Deep Fusion Model Based Enhanced Convolution Neural Networks for MRI Brain Image Classification System

J. Andrews, A. Jayachandran, T.Sudersson Rama Perumal

Abstract: ***Magnetic Resonance (MR) Imaging is a popular non-invasive modality for the visualization of different abnormalities in the brain due to its good soft-tissue contrast and accessibility of multispectral images. Using information from MR images, CAD systems have been developed to benefit doctors in rapid diagnosis. CAD systems can provide the diagnosis depending upon the specific attributes present in the medical images. The present study proposes a comprehensive method for the diagnosis of the cancerous region in the MRI images. Here, after image noise reduction, optimal image segmentation based on Support Vector Neural neural algorithm is utilized. Afterward, an optimized feature extraction and feature selection based on a modified region growing optimization algorithm are proposed for improving the classification accuracy of brain images. Further, it is also proposed that the input MR brain image be de-noised using a non-local Euclidean median in non-subsampled contourlet space. The classification accuracy of MRG with SVM is 74.24%, MRG with CNN is 82.67% and MRG with ANN is 62.71% and our proposed method MRG with MBCNN is 91.64%.***

Keywords: ***MRI image, CNN, Classification, Denoising, Texture.***

I. INTRODUCTION

The brain is a crucial part of the human body which plays an important role in controlling all parts of the human organ. Sometimes the brain is affected by the unnatural growth of abnormal cells in the tissues. This abnormal growth of cells is called Brain tumor which can be cancerous or noncancerous. Uncontrolled brain tumor leads to death to the patients. So, it is necessary to detect the tumor as early as possible to reduce the chances of death of the patient. Human Brain is made up of numerous number of cells called as neurons. Each cell carries a different function from another. The term growth of a cell includes cell division and cell reproduction. When the cycle of growth of cell fails to control then the cell grows and divides very often irregularly.Then these excess cells make a mass of tissues and termed it as a tumor[1-3]. Thus a brain tumor, can be defined as a collection of abnormal cells developed inside the brain. Skull of the brain is very hard and has limited space. Any growth inside the brain builds up many problems. Tumors of the brain can be classified as cancerous (malignant) ornon-cancerous (benign). As these cell tumors starts to grow they creates a pressure within the skull to increase. Which damages the brain and it is also a life-threatening. There are two types f brain tumors, primary and secondary. A tumor which forms in the brain is termed as primary brain tumor. When the tumor is occurring due to the cancer cells of another organ which is spread to the brain is known as secondary or metastatic brain tumor. Primary brain tumors are more usually occurs in children and older adults. Secondary brain tumor is often found on adults. The MRI sequence images are used here as they represent a particular appearance of tissue which depicted in terms of no. of radio-frequency and gradients[4-5].

This provides different sequences showing different contrast levels between tissues which helps in diagnosis diseases. This builds a need for classification or separation of MRI sequences into number of different slices namely proton-density (PD) weighted, T1-weighted, T2-weighted, diffusion-weighted,flow sensitive and 'miscellaneous'. In our proposed work 3 main slices for detection of brain tumor used are:

- T1-weighted MRI: Since T1 w allows for an easy annotation of the healthy tissues, it has become the most commonly used sequence images for the brain tumor structure analysis.
- T2-weighted MRI: T2- weighted images reflect the decay speed of magnetic moment in the transverse relaxation.
- PD-Proton Density-weighted MRI: These images reflect the difference between proton density.

Contours usually contain key visual information of an image. In computer vision, contours have been widely used in many practical tasks. Although quite a few contour detection methods have been developed over the past several decades, contour detection is still a challenging problem in the image field. Among the non-learning approaches, many early methods, such as the famous Canny detector, find contours by extracting edges where the brightness or color changes sharply. However, such methods usually employ regular kernels, e.g., Gaussian filter and Gabor filter , to measure the extents of local changes, and thus can hardly deal with textures.

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To address this problem, many texture suppression methods have been proposed. Examples are the method based on non classical receptive field inhibition, the method

based on sparseness measures, the method based on surround-modulation, etc. It has been validated that texture suppression can help improve contour detection performance. Nonetheless, these methods still mainly use low-level local features. Moreover, some of them are computationally heavy, which leads to difficulties in practical applications[6-8].

Magnetic Resonance (MR) Imaging is a popular non-invasive modality for the visualization of different abnormalities in the brain due to its good soft-tissue contrast and accessibility of multispectral images. Using information from MR images, CAD systems have been developed to benefit doctors in rapid diagnosis. CAD systems can provide the diagnosis depending upon the specific attributes present in the medical images. Typically, these systems usually employ the steps of preprocessing, attribute extraction, selection, and classification for categorizing normal/ abnormal brain MR images. Numerous methods have been proposed in the literature that employs classical machine learning algorithms for the detection of abnormal brain images. These studies have proposed solutions based on K-nearest neighbour (k-NN), Support vector machine (SVM), Kohonen-Hopfield neural network (KHNN), and Artificial neural networks (ANN), etc[9-10]. This paper is organized as follows; section II states about the existing work associated with MRI brain image segmentation. Section III describes about the proposed framework consists of preprocessing, feature extraction, feature selection, similarity measure and classifier. Section IV contains experimental results. The summarization of the proposed system is given in section V.

II. METHODOLOGY

The proposed system fusses and registers the three MRI scan images, by extracting Gray Level Run Length Matrix (GLRLM) and Centre-Symmetric Local-Binary Patterns (CSLBP) and features are stored in the database, CNN classifier is used to divide the brain images as Benign tumor , Malignant tumor and Normal.

A. Image Enhancement and Noise Removal

This section provides some techniques to enhancement of MRI which can perform image enhancement and noise removal techniques that enhance quality of the images for better segmentation accuracy. This primary stage plays a significant role to detect, trace and extract the brain tumor region from hemisphere. Because in this step images are changes to finer, sharper and enhanced. The enhanced image is finer than the original one for the specific application and gives the more accurate segmentation. The main objectives of this step is improve image and quality[11].

Mostly segmentation process depends on the sharp transition of image intensity level. A blur or noisy image is not appropriate for extract information. The average filter has been applied in this method for smoothing the images by reducing the image intensity values variation from one pixel to another. An average filter is a linear smoothing filter that was done by the value of each pixel in an image replaced with the average of the gray levels with a filter mask. In this proposed method, 5x5 filter mask was used for filtering approach that enhanced the image quality and reduced noise. This filter operation had done by the convolution sum of the filter mask with corresponding intensity values in an image[12].

2.2 Segmentation of brain tumor region using Optimal Thresholding

As compared with other methods, region growing results with faster and accurate segmentation. Region growing methods can correctly separate the regions that have the same properties. It can provide the original images which have clear edges for the good segmentation results with less time compared to other methods. The approach is more innovative and novel as we can place the seed points inside the edge of the affected region and not on the centre point of the affected region. This method can be carried out manually or automatically. By using region-growing method brain tumor region is segmented [13-14]. Here the seed point is manually selected and corresponding pixels are grouped by comparing seed pixel with neighboring pixels. Consider if the selected seeds forms n number of regions. $RR1, RR2, RR3, \ldots RRi$. For each repetition, one pixel will be added into the regions. Now using the region RRiafter m steps and not allotted set of pixel, it is given in Eqn(1)

$$L = \left\{ u \bigcup_{i=1}^{n} RR_i \,/\, I(u) \bigcap \bigcup_{i=1}^{n} RR_i \neq \phi \right\} \qquad (1)$$

Where, $I(u)$ is the adjoining neighbor of pixel u , uєL means $I(u)$ maps exactly one RRi and $i(u) = \{1,2,..,n\}$ with satisfying the condition, $I(u) \cap RRi \neq \emptyset$ and $\delta(u)$ finds the difference from the neighboring regions of u. $\delta(u)$ Can be expressed as per Eqn(2):

$$\delta(u) = \left| g(u) - meany \in RR_i(u) g(y) \right|$$
$$\delta(u) = \min u \in L \left\{ \delta(u) \right\} \qquad (2)$$

Where, $g(u)$is gray-scale value of pixel of existing boundary pixels and $u \in L$ follows that and u belongs to RRi,the above procedure continued till all the pixels are assigned. Our "ideal thresholding approach" sections the picture by thresholding the distinction lattice of the likelihood delineate, while taking into tally the pixel's tissue compose and quality of its probability. The key thought behind our approach is to distinguish all pixels whose shading attributes are like those of the seed pixel, before iteratively refining the division limit. The refinement is by basic thresholding of the distinction lattice, Q, which is a grid of the contrast between the two most noteworthy probabilities for every pixel, and gives a moment level of

tissue membership probability and this can be communicated as per Eqn(3)

$$Q = P_{\max 1} - P_{\max 2} \qquad (3)$$

where $P_{\max 1} = \max(P)$ and $P_{\max 2} = \max(P)$, $P \neq P_{\max 1}$

The region of interest (ROI) pointis defined as the region in Q and the next step is to iteratively threshold the ROI.At each step the mean of the segmented ROI,where the seed point is located is calculated. Theoretically if the mean value will decrease ,the threshold value also decrease. The optimal threshold is defined as the threshold value where the mean values become 'stable' without any sudden decreases or increase. The segmented region can be obtained by thresholding the ROI with the optimal threshold value. Experimentally, the suitable values for the threshold τ, and step size are 0.1,0.01 respectively. **Pseudo code for the proposed segmentation approach is as follows.**

Input: 4D probability map, P

Output: Segmented lesion region, $I_{x,y}$

Procedure:

1 Compute probability difference matrix, Q

2 Based on probability map of seed pixel, identify ROI

3 Set $\phi = \max(Q)$

4 Set $\tau = 0.1$

5 Set $step = 0.01$

6 Set $th = \phi$

7 While $th > -\tau$

$seg = ROI > th$

$segmean = mean(seg)$

$th = th - step$

end

8 Identify optimal threshold, th_{opt} based on $segmean$

9 $I_{x,y} = ROI > th_{opt}$

10 Perform morphological operations on $I_{x,y}$

Finally, the segmented MRI image $I_{x,y}$ for the pre-processed image D_n will be generated using our proposed hybrid segmentation method and the following section illustrate the feature extraction for the segmented image $I_{x,y}$

III. FEATURE EXTRACTION AND CLASSIFICATION

The Feature extraction approach is one of the important methods to classification accuracy. It extracts the relevant information of brain image and it is formed in a feature vector. The obtained feature vector is applied to retrieval process or classification process. In this paper, from the MRI brain image three types of features are extracted on the basis of their shape, margin and their density. The shape features provide the boundaries of the MRI brain image; margin features used to describe the margin characteristics of the MRI brain image and finally the third feature of density feature represents the brightness variation of the MRI brain image. Finally, the obtained three features are formed into a single feature vector. MRI Brain image is represented in gray levels where density degree is denoted by their brightness variation of MRI image. Density features are obtained through the following steps: First, separate or divide the MRI brain into two regions are inner and outer regions. Inner region minor axis is equal to the half minor axis of the outer region. Second, calculate the average brightness of the inner and outer region. Finally, calculate the density degree for MRI images using the Eqn(4).

$$DensityDegree = \frac{\varphi_{inner}}{\varphi_{outer}} \quad (4)$$

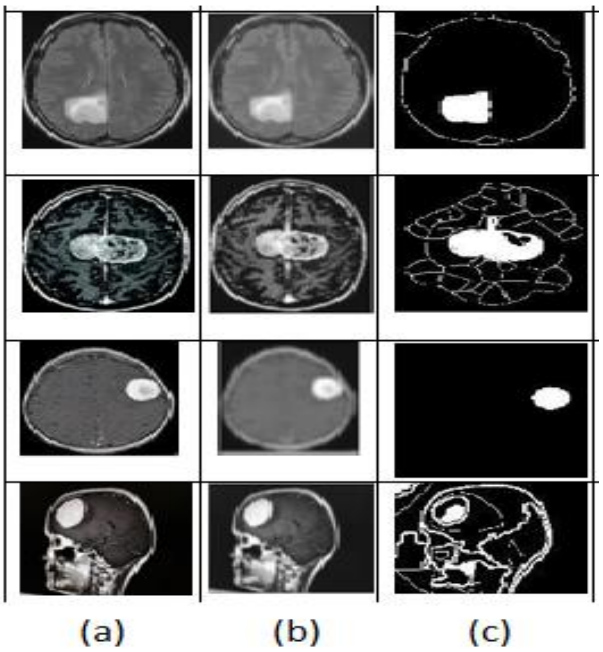

Fig 1 Segmentation results (a) original image (b) Preproessed image (c) Segmented image

Mostly, the effective classification is subjective to the image features which are associated with an edges and the depth of the network. Hence above mentioned pre-processing techniques are applied to the incoming image sequences to preserve the features edge and the connectivity of each edges for better classification. We boosted our network to the maximum in all possible ways and hence named as Maximum Boosted Convolutional Neural Network.

Classification of diseases is a crucial aspect in disease categorization through image processing techniques. The categorization of diseases according to pathogen groups is a significant research domain and potentially a challenging area of work.. Classification and detection are very similar, but in classification primary focus is on the categorization of various diseases and then the classification according to various pathogen groups. It consists of two stages such as training phase and testing phase. Mostly, the effective classification is subjective to the image features which are associated with an edges and the depth of the network. Hence above mentioned pre-processing techniques are applied to the incoming image sequences to preserve the features edge and the connectivity of each edges for better classification. We boosted our network to the maximum in all possible ways and hence named as Maximum Boosted Convolutional Neural Network. CNN structure normally includes convolutional layer, max-pooling layer with an activation function and a fully connected layer.

If the input of 2D convolutional layer is $I(x, y)$, and the corresponding feature map $s(x, y)$ will be obtained by convolving the input data
with a convolution kernel $w(x, y)$ of size $m \times n$, it is defined in Eqn(5).

$$s(x,y) = \sum_{m=0}^{M-1}\sum_{n=0}^{N-1} I(m,n) * w(x-m, y-n) \quad (5)$$

IV. DEEP FUSION MODEL

The two individual MBCNN features are fused and combined with LSTM for learning the deterministic spatial feature information of each image sequences in series of time to realize FER task. As shown in Fig.1, the proposed model is a composition of two deep learning structures. On the one hand, the proposed MBCNN has the ability to extract features and on the other hand, LSTM models the contextual information of arbitrary sequences in each time step. Besides the pre- processing techniques forms two input layer and fed into to the first convolutional layer of two individual MBCNN base model. The successive convolutional layers with batch normalization and activation function followed by fully connected layer forms the feature sampling layer which establish feature map of each expression.The two MBCNN feature layers are fused and it is given as per Eqn(6)

$$F(x) = \{f(Im)wi \oplus f(In)wj\} \quad (6)$$

where $F(x)$ is the output of fusion layer, $\oplus$ is the operation of matrix addition, $f(Im)$ is the mth equalised image features, and $f(In)$ is the nth edge enhanced features obtained from the original image sequence after pre-processing. More specifically, the knowledge of each expression features are transferred from the fused MBCNN to the LSTM model. Now LSTM feature learning layer generates new representative feature vector. Furthermore, Global Average Pooling (GAP) is considered which globally reduces the dimensionality of spatial features by averaging all the feature vectors obtained from the previous layer. According to [48], GAP avoids over fitting as it is a structural regularizer and no parameters are needed to optimize. Hence it produce the confidence feature maps and better approximation of expression categories. Finally, the softmax layer classifies and predicts the probability of each expression labels based on the input and learned feature maps. In multi-class facial expression classification, the softmax has an ability to classify a non-linear functions easily. However, it increases the generalization of our model. The Softmax layer is given as per Eqn(7)

$$P(x)_j = \frac{e^{x_j}}{\sum_{i=1}^{N} e^{x_i}} \quad (7)$$

The performance of MRI Brain image classification was evaluated on collected images from National Cancer Institute database (http://cancerimagingarchive.net.. Here, the dataset composed comprises of 20 different patients with 200 MRI images. Three orders of MR images has considered for each patient i.e., T1, T2 and FLAIR. However, each volume holds a dissimilar number of slices that is 100–150. In this paper divide the framework into two categories where 100 abnormal and 40 normal images respectively. Classifier performance evaluation in this work is conducted with widely used statistical measures, sensitivity, specificity and accuracy, it is defined in Eqn(8) [15-16].

$$Sensitivity = \frac{Tp}{Tp + Fn}$$

$$Specificity = \frac{Tn}{Tn + Fp}$$

$$Accuracy = \frac{Tp + Tn}{Tp + Fp + Tn + Fn} \quad (8)$$

The experimental results of sensitivity, specificity and accuracy are given in Figure 2.Experimental results are also validated using k-fold cross validation method, the overall results are summarized in table 1

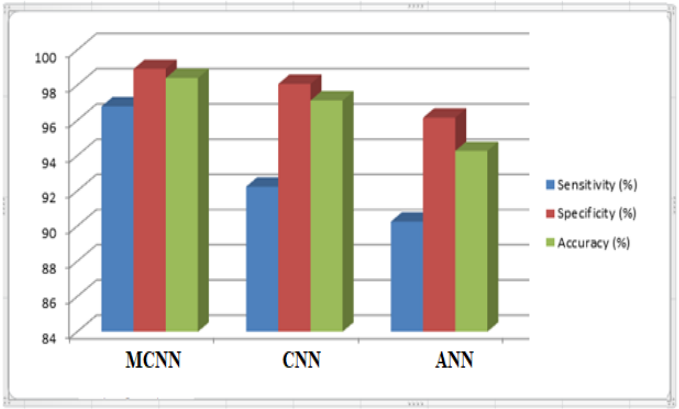

Figure 2 Experimental results of proposed method

Table 1 Overall summarized result of proposed MRG with different classifiers using k-fold method

Methods	Sensitivity(%)	Specificity (%)	Accuracy (%)
ANN	62.4	63.5	62.7
SVM	74.4	72.5	74.24
CNN	82.65	82.7	82.67
MBCNN	91.6	92.2	91.64

V. CONCLUSION

The development of the computer-aided detection systems in recent years turned them into a nondestructive and popular method for the cancer diagnosis in MRI images. The method includes different parts of image processing: in the first step, the original images have been pre-processed by a anisiotropic filter for the noise elimination. Afterward, an optimized image segmentation based on region growing algorithm is used for segmenting the cancer area from the background. Then, several features are extracted for improving the process of classification accuracy. To achieve an optimal feature extraction, an optimal method is used for selecting the useful features and for pruning the remained useless features. After feature extraction, they trained into an SVNN classifier to diagnosis what input image is cancerous or healthy. The image segmentation and the feature selection parts are optimized based on the newly introduced grasshopper optimization algorithm.

In future, optimal feature selection method has to be implemented, which should be followed with the development of improved deep learning architecture that may give higher potential in tumor detection and classification.

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