

Hybrid enhanced ICA & KSVM based brain tumor image segmentation

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ABSTRACT

Medical image processing is an important aspect in diagnosis and treatment strategy. The tremendous volume of medical data has accelerated the need for automated analysis of this image, more so in the case Magnetic Resonance Imaging (MRI). An improved K-means algorithm and EM algorithm have been combined in the proposed approach to produce a hybrid strategy for better clustering and segmentation using Enhanced ICA. A classifier for based on Support Vector Machine (SVM) has been formulated and employed for the classification of brain tumors in Magnetic Resonance Images (MRI). The proposed SVM classifier used a kernel in the form of Gaussian radial basis function kernel (GRB kernel) to improve the classifier performance. The performance of the classifier has been validated through expert clinical opinion and calculation of performance measures. The results amply illustrate the suitability of the proposed classifier.

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1. INTRODUCTION

The number of medical imaging techniques that align with computer and segmentation algorithms have increased. These techniques are examined and validated by researchers through the years. Analytic methodologies [1] have been applied for clinical analysis like cancer tumor staging. Human interpretation of images used to grade the tumors may vary with each reader as it depends on the visual features of lesions. Hence, these approaches play an important role in identifying and grading the tumor. Therefore, an automated image analytic process is used to classify the brain tumors which are capable of quantitatively assisting in a better objective diagnosis. Since a tumor does not have a pre-defined characteristic, it is important that these lesions be differentiated into a normal and cancerous tumor, accurately. Thus, the brain tumor image analysis is a challenging task. The process used for image analysis to diagnose cancer is different from the recent works on the genetic analysis of tissue samples [2].

The morph metric methods use methods that find the correlations between brain shape and disease severity, by statistically identifying and characterizing structural differences among people. Owing to the improvement in resolution of anatomical human brain scans and image processing techniques, many approaches to characterize the differences in shape and neuro-anatomical configuration of different brains have emerged in the recent times. The morph metric analysis of brain's magnetic resonance images (MRI) have gained popularity to examine the neuroanatomical correlates of a normal brain development and neurological disorders. Since, MRI is the best medical imaging technology for diagnosing pathological brains by providing details MR images from different modalities. These MR images can be used to study and compare brain tumors on preoperative and postoperative, in addition to be used to determine the resection extent [3]. The brain shape of different patients suffering from schizophrenia, autism, *alzheimer*, dyslexia and

Turner's syndrome has been studied by researchers. Segmentation is commonly required as a preliminary stage while analysing the medical images for computer-aided diagnosis and therapy. However, the intrinsic nature of the images makes medical image segmentation, a complex and challenging task. The precise segmentation of the brain is important due to its complicated structure. Some of the prominent image processing techniques that have been proposed for the segmentation of brain MRI are threshold, region-growing and clustering. The distribution of tissue intensities in brain images seems very complex that create difficulties in threshold determination. This makes the threshold methods restrictive and therefore, it has to be combined with other methods. The region growing technique, is an extension of the threshold method, that is, it is a combination of threshold method and connectivity conditions or region homogeneity criteria. Here, the anatomical information should be precise so as to successfully locate the single/multiple seed pixels for each region and combine it with their associated homogeneity. Another popular method used for medical image segmentation is clustering. Some typical clustering methods include fuzzy c-means (FCM) clustering and expectation maximization (EM) algorithms.

In the proposed algorithm, improved K-means algorithm is combined with EM algorithm, to produce a hybrid strategy for an enhanced clustering. This algorithm aims to use the well distributed cluster that is derived from the K-means along with the compactness of clusters that is provided by EM. The initial clusters are provided by improved K-means algorithm. These clusters produce centers which are widely spread in the given data. The centers are then used as initial variable for EM to find the local maxima through different iterations. This is followed by modification of Gaussian mixture model and enhancement of ICA segmentation approach. Next, the tumors are classified as benign and malignant using Kernel SVM. The discrete wavelet transforms (DWT) is used to extract the features [4], [5] which are further reduced to improve the classification accuracy using the Principal Component Analysis (PCA). After the features are extracted, SVM classifier is used to classify them.

In this paper, the Gaussian radial basis function kernel (GRB kernel) is used to analyse the classification. Various performance measures [6]-[8] and expert clinical opinions have been used to validate the classification method/algorithm.

2. REVIEW OF LITERATURE

Various segmentation approaches have been reported in the literature and have been studied over a period of time. Emphasis have been given to the segmentation of brain MR images. Some of the recent works mentioned in the literature have been A pixel classification based brain magnetic resonance images segmentation has been presented by A. In [9], where automatic segmentation of brain into four classes like background, cerebrospinal fluid, grey and white matter is performed. An unsupervised and knowledge based skull stripping algorithm for brain magnetic imaging termed as S3 bases on brain anatomy and image intensity characteristics was performed in [10]. In [11], P.Moeskops *et.al.* used adaptive intensity threshold, after which morphological operations is carried to boost robustness. An automatic segmentation method which is based on the Convolution Neural Networks (CNN) and explores small 3×3 kernels is described in [12]. Here intensity normalization is used with data augmentation, as the processing step that provides effective results for brain tumor segmentation in magnetic resonance images. The detection of human brain tumor using magnetic resonance image segmentation and morphological operators has been presented in [13]. Here the tumor cells were separated from normal cell using morphological operators combined with conventional image processing techniques. Microwave imaging was used in [14] to detect the brain tumor and localization of a deep brain RF source. Here, Levenberg-Marquadi iterative scheme was used as microwave imaging techniques to solve the inverse scattering problem for the head of the phantom in 403.5MHz medical radio band. It was seen through the simulation results that at least 45 dB SNR was required for small tumor detection. Here, a localization method based on microwave imaging is used for deep brain RF source. A semi-supervised clustering technique that uses the concept of multi objective optimization for segmentation of magnetic resonance brain image in intensity space is proposed by A.K. In [15] the intensity values were used as features and a modern objective optimization technique which uses the concept of simulated annealing is implemented to optimize the three cluster validity indices. Its performance was compared with approaches like FCM, Expectation maximization, fuzzy-VGAPS clustering techniques. An empirical wavelet transform (EWT) method to extract the features of brain SPECT image and assist in brain tumor detection was proposed in [16]. The image is decomposed into a number of sub-band images using EWT, while segmentation is done using the fuzzy C- means clustering, to achieve better accuracy. The Support vector machine classifier was used. A spatial fuzzy C-means (SPFCM) algorithm was presented in [17] for segmentation of magnetic resonance images. Here, the spatial information from the neighborhood of each pixel is employed and realized by defining a probability function. The SPFCM algorithm helped to solve the problem related to sensitivity to noise and intensity in homogeneity in magnetic resonance imaging

data and hence improve the segmentation results. The authors proved that the SPFCM had a better performance than some of the FCM based algorithms. A classification method to classify brain magnetic resonance images as normal and abnormal using wavelets texture features and k-means classifier was proposed in [18]. Here, the Euclidean distances were measured between feature vector of test magnetic resonance image and k-means classifier was fed with reference magnetic resonance images. A four phase hybrid approach was presented in [19] which can be used for brain tumor detection and classification in magnetic resonance images. The first phase includes, image pre-processing through noise filtering and skull detection. In the second phase, the features are extracted using gray level co-occurrence matrix. Normal and abnormal classification of inputs using least square support vector machine classifier with multilayer perception kernel is dealt in the third phase. The fourth phase was segmentation of tumor, for which authors used fast bounding box. This implementation was found to be 96.3% accurate. The performance analysis of different methods of tumor detection was described in [20]. A comparative study between different methods for tumor detection was described by the authors while emphasizing on the role of segmentation in medical imaging. They showed that segmentation works efficiently in detecting and extracting the tumor from magnetic resonance imaging.

3. PROPOSED APPROACH

There are many important applications of blind source separation through independent component analysis in many areas like signal processing and medical signal processing. Many computer aided algorithms have been proposed over the years, that can be implemented to analyze magnetic resonance images, like Eigen image analysis, principal component analysis (PCA) and fuzzy C method etc. Eigen image analysis is better when it comes to offering an effective segmentation and feature extraction. However, when it comes to satisfactory segmentation of brain tissues, the neural network based methods prove to perform better. These methods provide better performance when compared to the classical maximum likelihood methods. There has been a rise in the multi-spectral images, due to which many segmentation and analysis procedures having their base on orthogonal projection, Kalman filter, etc have been subjected to enhancement over the years. These procedures however, possess a drawback, that they require prior knowledge. Therefore, the independent component analysis (ICA) segmentation method provides better performance in the segmentation of brain tissues.

ICA can be used to identify linear non-orthogonal coordinate systems. The data's second and higher order statistics determine the direction of axis corresponding to the coordinate systems. The transformed variables that are found by the linear transformation of data by ICA are such that they are statistically independent from each other as far as possible. This means that the ICA, just like principal components analysis (PCA) technique, is useful in finding the data structure. The ICA, however, has a drawback of assuming the sources to be independent. Due to this the concept of mixture models have been introduced so that the data observed can be characterized into different mutually exclusive classes. One of the imperative step in ICA is choosing a proper search space. Hence, the generalization considerations are generally preceded by dimensionality reduction procedures in ICA. This improves the generalization performance of ICA along with a reduction in the computational complexity. Expectation maximization algorithm (EM) is used to estimate the probability densities through expectation maximization clustering. The EM algorithm is based on the search of maximum chances of parameter estimates which can be made when the data model is dependent on certain latent variables. In the algorithm presented in this paper, the initial clusters are identified using K- means algorithm after which expectation (E) and maximization (M) steps are performed alternatively to converge into a result through iteration. The latent variables are used in the same way as they were observed to compute the expectation of chances (E). The results of the last E step are used to compute the maximum probability in the maximization (M) step.

Mathematically for a given training dataset

$$\{x(1), x(2), \dots, x(m)\} \quad (1)$$

And model

$$p(x, z) \quad (2)$$

Where z is the latent variable, we have:

$$l(\theta) = \sum_1^m \log p(x; \theta) \tag{3}$$

$$= \sum_1^m \log \sum_z p(x; z; \theta) \tag{4}$$

Where, x, y, z and θ represent the log likelihood. Since z is an unknown latent variable, approximations have been used, which are formed in E and M steps described above. It can be mathematically written as: E Step, for each i :

$$Q_i(z^{(i)}) = p(z^{(i)} / x^{(i)}; \theta) \tag{5}$$

M Step, for all z :

$$\theta := \arg \max_{\theta} \sum_i \sum_z (t) Q_i(z^{(i)}) \log \frac{p(x^{(i)}, z^{(i)}; \theta)}{Q_i(z^{(i)})} \tag{6}$$

Where Q_i the posterior distribution of is $z^{(i)}$'s given the $x^{(i)}$ s.

Conceptually to incorporate the spatial information into GMM, as a typical variation of GMM is proposed by using the MRF model as a prior. Different from GMM, each pixel i in MODIFIEDGMM is characterized by its probability vector

$\pi_i = (\pi_i^1, \pi_i^2, \dots, \pi_i^c)^T$ where π_i^k denotes the probability of the i^{th} pixel belonging to the k^{th} cluster.

In modified GMM, the corresponding mixture model of x_i is assumed as

$$p(x_i / \pi, \theta) = \sum_{k=1}^c \pi_i^k p(x_i / \theta_k) \tag{7}$$

where $p(x_i / \theta_k)$ is a Gaussian distribution with parameters $\theta_k = \{u_k, \Sigma_k\}$.

To take the spatial dependence into account, the prior distribution of π is given by the MRF model through a Gibbs density function

$$p(\pi) = \exp\left(-\beta \sum_{i=1}^N V_{N_i}(\pi)\right) / Z \tag{8}$$

where Z is a normalizing constant and β is regularization parameter.

The clique potential function of the pixel label vectors π_m is given by $V_{N_i}(\pi)$ which lies within the neighborhood N_i of the i^{th} pixel

$$V_{N_i}(\pi) = \sum_{m \in N_i} |\pi_i - \pi_m|^Z \tag{9}$$

Notice that the $\pi = \{\pi_1, \pi_2, \dots, \pi_k\}$ in GMM is shared by all pixels, whereas in MODIFIEDGMM π_i is different for each pixel i and depends on its neighboring pixels. In MODIFIEDGMM, the modified EM algorithm is utilized to obtain the maximum a posteriori (MAP) estimation of the parameters.

Subsequently the ICA is done at the following levels

1. Enhancement of energy criteria: Eigen values are used to determine the effectiveness of the features. These eigen values are indicative of the original data; the eigen value spectrum on the other hand indicates the energy of the original data. The information that represents the original data needs to

be preserved to the maximum extent while transforming from a high dimensional space to a lower dimensional space.

2. Improvement of magnitude criteria: In order to implement the ICA in this regard, it should be done in a reduced PCA space so that the small valued trailing eigen values are not included. Therefore, these criteria favours low dimension spaces whereas the small valued trailing eigen values are excluded.

An improved performance is achieved in the proposed work by using dimensionality reduction procedures that aim at balancing the energy and magnitude criterion. ICA, an extension to the co-variance based PCA is used to solve BSS problems like cocktail party problem. The observed signals are made up of linear combination of original signals and a matrix mixture.

It can be represented as

$$X = AS \quad (10)$$

$W=A^{-1}$ inverse is computed to obtain mixing matrix A. The IC is obtained as:

$$\hat{S}_{=WX}, \quad (11)$$

$$\hat{S}_{=S} \quad (12)$$

The suspicious regions need to be segmented from an IC. Assuming t_{ij} to be the (i, j) 'th element of a co-occurrence matrix W that considers the gray level transitions between two adjacent pixels. The equation is written as:

$$t_{ij} = \sum_{l=1}^M \sum_{k=1}^N \delta(l, k) \quad (13)$$

Where

$$\delta_{d,\theta} = \begin{cases} 1 & \text{if } 1(1+1,k)=i, I=I(l,k)=i, I(I, K+1) \text{ and / or } I(1,k), I(1+1,k)=j \\ 0 & \text{Otherwise} \end{cases} \quad (14)$$

The probability of a transition of this gray level from i to j can be defined as

$$P_{ij} = \frac{t_{ij}}{\sum_{i=0}^{L-1} \sum_{j=0}^{L-1} t_{ij}} \quad (15)$$

Here, t represents the threshold that partitions the co-occurrence matrix that is defined by (13). The co-occurrence matrixes are first grouped into 4 quadrants namely A, B, C and D, after which they are grouped into foreground and background objects. The ones having pixels with intensity level greater than threshold fall into the foreground object category while those with pixel intensity less than threshold fall into the background category. The transitions within background and foreground are represented by A and C quadrants while the transitions across boundaries between foreground and back grounds are represented by B and D quadrants. The following equations represent the probabilities associated with each of these quadrants.

$$P_{A=}^t = \sum_{i=0}^t \sum_{j=0}^t P_{ij} \quad P_{B=}^t = \sum_{i=0}^t \sum_{j=t+1}^{L-1} P_{ij}$$

$$P_{C=}^t = \sum_{i=t+1}^{L-1} \sum_{j=0}^t P_{ij} \quad P_{D=}^t = \sum_{i=t+1}^{L-1} \sum_{j=t+1}^{L-1} P_{ij} \quad (16)$$

The cell probabilities can be used to obtain the probabilities in each quadrant:

$$P_{ij/A}^t = \frac{P_{ij}}{p_A^t} \quad P_{ij/B}^t = \frac{P_{ij}}{P_B^t} \quad P_{ij/C}^t = \frac{P_{ij}}{P_C^t} \quad P_{ij/D}^t = \frac{P_{ij}}{P_D^t} \quad (17)$$

In the proposed work, a local entropy based threshold has been employed to segment the tumor. Since the local transitions from background to background (BB) and objects to objects (FF) are represented by quadrants A and C respectively, the mathematical definition of local entropies can be written as:

$$H_{BB}(t) = - \sum_{i=0}^t \sum_{j=0}^t P_{ij/A}^t \cdot \log P_{ij/A}^t \quad (18)$$

$$H_{FF}(t) = - \sum_{i=t+1}^{L-1} \sum_{j=t+1}^{L-1} P_{ij/C}^t \cdot \log P_{ij/C}^t \quad (19)$$

The second-order local entropy can be obtained by summing up the local within-class transition entropies of the foreground and the background and can be written as

$$H_{LE}(t) = H_{BB}(t) + H_{FF}(t) \quad (20)$$

Maximizing the above equation results in a threshold based on local entropy, using which the tumor can be segmented

$$t_{LE} = \arg \left\{ \max_t H_{LE}(t) \right\} \quad (21)$$

3.1. Method

The proposed approach is to be coded using Matlab. The steps involved in the process can be listed as below.

- a. Populating the required images for analysis from databases like Brain Tumor Disease database and images sourced from other super specialty hospitals.
- b. Performing preprocessing operations like noise removal, edge detection and thresholding to remove the back ground and other clinically irrelevant things in the context of the proposed analysis
- c. Designing an Enhanced ICA Mixture Model (EICAMM) for automatic segmentation of brain.
- d. Designing a Classifier based on Support Vector Machine (SVM) for classifying and correlating different neurological disorders.
- e. Designing a Graphical User Interface (GUI) using Matlab for loading the required image for analysis, processing the results and presenting the interpretation.
- f. Validating the results by comparing with standard data sets and expert clinical opinion
- g. Performing Receiver Operating Characteristic (ROC) analysis to validate the performance of the classifier.

4. RESULTS & DISCUSSIONS

The following section summarizes the results of the proposed segmentation approach. The proposed was coded in Matlab R 2012 a and the validity of the segmentation is demonstrated with the help of evaluation parameters. The ground truth images for validation were obtained through manual segmentation. The following images listed in Figure 1 have been considered for testing and validation. To have a true representation the images are of different sizes and intensity values.

The histogram profile of the images serves to give a trend in distribution of intensity values and help in the initial stages of the choosing the threshold. The histogram of the images is illustrated in the Figure 2. The below shown are the histogram profiles, clearly illustrates that the test image have different intensity profile and variant pixel distribution. This pixel distribution is also influenced the type and the location of the

tumor too. Similarly the size of the tumor also plays a crucial role in defining the intensity profile. The intensity profile of a particular region can also give an inclination towards percentage of scattered elements. Edge detection refers to the progression of identify and locate sharp discontinuities in an image.

Edge is a basic and important feature of an image. Image is a combination of edges. Detecting edges is one of the mainly significant features in image segmentation. Edge detection is a vital step as it is a process of identifying and locates sharp dis-continuities in a representation. The edges of the test images as identified using Prewitt edge detector is illustrated through Figure 3. The complexity of medical image segmentation can be clearly understood from the above images. Even though we are using a similar edge detector we can see an appreciable difference in performance between different images. It can be clearly observed that the edges are neatly demarcated in image (b) where as in image (c) the edges appeared to merge and in the case of image (a) it appears to be cluttered and distorted. It can be observed from the intensity profile and edges that test images present a very complicated task for segmentation. The results of the segmentation of these test images using the proposed approach are depicted using the Figure 4.

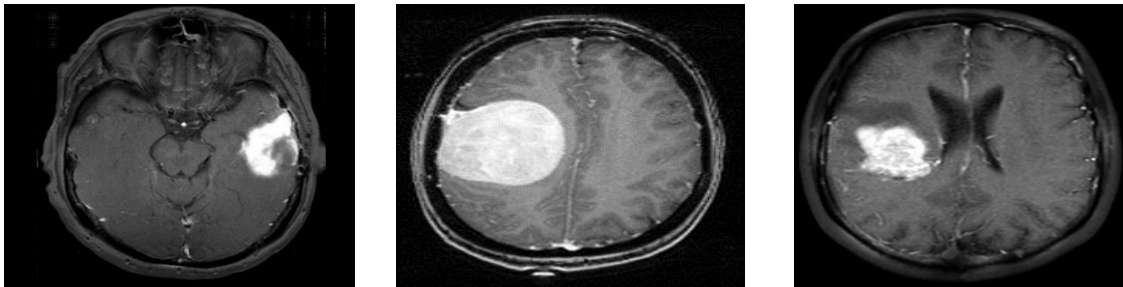
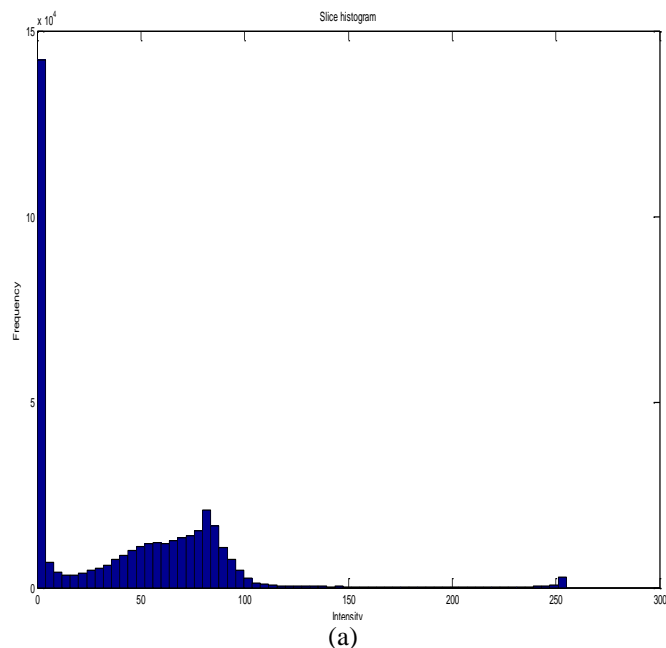


Figure 1. Image (a), image (b) and image (c) considered for evaluation



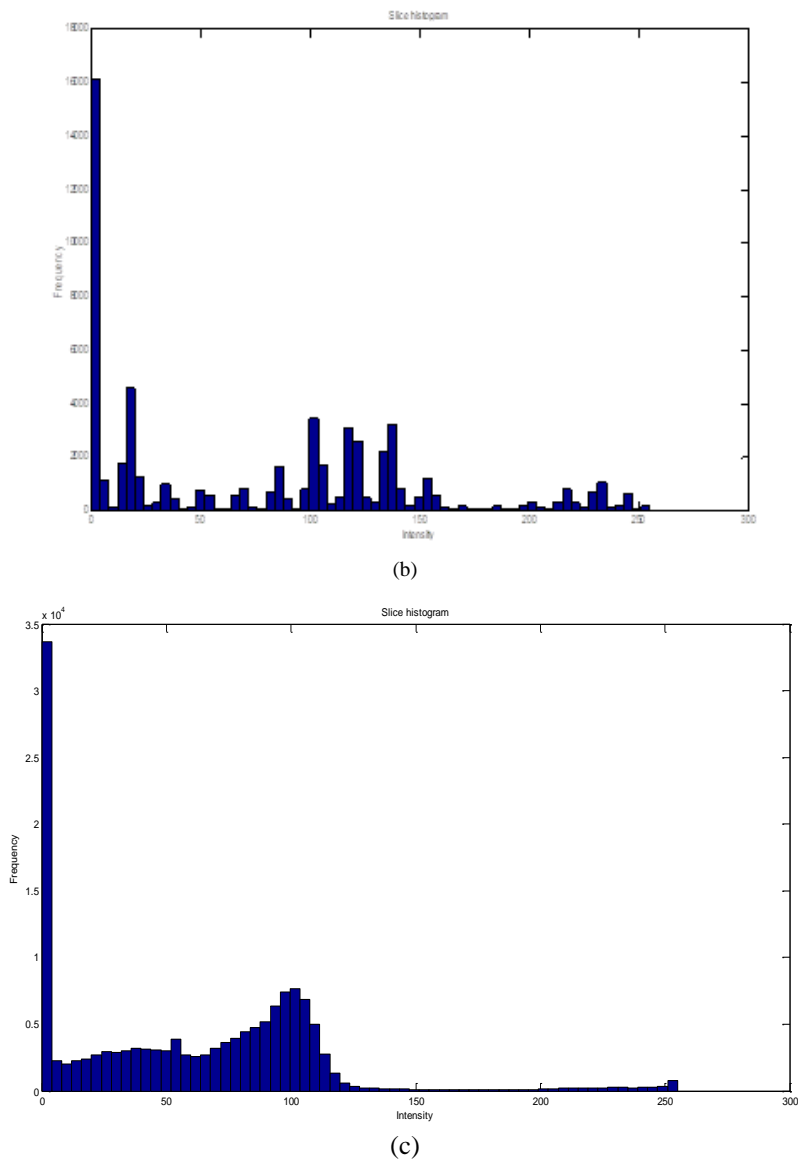


Figure 2. Histograms of image (a) Image (b) image (c)

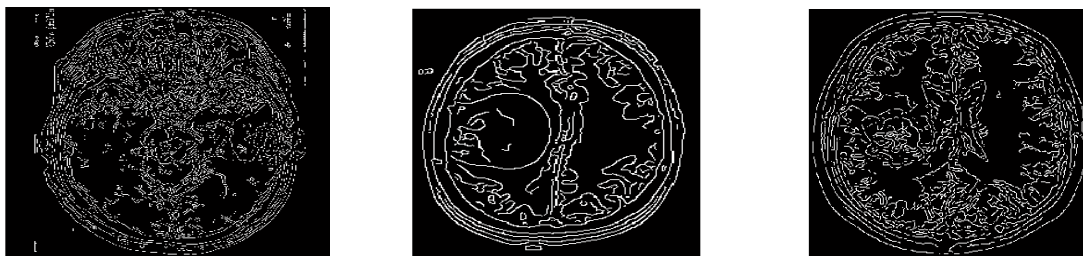


Figure 3. The edges identified for test images using prewitt operator of image (a) image (b) image (c)

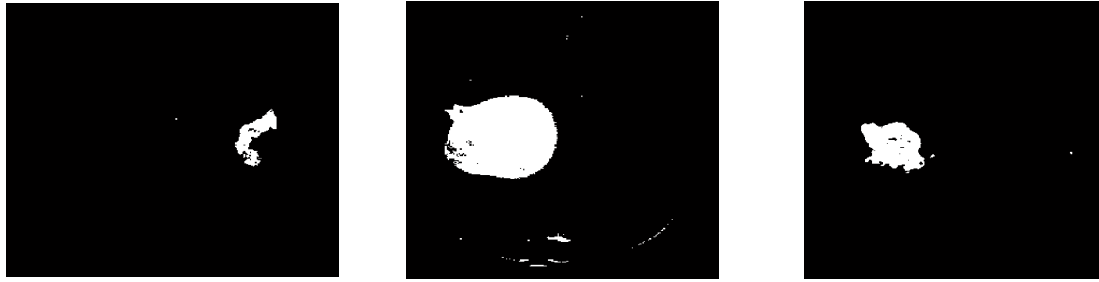


Figure 4. Tumor in image (a), image (b), and image (c) are segmented using the proposed approach

Through Figure 4, it can be clearly observed through visual inspection that the proposed approach has delivered a neat and clean segmentation. The performance is clearly visible in image (a) and image (c), while in image (b) we can observe some of the background elements have also been included. To illustrate the effectiveness of the segmentation a sample illustration of intensity profiling of the segmented tumor image (b) is given in the Figure 5. It can be clearly observed from the figure there is a neat distribution of the segmentation indicating clear profiling. The validity of the segmentation is evaluated through evaluation parameters discussed in section 4, these are computed by comparing the segmented image with the ground truth obtained using manual segmentation. The results of evaluation are listed using the Table 1.

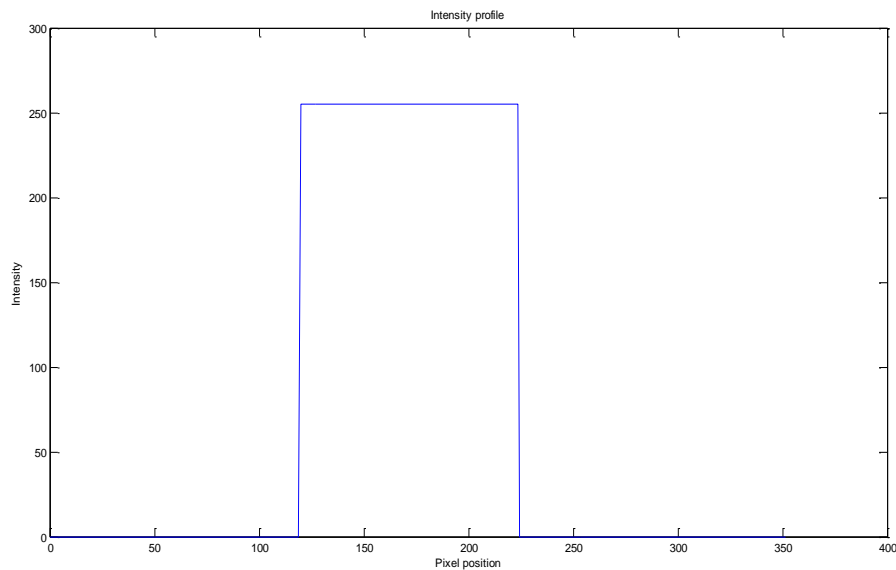


Figure 5. Intensity profile distribution of segmented image (b)

Table 1. Evaluation parameters for the proposed segmentation approach

Image	PRI	VOI	GCE	JID	JD	PSNR
Image (a)	0.99	0.041	0.004	0.83	0.16	62.15
Image (b)	0.96	0.231	0.012	0.87	0.12	45.58
Image (c)	0.99	0.041	0.004	0.91	0.05	60.15

From the Table 1, it can be inferred that the proposed method has delivered in terms of all the evaluation parameters. It is also interesting to observe that the image (a) which produced cluttered has in fact been segmented better than the other two images as evident from the evaluation parameters.



Figure 6. Overlap images of segmented images with ground truth images

The overlap images of ground truth images and the segmented images illustrated using Figure 6 also clearly points to near perfect segmentation achieved with the help of the proposed approach.

In the presented work, a classifier based on Kernel based support vector machine (KSVM) has been implemented. Here, after a tumor is segmented, analysis is done using thirteen different parameters extracted using DWTs. For this, a DB5 wavelet is used. After the extraction of these parameters, a PCA analysis is employed that reduced the dimensionality of the parameters for the extracted data set. After the PCA analysis, a Gaussian radial basis (GRB) kernel is employed for kernel based support vector machine classification.

There are more than 120 types of brain tumors which differ in origin, location, size, characteristics of the tumor tissues, as defined by the World Health Organization (WHO) classification system [21]-[23]. Out of these, we have considered three types of malignant tumors. The first one is Glioblastoma: primary malignant brain tumors classified as Grade IV and developed from star-shaped cells, called astrocytes that support nerve cells, which usually starts from cerebrum. Sarcoma tumor has a grade that varies from 1 to IV. This tumor arises in the connective tissues like blood vessels. The next one is Metastatic bronchogenic carcinoma, a secondary malignant brain tumor that spreads to the brain from bronchogenic carcinoma lung tumor. 66 human brain MRIs along with 22 normal and 44 abnormal images make up the data set. These include glioblastoma, sarcoma and metastatic bronchogenic carcinoma tumors collected from Harvard Medical School website (<http://med.harvard.edu/AANLIB/>). The brain MRIs were in axial plane, T2-weighted and 256 _ 256 pixels. Figure 7 shows a sample of the data set.

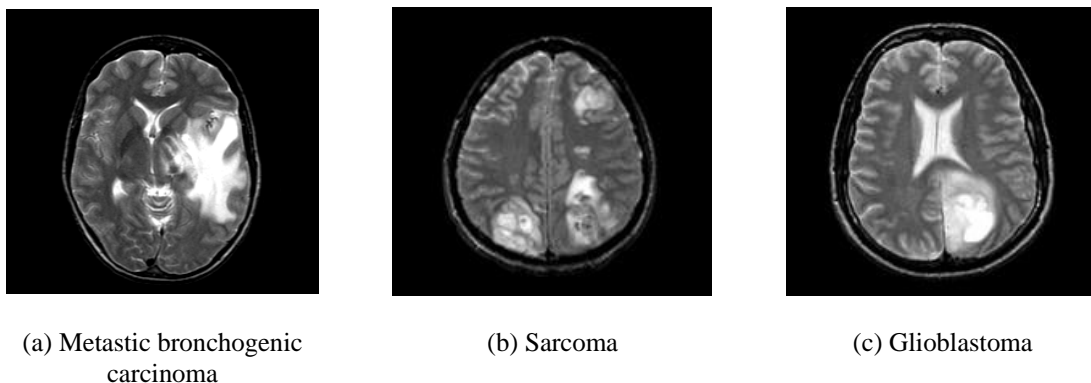


Figure 7. Sample of data set

Two data sets were formed to validate the proposed classifier. These two data sets included a total of 40 images (20 images each) and were heterogeneous with both normal and abnormal images. The term 'True positive' is used to categorize correct classification of abnormality while 'true negative' is used to categorize correct classification of normal image. Similarly an incorrect classification of abnormality is classified as 'False negative' and incorrect classification of normality is categorized as 'False positive'. The Table 2 shows the performance of the proposed classifier.

Table 2 Performance of the proposed classifier

Data set	Number of True Positive (TP)	Number of False Positive (FP)	Number of True Negatives (TN)	Number of False Negatives (FN)
DS-1	14	1	4	1
DS-2	15	0	5	0

The ability of the classifier is defined by the accuracy with which it discriminated between healthy and diseased states. The proposed classifier has an accuracy of 0.9 or 90% for data set DS1 while it is 1 or 100% for data set DS2. The sensitivity is another parameter which is used to define the classifier performance. It is nothing but the fraction of actual positives that have been correctly predicted. The sensitivity of the proposed classifier is 0.93(93%) and 1(100%) for dataset DS1 and dataset DS2 respectively.

The fraction of actual negatives that are correctly classified is identified by the specificity of the classifier. For the proposed classifier, the specificity is 0.80(80%) and 1(100%) for data set DS1 and DS2 respectively. The probability of the classifier that it will provide correct classification for images under test is quantified using positive predictive value (PPV) and negative predictive value (NPV) parameters. The portion from image data set which correctly classifies tumor as malignant is indicated by PPV while the NPV indicates the proportion of samples with negative results that resulted in correct classification of benign tumors.

MCC or Matthew's correlation coefficient can be used to quantify the performance of classifier. MCC value of +1 represents perfect classification and 0 represents a very poor classification and -1 indicates a total disagreement between actual and observed classification. For data set DS1, MCC is 0.733 while that for DS2 is 1. The performance of the proposed classifier in terms of the performance measures has been summarized using the Figure 8.

A total of forty images comprising both malignant and benign tumors have been considered for validation. The performance of the classification was quantified with the help of different measures like accuracy, sensitivity, specificity, PPV, NPV and MCC. The performance measure validates and demonstrates the suitability of the proposed classifier in identifying different types of brain tumors considered in this study.

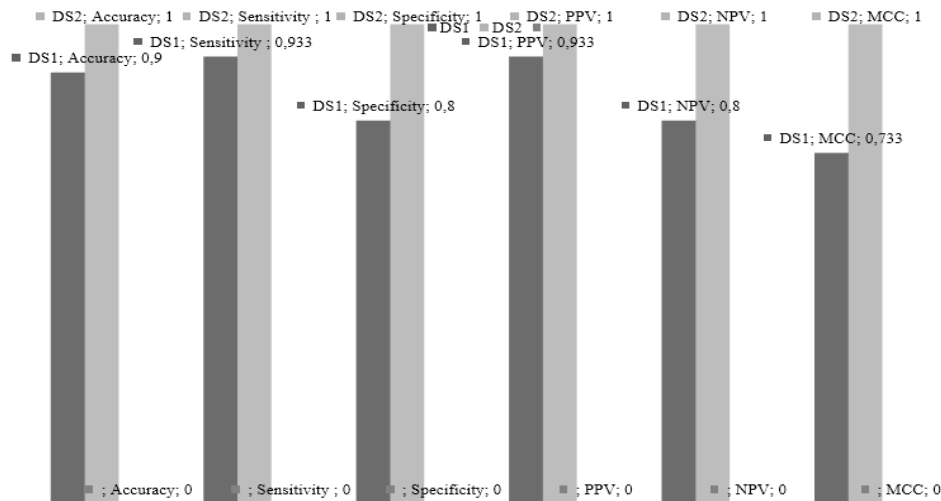


Figure 8. Classifier performance

5. CONCLUSION

Human way on interpreting and making a cognitive analysis of an image is very complex and involves lot of computation power. The primary issue with visual interpretation is that there is a wide difference in sense of perception between different users. In this work we have used enhanced ICA and successfully proposed automatic segmentation of brain tumors in MRI. The segmentation results have been evaluated through different performance measures. Likewise, a kernel-based classifier has been evaluated by expert clinical opinion to successfully classify the tumor as benign or malignant. Also, the classifier's performance has been validated with the help of different performance measures. It can be inferred from the

results that the classifier's performance is satisfactory in different performance indices and demonstrates its suitability in classifying tumors. The performance of the proposed classifier can be validated through its ROC performance and AUC.

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