

Virtual Instrumentation Based Brain Tumor Detection, Analysis and Identification

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ABSTRACT

End to end mechanism of automating the tumor detection and classifying the tumor cells is carried out in this paper. Denoising followed by image enhancement and segmentation is used for tumor detection. Comparative evaluation of segmentation techniques is carried out which include Thresholding, Watershed algorithm, K-means, Fuzzy C. Performance of segmentation algorithm is evaluated by accuracy analysis. Fuzzy C is proved to be the best segmentation technique for brain tumor detection. Different parameters are extracted from the detected tumor which is used to train the Support Vector Machine. Designed Support Vector Machine is then used to determine tumor type whether benign or malignant.

Keywords: Brain Tumor, Image processing, MRI, Filtering, Segmentation, SVM

I. INTRODUCTION

The uncontrolled growth of cell results in a tumor. Tumor detected at an early stage helps in saving persons life. For brain tumor detection, a person undergoes MRI scanning. MRI image obtained is further analyzed by doctors visually to detect the presence of a tumor. However, a considerable variation is observed among doctors which results in variable conclusion. Detection of tumor type whether benign or malignant requires a biopsy to be carried. This is extremely time consuming. Medical imaging hence plays a very important role where the results are obtained in less time and are more accurate and reliable compared to manual testing.

In the last few years, researchers have developed several techniques which automate the process of tumor detection and analysis.

Benson C.C. et al.[25] proposed a watershed algorithm based on different feature combination such as color,

edge, orientation, and texture. The over segmentation problem is overcome by using a marker-based watershed algorithm where markers were found manually. The accuracy is calculated by Dice and Tanimoto coefficient.

Guang Yang et al.[3] proposed a method where discrete wavelet transform is used to distinguish between tumor grades. The comparison is done on different window size and found that Coif wavelet produces the best clustering result. Besides, it is also found that the sub spectral analysis is sufficient to distinguish grades of the tumor.

Sergio Pereira et al.[2] proposed a Convolutional Neural Network based method for segmentation of brain tumor. Heterogeneity in MRI images is addressed using intensity normalization. The variation in the structural components in a brain tumor was handled by data augmentation. It is found that small kernel proves to be more efficient and are less prone to overfitting.

II. PROPOSED METHOD

Fig 3.1 shows design flow required for tumor detection.



A. Image and Database

Brain tumor images can be MRI images or CT scan images. MRI images are usually preferred over CT scan. This is because ionizing radiations are not used while carrying out MRI imaging besides MRI image depicts anatomy and evaluate structure in much greater details as compared to CT scan[1]. MRI images are therefore used for carrying out an evaluation of segmentation techniques.

Images of MRI are taken from figshare.com where images from 3064 patients are available. Each. mat file in above dataset consists of brain image, extracted tumor image, and its type. This image data set is used to train the Support Vector Machine.

B. Pre-processing

MRI images are highly affected by Rician noise. MRI images are also subjected to uneven contract. Proper intensity standardization along with noise removal is required before any analysis is carried out on the image. Pre-processing stage hence consists of denoising followed by image enhancement and sharpening.

The advantage of the designed pre-processing stage is that it doesn't over smoothen or blur the image instead helps in maintain the image features unlike other pre-processing technique

Denoising

MRI images are highly affected by Rician noise. Hard wavelet denoising technique with two level of decomposition is used. This is because the Peak Signal to Noise Ratio is maximum and Mean Square Error is minimum with Hard wavelet transform denoising technique when compared with Median filter, Weiner filter, and Soft wavelet transform.[1]

In Hard wavelet denoising technique, the signal is split into lower and upper sidebands. The detailed coefficient is then subjected to thresholding. The universal thresholding technique is used for calculating the threshold.

$$\lambda_{j} = \frac{\delta\sqrt{2\log(N)}}{\sqrt{\log_{2}^{j+1}}} \tag{1}$$

The coefficient less then threshold value are reduced to zero while coefficient greater then threshold is left unchanged.

$$y = x if |x| > \lambda (2)$$

$$y = 0 if |x| < \lambda$$

Where y is the output signal, x is the input and λ is the threshold value





Fig 2.1: Image with Rician noise

Fig 2.2: Filtered Image



Fig 2.3 : Filtered Image Fig 2.4 : Enhanced Image

Image Enhancement

MRI images suffer from poor contrast. Besides luminance non-linearity is also introduced by imaging devices. Enhancing the image contrast is necessary before any further processing.

Enhancing the image is carried out by combining the histogram process with gamma correction[4]. Cumulative histogram is initially calculated using-

$$C(h_i) = \sum_{i=1}^k hist(r_i)$$
(3)

Where i is the gray level of image and $hist(r_i)$ is a discrete function which defines the intensity levels of a digital image.

Median, minimum and maximum values are then calculated to determine the value of gamma-

$$g = log\left(\frac{median - minimum}{maxium - median}\right)$$
(4)

The gamma values are then used to enhance the contrast of the image. The enhanced image is –

$$G(x,y) = f(x,y)^{\frac{1}{g}}$$
(5)

Where G(x, y) is enhanced an image, f(x, y) is the original image and g is the value of gamma.

Sharpening

Edges, play an important role in tumor detection to separate the normal cells from tumor cells. This highfrequency information about the edges is enhanced using sharpening.

First and second order derivatives are highly sensitive to noise and less sensitive to delicate edges.[5] Hence, Canny edge detection technique is used for sharpening. Firstly Sobel operators are used.

$$Kernel1 = \begin{bmatrix} -1 & 0 & 1 \\ -2 & 0 & 2 \\ -1 & 0 & 1 \end{bmatrix}$$
$$Kernel2 = \begin{bmatrix} 1 & 2 & 1 \\ 0 & 0 & 0 \\ -1 & -2 & -1 \end{bmatrix}$$
(6)

The gradient obtained are used to determine the magnitude and angle.

$$|G| = \sqrt{G_X^2 + G_Y^2} ,$$

$$\theta = \arctan\left(\frac{|G_y|}{|G_x|}\right)$$
(7)

Where G_y and G_x are gradients in x and y-direction respectively.

The non-maximum suppression is carried out followed by hysteresis thresholding where values below the threshold are suppressed. The image obtained by sharpening is added with the enhanced image to get the complete pre-processed image.





Fig 2.5 : Enhanced Image

Fig 2.6 : Enhanced and Sharpened Image

A. Post-processing.

Post-processing concentrates on the segregating the tumor cells from the normal cells. This is done by skull tripping followed by segmentation and morphology.

Skull Tripping

Skull tripping is used to separate brain tissue from the non brain tissue. Skull tripping is done firstly by binarizing the image using the threshold value. Filling and erosion are carried out on the binarized image to obtain the mask. The mask generated is then used to trip of the skull, separating the brain tissue.[20]





Fig 2.6: Enhanced and Sharpened Image

Fig 2.7: Skull tripped Image

Segmentation

Comparative analysis of five different techniques is carried out this involves Thresholding, Watershed, Kmeans, and Fuzzy C.

Thresholding

Thresholding divides the pixels based on its intensity levels. In MRI images, the tumor part as high intensity and solidity compared to the other brain tissues. The histogram is used to determine the value of threshold which separates the high-intensity tumor part from the nontumor ones.

$$y(x, y) = 1 \quad if \ f(x, y) > \lambda \tag{8}$$

$$y(x, y) = 0 \quad if \ f(x, y) < \lambda$$

Where y((x, y)) is threshold image, f(x, y) is the original image and λ is the value of the threshold.

This technique is easy to implement but is inefficient while detecting cancerous tumor and tumor in an early stage.

Watershed

Watershed algorithm is based on topological interpretation.

A pixel with similar intensity appears to be like basins. Filling of basin starts from the local minima of individual basins and stops when it reaches a peak point of the basin. The entire image gets divided into lines called watershed lines. The internal and external markers are determined where internal marker defines the area of interest and external marker defines the background.[25].Morphological operates than separate the tumor cells from the normal ones.

K-means

It is unsupervised learning method which groups pixels depending on its characteristics. K-means is an iterative process which consists of four major steps. It starts with finding the number of cluster 'k' whose centroids are randomly chosen. Euclidean distance is calculated between the pixel and the cluster. Grouping of pixels into a cluster is done based on the shortest distance. The centroid is the re-calculated and process continues until the centroid remains unchanged.[19]

The formula is used to compute cluster means m-

$$M = \frac{\sum_{i:c(i)=k} x_i}{N_k}, k = 1, \dots, k$$
(9)

While the distance between the pixel and cluster is determined by-

 $D(i) = \arg \min \|x_i - M_k\|^2, i = 1, \dots, N$ (10)

It is observed that the algorithm is fast and offers best results with discrete data set.

Fuzzy C

Fuzzy C is an iterative algorithm where identical data points are grouped into clusters. An iterative action is carried out on following objective function-

$$F = \sum_{p=1}^{N} \sum_{q=1}^{C} \mu_{pq}^{m} |x_{p} - c_{q}|^{2}$$
(11)

Here N represents total pixels, C represents the cluster number m is the factor of fuzziness. p is the pixel in N and q is the cluster in C denoted by xp and cq respectively.

After every iteration, the value of F reduces which indicates that the algorithm produces fair separation of pixels into required clusters.[24] The algorithm is quite efficient than K-means but the time required for clustering is very large.

C. Support Vector Machine.

Support Vector Machine(SVM) is based on the concept of decision planes which helps to separate set of items having dissimilar properties. Classifying

tumor as benign or malignant is done by SVM. It involves two steps training and testing.

Training

To train the Support Vector Machine, features are extracted from the database images. Statistical features include mean, entropy, standard deviation, skewness, kurtosis, contrast, energy, and correlation will regional feature includes area, perimeter, major and minor axis and eccentricity[26]. These are then used to train the Support vector machine.

Statistical features-

Mean

Mean gives a contribution of individual pixel intensity. It is given by formula-

$$M = \frac{1}{m * n} \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} f(x, y)$$
(12)

Where m and n represents number of rows and columns.

Entropy

Entropy is used to determine the randomness of the image texture. It is given by following formula-

$$E = -\sum_{x=0}^{m-1} \sum_{y=0}^{n-1} f(x, y) \log_2 f(x, y)$$
(13)

where m and n represent the number of rows and columns.

Std deviation

It can serve as a measure of inhomogeneity.

$$SD = \sqrt{\frac{1}{m * n} \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} (f(x, y) - M)^2}$$
(14)

where m and n represents the number of rows and columns and M is the mean

Skewness

A measure of symmetry is determined by skewness. It is given by formula-

$$S(X) = \frac{1}{m * n} \frac{\sum (f(x, y) - M)^3}{SD^3}$$
(15)

Where SD is the std deviation and M is the mean and m and n represents a number of rows and columns

Kurtosis

Kurtosis determines the shape of a random variable's probability distribution.

$$K(X) = \frac{1}{m * n} \frac{\sum (f(x, y) - M)^4}{SD^4}$$
(16)

Where SD is the std deviation and M is the mean and m and n represents the number of rows and columns

Contrast

Contrast measures intensity of a pixel and its neighbor over the image. It is given as-

$$Contrast = \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} (x-y)^2 f(x,y) \quad (17)$$

where m and n represents the number of rows and columns

Energy

This parameter measures the similarity between of an image

Energy =
$$\sum_{x=0}^{m-1} \sum_{y=0}^{n-1} f^2(x,y)$$
 (18)

Correlation

Spatial dependencies between the pixels are described by Correlation

$$\text{Correlation} = \frac{\sum_{x=0}^{m-1} \sum_{y=0}^{n-1} (x, y) f(x, y) - M_x M_y}{\sigma_x \sigma_y} \quad (19)$$

where M_x and σ_x are the mean and standard deviation in the horizontal spatial domain and M_y and σ_y are the mean and standard deviation in the vertical spatial domain.

Homogeneity

It is used to determine the textured and non-textured feature of the image

Homogeneity =
$$\sum_{x=0}^{m-1} \sum_{y=0}^{n-1} \frac{1}{1+(x+y)^2} f(x,y)$$
 (20)

Regional parameter-

Area

Image after symentation represents total number of black and white pixels[19].The binary image representation is given by-

$$I = \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} (f(0) + f(1))$$
(21)

The image is 256*256 hence the value of m and n is 256. To calculate area number of white pixels needs to be considered

Area =
$$0.256 * \sum \sum f(0) mm^2$$
 (22)

Major and minor axis

The major axis is the length (in pixel) of the largest axis of the tumor ellipse and the minor axis is the length (in pixel) of the smallest axis of the tumor ellipse.



Figure 2.8

Perimeter

It is the no of pixels that form the edge of the tumor image.

Eccentricity

It is defined as the ratio of the axis length which includes major and minor axis.

Testing

In testing, the tumor detected test image undergoes the similar feature extraction which is then used by SVM to classify the tumor whether malignant or benign.

III. EVALUATION AND RESULT

Evaluation and result of segmentation Algorithm:

The following image shows the few sample outcomes of the segmentation algorithm.

In Fig 3.1, A represents the skull tripped MRI image, B shows tumor detection obtained by thresholding, C shows tumor detection obtained by watershed, D shows tumor detection obtained by K means and E shows tumor detection using Fuzzy C.

The evaluation metrics used to evaluate the techniques are sensitivity, specificity, and accuracy[23].

Accuracy is the degree of correctness of diagnostic the test on a condition. Accuracy is given by following formula-

$$Accuracy = \frac{TN + TP}{TN + TP + FN + FP}$$
(23)



Figure 3.1 Output of segmentation algorithm

Specificity determines how good the test is at identifying the normal condition. Specificity is given by following formula-

Specificity =
$$\frac{\text{TN}}{\text{TN} + \text{FP}}$$
 (24)

Sensitivity is used to determine the goodness of the test in detecting the diseases. Sensitivity is given by following formula-

Sensitivity =
$$\frac{\text{TN}}{\text{TN} + \text{FN}}$$
 (24)

The below table shows the comparative analysis of the segmentation algorithm –

Methods		Specificity	Sensitivity
	Accuracy		
Thresholding	80.78%	83.33%	86.61%

Watershed	78.82%	84.76%	75.91%
Kmeans	88.17%	88.90%	65.78%
Fuzzy C	91.09%	91.56%	71.78%

 Table 3.1 Comparison of segmentation techniques

The comparison of the segmentation algorithm is also done using timing parameter and area analysis.

The following graph shows timing analysis of the four segmentation algorithm on 35 images. The y-axis shows time in seconds for every image on x-axis -





It is observed that the Fuzzy C algorithm requires the maximum time compared to rest of the algorithm.

The following graph shows area analysis of the four segmentation algorithm on 35 images which is compared to the true area. The y-axis shows the area (in pixel) for every image on x-axis –



Figure 3.2 Area analysis of detected tumor

It is found that the area of the detected tumor in Fuzzy C highly resembles the actual tumor area. In kmeans, the area of detected tumor slightly resembles the actual tumor area. On the other hand, the area detected by threshold and watershed highly various in comparison with the actual tumor area. Thus the accuracy of fuzzy C is high as proved in Table 1.

Evaluation and result of SVM:

SVM is trained with 3064 images taking into consideration the statistical and regional parameters. 35 test images are used to check the designed SVM. The classification of the tumor into benign and malignant is proved accurate in 32 cases out of 35 cases which results in an accuracy of 91.42%.

IV. CONCLUSION

In this paper, the main focus was to design a model to detect tumor with accuracy and classify them into benign and malignant. For detecting a tumor, preprocessing(denoising and image enhancement) and post-processing (segmentation and morphology) is carried out wherein four different segmentation algorithm are compared based on accuracy, sensitivity, specificity and timing analysis. It is observed that the thresholding and watershed methods of tumor detection are inefficient in detecting an early-stage tumor, besides the cancerous tumor are also not accurately detected by these methods. K means on the other side, provide better accuracy compared to the threshold and watershed but is less accurate compared to Fuzzy C. Fuzzy C is highly accurate and proves to be the best tumor detection algorithm. Support Vector Machine is trained to test and classify a tumor as malignant and benign. It proved to be 91.42% accurate. This research can be extended further to identify the cancerous cell inside the tumor.

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