

EFFICIENT BRAIN TUMOR SEGMENTATION IN MRI IMAGES USING WAVELETS AND NEURAL NETWORKS

J.Jefferson Thomas^[1], S.Hashbas^[2],M.Caroline Viola Stella Mary^[3],
J.Monica Esther*

ABSTRACT

Brain tumor extraction and its analysis are challenging tasks in Medical image processing because brain image is complicated. Segmentation plays a very important role in the medical image processing. In that way MRI (Magnetic Resonance Imaging) has become a useful medical diagnostic tool for the diagnosis of brain and other medical images. In this project we are presenting a segmentation algorithm using Wavelets and Neural Networks.

I INTRODUCTION

In the fast moving world, Brain tumor is one of the major causes for the increase in Mortality among children and adults. Brain tumor is one an abnormal mass of tissue in which cells grow and multiply, seemingly unchecked by the mechanisms that control normal cells. The complex brain tumors can be separated into two general categories depending on the tumors origin, their growth pattern and malignancy. Primary brain tumors are tumors that arise from cells in the brain or from the covering of the brain. A secondary or metastatic brain tumor occurs when cancer cells spread to the brain from a primary cancer in another part of the body. Most Research in developed countries show that the number of people who develop brain tumors and die from them has increased over past three decades.

II RELATED WORK

A computer software system is designed for segmentation and classification[1] of benign and malignant tumour slices in brain computed tomography images. In this study, the authors present a method to select both dominant run length and co-occurrence texture features of wavelet approximation tumour region of each slice to be segmented by a support vector machine. Two-

dimensional discrete wavelet decomposition is performed on the tumour image to remove the noise. The images considered for this study belong to 208 tumour slices. Seventeen features are extracted and six features are selected using Student's t-test. This study constructed the SVM and probabilistic neural network (PNN) classifiers with the selected features. The classification accuracy of both classifiers are evaluated using the k fold cross validation method. The segmentation results are also compared with the experienced radiologist ground truth. Quantitative analysis between ground truth and the segmented tumour is presented in terms of segmentation accuracy and segmentation error. The proposed system provides some newly found texture features have an important contribution in classifying tumour slices efficiently and accurately. The experimental results show that the proposed SVM classifier is able to achieve high segmentation and classification accuracy effectiveness as measured by sensitivity and specificity.

Volumetric segmentation[2] of subcortical structures such as the basal ganglia and thalamus is necessary for non-invasive diagnosis and neurosurgery planning. This is a challenging problem due in part to limited boundary information between structures, similar intensity profiles across the different structures, and low contrast data. This paper presents a semi-automatic segmentation system exploiting the superior image quality of ultra high field MRI. The proposed approach utilizes the complementary edge information in the multiple structural MRI modalities. It combines optimally selected two modalities from susceptibility-weighted, T2-weighted, and diffusion MRI, and introduces a tailored new edge indicator function. In addition to this, we employ prior shape and configuration knowledge of the sub cortical structures in order to guide the evolution of geometric active surfaces. Neighboring structures are segmented iteratively, constraining over segmentation at their borders with a non-overlapping penalty. Several experiments with data acquired on a 7T MRI scanner demonstrate the feasibility and power of the approach for the segmentation of basal ganglia components critical for neurosurgery applications such as deep brain stimulation surgery.

Multilevel thresholding[3] amounts to segmenting a gray-level image into several

J.Jefferson Thomas^[1], PG/IT Student, Francis Xavier Engineering College, jeffitcian@gmail.com.
S.Hashbas^[2], PG/IT Student, Francis Xavier Engineering College, asbasmtch@gmail.com M.Caroline Viola Stella Mary^[3], Professor, IT Department, Francis Xavier Engineering College, carolsam67@gmail.com J.Monica Esther*, Assistant Professor, IT Department, Francis Xavier Engineering College, evervictory@gmail.com

distinct regions. This paper presents a 2D histogram based multilevel thresholding approach to improve the separation between objects. Recent studies indicate that the results obtained with 2D histogram oriented approaches are superior to those obtained with 1D histogram based techniques in the context of bi-level thresholding. Here, a method to incorporate 2D histogram related information for generalized multilevel thresholding is proposed using the maximum Tsallis entropy. Differential evolution (DE), a simple yet efficient evolutionary algorithm of current interest, is employed to improve the computational efficiency of the proposed method. The performance of DE is investigated extensively through comparison with other well-known nature inspired global optimization techniques such as genetic algorithm, particle swarm optimization, artificial bee colony, and simulated annealing. In addition, the outcome of the proposed method is evaluated using a well known benchmark—the Berkley segmentation data set with 300 distinct images.

This paper[4] suggests that fractal texture feature is useful to detect pediatric brain tumor in multimodal MRI. In this study, we systematically investigate efficacy of using several different image features such as intensity, fractal texture, and level-set shape in segmentation of posterior-fossa (PF) tumor for pediatric patients. We explore effectiveness of using four different feature selection and three different segmentation techniques, respectively, to discriminate tumor regions from normal tissue in multimodal brain MRI. We further study the selective fusion of these features for improved PF tumor segmentation. Our result suggests that Kullback–Leibler divergence measure for feature ranking and selection and the expectation maximization algorithm for feature fusion and tumor segmentation offer the best results for the patient data in this study. We show that for T1 and fluid attenuation inversion recovery (FLAIR) MRI modalities, the best PF tumor segmentation is obtained using the texture feature such as multi-fractional Brownian motion while that for T2 MRI is obtained by fusing level-set shape with intensity features. In multimodality fused MRI feature offers the best PF tumor segmentation performance. We use different similarity metrics to evaluate quality and robustness of these selected features for PF tumor segmentation in MRI for ten pediatric patients.

The generalized algorithm[5] initiates k cluster centroids by randomly selecting k feature vectors from X. Later, the feature vectors are grouped into k clusters using a selected distance measure such as Euclidean. The clustering procedure stops only when all cluster centroids tend to converge. Similarity is measured by distance and defined by an N dimensional feature space. Feature distance calculation differs from

spatial distance calculation. Feature distance calculation is based on features such as color or intensity and texture while spatial distance calculation is based on x, y (width, height) coordinates. Devising an appropriate distance calculation method is an important task since it greatly affects final clustering result. Clustering algorithms may be generally classified into four main categories which are hierarchical, overlapping and exclusive.

The image of the brain[6] is acquired through MRI technique. If the histograms of the images corresponding to the two halves of the brain are plotted, a symmetry between the two histograms should be observed due to symmetrical nature of the brain along its central axis. On the other hand, if any asymmetry is observed, the presence of the tumor is detected. After detection of the presence of the tumor, thresholding can be done for segmentation of the image. Segmentation is done by calculating the threshold point. The differences of the two histograms are plotted and the peak of the difference is chosen as the threshold point. Using this threshold point, the whole image is converted into binary image providing with the boundary of the tumor. The binary image is now cropped along the contour of the tumor to calculate the physical dimension of the tumor. The flowchart below depicts the stages of the work reported in the present communication.

III PROPOSED SYSTEM

A. Preprocessing

The image of the brain obtained through MRI is loaded by using the command 'imread' in MATLAB. The image is then converted into gray color image, i.e., 2D image. The gray color image consists of pixel intensity between 0-255 where 0 represents black and 255 is used for white.

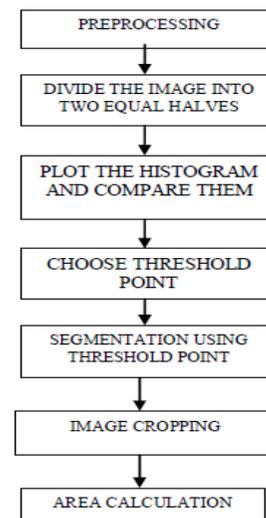


Fig1 .-Working methodology of Histogram Thresholding algorithm

B. Division the image

After converting the image into gray color image, it is divided into two equal halves along its central axis. The following algorithm is applied to achieve this: The image pixels are stored as a variable (say P) where P shows the values of the pixels in a 2D matrix (row – column) form. Number of rows and columns are assigned some other variables. The column value is divided by 2 and assigned another variable name (say S) Form new matrix using for loop by rows from 0:1:Q as outer loop and columns from 0:1:S as inner loop. Using the command ‘imshow’, the image is constructed based on the new matrix. This image will be the halves of the original image. For the other half of the image, the column value from S:1:R is considered as the inner loop.

C. Plot the histogram and compare them

Histogram is a plot between number of pixel and pixel intensity. To plot the histogram, bar graph can be used. The histogram code operates by first reading the grayscale value at the first entry and coming up with pixel intensity between 0 and 255. It increments the total number of pixels and then it will move on to the next row or column entry until it finishes reading all the raster data. However, while it is reading each entry, if it picks up pixel intensity value more than once it will increment that particular value. MATLAB command used for this is ‘bar()’. Finally the two histograms are compared to detect the tumor and hence the tumor.

D. Choose threshold point

The difference of the two histograms is calculated and the resultant difference is plotted using bar graph to select the threshold point.

E. Segmentation using threshold point

A zero matrix of same size of original image matrix is considered. Each pixel value of the image matrix is compared with the threshold point. If the value of pixel is greater than threshold, coordinate of c matrix is assigned a value 255 otherwise 0 is assigned to that. This process is repeated till all the pixel values are compared to threshold point. Matrix is then transformed into image using ‘imshow’ command.

F. Image cropping

Cropping is the process of selecting desired region from an image that is to be processed. The image shows the desired tumor portion. This cropped image is used to calculate the tumor area.

G. Area calculation

Area of an image is the total number of the pixels present in the area which can be calculated in the length units by multiplying the number of pixels with the dimension of one pixel. To calculate the number of pixels in the cropped image the function Bwarea is used. This function calculates the number pixels present in the image.

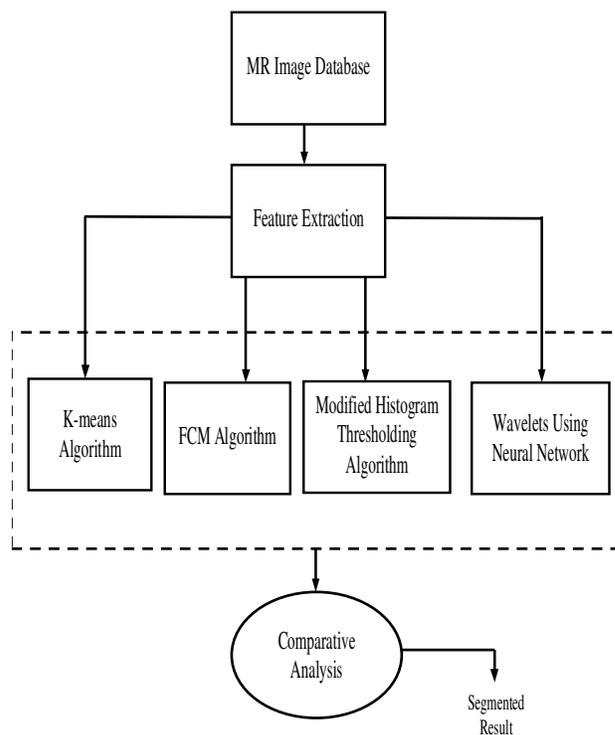


Fig2 . – System Architecture

IV RESULT AND DISSCUION

Fuzzy C-means Algorithm sample output

Fuzzy C-means clustering (FCM) is an unsupervised data clustering method in which each data point belongs to a cluster to a degree specified by a membership value.

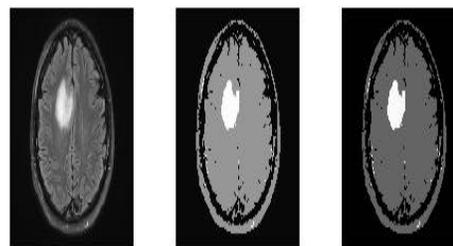


Fig3 Brain MRI Image segmented by Fuzzy C-means algorithm with Tumor

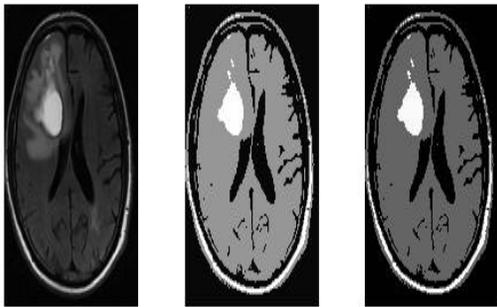


Fig4 Brain MRI Image segmented by Fuzzy C-means algorithm with Tumor

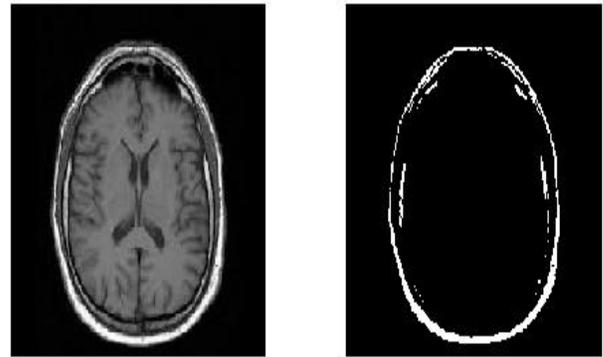


Fig8 Brain MRI Image segmented by K-means algorithm without Tumor

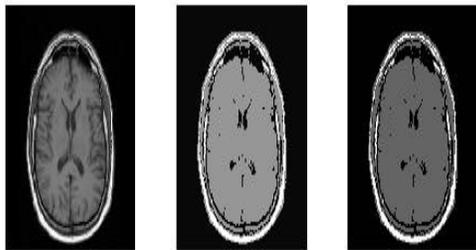


Fig5 Brain MRI Image segmented by Fuzzy C-means algorithm without Tumor

Modified Histogram Thresholding algorithm

A diagram consisting of rectangles whose area is proportional to the frequency of a variable and whose width is equal to the class interval.

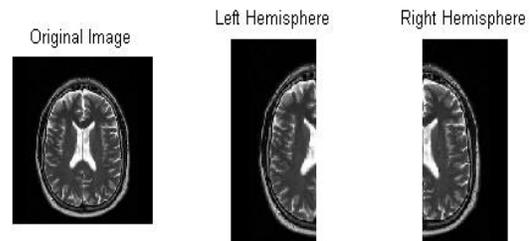
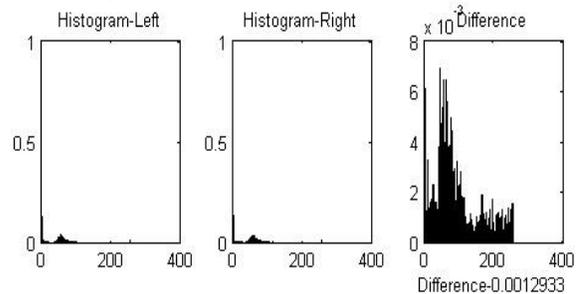


Image-1



K-means Algorithm Sample Output

K means clustering is the most widely used and studied method among the clustering formulations that are based on minimizing a formal objective function.

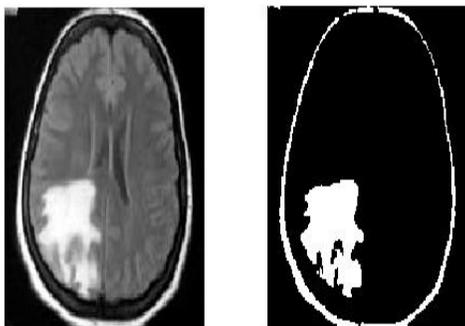


Fig6 Brain MRI Image segmented by K-means algorithm with Tumor

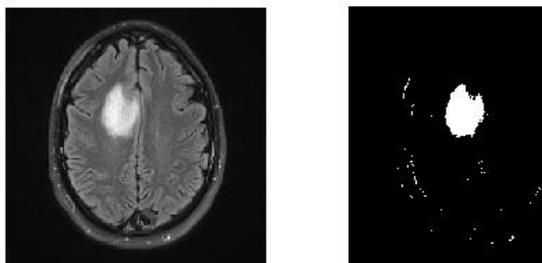


Fig7 Brain MRI Image segmented by K-means algorithm with Tumor

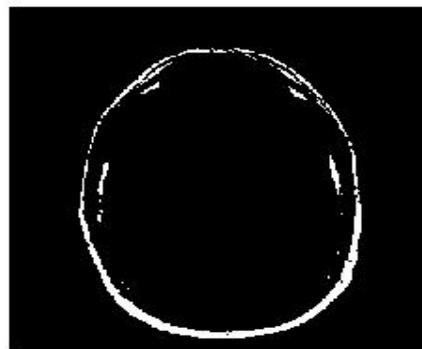


Fig9 Brain MRI Image segmented by Modified Histogram Thresholding Algorithm without Tumor

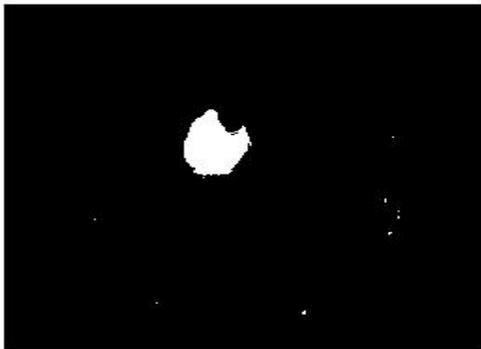
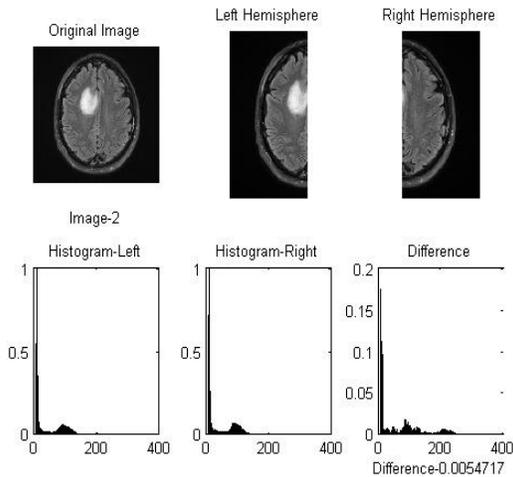


Fig10 Brain MRI Image segmented by Modified Histogram Thresholding Algorithm with Tumor

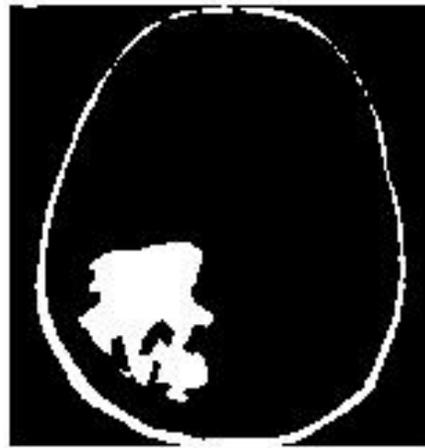
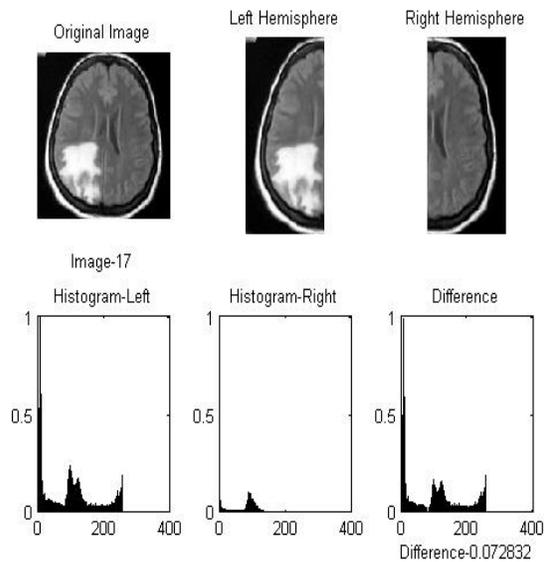


Fig11 Brain MRI Image segmented by Modified Histogram Thresholding Algorithm with Tumor

V CONCLUSION

In this project a technique to detect presence of brain Tumour based on thresholding technique has been developed. The segmentation of the brain is also being done while detecting the presence of the tumor. The physical dimension of the tumor which is of utmost importance to the physicians can also be calculated using the present technique.

As a future enhancement determining the contour of the Brain Tumour and the size of the tumour may help the physicians in diagnosing the intense of the disease. Various techniques for contour detection may be implemented to produce a cost effective and reduced time complexity method.

A Support Vector Machine (SVM) is a discriminative classifier formally defined by a separating hyperplane. In other words, given labeled training data (supervised learning), the algorithm outputs an optimal hyperplane which categorizes new examples.

An SVM model is a representation of the examples as points in space, mapped so that the examples of the separate categories are divided by a clear gap that is as wide as possible. New examples are then mapped into that same space and predicted to belong to a category based on which side of the gap they fall on.

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