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SECTUBIM: Automatic Segmentation And Classification of Tumeric Brain MRI Images using FHS (FCM, HWT and SVM)

Arpan Batra[1], Dr. Geeta Kaushik[2]
M.Tech Student[1], Associate Professor[2]
Department of Electronics and Communication
Maharishi Markandshwar University, Mullana, Haryana, India

Abstract:
Abnormal development in any form fluid- fill or solid form of the tissue is termed as tumor. Gliomas are the Brain Tumors that are categorized into Malignant and Benign tumors. Benign tumors are less harmful than the Malignant tumor as benign are not having the capability of spreading by its own to other parts of the body. Whereas on the other hand Malignant tumors are cancerous tumors and are suspected to grow unconditionally. Gliomas are of two grades Low Grade Gliomas (LGG) and High Grade Gliomas (HGG). HGG are more harmful and destructive then LGG. Four stages are there to detect the tumor namely pre-processing, feature extraction, segmentation and classification. The proposed algorithm is combination make use of the FCM clustering and SVM classifier for classification of the tumor along with BCFCM for bias field correction and HAAR wavelet transform for feature extraction.

Keywords: Malignant, MRI, Glioma,Segmentation, Classification, BCFCM, FCM, SVM, Wavelet Transform, DSC and PPV

I. INTRODUCTION

Image processing is the phenomenon of in which image is enhanced by use of some operations and also the image is converted into digital form. Image processing is the powerful way to extract the important information from the image. Medical image processing is providing great help to doctors for proper diagnosis of the disease at very early stages. These techniques are very efficient and time saving. Magnetic resonance imaging is a scanning technique for extracting important information of the soft tissues of the body. Automatic segmentation and classification of the MRI images for detection of the brain tumor is playing a significant role for saving life of millions of people as this helps in providing the clear picture of the tumor portion and the size of the tumor inside the body. It is difficult to extract information regarding the tumor until and unless MRI images are efficiently and properly segmented and classified. For detecting tumor, first enhancement of the MRI Image by removing the unwanted noise needs to be done. After enhancing the image, segmentation needs to be performed. Fuzzy C – Means clustering is used for segmenting the enhanced image. Tumor portion is extracted using different extraction technique. In proposed work Haar Wavelet Transform is used for extracting the important features. In last classification is done to classify the images. Support Vector Machine is used for classifying the extracted feature. Development of the hybrid technique that uses different techniques to provide efficient result in terms of the tumor detection is the main objective of the proposed work.

II. PROPOSED CONCEPT

Detection of tumor is very essential at early stages of the tumor gwoth as delay in detectin and treatment can lead to death of the patient. Therefore automatic segmentation and clasiification came into picture. Proposed work has been divided into four stages namely pre- processing, segmentation, feature extraction and segmentaion. Below is the block diagram of the method.

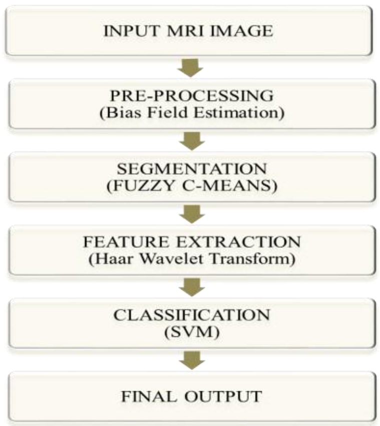


Figure.1. Flow Diagram of Proposed Method

Input image is the MRI image in DCIM format. Different stages for tumor detection are

A) PRE-PROCESSING - BCFCM Bias Field Corrected FCM

Pre-Processing is the process of enhancing the input image by removing the unwanted noise. Image filtering and noise removal results in the good quality of image. For enhancing the image first bias field estimation is done. Bias field is the undesirable low frequency signal that result in the blurriness of the image. BCFCM technique is used for getting the good quality image. The observed MRI signal is modeled as a product of the true signal generated by the underlying anatomy, and a spatially varying factor called the gain field

$Y_k = G_k X_k \ \forall k \in \{1,2,\ldots,N\}$.. (1)

where X_k and Y_k are the true and observed intensities at the k^{th}voxel, respectively, is the gain field at the k^{th}voxel, and is the total number of voxels in the MRI volume

The application of a logarithmic transformation to the intensities allows the artifact to be modeled as an additive bias field

$y_k = x_k + \beta_k \; \forall k \in \{1,2,\ldots,N\}$ ……………………… (2)

where x_k and y_k are the true and observed log-transformed intensities at the k^{th} voxel, respectively, and β_k is the bias field at the k^{th} voxel.

Bias Field is estimated by making use of the zero gradient condition for the bias field estimator that is expressed by

$$\beta_k^* = y_k - \frac{\sum_{i=1}^{C} u_{ik}^{p} v_i}{\sum_{i=1}^{C} u_{ik}^{p}} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots (3)$$

BCFCM algorithm

Step1 Initialize the process

Step2 Keep constant in FCM objective function, must be larger than 1

Step 3 Convert input image to long array

Step 4 Calculate initial Bias field estimate

Step 5 Set Partition matrix

Step6 Calculate Cluster updates storage

Step7 Calculate distance to class means for each (bias corrected) pixel and neighbors

Step 8 Estimate the (new) Bias-Field

Step9 Use Low-pass filter Bias-Field as regularization

Step 10 Reshape Partition table to image

Step11 Reshape bias field to image

B) SEGMENTATION – FCM Fuzzy C Means Clustering

Segmentation simply means dividing the image into small regions depending upon the number of regions required. In the proposed method, FCM is used to segment the image into 3 clusters. One of the two basic properties of intensity values discontinuity and similarity makes the base for Segmentation process. After clustering samples belonging to same cluster are more similar when compared to the samples of other cluster. FCM make use of partial membership that means every piece of data belongs to one or more cluster.

The main objective of FCM clustering is to minimize the below

$$J_m = \sum_{i=1}^{N}\sum_{j=1}^{C} u_{ij}^{m} \left\|x_i - c_j\right\|^2, \; 1 \le m \le \infty \ldots\ldots (4)$$

where *m* is any real number greater than 1,

u_{ij} is the degree of membership of x_i in the cluster *j*,

x_i is the *i*th of d-dimensional measured data,

c_j is the d-dimension center of the cluster,

$\left\|x_i - c_j\right\|$ is the Euclidean distance between i^{th} data and j^{th} cluster center.

Degree of membership is defined as

$$u_{ij} = \frac{1}{\sum_{k=1}^{C}\left(\frac{\left\|x_i - c_j\right\|}{\left\|x_i - c_k\right\|}\right)^{\frac{2}{m-1}}} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (5)$$

and cluster center c_j as

$$c_j = \frac{\sum_{i=1}^{N} u_{ij}^{m} . x_i}{\sum_{i=1}^{N} u_{ij}^{m}} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (6)$$

FCM algorithm

Step 1 Need to decide how many clusters we need. Here 3 clusters approach is implemented.

Step 2 Initialize $U=[u_{ij}]$ matrix, $U^{(0)}$

Step 3 At t-step: calculate the centers vectors $C^{(t)}=[c_j]$ with $U^{(t)}$

$$c_j = \frac{\sum_{i=1}^{N} u_{ij}^{m} . x_i}{\sum_{i=1}^{N} u_{ij}^{m}} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (7)$$

Step 4 Update $U^{(t)}$, $U^{(t+1)}$

$$u_{ij} = \frac{1}{\sum_{k=1}^{C}\left(\frac{\left\|x_i - c_j\right\|}{\left\|x_i - c_k\right\|}\right)^{\frac{2}{m-1}}} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (8)$$

Step 5 If $\left\|U^{(t+1)} - U^{t}\right\| < \varepsilon$ then STOP; otherwise return to step 2, where ε is the termination criterion between 0 and 1.

C) FEATURE EXTRAXTION – HAAR Wavelet Transform

Feature extraction is the process of separating the important data from the main image. For brain tumor images, feature extraction is done for extracting the tumor portion. That extracted portion of the image is used by the classifier for classification of the tumor or non-tumor MRI images. In proposed concept, Haar Wavelet Transform has been used for extracting the important features. Alfred proposed the first wavelet that is named as Haar wavelet. Only addition and subtraction are required for its forward and reverse transform. Haar Wavelet is not differentiable because it is not continuous.

Haar wavelet family for $q \in (0,1)$ is defined by

$$h_i(q) = \begin{cases} 1 & 0 \le q \le 0.5 \\ -1 & 0.5 \le q \le 1 \\ 0 & otherwise \end{cases} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (9)$$

Haar wavelet Transform algorithm

To calculate the Haar transform of an array of n samples:

Step 1 Divide the samples into pairs and then calculate the average of each pair of samples. Total averages numbers should be exactly half of the total samples.

Step 2 Calculate the difference between each average and the samples it was calculated from. (n/2 differences)

Step 3 Write average values in the first of the array.

Step 4 Write differences values in the second half of the array.

Step 5 Repeat the process on first half of the array followed by again first half until last values resolves. All times array size should be power of two.

D) CLASSIFICATION – SVM Support Vector Machine

For classifying the extracted portion of MRI image into a tumor image or a normal image, classifiers are used. In the proposed concept SVM classifier is used. SVM gives better results because it is a binary classifier based on supervised learning's. Support vector machine (SVM) comprise a subgroup of discriminative methods which their label inferring models are SVM scoring functions. SVM classifies between two classes by constructing a hyperplane in high-dimensional feature space which can be used for classification. Hyperplane can be represented by equation-

w.x+b=0……………………………………………… (10)

w is weight vector and normal to hyperplane. b is bias or threshold.

SVM Algorithm

Step 1 Data setup: our dataset contains two classes (tumor &non tumor), each N samples.

Step 2 SVM with linear kernel (-t 0). We need to determine the best available parameter value C using 2-fold cross validation.

Step 3 After determining the best parameter value for C, we train the entire data again using this parameter value.

Step 4 Plot support value

Step 5 Plot decision value.

III. DEFINITIONS AND EVALUATION PARAMETERS

Some of the important definitions that are useful in defining the evaluation parameters are:

- True positive – Tumor image correctly identified as tumor image (T_P)
- False positive – Non Tumor image incorrectly identified as tumor image (F_P)
- True negative – Non Tumor image correctly identified as Non Tumor image (T_N)
- False negative - Tumor image incorrectly identified as Non Tumor image (F_N)

For evaluating the performance of the proposed method, five parameters are calculated. These parameters calculations are done using predefine formulas. Accuracy - Accuracy is the probability that a diagnostic test is correctly performed. It is calculated by

$$Accuracy = \frac{T_P + T_N}{T_P + F_N + T_N + F_P} * 100\% \quad \ldots\ldots\ldots\ldots\ldots (11)$$

Sensitivity – Sensitivity is the probability of positive for a diagnostic test. It is also termed as true positive fraction. The percentage of sensitivity is given by

$$Sensitivity = \frac{T_P}{T_P + F_N} * 100\% \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (12)$$

Specificity - Specificity is the probability of negative for a diagnostic test. It is also termed as true negative fraction. The percentage of specificity is given by

$$Specificity = \frac{T_N}{T_N + F_P} * 100\% \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots (13)$$

Dice Similarity Coefficient – DSC measures the overlap between the manual and the automatic segmentation. It is defined as

$$DSC = \frac{2T_P}{F_N + F_P + 2T_P} * 100\% \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (14)$$

Positive Predictive Value - PPV is a measure of the amount of FP and TP, defined as,

$$PPV = \frac{T_P}{F_P + T_P} * 100\% \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (15)$$

IV. RESULTS

- Input image – MRI images in DCIM format is used as input image.

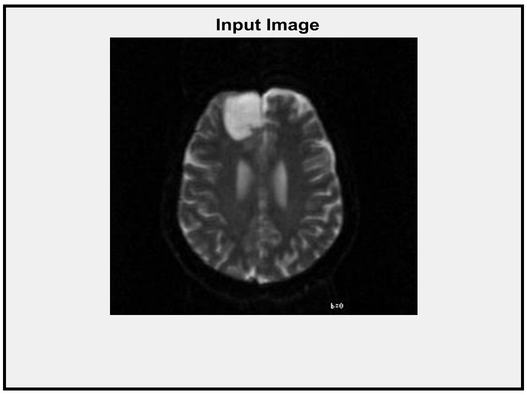


Figure.2. Input MRI Image

- Bias estimated output – Bias estimated output showing the image with components those results in blurring the image or reducing the image quality.

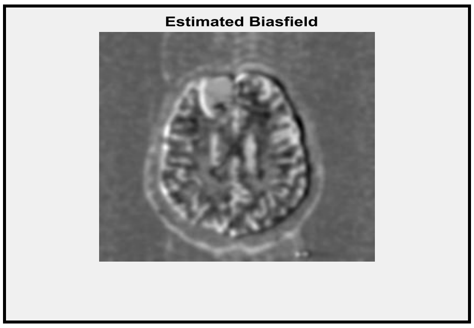


Figure.3. Bias Estimated Output

- Bias corrected image output – Bias corrected image is obtained by subtracting the bias estimated output from original image. Therefore bias estimated image is enhanced image when compared to original image.

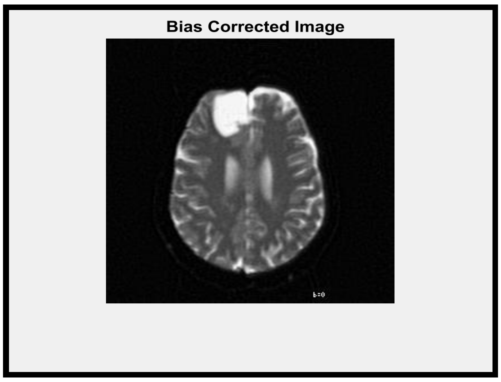


Figure.4. Bias Corrected Image

- Labeled by cluster index image output - Image is divided into 3 clusters as shown in the below image.

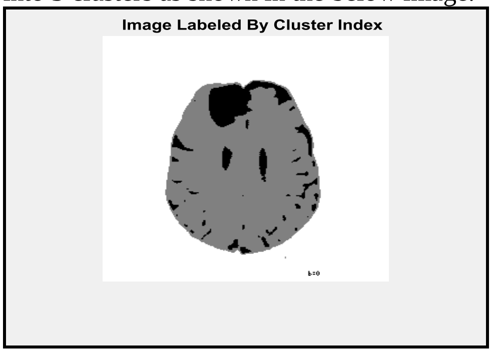


Figure.5. Labeled By Cluster Index Image

- Brain Tumor Segmentation Image output – Segmentation image is highlighting the tumor portion of the Image.

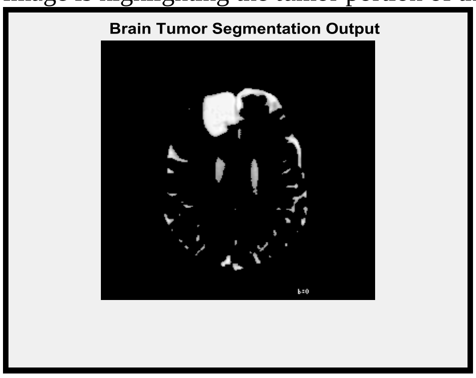
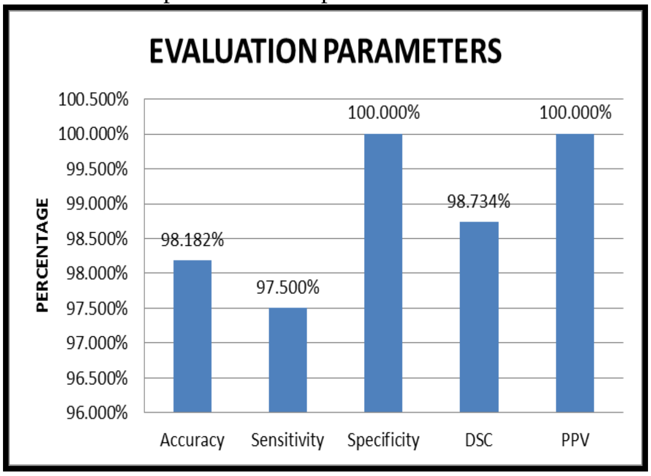


Figure.6. Brain Tumor Segmentation Image

- Classification output – SVM Classifier classifies the image into tumor or non-tumor images.

Figure.6. Classification output

- Evaluation parameters output



Graph - 1 Parameter Values

- Comparison - Table below shows the comparison of the proposed approach with some of the existing approaches in term of accuracy.

Table.1. Comparison of different methodology's accuracy

Approach	Methodology	Dataset size	Accuracy (%)
Praveen G.B [7]	LS-SVM + MLP	100	96.63
Shenbagarajan [8]	ACM + ANNLM	80	93.74
R. Mishra [11]	Wavelet packets + ANN	Six images	95
E. A. El-Dihshan[12]	DWT + PCA + ANN	70	97
Antonie L [9]	SVM	50	70
Chaplot S. [10]	Wavelets+SVM	52	98
Proposed	FCM + HWT+ SVM	55	98.2

V. CONCLUSION

Brain tumor detection in early stages with high percentage of accuracy is possible only by using automatic segmentation and classification of the MRI images. In this paper, hybrid approach is used for detecting the turmeric brain images by making use of Fuzzy C Means clustering for segmentation, Haar Wavelet Transform for feature extraction and Support Vector Machine for classification. Proposed methodology is able to achieve 98.2 percent of accuracy when tested with 55 samples of images. Along with accuracy four other parameters namely sensitivity, specificity, positive predictive value and dice similarity coefficient are also calculated for measuring the performance. As a future scope, the proposed approach can be tested with large size of dataset.

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