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An Automated Detection and Segmentation of Tumor in Brain MRI using Machine Learning Technique

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Abstract: ***Magnetic Resonance Imaging can be helpful in detecting brain tumor. It has advantages over procedures like Computed Tomography scan as it does not involve use of ionizing radiation due to which exposure of a person to such risks and related side effects can be prevented. Whatever be the technique of the imaging process, the one with the maximum accuracy must be preferred. Detection of brain tumor occurs in various stages like pre-processing, segmentation, feature extraction and classifier. For this to happen, k-mean segmentation approach is applied. Gray Level Co-Occurrence Matrix and Discrete Wavelet Transform are helpful in extraction of the tumor feature. Two types of classifiers are used for classification namely Support Vector Machine and Hidden Markov Model. Then the comparison is done based on performance parameters like sensitivity, specificity and accuracy. After calculating the results, the values of performance parameters are compared. The proposed technique has been found to perform well in terms of accuracy as compared to previous technique.***

Keywords: Brain tumor, Gray Level Co-Occurrence Matrix, Hidden Markov Model, K-Mean, Magnetic Resonance Image, Principal Component Analysis, Support Vector Machine

1. Introduction

Brain is one of the vital organs of body system. It controls activities and processes, integrates and coordinates the information it receives from different body organs. At the same time, it also makes decision and sends instructions to perform tasks accordingly. Brain tumor is identified as a situation in which the cells existing within the brain tissue becomes capable of uncontrolled proliferation. Sometimes tumors also arise from meninges as well as vessels supplying the brain tissues. Tumors are broadly classified as malignant and benign. Benign tumor cells divide slowly whereas malignant cells have got the capacity to divide endlessly as well as migrate to remote organs and thereby producing a new tumor wherever they get lodged by a process called metastasis. World Health Organisation (WHO) has classified the brain tumor into four grades ranging from grade I to grade IV which are determined only by means of proper histopathological examinations of the tissue extracted from the affected region [1]. The signs and symptoms of brain tumors vary depending upon type, size as well as the position where the tumor is located. Some of the general signs and symptoms of brain tumor are headache, seizures, memory loss, confusion, depression, weakness, numbness, nausea and vomiting. Depending upon location of tumor patients exhibit various symptoms like facial numbness, disbalancing, swallowing problems, speech problems, reading and writing difficulties and so on [2]. According to a research conducted by International Agency for Research on Cancer (IARC) which is a part of WHO, an estimated 296851 new cases of brain tumor cancer were reported in 2018. And their calculations say that the average number of such new cases is likely to pile up to 309040 by 2020. Statistics show that about 241037 deaths had occurred worldwide due to brain cancer in 2018. The data is available on Global Cancer Observatory (GCO) website [3, 4]. Thus there is a rising demand for digital image processing for early diagnosis and hence treatment of complicated diseases like brain tumor, renal stones, breast cancer, lung cancer, ovarian cancer, etc. The diagnosis of brain cancer even by some radiologists is an extremely complicated job. A number of imaging techniques are used for the scanning of a particular body part like Computed Tomography (CT) scan, X-rays and Magnetic Resonance Image (MRI). Among all, MRI is the best imaging techniques for the detection and identification of the proper location and size of the tumor in the brain as it provides detailed pictures of brain and nerve tissues in multiple plains. Also MRI is non-invasive and does not use any kind of ionising radiation. These pictures are then interpreted in detail by the radiologists. In the case of suspected brain tumor, the radiologists do the evaluation manually and make a report about the exact location and size of tumor in the brain. This report is very much important for the diagnosis and treatment planning, for performing major brain surgeries and prescribing medication accordingly. As it is a manual evaluation, the accuracy of the report may vary depending upon the experience of radiologists. Also, manual analysis is time consuming. Since the existing techniques till date have not shown satisfactory results, to reduce time and increase accuracy, automated analysis has to be done. Such an updated technique can help minimise the mortality rate due to brain tumor and associated complications, if the patient survives [5]. For this, proper image segmentation is very crucial. Various studies have been carried out in past few years in the field of brain tumor image processing as there is a need of early detection and diagnosis of brain tumor. That can be achieved only by using proper image processing techniques. The image processing and image improvement techniques are used for the detection of cerebral cancer. These techniques are used for the improvement of the picture quality for medical image processing. For highlighting the characteristics of the MR pictures, contrast adjustment and threshold approaches are used. Techniques such as Histogram, Edge Recognition, Segmentation and Morphological operations are used for the recognition and categorization of brain tumors [6]. To get precise outcomes, the MR images must be in accurate format and do not contain any unnecessary information. These objectives can be achieved by inculcating image pre-processing. Image pre-processing technique involves several procedures such as elimination and minimization of unwanted noise, redevelopment of images, up-gradation of the images, and translation to grayscale [7]. Signal to noise ratio (SNR) is improved with the application of anisotropic diffusion filter. In this process, inner parts of the images are smoothed, while the edges are preserved by the application of edge strengths and noise reduction statistics. MR images of all patients are aligned to the same co-ordinate system. Choosing MR weighted image as the reference image, other channels are registered. The non-cerebral tissue parts that are not of interest in the study have to be removed. It may include the elimination of skin, subcutaneous tissue, fat and muscle from MRI connecting medical images. In this way, the quality of image is improved. As a result, the interpretation and hence, the diagnosis becomes more precise. In the process, a picture is divided into various segments and each segment has same qualities, as far as texture, color, intensity and gray scale levels are concerned [8]. The useful information is extracted in the form of shape, color, texture and other properties and these are then studied. Image classification is a cumbersome task, as it includes several processes like object division, characteristic extraction, image detection and much more. It is very difficult to classify the image because of its complexity. Image segmentation is used to partition MR images on the basis of similarity in terms of texture, color, intensity, contrast, etc. Different methods for image segmentation are threshold-based segmentation, clustering-based segmentation, edge-based segmentation and region-based segmentation. As the MR images contain different brightness level and have high contrast level, threshold-based segmentation method is used. It is simple and effective method. It partitions the MR image into foreground and background. It isolates the objects by converting grayscale images into binary images [9]. Otsu's method and k-means clustering methods are commonly used threshold-based segmentation techniques [10]. K-mean clustering is widely used to divide the information into k clusters. The quality depends upon the values of k. Principal Component Analysis (PCA) is a statistical technique which is used to reduce dimensions of data before k-mean clustering. It can decrease the computation cost. Feature extraction is defined as the transformation of input data into set of features. In this article, Discrete Wavelet Transform (DWT) and Gray Level Co-Occurrence Matrix (GLCM) are used for extracting tumor features. Wavelet transform is used as it provides well localization in both spectral and spatial domains [11]. This is used to extract the coefficient of wavelet from cranium MR pictures. 2D discrete wavelet transform generates four sub-bands. These are Low-Low (LL), Low-High (LH), High-High (HH) and High-Low (HL) sub-bands. GLCM is the statistical method of extracting the textures that consider the spatial relationship of the pixels from the calculated matrix [12]. Using GLCM statistical features like mean, entropy, root mean square (RMS), variance, smoothness, kurtosis, skewness and inverse difference movement (IDM) are calculated.

Support Vector Machine (SVM) is a concept of supervised learning and machine learning. It gives better performance when the number of training samples is very small and the dimension of feature space is very high [13]. A dataset is divided into uniform subsets repeatedly for calculating the class members through Decision Tree (DT) classifier. In every intermediary state, the acceptations and rejection of class labels are achieved through the hierarchical classifier. The node partitioning, identification of terminal nodes and allocating the class label to terminal nodes are the three major parts of this classifier. With the help of SVM, a hyperplane or a suit of hyperplanes is generated in high dimensional space for performing classification [14]. The hyperplane located remotely from the adjacent training data end of some class supports in the attainment of the good division [15]. The generalization of the error of the classifier is less in the case when the margin is large. Depending upon the chosen hyperplane and kernel parameters, high performance and accuracy are achieved. Hidden Markov Model (HMM) is a concept of reinforcement learning and machine learning. It depends upon decision making ability in sequence, as the output depends on the state of the current input and the next input depends on the output of the previous input. It gives best suitable results on the basis of maximum rewards in a particular situation. It is a statistical model where the system is being modelled with hidden states. For this, knowledge of basic probabilities is needed but not background knowledge as past states are totally independent of future states [16]. HMM is commonly used in the field of Artificial Intelligence (AI), Pattern recognition and computer vision application. One of the advantages of HMM is that complex model can be built-in a small dataset without incorporating noise in the data [17]. In this article, two concepts of machine learning approaches have been proposed which are SVM and HMM. These have been proposed to segment the tumor region of the brain from the surrounding normal tissue. For the effective analysis of MR images, skull stripping is done to remove the non-cerebral region from MR images which are not the region of interest in this study. At last, comparison is done on the basis of performance parameters like sensitivity, specificity and accuracy. The observed results can be used as a second opinion for assistance from radiologists. As a result, the recognition of exact tumor location and size is done after proper clinical examination of the patient. The major problem is lack of publicly available datasets. The dataset of four different patients have been collected from a hospital. From the entire database, 20 MR images having tumor have been sorted out and used in this study. MR images are then made noise invariant and stripping of skull is done. Detailed study of various techniques/algorithms is done for detection of healthy and unhealthy tissues using MRI. The segmentation has been done from both proposed (HMM) and existing (SVM) technique. The values of performance parameters are calculated and compared. The proposed technique has been found to perform well in terms of accuracy as compared to previous technique.

2. Background and Related Work

For the successful treatment and recovery as well as to minimise mortality among patients, early diagnosis of brain tumor plays a significant role. Brain tumor detection and classification is an essential technique for early diagnosis and thereby planning of treatment. In medical imaging, many researchers have presented different brain tumor detection and segmentation techniques. The background work and latest articles have been studied and detailed analysis done. The author presented a hybrid method for categorization of brain tumor into normal and pathological brain with high sensitivity, specificity and accuracy using genetic algorithm (GA) and SVM [18].In [19]'a strategy for detecting and extracting brain tumor from MR images of brain using Matrix Laboratory (MATLAB) software. Basic image processing methods like noise removal functions, segmentation and morphological operations are done in this. Whereas, [20] proposed a novel automated brain tumor recognition technique from the pictures which included noise in them. The Edge Adaptive Total Variation De-noising (EATVD) technique was performed to de-noise the image and preserve edges within the de-noising process. The segmented areas were converted into GLCM for the extraction of features. During this process, distinctive features like power, homogeneity, correlation and contrast were retrieved. Multi-class SVM was used for the detection of tumor in images. On evaluating the results, it was observed that the amount of precision was increased within the noisy images when the tumor was extracted using these steps. The result showed that the peak signal to noise ratio (PSNR) was above the traditional methods. On the other hand, the article [21] proposed a generalized method of classification of brain neoplasm, which was based on rectangular window image cropping method. DWT was used to extract features, PCA was used to reduce dimension of the image and SVM was used to classify the tumor types. According to, [22] automated brain tumor interpretation was done on the basis of an organised and explicit two-tier classification of brain MRI images and various proposed techniques. In this, information was identified with normal anatomical structures and abnormal tissues to be treated, which was extracted from brain tumor segmentation on MRI. For the successful segmentation, the proposed system used k-means algorithm. In this system, the features retrieved from the discrete wavelength transform blend wavelets were trained by self-organising map neural network. As a result, the resultant filter factors were trained by the k-nearest neighbour. Thus, the two-tier classification system gave preferable performance over the existing classification methods. After validating the experimental results with the help of real data sets, the proposed system was found to show enhanced performance as far as parameters such as sensitivity, specificity and accuracy were concerned when compared to those of the existing SVM based classification system. At last, the research team presented a hybrid method to improve the quality of detection of brain tumor using Hidden Markov Random Fields (HMRF) and threshold methods. These methods have been applied on MR images of 3 different patient data sets. This gave high accuracy of MRI brain tumor images. Using these methods, size of brain tumor could be calculated as a future work [16].

3. Proposed Work Methodology

In this section, brain MR images have been used for performing various stages of brain tumor detection. Tumor localization and classification both are crucial steps for detecting brain tumor. In the existing techniques (SVM), tumor localization and classification is done but with high complexity due to which execution time is very high. To overcome this bottleneck and to meet the future needs, HMM is proposed, which reduce the execution time and gives more accuracy. The detailed flow chart using machine learning approach is given in Figure 1.

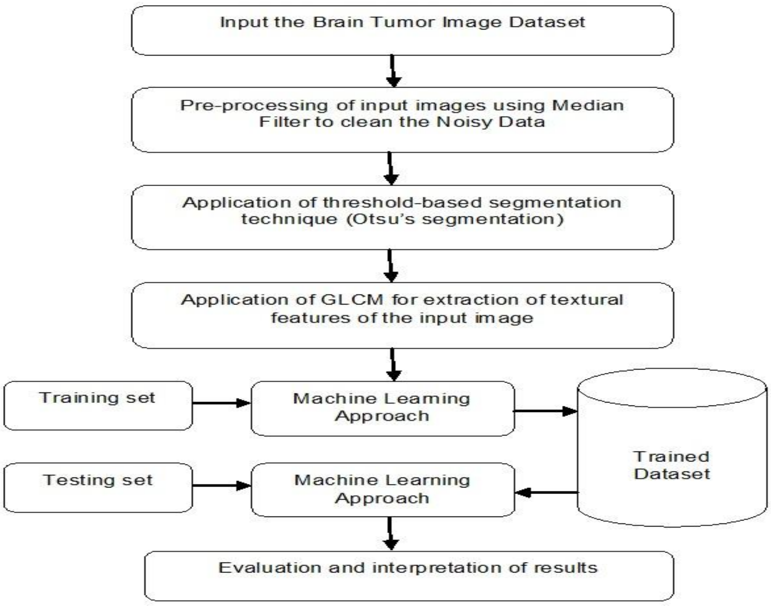

Figure 1: Proposed Methodology Flow Chart

The implementation details are discussed in following sections.

3.1. Brain MR Images

In this study, real dataset of four different patients diagnosed with having brain tumor has been collected from a reputed hospital. The data was acquired from the Midnapur Diagnostics Private Limited at R. G. Kar Medical College and Hospital, Kolkata (West Bengal), India. Midnapur Diagnostics Pvt. Ltd is a joint venture project with the Department of Health and Family Welfare, Govt. of West Bengal, India. From the entire dataset, 20 MR images with visible brain tumor have been incorporated for research purpose. Medical images obtained from the hospitals are in Digital Imaging and Communication in Medical (DICOM) format. Medical image can be studied and viewed easily using RadiAnt DICOM Viewer software. It has functions like multi-planar reconstruction (MPR), 3D volume rendering, adjustment of image window, splitting screen, transformation etc. These image formats are large in size/series. For easy access of these data, they are converted into any file format like JPEG, JPG, BMP, TIFF, PNG as analysis of images in DICOM format is a tiresome process [10]. And it is converted by using DICOM converter software. On converting DICOM to any desired format, dimension of image may vary depending upon the size of image but bit-depth and resolution will remain same in all converted images. Here, bit-depth is 24, resolution is 96×96 dpi and color representation is in RGB format. All images are resized to 200×200 pixel size.

3.2. Image Pre-processing

In order to get precise outcomes, MR images must be in accurate format and does not contain any unnecessary information. Skull stripping is done to remove non-cerebral tissue parts that are not of interest in this study. Brain MR Image is converted from RGB to gray scale. Basically, all MR images may contain salt and pepper noise in addition other noise. This noise is unwanted and needs to be removed. Median filter is used to remove the salt and pepper noise as it is non-linear and gives better results compared to mean filter. It maintains the sharpness of the boundaries and preserves fine details of the MR image. The values of noise parameters are given as: sigma is 0.05, offset is 0.01 and mean is 0. Erosion and dilation filter size is 2. Signal to noise ratio (SNR) is improved using anisotropic diffusion filter.

To calculate SNR, steps are as follows:

3.2.1. Signal power (P_{signal}) as the mean of pixel values which is given as:

$$P_{signal} = \frac{\text{sum (signal amplitude}^2)}{\text{signal row size} \times \text{signal column size}} \quad (1)$$

3.2.2. Noise power (P_{noise}) as the standard deviation or error values of the pixel values which is given as:

$$P_{noise} = \frac{\text{sum (noise amplitude}^2)}{\text{noise row size} \times \text{noise column size}} \quad (2)$$

3.2.3. Take the ratio of above steps and results are expressed in decibel unit which is given as:

$$\text{SNR} = 10\log_{10}\frac{P_{signal}}{P_{noise}} \quad (3)$$

3.3. Segmentation

In this article, threshold-based segmentation (Otsu’s segmentation) is done to convert gray scale image to binary and to extract the region of interest. It is called Otsu’s binarization for segmentation. The default value of threshold is 0.1.Image in SRGB format is again converted to lab form to get the cluster value k using k-mean clustering segmentation. Then, the image is classified in (a×b) color space. It creates 3 clusters, as image has 3 colors. Distance is measured using Euclidean Distance Matrix given as:

$$\text{Distance } [(x, y), (a, b)] = (x - a)^2 + (x - b)^2 \quad (4)$$

Every pixel in the image is being labelled and cluster mean is calculated. The results of clustering are Results of clustering are stored in the blank cell array. This process is repeated until there is change in mean [7].

3.4. Feature Extraction

Haralick et. al in 1973, proposed GLCM to measure textures. It is a matrix, where number of rows and columns are equal to number of gray level. Generalised form of GLCM is shown in Figure 2.

In this article, DWT and GLCM are used to extract tumor features, as they give well localization in both spectral and spatial domain. The first step is to analyze texture or retrieve data from the histogram picture brightness. In next step, second-order textural features are extracted. The probability density function $P(i, j\backslash d, \theta)$ is the probability matrix of two pixels, which are located at distance d and direction θ have a gray level values i and j. GLCM matrix $\emptyset(d, \theta)$ is given as:

$$\emptyset(d, \theta) = [P(i, j\backslash d, \theta)], \quad 0 < i, j \leq N \quad (5)$$

Here N is the maximum gray level. μ is mean value of P, σ is standard deviation of P and $P_x(i)$ is the i_{th} entry obtained by summing the rows of P(i,j).

$$P(i, j) = \sum_{j=1}^{N-1} P(i, j) \quad (6)$$

Gray Level	0	1	2	3
0	# (0,0)	# (0,1)	# (0,2)	# (0,3)
1	# (1,0)	# (1,1)	# (1,2)	# (1,3)
2	# (2,0)	# (2,1)	# (2,2)	# (2,3)
3	# (3,0)	# (3,1)	# (3,2)	# (3,3)

Figure 2: Generalised Form of GLCM

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The statistical features like mean, standard deviation, entropy, root mean square (RMS), variance, smoothness, kurtosis, skewness and IDM are then calculated and are shown in Table 1.

Table 1; Different Statistical Textural Features using GLCM Technique with Their Mathematical Formula.

S. No.	Statistical Textural Features Using GLCM	Formulae
1	Mean	$\mu_x = \sum_{i=0}^{N-1} iP_x(i)\ , \mu_y = \sum_{j=0}^{N-1} jP_y(j)$
2	Standard Deviation	$\sigma_x^2 = \sum_{i=0}^{N-1}(P_x(i) - \mu_x(\text{i}))^2\ ,\ \sigma_y^2 = \sum_{j=0}^{N-1}(P_y(j) - \mu_y(j))^2$
3	Contrast	$Contrast = \sum_{n=0}^{N-1} n^2 \left\{\sum_{i=1}^{N}\sum_{j=1}^{N} P(i,j)\right\}$
4	Correlation	$Correlation = \frac{\sum_i \sum_j (i \times j)P(i,j) - \mu_x \times \mu_y}{\sigma_x \times \sigma_y}$
5	Angular second moment/ Energy	$ASM = \sum_i \sum_j \{P(i,j)\}^2$
6	Homogeneity/ Inverse difference moment (IDM)	$IDM = \sum_i \sum_j \frac{1}{1+(i-j)^2} P(i,j)$
7	Entropy	$Entropy = -\sum_i \sum_j P(i,j) log\,(P(i,j))$
8	Variance	$Variance = \sum_i \sum_{\text{j}} (i-\mu)^2 P(i,j)$
9	Skewness	$s = \frac{E(x-\mu)^3}{\sigma^3}$
10	Kurtosis	$k = \frac{E(x-\mu)^4}{\sigma^4}$

3.5. Machine Learning Approach

In this article, tumor is detected by using two machine learning approach SVM and HMM.

3.5.1. Existing Algorithm

SVM can be used for both linear as well as non-linear data. Mapping of non-linear data into linear feature space can be done by using kernel function (K). To describe SVM a set of linearly separable data and its class are considered. The decision function is represented as:

$$f(x) = sgn\left(\sum_{i=1}^{N} \alpha_i \gamma_i K(x_i \cdot x) + b\right) \qquad (7)$$

It is observed that the maximal marginal classifier is found in the linear space. In SVM training, a convex quadratic programming (QP) is solved with the help of equality and inequality constraints that are obtained by the objective of margin maximization. Using appropriate kernel and hyper parameters, the best training model is found. In SVM based classification, the correct class is selected on the basis of award and penalty. The memory space required for SVM is determined by the product of number of support vectors and number of feature values. SVM has larger model size which can be improved by selection of hyper parameters [23].

3.5.2. Proposed Algorithm

HMM is a machine learning tool which represents probability distribution over observable sequences. This tool got its name from its two exclusive properties:

It speculates the result produced by a process at time t while the state Z_t remains hidden from the observer. It also speculates the state of the process satisfying the Markov property and is given the value of Z_{t-1}, while the current state remains independent of all the states prior to t-1. Bayesian network maps the relationship between events in terms of probability. It shows how the occurrence of certain events influences the probability of other events occurring. Bayesian network representing hidden states in gray is shown in Figure 3.

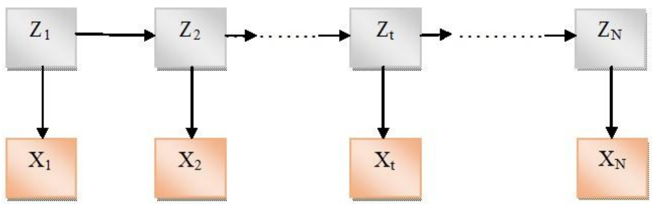


Figure 3: Bayesian Network Representing Hidden States in Gray

The joint distribution of a sequence of states and observations can be given as:

$$P(X_{1:N}, Z_{1:N}) = P(Z_1)\prod_{t=2}^{N} P\left(\frac{Z_t}{Z_{t-1}}\right)\prod_{t=1}^{N} P\left(\frac{X_t}{Z_t}\right) \qquad (8)$$

HMM is characterized by five distinct parameters:

1. Number of states in the model, K
2. Number of distinct observations, Ω
3. Model of state transition, A: It is also called transition matrix of [K*K] whose element is $A_{ij\,\in\{1......K\}}$ given as:

$$A_{ij} = P\left(\frac{Z_{t,j} = 1}{Z_{t-1,i} = 1}\right) \qquad (9)$$

Conditional probability is given by below equation:

$$P(Z_t|Z_{t-1}) = \prod_{i=1}^{K}\prod_{j=1}^{K} A_{ij}^{Z_{t-1,i}Z_{t,j}} \quad (10)$$

4. Model of observation, B: It is also known as emission probability of [Ω×K] matrix whose element is B_{kj} which is given as:

$$B_{kj} = P(X_t = k|Z_t = j) \quad (11)$$

Conditional probability is given by following equation:

$$P(X_t|Z_t) = \prod_{j=1}^{K}\prod_{k=1}^{\Omega} B_{kj}^{Z_{t,j}X_{t,k}} \quad (12)$$

5. Distribution of initial state, π: It has K×1 vector as$\pi_i = P(Z_{1i=1})$and conditional probability is given by below equation:

$$P\left(\frac{Z_1}{\pi}\right) = \prod_{i=1}^{K} \pi_i^{Z_{1i}} \quad (13)$$

Based upon the above five parameters, an HMM can be specifically abbreviates as:

$$\lambda = (A, B, \pi) \quad (14)$$

HMM can be used in real world applications. While doing the research, three problems faced were:

1. The way the problem, that the model produces is computed, forms a part of the exact inference which can be solved by forward filtering.
2. Finding the most probable sequence of hidden states is the second milestone which can be solved by using Viterbi algorithm. Calculation of probability of being in state forms a related problem which can be solved by means of forward-backward algorithm as it calculate the filtered and smoothed marginal which can then be used to present the exact inference.
3. Adjustment of the model parameters to maximise the probability of observation, becomes the third problem which can be solved using Baum-Welch algorithm [24].

4. Experimental Results

The proposed algorithm is simulated using MATLAB R2016a version with 4 GB HDD and 4 GB internal RAM as hardware devices. All stages of brain tumor detection are done with Graphics User Interface (GUI) MATLAB guide. All MATLAB programs work as per GUI MATLAB guide. Here, a variety of combinations of filters and image processing techniques have been implemented to get best possible results which can help in detection of brain tumors at early stages [9]. Graphical User Interface Development Environment (GUIDE) Quick Start Dialogue box opens after typing GUIDE in command window or start menu by selecting MATLAB> GUIDE (GUI BUILDER) as shown in Figure 4.

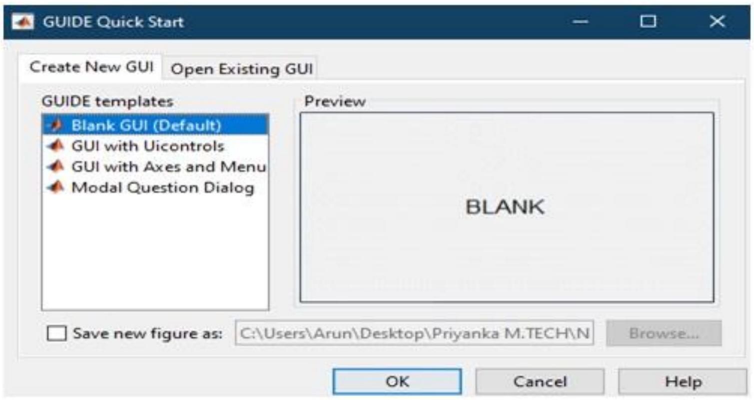
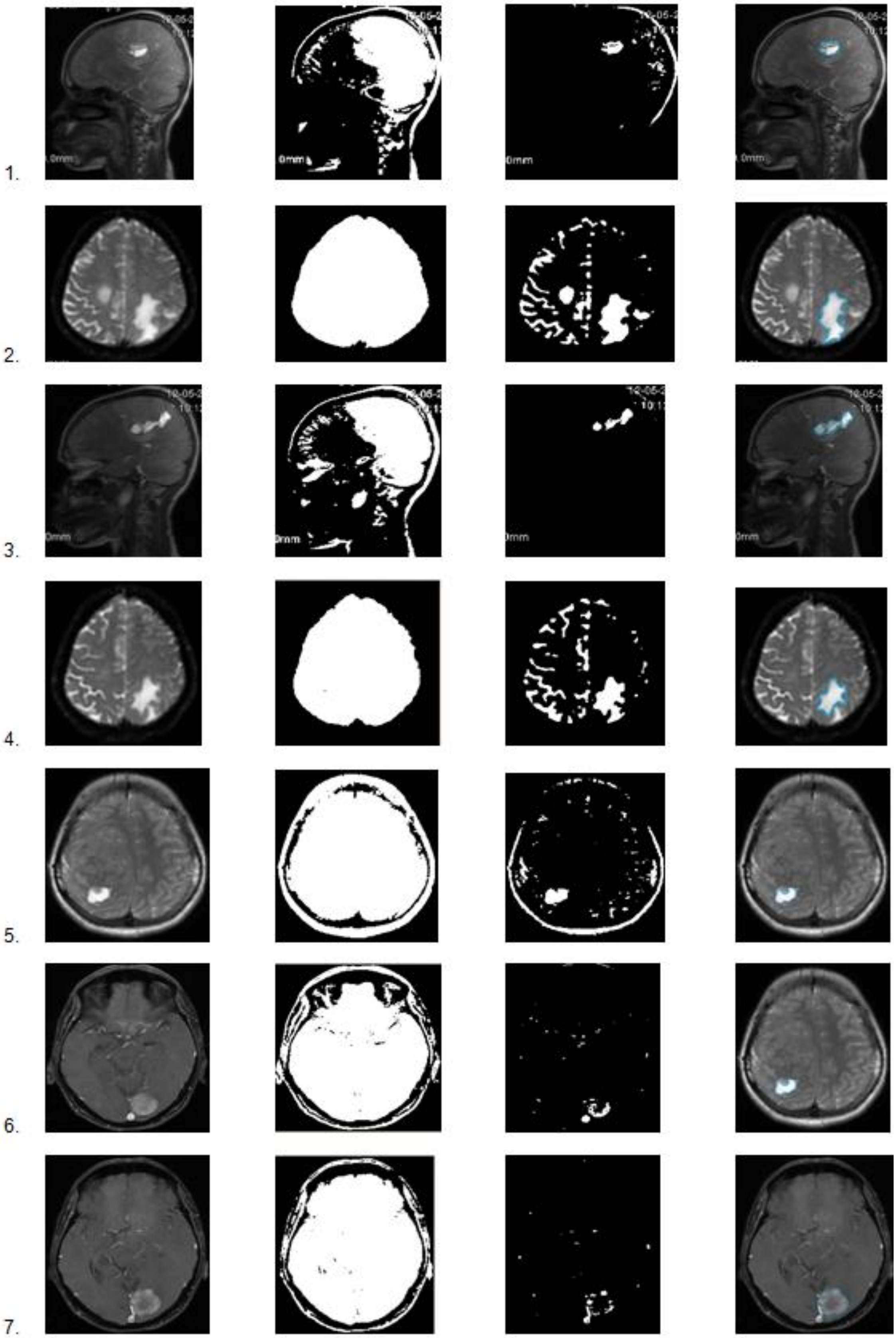


Figure 4: GUIDE Quick Start with Blank Function File

When GUI is saved, GUIDE generates two types of files. They are Matlab Interface figures (FIG-file) and Mat-file. FIG-file with extension as .fig contains all details of GUI layout and components like push buttons, sliders, toolbars, etc. Mat-file has .mat extension which is a code file where code is written in call-back function. Fig and Mat file must be saved with the same name and in the same folder. Figure 5(a) shows real dataset of MRI brain images diagnosed with having brain tumor has been collected from reputed hospital, Figure 5(b) shows the output of MR image using Otsu's threshold method, Figure 5(c) shows segmented brain MR images by proposed algorithm which is described in this paper and Figure 5(d) shows the exact marked (encircled in blue) location of brain tumor in brain MR images.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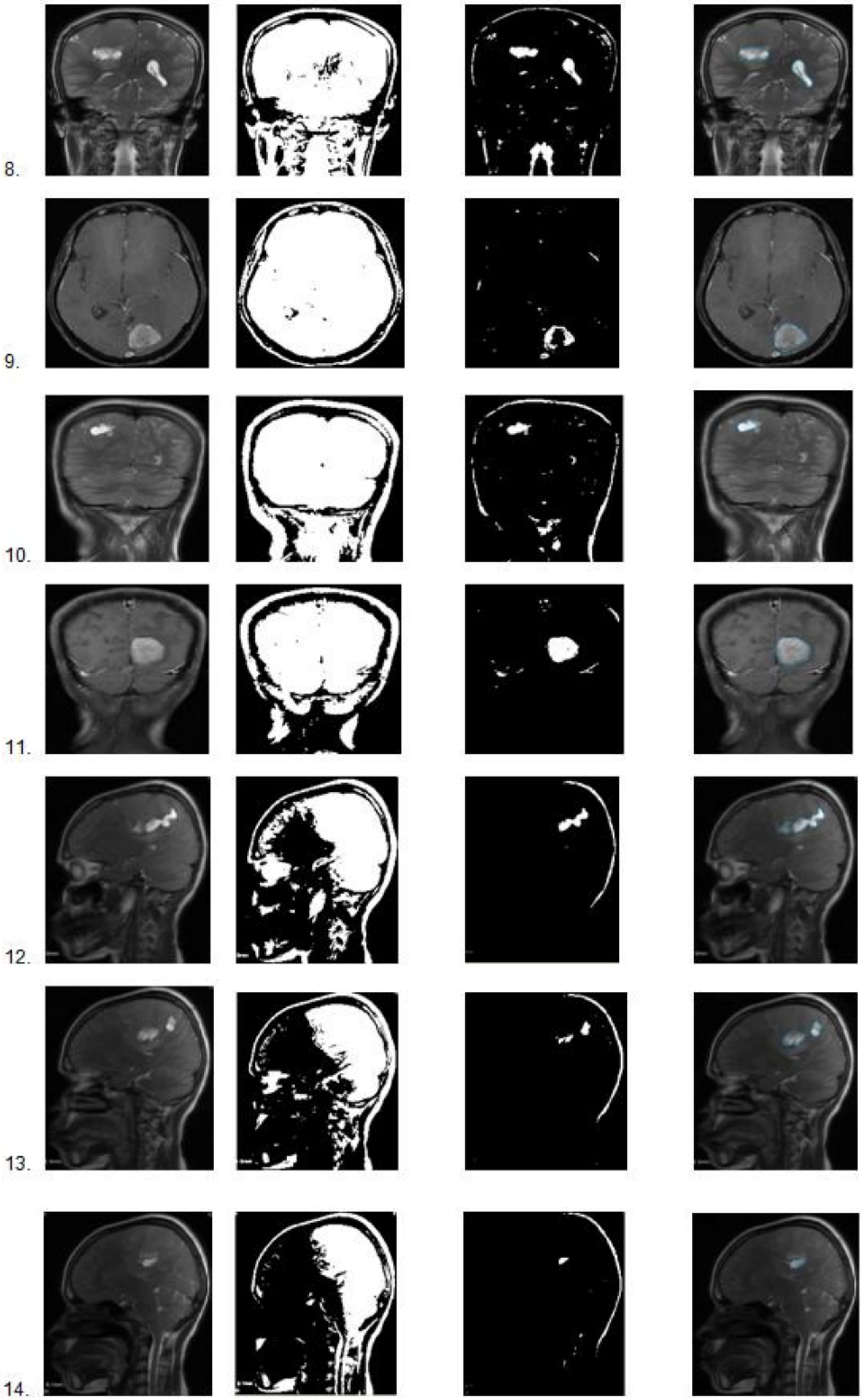
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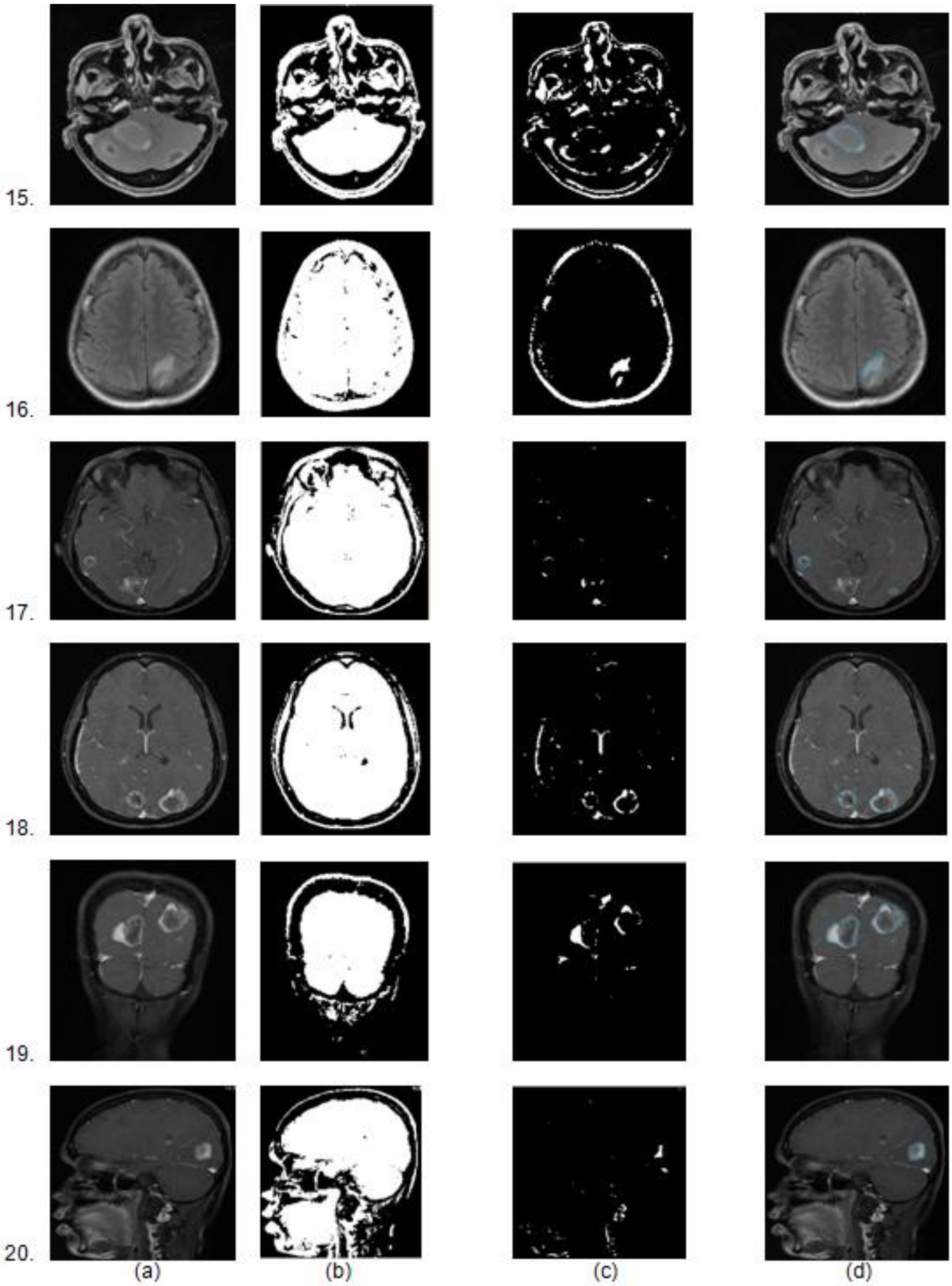

Figure 5 (a) MRI Brain Images with Tumor **(b)** Otsu's Threshold Image **(c)** Tumor Segmented Brain MR Image by Proposed Method **(d)** Exact Marked Location of Brain Tumor in Brain MR Image

Performance Analysis

1. **Accuracy:** It is the ratio of correctly classified number of points to the total number of points multiplied by 100. Accuracy (A) can be represented as:

$$A = \frac{\text{Number of points correctly classified}}{\text{Total number of points}} \times 100 \tag{15}$$

2. **Specificity:** It is the ratio of related occurrence and extracted occurrence. It is also called positive predictive value.

$$\text{Specificity} = \frac{\text{True positive}}{\text{True positive} + \text{False positive}} \tag{16}$$

3. **Sensitivity:** It is the ratio of related occurrence and total sum of related instances.

$$\text{Sensitivity} = \frac{\text{True positive}}{\text{True positive} + \text{False negative}} \quad (17)$$

Comparison of HMM and SVM on the basis of Performance Analysis

From Table 2, Figure 6, Figure 7 and Figure 8 shown below, it is clearly recognizable that the proposed algorithm (HMM) produces better accuracy, sensitivity and specificity values when compared with the existing algorithm (SVM). It is concluded that the average accuracy, specificity and sensitivity of the HMM is 78.5%, 60% and 53% respectively and the average accuracy, specificity and sensitivity of SVM is 56.5%, 46% and 49% respectively. From this, it is observed that HMM has high performance measures than SVM. The highest measured accuracy of HMM is 90% and that of SVM is 80%. It is concluded, that there is 10% more accuracy in proposed algorithm than that in existing algorithm. The highest measured specificity of HMM and SVM is same i.e. 100%. The highest measured sensitivity of HMM is 100% and that of SVM is 80%. From this, it is calculated that there is 20% more sensitivity in proposed algorithm than that in existing algorithm. Based on all calculated parameters, it can be inferred that HMM is better than SVM. Prevention is better than cure. This can only be achieved with the help of some technique that can help in early diagnosis of any illness and that to with maximum possible accuracy and specificity. As the time passes by, an increasing trend has been observed in mortality rates due to brain tumors and related complications. Medical image processing gains widespread popularity due to various types of disease detection, prediction and classification. The processing and evaluation of normal, as well as abnormal images is the major objective of medical image processing, which helps in diagnosing the tumor affected regions from brain MR image dataset. Let us think of a situation where, medical image processing inculcates Artificial Intelligence. It can enable the automated image processing to challenging scenarios with least human intervention and maximum precision. Presently, how accurately and effectively, the existing techniques are diagnosing tumor images, depends on the techniques that are being used in various phases of tumor recognition.

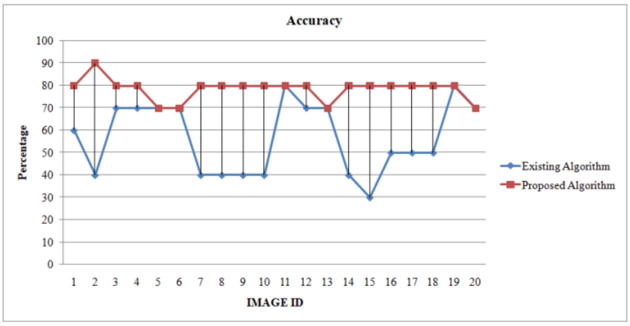

Figure 6: Overall Comparison of Accuracy Values between Existing Algorithm and Proposed Algorithm

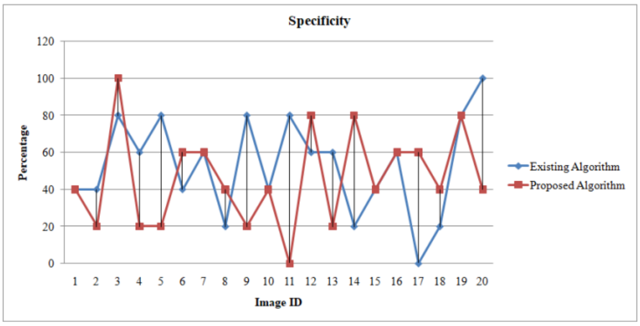

Figure 7: Overall Comparison of Specificity Values between Existing Algorithm and Proposed Algorithm

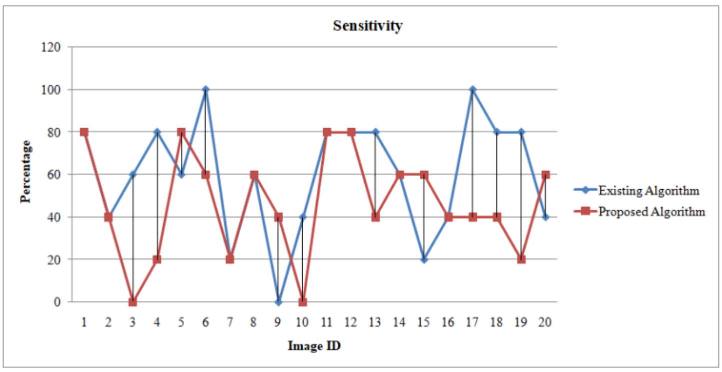

Figure 8: Overall Comparison of Sensitivity Values between Existing Algorithm and Proposed Algorithm

Table 2: Overall comparison of performance on the basis of parameters like accuracy, specificity and sensitivity

Image ID	Support Vector Machine (Existing Algorithm)			Hidden Markov Model (Proposed Algorithm)		
	Performance Parameters					
	Accuracy (%)	Specificity (%)	Sensitivity (%)	Accuracy (%)	Specificity (%)	Sensitivity (%)
1	60	40	80	80	40	80
2	40	20	40	90	40	40
3	70	100	0	80	80	60
4	70	20	20	80	60	80
5	70	20	80	70	80	60
6	70	60	60	70	40	100
7	40	60	20	80	60	20
8	40	40	60	80	20	60
9	40	20	40	80	80	0
10	40	40	0	80	40	40
11	80	0	80	80	80	80
12	70	80	80	80	60	80
13	70	20	40	70	60	80
14	40	80	60	80	20	60
15	30	40	60	80	40	20
16	50	60	40	80	60	40
17	50	60	40	80	0	100
18	50	40	40	80	20	80
19	80	80	20	80	80	80
20	70	40	60	70	100	40
Average (%)	**56.5**	**49**	**46**	**78.5**	**53**	**60**

5. Conclusion

Detecting the brain tumor from MRI images is the major aim of this study. The existing approaches can localize and categorize tumor portion from MR images with high execution time and low accuracy. Due to its complexity, that methodology was not able to yield satisfactory results. To avoid this bottleneck and to meet the need of high accuracy rate with least execution time, there is a need to design a relatively more effective technique. To achieve this goal, median filter is applied to de-noise the MR images. The threshold-based segmentation (Otsu's segmentation) technique is applied for the image segmentation which removes non-brain tissue region from the MR image. The textural feature extraction algorithm called GLCM is applied for the feature extraction. For the localization and categorization of the tumor region from an MR image, the machine learning algorithm is applied in the final phase. Computer vision and machine learning toolbox are used by the proposed technique when implemented in MATLAB simulator. For detecting the tumor portion, the performances of proposed and existing techniques are compared on the basis of performance parameters like accuracy, specificity and sensitivity in terms of lesion localization and characterization and then the comparison results are analysed. On the basis of average accuracy calculated for 20 MR images of the patients having brain tumor, the result shows that the proposed HMM is giving accuracy of 78.5%. Whereas, the conventional techniques using SVM have shown an accuracy of 56.5%. After calculating the results, it has been observed that HMM performs well in terms of accuracy and execution time as compared to SVM. Hence, to improve efficiency of the brain tumor detection, SVM classifier can be replaced with proposed work i.e. HMM classifier. Therefore, the proposed work is today's need in the field of bio-medical image processing. This approach can be implemented by engineers in near future for detection of brain tumor. This proposed AI based bio-medical image processing system can be a boon for the patients in coming future.

6. Future Scope

Proposed techniques can be replaced by hybrid techniques for detection and classification of the brain tumor. It can be further extended using other Artificial Intelligence techniques and can be implemented with python, big data analytics and data mining methods.

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