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A Hybrid Enhanced ICA Approach for Segmentation of Brain MR Image

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Abstract: Medical imaging and analysis has become an integrated tool for effective and efficient management of any disease. The significance of medical imaging is diagnosing. Diseased state of human brain is huge. One such diagnosis is identification and extraction of brain tumor. The utility of any image is influenced by the quantity and quality of information that can be extracted lent of it. The processing power of humans are tremendous and they posses every complex interpreting skill. Humans are capable of performing cognitive analysis of an image. Some of the typical issues in regard to visual interpretation and manual analysis include wide difference in sense of perception between different users, human fatigue and for most of the time human one capable of providing a qualitative analysis rather than a quantifying one. A computer based image analysis accounts for most of these problems and can help in saving crucial time needed to respond to a medical emergency. Effective image processing methods can serve as potent tools that can help in an affordable and effective healthcare practices. This research work illustrates one such tool that will significantly contribute towards the analysis and the interpretation of MRI images for tumor detection and classification. An enhanced and modified Gaussian mixture mode model and the ICA segmentation approach has been employed for segmenting brain tumors in MR images.

INTRODUCTION

The amount of information presented by an image is enormous and it is considered as one of the best medium for explicit convey of information. Image processing tool are of vital importance to extract and analysis this information. With the advent of machine learning understanding these images and extracting useful information out of them has become a crucial task. Image segmentation is the most critical stage of data processing, because a good classification is dependent on the features extracted from the segmented images. It plays a crucial role in determining the sensitivity of the entire system. It is important to design new segmentation approaches and employ effective classifiers for segmenting and analyzing medical images. Human brain is one of the most complex structures and poses serious challenges in imaging and analysis. Accurate segmentation and classification of brain images still remains one of the most critical challenges in the automated analysis and machine learning approaches. This especially more true in the case of brain tumors which increases the complexity manifold because if their location, morphology and sizes. How well a tumor can be alienated and segmented plays an important role in determining further clinical evaluation and analysis. Even though Magnetic Resonance Imaging (MRI) is the most preferred imaging procedure for analysis of brain images, it has several limitations too. Some of the typical challenges encountered in segmenting brain tumors from magnetic resonance images are listed here. Magnetic resonance images are often are susceptible to rician distribution noise which can be attributed to MRI system. This noise tends to vary the intensity levels of magnetic resonance images and hence, inhibit the process of segmentation. Magnetic resonance images also suffer from non-homogeneity of radio frequency waves which can result in shading effect. This intensity in homogeneity is also called as bias field or shading artifact. Another important issue that has to be tackled in MRI images is partial volume effect. The partial volume effect can be attributed to the presence of more than one type or class of tissues that occupies one pixel of an image. When such a partial volume effect encountered the pixels are called as mixels. The automation of segmentation for magnetic resonance images is also complicated for the fact that the tumor tissues differ from patient to patient. They have different gray level intensities and have strikingly similar appearance to normal tissues. Usually, statistical modeling will be employed to categorize and classify normal and abnormal tissues. Currently, much of the segmentation of brain tumor in magnetic resonance images is carried out manually by radiologists. The reliability of such an approach is purely influenced by knowledge and skill of the radiologist. In addition, to this the process is tedious, consumes huge amount of time and is highly subjective in nature in terms of classification. Adding to this, the shortage of radiologists is also compounded by the sheer volume of magnetic resonance images and very specifically the sensitivity of human eye in interpreting large number of images plays a very crucial role is the accurate classification of brain tumors. Invariably, there is decrease in sensitivity with increase in number of images when problem is more pre-dominant and when only small number of slices are affected. Hence, there is a huge need for automated systems that are capable of analyzing and classifying medical images. So, in spite of all challenges posed by magnetic resonance images there is a strong demand for designing and developing automated detection and classification of brain tumors. Image segmentation is the first and foremost step in any automated image analysis and classification.

Image segmentation techniques can be classified (Dass *et al*., 2012) into the following categories: edge-based, threshold based, region-based, neural network based, cluster-based and hybrid (Pal and Pal, 993) image segmentation based on thresholding is one of the oldest and powerful technique, since the threshold value divides the pixels in such a way that pixels having intensity value less than threshold belongs to one class while pixels whose intensity value is greater than threshold belongs to another class (Kang *et al*., 2009). Segmentation based on edge detection attempts to resolve image by detecting the edges between different regions that have sudden change in intensity value are extracted and linked to form closed region boundaries. Region based methods (Kaganami and Beij, 2009), divides an image into different regions that are similar according to a set of some predefined conditions. The neural network based image segmentation techniques reported in the literature (Zhu *et al*., 2009) can mainly be classified into two categories: supervised and unsupervised methods. Clustering is an unsupervised learning technique, where one needs to know the number of clusters in advance to classify pixels (Dehariya *et al*., 2010). A similarity condition is defined between pixels and then similar pixels are grouped together to form clusters. The hybrid approaches (Ozisik, 2004) employ any two of the above methods and are characterized by the application for which they are adopted. These hybrid methods utilize advantages of those two methods and avoid inherent limitations.

The segmentation of human brain throws complex challenges that have to be effectively surmounted. So in the proposed approach an improved k-means algorithm and EM algorithm are combined to formulate a hybrid strategy for better clustering. The proposed approach aims to exploit the capability of providing well distributed cluster of k-means and the compactness of clusters provided by EM. The initial clusters are provided by the improved k-means algorithm. This initial clustering operation results in centers which are widely spread in the given data. These centers form the initial variable for EM which subsequently uses these variables and iterates to find the local maxima. This is subsequently used for enhancing and modifying Gaussian mixture mode model and the ICA segmentation approach that follows it.

Literature review: A variety of segmentation approaches have been reported in the literature and the topic has been extensively studied over a period of time. Very specific emphasis has also been given on segmentation of brain MR images. This section reviews some of the recent works reported in the literature. Chaudhari *et al*. (2015) presented pixel classification based brain magnetic resonance images segmentation. The researchers performed automatic segmentation of brain into four classes namely background, cerebrospinal fluid, grey and white matter. Roy and Maji (2015) proposed an unsupervised and knowledge based skull stripping algorithm for brain magnetic resonance imaging termed as S3 which is based on brain anatomy and image intensity characteristics. The researchers used adaptive intensity thresholding followed by morphological operations for increased robustness. Moeskops *et al*. (2016) described a method for automatic segmentation of magnetic resonance brain images into a number of tissue classes using a convolution neural networks. Pereira *et al*. (2016) described an automatic segmentation method based on Convolutional Neural Networks (CNN), exploring small 3×3 kernels. The researchers used intensity normalization as a preprocessing step which proved together with data augmentation to be very effective for brain tumor segmentation in magnetic resonance images. Nandi (2015) presented the detection of human brain tumor using magnetic resonance image segmentation and morphological operators. Then morphological operators along with basic image processing techniques were used for separating tumor cells from normal cells. Chandra and Balasingham (2015) presented the detection of brain tumor and localization of a deep brain RF source using microwave imaging. They authors used Levernberg-Marquadt iterative scheme as microwave imaging technique to solve the inverse scattering problem for the head of the phantom in 403.5 MHz medical radio band. The simulation results showed that at least 45 dB SNR was required for small tumor detection. The authors presented a localization method based on microwave imaging for deep brain RF source. Alok *et al*. (2015) proposed a semi-supervised clustering technique that used the concepts of multi objective optimization for segmentation of magnetic resonance brain image in intensity space. The intensity values of brain pixels were utilized as the features. A modern multi objective optimization technique based on the concept of simulated annealing was used to optimize the three cluster validity indices. The performance of the approach was compared with other techniques like FCM, expectation maximization, fuzzy-VGAPS clustering techniques. Jambholkar *et al*. (2015) proposed an Empirical Wavelet Transform (EWT) method for feature extraction of brain SPECT image and also assisted in brain tumor detection. EWT decomposed the image into a number of sub-band images and Fuzzy C-Mean (FCM) clustering algorithm was used for segmentation to achieve higher accuracy. Support vector machine was used as a classifier. Adhikari *et al*. (2015) presented a Spatial Fuzzy C-Means (SPFCM) algorithm for segmentation of magnetic resonance images. They employed spatial information from the neighborhood of each pixel and realized by defining a probability function. The resulted SPFCM algorithm solved the problem of sensitivity to noise and intensity inhomogeneity in magnetic resonance imaging data and improved the segmentation results. The authors showed that SPFCM was superior in performance when compared to some FCM based algorithms. Gonal and Kohir (2015) proposed a classification method that classifies brain magnetic resonance images as normal or abnormal by using wavelets texture features and k-means classifier. The Euclidean distances measured between feature vectors of test magnetic resonance image and reference magnetic resonance image were fed to k-means classifier for classification. Praveen and Agrawal (2015) presented a four phase hybrid approach for brain tumor detection and classification in magnetic resonance images. The image pre-processing includes noise filtering and skull detection as the first phase. Feature extraction using gray level co-occurrence matrix was the second phase. The third phase dealt with normal or abnormal classification of inputs by using least square support vector machine classifier with multilayer perception kernel. The researchers used fast bounding box for segmentation of tumor. The classification accuracy was found to be 96.63%. Handore and Kokare (2015) described the performance analysis of various methods of tumor detection. The researchers described comparative study of various methods for tumor detection. The researchers showed that image segmentation plays an important role in medical imaging. They also described that segmentation can work efficiently in detecting and extracting the tumor from magnetic resonance image. Dawngliana, etc., proposed hybridized multilevel thresholding and level set method for automatic segmentation of brain tumor in magnetic resonance Image. The researchers interfaced the initial segmentation from multilevel thresholding and extracted a fine portrait using level set method with morphological operations.

MATERIALS AND METHODS

Proposed approach: Blind source separation by independent component analysis has shown significant applications in the domain of signal processing, medical signal processing and medical image processing. Over the years, many types of computer systems assisted methods have been developed and implemented for analyzing magnetic resonance images. The methods include Eigen image analysis, Principal Component Analysis (PCA) and fuzzy C-means method.

Eigen image analysis are found to be more effective in segmentation and feature extraction while the performance of neural network appears to be satisfactory in segmenting brain tissues. These methods provide better performance when compared to the classical maximum likelihood methods. With the advent of multi spectral images different segmentation and analysis procedures based on orthogonal subspace projection, kalman filter, etc. have evolved over a period of time. But the typical issue with these procedures is the requirement of prior knowledge. In this context segmentation approach based on Independent Component Analysis (ICA) which is an unsupervised texturing method provides greater advantage in the segmentation of brain tissues.

One typical disadvantage of ICA is its assumption that the sources are independent. In order to relax this assumption the concept of mixture models have been introduced. In the case of mixture model, the observed data is characterized into several mutually exclusive classes. In order to improve the generalization performance of ICA it is imperative to choose a proper search space.

Given a set $\{x_i, i = 1, 2, ..., N\}$ where, xi is the gray value of the ith image pixel modeled as i.i.d and N is the total number of the image pixels. GMM assumes a mixture model consisting of c Gaussian density components with the parameters $\theta_k = \{u_k, \Sigma_k\}$ in the kth component. In GMM, the probability density of xi is formulated by:

$$p(x_i \,|\, \pi, \theta) = \sum_{k=1}^{c} \pi_k p(x_i \,|\, \theta_k) \qquad (1)$$

where, $\theta = \{\theta_1, \theta_2, ..., \theta_c\}$ is the parameters of all the components and π_k is the mixing weight of the kth component, satisfying $\pi_k > 0$ and $\Sigma^c_{k=1} \pi k = 1$. The kth Gaussian is denoted by:

$$p(x_i \,|\, \theta_k) = \frac{1}{\sqrt{(2x)\,|\sum_k|}} \exp\left(-\frac{(x_i - u_k)^T \sum_k^{-1} (x_i - u_k)}{2} \right) \qquad (2)$$

where, u_k and Σ_k are the mean and the covariance matrix, respectively. The parameters $\{\theta, \pi\}$ can iteratively be estimated by maximizing the likelihood function using the proposed hybrid expectation-maximization.

In the proposed improvement, a computationally less complex approach is suggested to identify better initial clusters thereby enhancing the efficiency and performance of the clustering operation. The steps involved in the implementation of the improved k-means clustering are mentioned below.

Step1: Considering middle point in each data set as the initial centroids.

Step 2: Computing the Euclidean distance for each data point from the origin.

Step 3: Sorting the obtained data point using the distance computed.

Step 4: Portioning the sorted data points in to K equal sets.

Step 5: Considering the middle point in each set as the initial centroid.

Step 6: Computing the distance between each data point to the all the initial centroids.

Step 7: Finding the closest centroid c_j and assign d_i to cluster j for each data point d_i.

Step 8: Setting the Cluster Id[i] =j.//j:Id of the closest cluster.

Step 9: Setting the nearest Dist[i] = $d(d_i, c_j)$.

Step 10: Recalculate the centroids for each cluster $j(1 \leq j \leq k)$.

Step 11: For each data point d_i, its distance from the centroid of the present nearest cluster is calculated. If this distance is less than or equal to the present nearest distance, the data point stays in the same cluster. The operation moves to step.

Step 12: For every centroid $c_j(1 \leq j \leq k)$ the distance $d(d_i, c_j)$ is computed.

Step 13: If convergence criteria are met then giving the clusters or going back to Step 2.

In EM, alternating steps of Expectation (E) and Maximization (M) are performed iteratively till the results converge. The E step computes an expectation of the likelihood by including the latent variables as if they were observed and maximization (M) step which computes the maximum likelihood estimates of the parameters by maximizing the expected likelihood found on the last E step. The parameters found on the M step are then used to begin another E step and the process is repeated until convergence. Mathematically for a given training dataset {x(1), x(2), ..., x(m) and model p(x, z). Where z is the latent variable, we have:

$$l(\theta) = \sum_1^m \log p\,(x; \theta) \qquad (3)$$

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

As can be seen from the above equation, the log likelihood is described in terms of x, z and θ. But since, z, the latent variable is not known, we use approximations in its place. These approximations take the form of E & M steps mentioned above and formulated mathematically below. E step, for each i:

$$Q_i(z^{(i)}) := P(z^{(i)}/x^{(i)}; \theta) \qquad (5)$$

M step, for all z:

$$\theta := \arg\max_{\theta} \sum_{i} \sum_{z(i)} Q_i\ (z^{(i)}) \log \frac{p(x)^{(i)},\ z^{(i)}; \theta}{Q_i\ (z^{(i)})} \qquad (6)$$

where, Q_i the posterior distribution of is's $z^{(i)}$ given the $x^{(i)}$. 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 modified GMM is characterized by its probability vector $\pi_i = (\pi^1{}_i, \pi^2{}_i, ..., \pi^c{}_i)^T$ where $\pi^k{}_i$ denotes the probability of the i th pixel belonging to the kth cluster. In Modified GMM, the corresponding mixture model of x_i is assumed as:

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

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 p is given by the MRF model through a Gibbs density function:

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

where, Z is a normalizing constant and β is regularization parameter. $V_{Ni}(\pi)$ is the clique potential function of the pixel label vectors πm within the neighborhood N_i of the ith pixel:

$$V_{Ni}(\pi) = \sum_{m \in N_i} |\pi_i - \pi_m|^2 \qquad (9)$$

Notice that the $\pi = \{\pi_1, \pi_2, ..., \pi_k\}$ in GMM is shared by all pixels whereas in modified GMM π_i is different for each pixel i and depends on its neighboring pixels. In modified GMM, the modified EM algorithm is utilized to obtain the maximum a posteriori (MAP) estimation of the parameters. The above will be considered as source for the ICA for further implementation of segmentation.

Evaluation of segmentation: The performance of the proposed segmentation approach is evaluated using different performance measures they are Probabilistic Rand Index (PRI), Variation of Information (VOI), Global Consistency Error (GCE), PSNR (Peak Signal to Noise Ratio), Dice coefficient (DCE) and Jaccard Distance (JD). The Probabilistic Rand Index (PRI) (Hanbury and Stottinger, 2008) counts the fraction of pairs of pixels whose labeling are consistent between the computed segmentation and the ground truth, averaging across multiple ground truth segmentations to account for scale variation in human perception. Consider a set of manually segmented (ground truth) images $\{S_1, S_2, ..., S_K\}$ corresponding to an image $X = \{x_1, x_2, ..., x_i, ..., x_N\}$ where a subscript indexes one of N pixels. S_{test} is the segmentation of a test image and then PRI is defined as:

$$PR(S_{test}\{s_k\}) = \frac{1}{\frac{N}{z}} \sum_{ij} [(l_j^{S_{test}})p_{ij} + I(l_i^{S_{test}} \neq l_j^{S_{test}})(1-p_{ij})] \qquad (10)$$

$$p_{ij} = \frac{1}{k} \sum_{1}^{k} I(l_i^k = l_j^k) \qquad (11)$$

The Global Consistency Error (GCE) (Hanbury and Stottinger, 2008) measures the extent to which segmentation can be viewed as a refinement of the other. Segmentations which are related in this manner are considered to be consistent, since, they could represent the same natural image segmented at different scales. Let S and S' be two segmented images, for a given point x_i (pixel), considering the classes (segments) that contain x_i in S and S'.These sets are denoted in the form of pixels by $C(S, x_i)$ and $C(S', x_i)$, respectively. The Local Refinement Error (LRE) is then defined at point x_i as:

$$LRE(S, S', x_i) = \frac{|c(s, x_i)/(s', x_i)|}{|C(S, x_i)|} \qquad (12)$$

Global Consistency Error (GCE) forces all local refinements to be in the same direction and is defined as:

$$GCE(S, S') = \frac{1}{N} \min\{LRE(S, S', x_i), LRE(S', S, x_i) \qquad (13)$$

The Variation of Information (VoI) (Chinnadurai and Chandrashekhar, 2010) metric defines the distance between two segmentations as the average conditional entropy of the segmentation given the other and thus roughly measures the amount of randomness in the segmentation which cannot be explained by the other. A clustering with clusters $X_1, X_2, ..., X_k$ is represented by a random variable X with $X = \{1, ..., K\}$ such that $p_i = |x_i|/ni \in X$ and $n = \Sigma_i X_i$ the variation of information between two clusters X and Y can be given by:

$$VI(X; Y) = H(X) + H(Y) - 2I(X, Y) \qquad (14)$$

where, H(X) is entropy of X and I(X, Y) is mutual information between X and Y. The mutual information of two clustering is the loss of uncertainty of one clustering if the other is given.

The Peak Signal to Noise Ratio (PSNR) (Sumi *et al*., 2010) is used to find the deviation of segmented image and from the ground truth image. Equation 6 represents the PSNR. In this equation Mean Squared Error (MSE) for two M*N monochrome images f and z and it is given by Eq. 16. MaxBits gives the maximum possible pixel value (255) of the image:

$$\text{PSNR} = 10\times\log_{10}\frac{\text{MaxBits}^2}{\text{MSE}} \quad (15)$$

$$\text{MSE} = \frac{1}{\text{M}\times\text{N}}\sum_{x=0}^{M-1}\sum_{y=0}^{N-1}((f(x,y)-z(x,\,y))^2 \quad (16)$$

Jaccard Distance (JD) which measures dissimilarity between sample sets is complementary to the Jaccard coefficient and is obtained by subtracting the Jaccard coefficient from 1. The Jaccard index, also known as the Jaccard similarity coefficient is a statistic used for comparing the similarity and diversity of sample sets. The Jaccards Coefficient is given by:

$$J = \frac{|A\cap G|}{|A\cup G|} \quad (17)$$

The jaccards distance is given by:

$$JD = 1\text{-}J \quad (18)$$

where, A and G are two set of data points. The Dice coefficient (DCE) (Estrada and Jepson, 2005) measures the spatial overlap between two segmentations. Conceptually that DCE is also a special case of the kappa statistic commonly used in reliability analysis. It is commonly used in reporting performance of segmentation:

$$\text{DCE} = \frac{2|A\cap G|}{|A|+|G|} \quad (19)$$

where, A and G are two set of data points.

RESULTS AND DISCUSSION

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 Fig. 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 Fig. 2-4.

The histogram profile 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 particualr 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 Fig. 5.

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 in Fig. 6-8.

Through Fig. 6-8 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 Fig. 9. 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 in Table 1.

From Table 1, it can be inferred that the proposed method has delivered in terms of all the evaluation

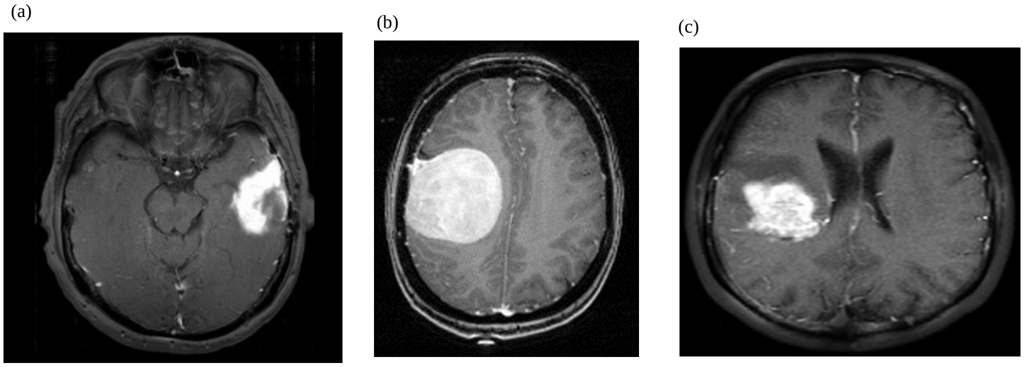

Fig. 1(a-c): Image, (a), Image (b) and Image (c) considered for evaluation

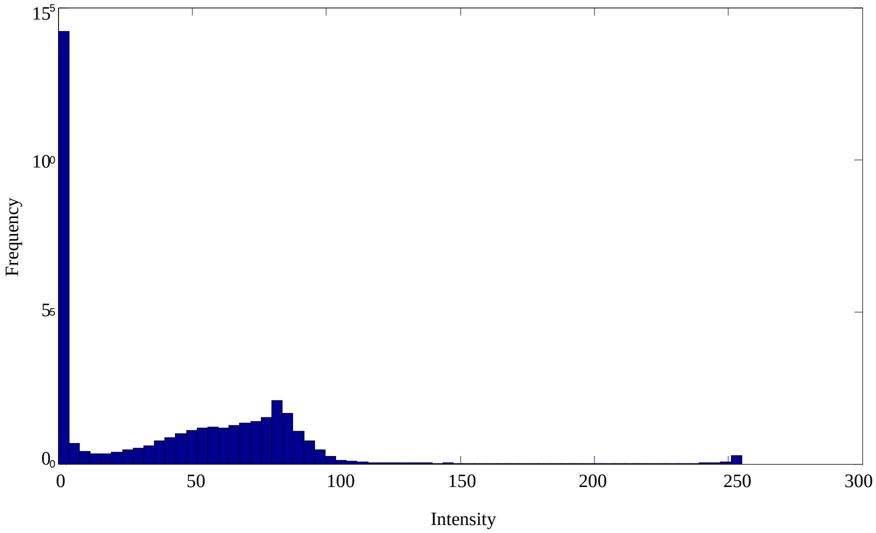

Fig. 2: Histogram of image (a)

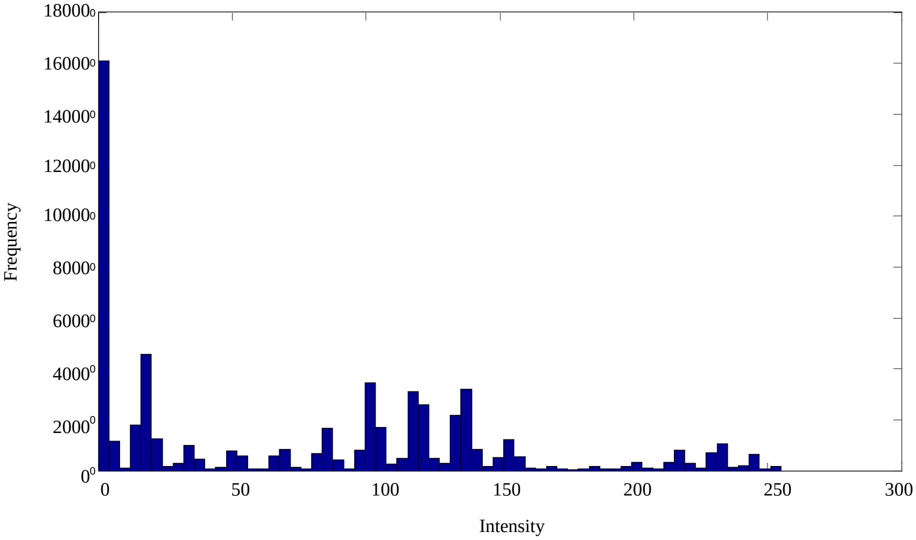

Fig. 3: Histogram of image (b)

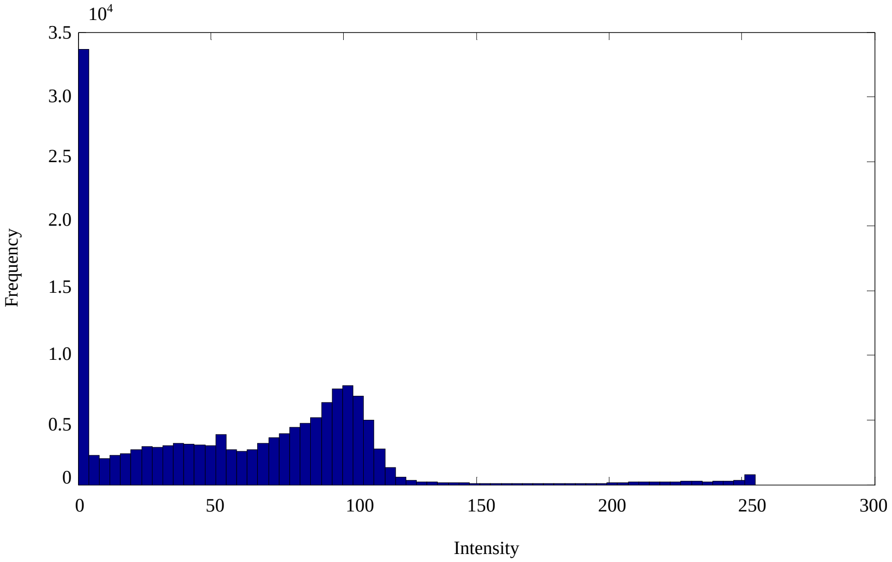

Fig. 4: Histogram of image (c)

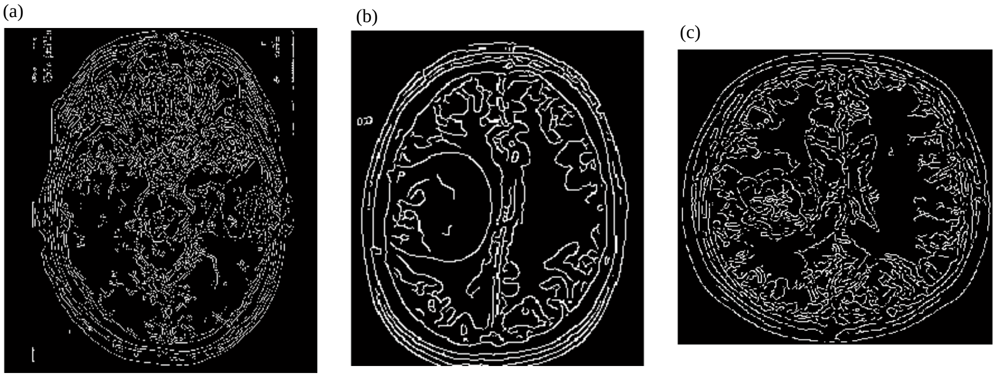

Fig. 5(a-c): The edges identified for test images using Prewitt operator

Fig. 6: Tumor in image (a) segmented using the proposed approach

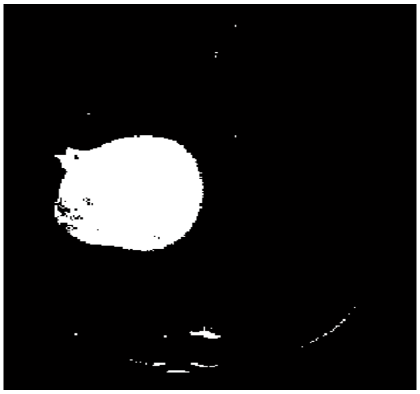

Fig. 7: Tumor in image (b) segmented using the proposed approach

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.

Probability random index being a measure of consistency indicates the closeness of the manually segmented image in the form of ground truth to that

Table 1: Evaluation parameters for the proposed segmentation approach

Image	PRI	VOI	GCE	DCE	JID	JD	PSNR
(a)	0.994077	0.0410444	0.00415916	4.11438e-06	0.830311	0.169689	62.1516
(b)	0.968306	0.2346870	0.01246980	7.54947e-08	0.879389	0.1206110	45.5802
(c)	0.994581	0.0413095	0.00459764	9.83213e-07	0.914530	0.0854701	60.1518

Fig. 8: Tumor in image (c) segmented using the proposed approach

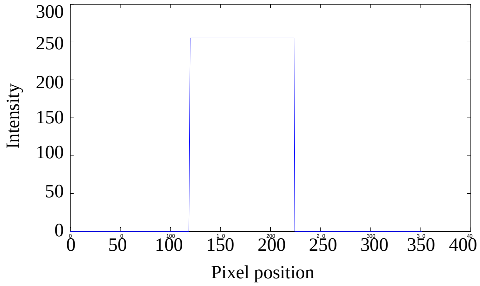

Fig. 9: Intensity profile distribution of segmented image (b)

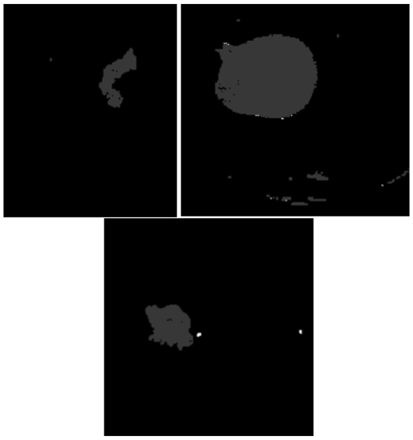

Fig. 10: Overlap images of segmented images with ground truth images

computed automatically the value of closure to 1 indicates the very high degree of consistency. From Table 1 it can be observed the probability random index of all the 3 images are high value and very closure to 1 this clearly count to the close correlation between the manual segmented image, image segmented by the proposed approach.

It can be observed from Table 1 the variation of information is very less to have a perfect segmentation and comparison with round truth image the variation of information should be close to zero, from Table 1 it can be observed that the variation of information is very close to zero for all the 3 images indicating very little randomness in segmentation the same cam be set for global consistency error which defines the refinement and ice coefficients which measure the overlap between two segmented images the value exhibited by the proposed segmented approach is very close to idle values.

Similarly Jaccard Distance and Jaccard index measures the similarity and diversity of the images under study, also have produced high desirable values this can be clearly observed from the Jacob index ≥0.8, subsequently reflects in Jacob index to <0.2 these two parameters also amplitude the effective number of the proposed approach.

It can also be observed from Table that PSNR vale is also high indicating that the proposed approach also not illuse any unnecessary noise in the image getting reflected by the high PSNR.

The overlap images of ground truth images and the segmented images illustrated using Fig. 10 also clearly points to near perfect segmentation achieved with the help of the proposed approach.

CONCLUSION

It can be safely concluded that the proposed approach provides better segmentation of brain tumors. Some of the important contributions are modifications to existing Gaussian Mixture Mode Models in the form of a hybrid Expected Maximum (EM) algorithm which can result in the formation of better initial clusters. Similarly the incorporation of Markov Random Field (MRF) will account for variations in spatial information. This enhances the performance of ICA by incorporating the designed Modified Gaussian Mixture Mode Model. The above approach can be used for segmentation and subsequent analysis of different neurological disorders In order to illustrate the performance of these segmentation approaches they one evaluated using different performance measures like PRI, VOI, GCE, PSNR, DCE and JD. The performance measures amply illustrate the capability of proposed method in delivering better segmentation.

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