decisions are required for the purpose of initiating and speeding up the recovery process. Computer aided detection of abnormal growth of tissues is primarily motivated by the necessity of achieving maximum possible accuracy [5]. Many neurological diseases and conditions alter the normal volumes and regional distributions of brain parenchyma (gray- and white matter) and cerebrospinal fluid (CSF). Such abnormalities are commonly related to the conditions of hydrocephalus, cystic formations, brain atrophy and tumor growth. There are also age-related differences in volumes of brain parenchyma and CSF. Brain tumor is one of the major causes for the increase in mortality among children and adults. A tumor is a mass of tissue that grows out of control of the normal forces that regulates growth [18]. The incidence of brain tumors is increasing rapidly, particularly in the older population than compared with younger population. Brain tumor is a group of abnormal cells that grows inside of the brain or around the brain. Tumors can directly destroy all healthy brain cells. It can also indirectly damage healthy cells by crowding other parts of the brain and causing inflammation, brain swelling and pressure within the skull [19]. Early detection and correct treatment based on accurate diagnosis are important steps to improve disease outcome. Brain abnormalities comprise a wide spectrum of conditions ranging from developmental errors to vascular accidents. This variability results in innumerable possibilities of findings on prenatal ultrasound, which could create some diagnostic dilemmas.

In our proposed technique, initially the input MRI image is pre-processed in order to eliminate the noise and make the image fit for rest of the processes. Here we use the skull stripping and image enhancement in the preprocessing stage. Subsequently, the pre-processed image is segmented using the modified Fuzzy C-means technique. In the modified FCM, we use hybrid objective function like FCM and kernel FCM. After the segmentation process, the feature such as mean, standard deviation, range and pixel orientation are extracted from the regions and is given to the support vector machine for training. In the final stage the image is classified as tumorous or normal with the help of the trained SVM.

The main contributions of this research paper includes,

- The main objective of this research is segmentation process. In this technique, we use hybrid objective function based on FCM and kernel FCM.
- Extraction of the feature vectors like mean, standard deviation, range and pixel orientation of the segmented regions.
- Train the feature vectors using the support vector machine.
- Efficiency is analyzed by means of the quality rate, sensitivity, specificity and the accuracy value.
- Comparison is effectively made with the classification techniques such as neural network, and Support vector machine.

The rest of this paper is organized as follows: A brief review of researches relevant to the Brain tumor detection and segmentation technique is presented in section 2. The proposed Brain tumor detection using Modified FCM technique is presented in Section 3. The detailed experimental results and discussions are given in Section 4. The conclusions are summed up in Section 5.
2. REVIEW OF RELATED WORK

Lots of researches have been performed for the segmentation of normal and abnormal tissues in MRI brain images. Some of the recent related works regarding the segmentation of brain tissues are reviewed in the following section.

R. B. Dubey et al. [20] developed a semi-automatic method that was developed for the segmentation of brain tumor from MR images. Replacing the constant propagation term by a statistical force overcome many limitations and result in convergence to a stable solution. Using the MR images that had tumors, probabilities for background and tumor regions were calculated from pre- and post-contrast difference image and mixture modeling fit of the histogram. The whole image was used for initialization of the level set evolution to segment the tumor boundaries. Result obtained on two cases presented different tumors with significant shape and intensity variability and showed that the method was an efficient tool for the clinic. Validity of the method was demonstrated by comparison with manual expert radiologist.

In order to improve robustness of automated image segmentation, especially in the field of brain tissue segmentation from 3D MRI towards classical image deteriorating including the noise and bias field artifacts that arise in the MRI acquisition process, Caldairou et al. [21] propose to integrate into the FCM segmentation methodology concepts inspired by the Non-Local (NL) framework. The key algorithmic contributions of this article were the definition of an NL data term and an NL regularization term to efficiently handle intensity inhomogeneity and noise in the data. The resulting energy formulation was then built into an NL/FCM brain tissue segmentation algorithm. Experiments were performed on both the synthetic and real MRI data, leading to the classification of brain tissues into grey-matter, white matter and cerebrospinal fluid and also indicated significant improvement in performance in the case of higher noise levels, when compared to a range of standard algorithms.

Shafaf Ibrahim et al. [22] presented a paper that compared the performances of Seed-Based Region Growing (SBRG), Adaptive Network-Based Fuzzy Inference System (ANFIS) and Fuzzy c-Means (FCM) in brain abnormalities segmentation. Controlled experimental data was used and was designed in such a way that prior knowledge of the size of the abnormalities was known. This was done by cutting various sizes of abnormalities and pasting it onto normal brain tissues. The normal tissues or the background were divided into three different categories. The segmentation was done with fifty seven data of each category. The knowledge of the size of the abnormalities by the number of pixels was then compared with segmentation results of three techniques proposed. It was proven that the ANFIS returns the best segmentation performances in light abnormalities, whereas the SBRG on the other hand performed all in dark abnormalities segmentation.

Mina Rafi Nazari et al. [23] have proposed a content-based approach for medical image retrieval. Then, a case study that describes the techniques of a CBIR system for retrieving digital human brain MRI database based on textural features retrieval, has been presented. Their aim is to distribute the facts of the CBIR approach to the applications of medical image management as well as to distinguish between normal and abnormal medical images based on features. Recognizing normal and abnormal images are the main indices and the abnormal images have been clustered to identify two certain abnormalities: Multiple Sclerosis and Tumoral images for the classification of database. Experimental results have shown that the proposed technique has performed a classification with an achievement of
95% and also when compared with the results of other recent works, the proposed technique was robust and effective.

Nandita Pradhan et al. [24] have proposed a technique for segmentation and identification of pathological tissues (Tumor and Edema), normal tissues (White Matter and Gray Matter) and fluid (Cerebrospinal Fluid) from Fluid Attenuated Inversion Recovery (FLAIR) magnetic resonance (MR) images of brain using composite feature vectors comprising of wavelet and statistical parameters, which is contrary to other researchers who have developed feature vectors either using statistical parameter or using wavelet parameters. Here, the intracranial brain image has been segmented into five segments using k-mean algorithm, which is based on the combined features of wavelet energy function and statistical parameters that reflect texture properties. In addition to tumor, edema has also been characterized as a separate class, which is important for therapy planning, surgery, diagnosis and treatment of tumors. By extracting the feature vectors from small blocks of 4x4 pixels of image corresponding to tissues of tumor, edema, white matter, gray matter and cerebrospinal fluid, the block processing of image has been performed and then employing a back propagation algorithm, the artificial neural network has been trained.

Jayashri Joshi et al. [25] have proposed a tumor segmentation scheme based on statistical structure analysis, where the structural analysis on both tumorous and normal tissues has been performed. The local textures in the images could disclose the normal ‘regularities’ of biological structures. Therefore, the textural features have been extracted using co-occurrence matrix approach. The analysis of level of correlation has permitted to reduce the number of features to the only significant component. The classification has been performed by employing an artificial neural network and fuzzy c-means. They have designed this approach in order to examine the differences of texture features between macroscopic lesion white matter (LWM) and normal appearing white matter (NAWM) in magnetic resonance images (MRI) from patients with tumor and normal white matter (NWM).

Chunming Li et al. [26] have introduced a region-based approach for image segmentation, which has the potential to deal with intensity inhomogeneities in the segmentation. Initially, the local clustering criterion function for the image intensities in a neighborhood of each point has been defined based on the model of images with intensity inhomogeneities. This local clustering criterion function has been then integrated with respect to the neighborhood center to provide a global criterion of image segmentation. In a level set formulation, this criterion defines an energy in terms of the level set functions that signify a partition of the image domain and a bias field that accounts for the intensity inhomogeneity of the image. Thus, by reducing this energy, the approach is capable of segmenting the image and estimating the bias field simultaneously and the estimated bias field can be employed for intensity inhomogeneity correction (or bias correction). The proposed approach has been validated on synthetic images and real images of different modalities and obtained good performance in the presence of intensity inhomogeneities. Experiments have revealed that the approach was robust to initialization, faster, and more accurate.

Manisha Sutar, and N. J. Janwe [27] have proposed a segmentation method based on an extension to the conventional fuzzy C-means (FCM) clustering algorithm. The segmentation method was a key component of an MR image-based classification system for tumors. A neighborhood attraction, which was dependent on the relative location and features of neighboring pixels, has been shown to enhance the segmentation performance. The degree of attraction has been optimized using a Particle Swarm Optimization model. Also, their paper has demonstrated the superiority of the proposed method.
3. PROPOSED TECHNIQUE FOR DETECTION OF TUMOUR USING MODIFIED FCM

Segmentation of medical imagery is a challenging task due to the complexity of the images, as well as to the absence of models of the anatomy that fully capture the possible deformations in each structure. Brain tissue is a particularly complex structure, and its segmentation is an important step for our proposed method. In our proposed method consists of four phases namely preprocessing, segmentation, feature extraction and final classification. Preprocessing phase is done using skull stripping and image enhancement. The novel method have used for segmentation process. Subsequently, we use some features like mean, variance, standard deviation Range and pixel orientation for feature extraction process. In the final classification we use the Support vector machine classifier to detect tumour or not. The Block diagram of the proposed technique is shown schematically in Fig 1.

Figure 1: Overall block diagram of our proposed approach
3.1 Preprocessing

Various preprocessing methods have been proposed to deal with the MRI brain images used for segmentation. In preprocessing process, the MRI images are converted into grey images. Subsequently, the grey images are smoothed using contrast adjustment.

3.1.1 Skull stripping

This is preprocessing step which is required to produce better results. Skull is outer part of the brain surrounding it i.e. the removal of its non-cerebral tissues. The main problem in skull-stripping is the segmentation of the non-cerebral and the intracranial tissues due to their homogeneity intensities. So it may affect the result of seed point selection. Some observations are required to find the range of gray value of skull portion. Firstly, the contrast adjustment images are converted into binary images and find crop locations using this binary image. Consequently, the contrast adjusted image is cropped for the tumor part of the brain image. Select a low threshold value for converting cropped contrast adjusted image to binary. The cropped contrast adjusted image is converted to binary image. Subsequently, apply the morphological operation 'thicken' to the binary image once. Finally, brain region is extracted using region based binary mask extraction.

Region-based binary mask extraction: Region-based extraction is performed by considering the properties of each block that satisfy some criteria. We have utilized one of two criteria. One criterion is to determine the max-min difference and the other is to find out the mean values of the blocks. Subsequently, the process results with a brain mask is applied to the original MRI data. Thus, we have obtained a brain MRI image with its brain cortex stripped.

3.1.2 Image enhancement

Image enhancement is the process of adjusting digital images so that the results are more suitable for display or further analysis. After skull stripping process, the brain cortex can be visualized as a distinct dark ring surrounding the brain tissues in the MRI images. The distinct dark ring surrounding the brain tissues are removed by image enhanced method. For example, you can remove noise or brighten an image, making it easier to identify key features. In our method, we use morphological operation 'thicken' to the binary image.

3.2 Segmentation

After preprocessing, the MRI images are given to segmentation process. Firstly, the images are partitioned into two clusters. The initial cluster centers are chosen randomly from the image dataset uniquely. Numbers of clusters is determined randomly. Given a dataset \( X = \{x_1, x_2, \ldots, x_n\} \), where the data point \( x_b \in \Xi \subseteq \mathbb{R}^p \) \( (b = 1, 2, \ldots, n) \) \( n \) is the number of data, and \( p \) is the input dimension of a data point.

The FCM algorithm minimizes the objective function for the partition of data set

\[
\sum_{j=1}^{c} \sum_{k=1}^{d} u_{ik}^m \|x_i - o_j\|^2
\]

In this equation, \( d \) is the number of samples in the vector \( X \), \( c \) is the number of clusters (or classes \( 1 \leq c \leq d \) \), \( u_{ik} \) is the element of the partition matrix \( U \) of size \( (c \times d) \) containing the membership function, \( o_j \) is the center of the \( i^{th} \) class (cluster), and \( m \) is a weighting factor, which usually takes the value of 2. The constraint on \( u_{ij} \) is \( \sum_{i=1}^{c} u_{ij} = 1 \).
In the existing work [28], they have used the objective function of KFCM. Also, they have included some modifications in FCM. As an enhancement of classical FCM, the KFCM maps the data set $X$ from the feature space or the data space $\Xi \subseteq \mathbb{R}^p$ into a much higher dimensional space $H$ (a Hilbert space usually called kernel space) by a transform function $\Xi \rightarrow H$. In the new kernel space, the data demonstrate simpler structures or patterns. According to clustering algorithms, the data in the space show clusters that are more spherical and therefore can be clustered more easily by FCM algorithms.

$$k(x, y) = \langle \varphi(x), \varphi(y) \rangle \quad \forall x, y \in \Xi$$  \hspace{1cm} (2)

Where $\langle \cdot, \cdot \rangle$ is the inner product for Hilbert space $H$. Such kernel functions are usually called Mercer kernels or kernel. Given a Mercer kernel $k$, we know that there is always a transform function $\varphi: \Xi \rightarrow H$ satisfies $x(x, y) = \langle \varphi(x), \varphi(y) \rangle$, although sometimes, we do not know the specific form of $\varphi$. Widely used Mercer kernels include the Gaussian kernel $k(x, y) = \exp(-\|x - y\|^2 / r^2)$ and the polynomial kernel $k(x, y) = (x \cdot y + d)^2$. They are both defined over $\mathbb{R}^n \times \mathbb{R}^n$. Clearly, due to the fact that we only know the kernel functions, we need to solve the clustering problems in the kernel space by only using kernel functions, i.e., the inner product of the transform function $\varphi$. Usually this is called “kernel trick” [29].

The objective function is defined as

$$u_{ij}^{KFCM} = \sum_{i=1}^{c} \sum_{j=1}^{d} u_{ij}^{FCM} \varphi(x_j) - \varphi(o_i) \| ^2$$  \hspace{1cm} (3)

In our proposed work, we are summing up the integrated objective functions of FCM and KFCM after taking the half value with respect to the values of $i$ and $k$.

The reformulated of final objective function in equation (1) and equation (3) is given by

$$O_{sum} = \sum_{i=1}^{c} \sum_{k=1}^{d} \left( \frac{u_{ij}^{FCM} + u_{ij}^{KFCM}}{2} \right) \left( 1 - k(x_j, o_i) \right)$$  \hspace{1cm} (4)

Here, $1 - k(x_j, o_i)$ can be considered as a robust distance measurement derived in the kernel space [30].

The cluster center matrix $v$ is randomly initialized and the fuzzy partition matrix $U$ is created by equation (5) for all feature vectors. The outline of the algorithm is following:

- **Step 1:** Initialize the cluster center matrix $O$, by using a random number generator and record the cluster centers. Set $k = 0$

- **Step 2:** Initialize the fuzzy partition matrix, $U^{(k=0)}$, $m$ is set to be 2.0

- **Step 3:** Increment $k = k + 1$. Compute $v$ by using (4)

- **Step 4:** Update objective function $u_{ij}^{FCM}$ and $u_{ij}^{KFCM}$ using equation (1) and (3)

$$O_{sum} = \sum_{i=1}^{c} \sum_{k=1}^{d} \left( \frac{u_{ij}^{FCM} + u_{ij}^{KFCM}}{2} \right) \left( 1 - k(x_j, o_i) \right)$$

- **Step 5:** If $\|U^{(k)} - U^{(k-1)}\| < \varepsilon$ then stop, else repeat 2 to 5
3.3 Feature extraction

The important function of feature extraction is to reduce the original dataset by evaluating some specific properties or features that differentiate one input pattern from another. The extracted features provide the characteristics of the input type to the classifier by considering the depiction of the significant properties of the image. The analyzing methods have been done so far has used the values of pixels intensities, pixels coordinates and some other statistic features namely mean, variance or median, which have much error in determination process and low precision and efficiency in classification.

Here, the statistic features we have chosen are Mean $M$, Standard deviation, Range and Pixel orientation functions. The feature extraction process is carried out by with some initial pre-processing. Each tissue segmented image is split into a limited number of blocks and the feature values are calculated for every block. The initial steps are as follows:

- Find the neighbor blocks of the entire divided blocks.
- Find the distance between all the neighbor blocks.
- Find the feature values of the blocks with distinct distance measure.
- Find the average value of all the computed blocks distance.
- Store all the features in a vector and fed as an input to the classifier.

Features can be extracted from the matrix to reduce feature space dimensionality and the formal definitions of chosen features from the matrix are done. The statistic feature’s formula is depicted as below,

**Mean:** The mean is defined as the sum of the pixel values divided by the total number of pixels values.

$$M = \frac{1}{pq} \sum_{i=1}^{p} \sum_{j=1}^{q} x(i, j)$$

**Standard Deviation:** The Standard Deviation $\sigma$ is the estimate of the mean square deviation of grey pixel value $x(i, j)$ from its mean value $M$. Standard deviation describes the dispersion within a local region. It is determined using the formula:

$$\sigma = \sqrt{\frac{1}{pq} \sum_{i=1}^{p} \sum_{j=1}^{q} (x(i, j) - M)^2}$$

**Range:** The Range $R$ has two elements. One is minimum pixel intensity value of inside a block and other one is maximum pixel intensity value of inside a block.

$$R = \text{Min. value of pixel intensity and Max. value of pixel intensity in a block}$$

**Pixel Orientation:** The pixel orientation has 2 elements, First element minimum angle inside block, and second one is maximum angle inside a block.

$$PO = \tan \left( \frac{y - m}{x - m} \right)$$

Where,

- $m$ is the point which we require to measure the value
- $y$ is a point in the Y-axis of first quadrant
- $x$ is a point in the X-axis of first quadrant
3.4. Final classification using SVM

To train the SVM classifier, we need some data features to identify the normal brain region and tumor affected brain. The data features will then train the classifier and the classifier will find whether the given MRI image is tumor or not. The data features which we have chosen for training the SVM classifier are mean, standard deviation, range and pixel orientation. After computing all the data features, we have to give the values to the classifier. For instance, if we are choosing five normal MRI images and five abnormal MRI images, we need to calculate all the six data features separately for all the MRI images we had chosen. After calculating all the five data features for every chosen MRI images, we have to give the result to the SVM classifier. Using those results we can train the classifier to identify the tumor and non-tumor from the given MRI image. After the SVM classifier is trained, we can give a new MRI image to find whether it has tumor or not. Thereafter, the five data features such as number of tumor in the brain region, maximum area of the tumor region, minimum area of the tumor region, total number of pixels in each tumor, maximum repeated pixel in the tumor region and maximum repeated pixel in the lung region are computed for the new MRI image. The computed values of all the five data features are then give to the SVM classifier.

The SVM classifier is then compare the values of all the five data features with the stored values of normal and abnormal MRI images. Because during training we have stored all the five data features of the five normal MRI images and five abnormal MRI images. After comparison, the SVM classifier will identify whether the given MRI image comes under normal category or abnormal category and give the result to us.

Support Vector Machine (SVM)

In most cases, we want to assign an object to one of several categories based on some of its characteristics in our real life situation. For instance, based on the outcome of several medical tests we want to say whether the patient has a particular disease or not. In computer science such situations are explained as classification issue.

The support vector machine (SVM) which was derived from the statistical theory is a powerful supervised classifier and is an accurate learning technique. The SVM was introduced in 1995. It gives successful classification outcomes in different application domains such as medical diagnosis [31, 32]. SVM works under the principle of structural risk reduction from the statistical learning theory. To maximize the margin between the classes and to minimize the true cost [33], its kernel is used to control the empirical risk and categorization capacity. A support vector machine can search an optimal separating hyper plane amid the members and non-members of a given class in a high dimension feature space [34]. There are many general kernel functions such as linear, polynomial of degree and Radial basis function (RBF). Among these kernel functions, a radial basis function proves to be useful because of the fact the vectors are mapped nonlinearly to a very high dimension feature space.

4. EXPERIMENTAL RESULTS AND DISCUSSION

This section illustrates the experimental results of our proposed Segmentation technique using brain MRI images with and without tumors. Our proposed approach is implemented in Matlab environment on Core 2 Duo, processor speed 1.6 GHz (matlab version 7.10). Here, we have tested our proposed tumor detection technique using medical images taken from the publicly available sources.
4.1. MRI image dataset description

The MRI image dataset that we have utilized in our proposed tumor detection technique is taken from the publicly available sources. This image dataset contains 75 brain MRI images like with tumor and without tumor. The Brain image dataset are divided into two sets such as, (1) Training dataset (2) Testing dataset. The training dataset is used to segment the brain tumor images and the testing dataset is used to analyze the performance of the proposed technique. In this, the 60 images are utilized for the training purpose and the remaining 15 images are utilized for testing purpose. The figure 2 shows some of the sample MRI images with tumor images and non-tumor images.

![Sample MRI image dataset](image)

Fig.2. Sample MRI image dataset, (a) MRI images without tumor (b) MRI tumor images

4.2. Experimental results

In this section, we present experimental results from real MR brain images using segmentation and classification algorithms. An MR image is initially segmented by modified fuzzy c-means algorithm, and then segmented image is classified using support vector machine. The proposed method can successfully segment a tumor provided that the parameters are set correctly. The proposed technique is designed for supporting the tumor detection in brain images with tumor and without tumor. The obtained experimental results
from the proposed technique are given in figure 3 and 4. In figure 3 and 4, the MRI image with and without tumor along with the intermediate results of original tumor image, skull stripped image, segmented MRI image.

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<th>Sl.No</th>
<th>Tumor Images</th>
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**Figure 3.** Experimental results of skull stripped image, enhanced image, segmented image of tumor images

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<thead>
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<th>Sl.No</th>
<th>Non - Tumor Images</th>
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**Figure 4.** Experimental results of skull stripped image, enhanced image, segmented image of non-tumor images
4.3. Performance analysis using evaluation metrics

Diagnosis tests include different kinds of information, such as medical tests (e.g. blood tests, X-rays, MRI), medical signs (clubbing of the fingers, a sign of lung disease), or symptoms (e.g. pain in a particular pattern). Doctor’s decisions of medical treatment rely on diagnosis tests, which makes the accuracy of a diagnosis is essential in medical care. Fortunately, the attributes of the diagnosis tests can be measured. For a given disease condition, the best possible test can be chosen based on these attributes. Sensitivity, specificity and accuracy are widely used statistics to describe a diagnostic test. In particular, they are used to quantify how good and reliable a test is. As well, the how the image segmentation process could be found out in terms of quality rate.

In testing phase, the testing dataset is given to the proposed technique to find the tumors in brain images and the obtained results are evaluated through evaluation metrics namely, sensitivity, specificity and accuracy. In order to find these metrics, we first compute some of the terms like, True positive, True negative, False negative and False positive based on the definitions given in table 1.

The evaluation of brain tumor detection in different images is carried out using the following metrics [35],

\[
\text{Sensitivity} = \frac{\text{True Positive}}{(\text{True Positive} + \text{False Negative})} \\
\text{Specificity} = \frac{\text{True Negative}}{(\text{True Negative} + \text{False Positive})} \\
\text{Accuracy} = \frac{\text{True Negative} + \text{True Positive}}{(\text{True Negative} + \text{True Positive} + \text{False Negative} + \text{False Positive})}
\]

Where, \(TP\) stands for True Positive, \(TN\) stands for True Negative, \(FN\) stands for False Negative and \(FP\) stands for False Positive. As suggested by above equations, Sensitivity is the proportion of true positives that are correctly identified by a diagnostic test. It shows how good the test is at detecting a disease. Specificity is the proportion of the true negatives correctly identified by a diagnostic test. It suggests how good the test is at identifying normal (negative) condition. Accuracy is the proportion of true results, either true positive or true negative, in a population. It measures the degree of veracity of a diagnostic test on a condition.

<table>
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<th>Experimental Outcome</th>
<th>Condition as determined by the Standard of Truth</th>
<th>Row Total</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Positive</td>
<td>Negative</td>
</tr>
<tr>
<td>Positive</td>
<td>TP</td>
<td>FP</td>
</tr>
<tr>
<td>Negative</td>
<td>FN</td>
<td>TN</td>
</tr>
<tr>
<td>Column total</td>
<td>TP+FN</td>
<td>FP+TN</td>
</tr>
</tbody>
</table>

\[N = TP+TN+FP+FN\]

Table 1. Table defining the terms TP, FP, FN, TN
4.5. Performance evaluation of the proposed technique in tumor detection

The performance of our proposed technique is evaluated by means of the Modified FCM algorithm in terms of the evaluation metrics value. Here, with the aid of the input MRI image training and testing dataset, the values of TP, FP, FN, TN, Sensitivity, specificity and accuracy are given in table 2. By analyzing the results, our proposed Modified FCM is better performance. The outcomes of the experimentation proved with 80% of accuracy in Modified FCM with detection of tumors from the brain MRI images.

Table 2. Detection accuracy of the proposed approach in training and testing dataset

<table>
<thead>
<tr>
<th>Evaluation metrics</th>
<th>Input MRI image dataset</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>TN</td>
</tr>
<tr>
<td>Our Proposed Approach</td>
<td>Training dataset</td>
</tr>
<tr>
<td></td>
<td>Testing dataset</td>
</tr>
</tbody>
</table>

The comparison graphs of normal and abnormal MRI images for training and testing dataset are plotted in figure 5 and figure 6. In comparison work, we have taken five different levels like actual, KFCM+NN, KFCM+SVM, FCM+NN, FCM+SVM. In training dataset, we have taken 60 images like tumor and non-tumor images. Figure 5 shows if value is 1, the MRI images are normal, as like the value is 2, the MRI images are abnormal. In testing dataset, we have taken 15 images like tumor and non-tumor images. Figure 6 shows if value is 1, the MRI images are normal, as like the value is 2, the MRI images are abnormal.

Figure: 5 Normal and abnormal comparison for different techniques in training dataset
4.6. Comparative analysis
We have compared our proposed tumor detection technique of modified FCM against the neural network and SVM techniques. For comparison analysis, we compare our proposed approach with neural network and support vector machine. The performance analysis has been made by plotting the graphs of evaluation metrics such as sensitivity, specificity and the accuracy. By analyzing the plotted graph, the performance of the proposed technique has significantly improved the tumor detection compared with neural network. The evaluation graphs of the sensitivity, specificity and the accuracy graph are shown in figure 7 and 8. The graphs have been plotted for different metric values for the combination of KFCM+ NN, KFCM+ SVM, FCM+NN and FCM+SVM. By analyzing the graphs, the specificity and sensitivity graphs shows better results of our proposed Modified FCM algorithm with SVM. But the accuracy level proved that the proposed algorithm graph is good (80%) in detecting the tumors in the brain MRI images.
5. CONCLUSION

In this paper, we have presented an effective modified fuzzy c-means segmentation technique for detection of brain tumor. The proposed technique consists of pre-processing, segmentation using modified FCM, feature extraction of the region and final classification. The MRI image dataset that we have utilized in our proposed image segmentation technique is taken from the publicly available sources. This image dataset contains 75 brain MRI images like with tumor and without tumor. The obtained results for the tumor detection are evaluated through evaluation metrics namely, sensitivity, specificity and accuracy. In order to find these metrics, we first compute some of the terms like, True positive, True negative, False negative and False positive. For comparative analysis, our proposed approach compared with neural network. From the results obtained, we could see that the modified FCM technique received a better quantity rate for all the input images. From the evaluation metrics, we can see that our technique achieved better results for specificity, sensitivity, and accuracy which proved the effectiveness of the proposed technique. The proposed technique, achieved the specificity, sensitivity and accuracy of 0.97, 0.88 and 0.95 respectively for the training dataset and 1, 0.4, 0.8 respectively for the testing dataset.

REFERENCES


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