

Segmentation and Classification of MRI Brain Tumor

Mukambika P. S.¹, Uma Rani K.²

M.Tech (2nd year) Student, Biomedical Signal Processing and Instrumentation, Dept. of IT, SJCE, Mysuru, Karnataka, India

Associate Professor, Dept. of IT, SJCE, Mysuru, Karnataka, India

Abstract - Bio-medical image processing is the most challenging and emerging field in medical diagnosis. Processing of MRI images is one of the difficult parts of this field. The present work presents the comparison study of two techniques used for tumor detection of MRI images. One is based on the Level set method that uses the non parametric deformable models with active contour to segment the brain tumor from the MRI brain images. The other one is the K-means segmentation algorithm. After the segmentation decision making is performed in two stages: Feature extraction using Discrete Wavelet Transform and Gray Level Co-occurrence Matrix, and classification using the Support Vector Machine. It is observed that the results of segmentation accuracies from the proposed methods are comparatively high with the existing method.

Key Words: Magnetic Resonance Imaging (MRI), Brain Tumor, Level set, K-means, Performance Evaluation, Discrete Wavelet Transform (DWT), Gray Level Co-occurrence Matrix (GLCM), Support Vector Machine (SVM).

1. INTRODUCTION

Automated and accurate classification of Magnetic Resonance (MR) brain images is extremely important for medical analysis and interpretation. The classification of MR brain images is becoming increasingly important in the medical field since it is crucial for treatment planning and diagnosing of abnormalities, measuring tissue volume to examine tumor growth and studying the anatomical structure and patient's following procedure [1]. Medical image analysis is an important biomedical application which is highly computational in nature and requires the aid of the automated systems [2]. These image analysis techniques are often used to detect the abnormalities in the human bodies through scan images.

Magnetic Resonance imaging scan of head is the most common test taken to confirm the presence of a brain tumor and for identifying its location for selecting treatment options. Compared to all the other imaging techniques, MRI is efficient in the application of brain tumor detection and identification, due to the high contrast of soft tissues, high spatial resolution, and absence of any harmful radiation [3]. Manual classification of magnetic resonance brain tumor images is a challenging

and time-consuming task. Manual classification is highly prone to error due to inter observer variability and human error. As a result, the classification results are highly inferior leading to fatal results.

2. DATASET

Dataset of MRI brain tumor images includes 17 benign and 24 malignant tumor images of different patients which are DICOM in nature. These images T2 weighted sequence images obtained from Philips, 3T machine, and are provided by JSS hospital, Mysuru. These images are labeled by the expert radiologist.

3. METHODOLOGY

Detection and classification of MRI brain tumor images involve four modules: Pre processing, Segmentation, Feature Extraction and Classification. The steps followed for the implementation are depicted in Fig-1. Skull removal is used for preprocessing, and the preprocessed image is given as input for the segmentation process. Two types of segmentation algorithms are used to extract the tumor regions: Level set method and K-means algorithm. Statistical textural features are obtained by using DWT and GLCM. The obtained features are classified using SVM as benign or malignant tumors.

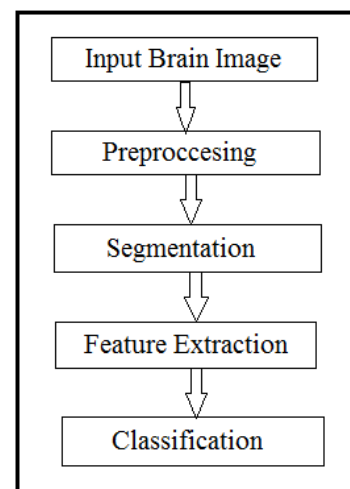


Fig -1: Block diagram

3.1 Preprocessing

MRI brain images cannot be fed directly as the input for the segmentation technique. Therefore skull removal is performed. Skull is the outer part of the brain. Morphology technique using double thresholding is applied to remove the skull out of the MRI brain images (SonaliPatil&Udupi2012). The binary image $b(x, y)$ of the original image $I(x, y)$ using double threshold is obtained by the equation 1.

$$b(x, y) = \begin{cases} 1; & 0.2 \leq I(x, y) \leq 0.7 \\ 0; & \end{cases} \quad (1)$$

3.2 Segmentation

Segmentation is the partition of a digital image into similar regions to simplify the image representation into something more meaningful and easier to analyze.

3.2.1 Level set method

Level set methods use non parametric deformable models with active contour energy minimization techniques which solve computation of geodesics or minimal distance curves. Level set methods are governed by curvature defining speeds of moving curves or fronts. There are large numbers of level set methods developed for segmentation of medical images and all most all these methods follow some common generic steps. First placement of an initial contour arbitrarily, outside or inside the region of interest, level set ϕ = signed Euclidean distance function of the contour and Function ϕ allowed to evolving according to first or second derivative partial differential equation (PDE), then it is reinitialized after a number of iterations and go to second statement until the function ϕ converges or = 0.

In the level set function as shown in Fig-2, a 2D curve r is represented by a 3D iso-surface ϕ . Let $r(t=0)$ be a smooth closed initial curve in the Euclidian plane R^2 and let $r(t)$ be a family of curves generated by moving $r(t=0)$ along its normal vector field with speed $F(k)$.

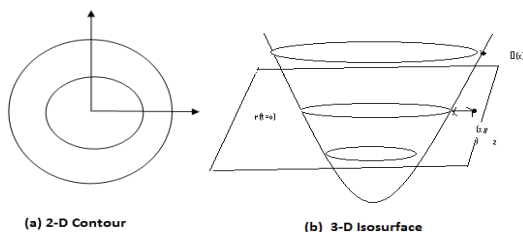


Fig-2: Contour and Level Set Evolution from Distance Function

The propagation front $r(t)$ is embedded as the zero levelset of $\phi(t=0)$ of the higher dimensional function ϕ . $\Phi(x, t=0)$, where $x \in R^2$ are the plots in the image space defined by,

$$\Phi(x, t = 0) = \pm d \quad (2)$$

where d is the distance from point x to $r(t=0)$ and sign depends on the position of the point x considering the initial surface $r(t=0)$. If x is outside (inside) the initial surface the sign is plus (minus).

3.2.2 K-means method

K-Means algorithm is one of the unsupervised clustering algorithm due to its efficiency and simplicity in clustering large data sets [4]. In traditional K-Means algorithm the numbers of clusters is defined and are initialized apriori. Next, k cluster centers are randomly chosen. Euclidean distance is generally considered to determine the distance between data objects and the cluster center. The distance between the each data point to each cluster centers are calculated. The data point is moved to particular cluster which has the shortest distance. The centroid is then reestimated. Again each data point is compared with all the centroids. The process continuous and at the end of loop, k -centroids change their point step by step until the centroids do not move any more. This algorithm works on basis of minimizing squared error function. The K-Means algorithm always converges to a local minimum. Local minimum found depends on the initial cluster centroids.

K-means clustering algorithm is summarized as,

1. Randomly initialize the N_c cluster centroid vectors.
2. Repeat
 - a) For each data vector, assign the vector to the class with the closest centroid vector, where the distance to the centroid is determined using,

$$d(z_p, m_j) = \sqrt{\sum_{k=1}^{N_d} (z_{pk} - m_{jk})^2} \quad (3)$$

where denotes the P^{th} data vector, denotes the centroid vector of cluster j and k subscripts the number of features of each centroid vector.

- b) Recalculate the cluster centroid vectors, using

$$V_j = \frac{1}{n_j} \sum_{d_j \in c_j} (i_j) \quad (4)$$

where denotes the number of data vectors in cluster j , stands for the centroid vector and c_j is the subset of data vectors that form cluster j , until a stopping criterion is satisfied.

The K-means clustering process can be stopped when any one of the following criteria are satisfied: when the maximum number of iterations has been exceeded, when

there is little change in the centroid vectors over a number of iterations or when there are no cluster membership changes.

3.3 Feature Extraction

Features are said to be properties that describe the whole image. It can also be referred as an important piece of information relevant for solving the computational task related to specific application. From the segmented image, features are computed to encode the useful diagnostic information.

3.4.2 Gray Level Co-Occurrence Matrix

A statistical method of examining texture that considers the spatial relationship of pixels is the GLCM, also known as the gray-level spatial dependence matrix. The GLCM functions characterize the texture of an image by calculating how often pairs of pixel with specific values and in a specified spatial relationship occur in an image, creating a GLCM, and then extracting the statistical measures from this matrix. GLCM calculates the co-occurrence matrix of an image by computing how often a pixel with a certain intensity i occurs in relation with other pixel, j at a certain distance d and orientation. The gray-level co-occurrence matrix can reveal certain properties about the spatial distribution of the gray levels in the texture image. In order to extract information concerning spatial distribution and its orientation, four co-occurrence submatrices can be calculated across four scanning directions θ ($0^\circ, 45^\circ, 90^\circ, 135^\circ$). The features extracted using GLCM method are:

Contrast: Contrast returns a measure of the intensity contrast between a pixel and its neighborhood. The contrast feature is a measure of the amount of local variations present in an image.

$$Contrast = \sum_{i,j} f(i,j)(i-j)^2 \quad (5)$$

Correlation: Correlation measures how correlated a pixel is to its neighborhood. It could also be described as a measure of linear dependencies among neighboring pixels in an image.

$$Correlation = \sum_{i,j} f(i,j)(i-\mu_i)(j-\mu_j)/\sigma_i\sigma_j \quad (6)$$

Energy: Energy can be defined as the quantifiable amount of the extent of pixel pair repetitions. Energy is a parameter to measure the similarity of an image. It is also referred to as angular second moment, and it is defined as.

$$Energy = \sum_{i,j} f(i,j)^2 \quad (7)$$

Homogeneity: Homogeneity measures the similarity of image pixels. It is inversely proportional to the contrast.

$$Homogeneity = \sum_{i,j} f(i,j)/(1+|i-j|) \quad (8)$$

3.4.1 Discrete Wavelet Transform

The input MRI images are decomposed into four sub-bands as smooth, horizontal, vertical and diagonal images in order to separate low and high frequencies by applying discrete wavelet transform (DWT). Decomposition may be either one level or two level decompositions [5]. The wavelet decomposition can be obtained by performing the filtering operations consecutively along horizontal and vertical directions. The other features extracted are:

Mean: The mean of an image is calculated by adding all the pixel values of an image divided by the total number of pixels in an image.

$$Mean(\mu) = \sum_{i,j} f(i,j)/N \quad (9)$$

Standard Deviation: The standard deviation is the second central moment describing probability distribution of an observed population and can serve as a measure of inhomogeneity. A higher value indicates better intensity level and high contrast of edges of an image.

$$SD(\sigma) = \sum_{i,j} \left(\frac{f(i,j)-\mu}{N} \right)^2 \quad (10)$$

Variance: Variance is a measure that is similar to the first order statistical variables called standard deviation. Variance is the square of standard deviation.

$$Variance = (\sigma)^2 \quad (11)$$

Entropy: Entropy is a measure of randomness of intensity image.

$$Entropy = -\sum_{i,j} f(i,j)\log(f(i,j)) \quad (12)$$

Inverse Different Moment: Inverse Difference Moment (IDM) is a measure of image texture.

$$IDM = \sum_{i,j} f(i,j)/|i-j|^k \quad (13)$$

Kurtosis: The shape of a random variable's probability distribution is described by the parameter called Kurtosis. For the random variable X , the Kurtosis is defined as.

$$Kurtosis = \sum_{i,j} \left((i-\mu_i) + (j-\mu_j) \right)^4 f(i,j) \quad (14)$$

Skewness: Skewness is a measure of the asymmetry of the data around the sample mean.

$$Skewness = \sum_{i,j} \left((i-\mu_i) + (j-\mu_j) \right)^3 f(i,j) \quad (15)$$

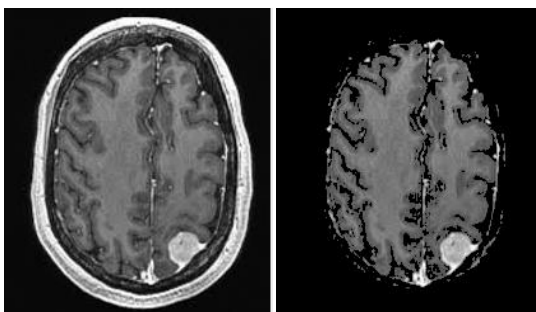
3.4 Classification

After extracting features using DWT and GLCM, they are directly given to the support vector machine (SVM) for the classification. The process involves two phases: Training phase and testing phase. In training phase the patterns in terms of features and class labels of benign and malignant tumor are fed to the classifier for training. In testing phase test pattern is fed and knowledge gained during training phase will classify the unknown pattern. SVM performs the robust non-linear classification with the kernel trick [6]. It finds the separating hyper plane in some feature space induced by the kernel function while all the computations are done in the original space itself. For the given training set, the decision function is found by solving the convex optimization.

4 RESULTS AND DISCUSSION

This section provides the experimental results of the present work.

Preprocessing results:

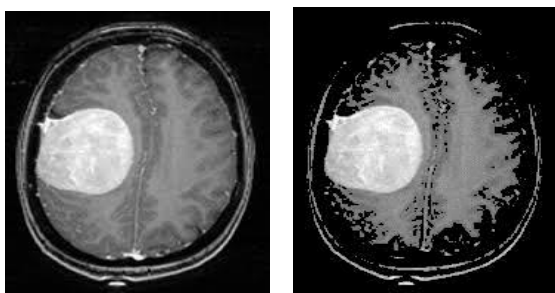


(3a)

(3b)

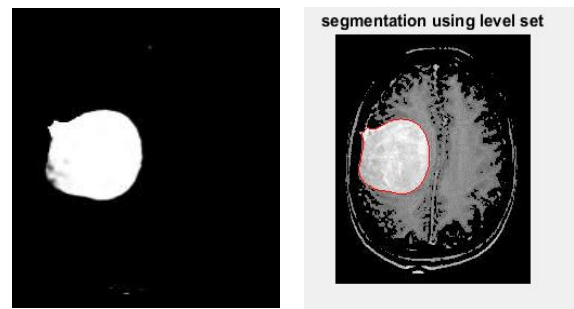
Fig-3: (3a) Input image (3b) Skull removed image

Segmentation results:



(4a)

(4b)



(4c)

Fig-4: Segmentation results using level set method
(4a) Input image (4b) Skull removed image
(4c) Segmented tumor

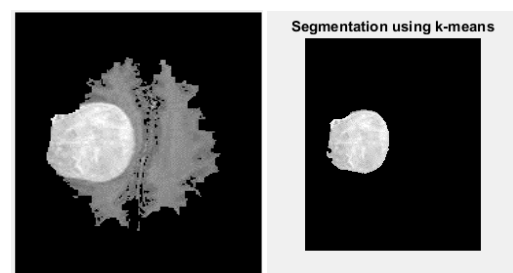
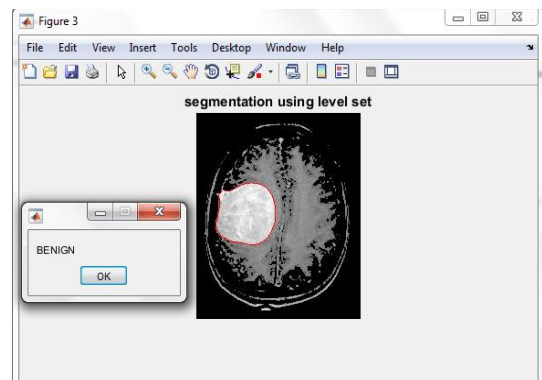
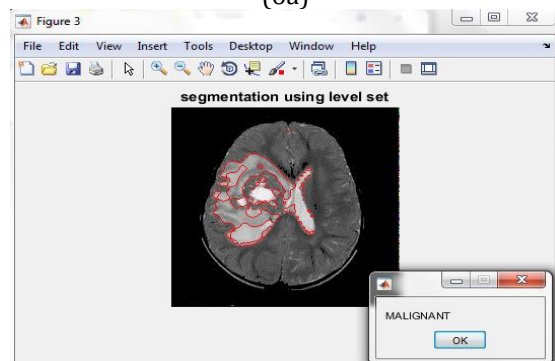


Fig-5: Segmentation results using K-means method

Classification results:

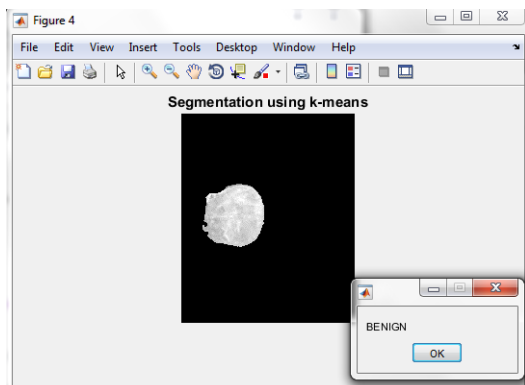


(6a)

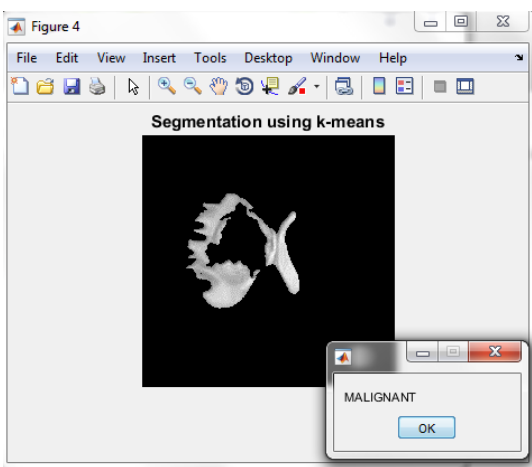


(6b)

Fig-6: Classification results using level set method
(6a) Benign (6b) Malignant



(7a)



(7b)

Fig-7: Classification results using K-means method (7a) Benign (7b) Malignant

- TP-Number of benign tumor region correctly detected in the MRI images.
- FP-Number of benign tumor region detected as malignant in the MRI images.
- TN-Number of malignant tumor region correctly detected in the MRI images.
- FN-Number of malignant tumor region detected as benign tumor region by the system.

Calculation of the accuracy, sensitivity and specificity is done according to these equations:

- $SENSITIVITY = TP / (TP + FN)$
- $SPECIFICITY = TN / (TN + FP)$
- $ACCURACY = TP + TN / (TP + TN + FP + FN)$

As the data base contains 41 MRI brain images of two cases (benign, malignant), the dataset is split. In order to split the feature subset into the training and testing sets, the Holdout method is selected, which is part of the model evaluation used to segregate training and test datasets, where two-third (70%) of the samples from all the classes are allocated to the training set and the remaining one-third (30 %) of the samples from all the classes are allocated to the testing set.

Table -1: Ratio of images used for training and testing

Class	Number of images	Training set (70%)	Testing set (30%)
Malignant	24	17	10
Benign	17	12	7
Total	41	29	17

Performance Analysis:

Evaluation of the proposed MRI brain images classification method is carried out by calculating the performance in terms of true positive, false positive, true negative and false negative. By using these matrices sensitivity, specificity and accuracy can be obtained.

		Predicted class	
		P	N
Actual Class	P	True Positives (TP)	False Negatives (FN)
	N	False Positives (FP)	True Negatives (TN)

Fig-8: Confusion matrix

Table -2: Performance Evaluation of SVM

Confusion matrix	SVM (Level set method)		SVM (K-means method)	
		TP=6	FN=1	TP=6
	FP=0	TN=10	FP=1	TN=8
Accuracy	94.12%		82.35%	
Sensitivity	100.00%		75.00%	
Specificity	90.01%		88.89%	

From the above results, it is clear that classifier performance of SVM for Level set method is better compared to classifier performance of SVM for K-means method.

5. CONCLUSIONS

This work presents an effective method to segment and classify the MRI brain images as benign or malignant. It

also presents a comparison study of two segmentation algorithms namely, Level set method and K-means algorithm. To differentiate malignant tumor region from benign tumor region, GLCM, Wavelet transform based features are extracted and are given to SVM classifier.

The experimental result shows that Level set algorithm gives better segmentation results compared to k-means algorithm.

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