An Efficient Image Analysis Framework for the Classification of Glioma Brain Images Using CNN Approach

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Abstract: The identification of brain tumors is multifarious work for the separation of the similar intensity pixels from their surrounding neighbours. The detection of tumors is performed with the help of automatic computing technique as presented in the proposed work. The non-active cells in brain region are known to be benign and they will never cause the death of the patient. These non-active cells follow a uniform pattern in brain and have lower density than the surrounding pixels. The Magnetic Resonance (MR) image contrast is improved by the cost map construction technique. The deep learning algorithm for differentiating the normal brain MRI images from glioma cases is implemented in the proposed method. This technique permits to extract the linear features from the brain MR image and glioma tumors are detected based on these extracted features. Using k-mean clustering algorithm the tumor regions in glioma are classified. The proposed algorithm provides high sensitivity, specificity and tumor segmentation accuracy.

Keywords: Brain, glioma, features, tumors, classifications.

1 Introduction

Progress in the use of information systems in medical field reduces the death ratio and helps the physicians to detect the diseases in patients at early stage with the aid of advanced medical devices. In this paper, information techniques will be used to detect the tumors in patients worldwide. The uncontrollable cells in human brain lead to the formation of the abnormal patterns. Depending on the location and density of the tumor pixels in brain region, the abnormal patterns are classified as benign or malignant [Sharma and Mukharjee (2013); Savary and Ravi (2015)]. The active cells in brain region are malignant and they cause the death if not treated properly and timely [Shrestha (2014); Ponnusamy and Samikannu (2018)]. These active cells do not follow any uniform pattern in brain and have higher density than the surrounding pixels. The benign tumors, also called low grade tumors, are classified into meningiomas and gliomas whereas malignant tumors, also called high grade tumors, are classified into Glioblastomas and

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astrocytomasuang [Josephine (2018)].

In general, radiotherapy or chemotherapy treatment will be given to the tumor affected patients based on the severity level of the tumors in the brain region [Liya and Kebin (2016)]. In present method, the tumors are detected using brain image modalities. The abnormal boundary pixels are detected using segmentation process. The tumor area in the brain can be detected with the help of different image modalities but the Magnetic Resonance Imaging (MRI) is the most powerful modality used in brain tumor detection. Fig. 1(a) Shows the image of a brain without tumor and Fig. 1(b) Shows the image of a brain with tumor.
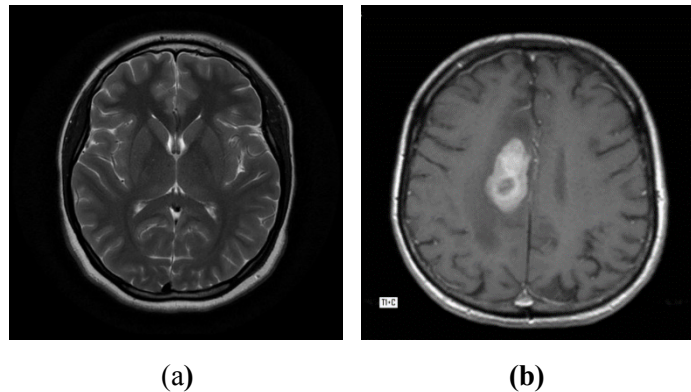

(a)   (b)

Figure 1: Images of brain (a) without tumor (b) with tumor

The conventional methods used to detecting and segmenting the tumor regions in the brain image are given in Section 2. Computer aided method for detecting the brain tumor is given in Section 3 and the Section 4 describes the findings from the simulation results. Section 5 is about the conclusion.

2 Literature survey

Josephine [Josephine (2018)] proposed an algorithm for the glioma image classifications using neural network classification approach. The authors used grey level features which were obtained from glioma source brain image and Genetic Algorithms (GA) were applied on the features to obtain optimized features. Different properties were classified using the neural network with the continuous training. The authors obtained 91.9% of sensitivity and 92.7% of specificity with 85.1% of average classification rate. Shil et al. [Shil, Polly, Hossain et al. (2017] used k-means clustering algorithm to obtain the threshold value for the segmentation process. Further, Discrete Wavelet Transform (DWT) was applied on the threshold image to extract feature values from the input images. The Principal Component Analysis (PCA) with Support Vector Machine (SVM) was used for the training and classification. The authors obtained 91.7% of sensitivity and 95.1% of specificity with 87.6% of average classification rate. Nilesh et al. [Nilesh, Arun, Har et al. (2017)] applied Berkeley Wavelet Transformation (BWT) on source brain MRI image to transform spatial domain pixels into multi resolution pixels. High sensitivity of 97.7% was achieved in the proposal with 94.2% and 96.5% of specificity

and segmentation accuracy achieved respectively.

The detection of tumors in the brain images using threshold technique was proposed by Isselmou et al. [Isselmou, Zhang and Xu (2016)]. Separating the tumor pixels from the brain images is achieved by threshold technique.

The tumor regions were identified in the threshold image by applying the morphological parameters. The proposed method achieves a sensitivity of 95% and a specificity rate of 96.1%. To detect the high contrast difference pixels in the brain MRI images Shanthakumar et al. [Shanthakumar and Ganeshkumar (2015)] proposed a method which separates the tumor pixels from the non-tumor background pixels using watershed separation technique. The proposed method achieves a sensitivity of 94%, an average classification rate of 92% for a specificity of 96%. Yazdani et al. [Yazdani, Yusof, Karimian et al. (2015)] proposed a method to detect the glioma images which is compared to different threshold algorithms. The proposed method achieved 91% of sensitivity, 94.1% of specificity for 87% of average classification rate.

3 Equations and mathematical expressions

3.1 Resources

Open access data BRATS 2015 used to test the performance of the proposed tumor detection methods. From this dataset, 176 brain MRI images (glioma images: 78; non-glioma images: 98) are assessed and categorized into training and testing phases. The training phase dataset contains 57 brain images (glioma images: 22; non-glioma images: 35) whereas the testing phase dataset contains 119 brain images (glioma images: 78; non-glioma images: 41). The manually segmented glioma brain images by the radiologist are present in the given website link.

3.2 Methods

A tumor regions detection technique from brain images is proposed in this paper. The cost map construction technique is applied on the test image to improve the image contrast for further processing. The linear features extracted from the brain MRI images are then classified for the detection of glioma tumors. The pixels having the abnormal property are classified and the brain MRI images are segmented using K-means clustering algorithm as illustrated in Fig. 2.
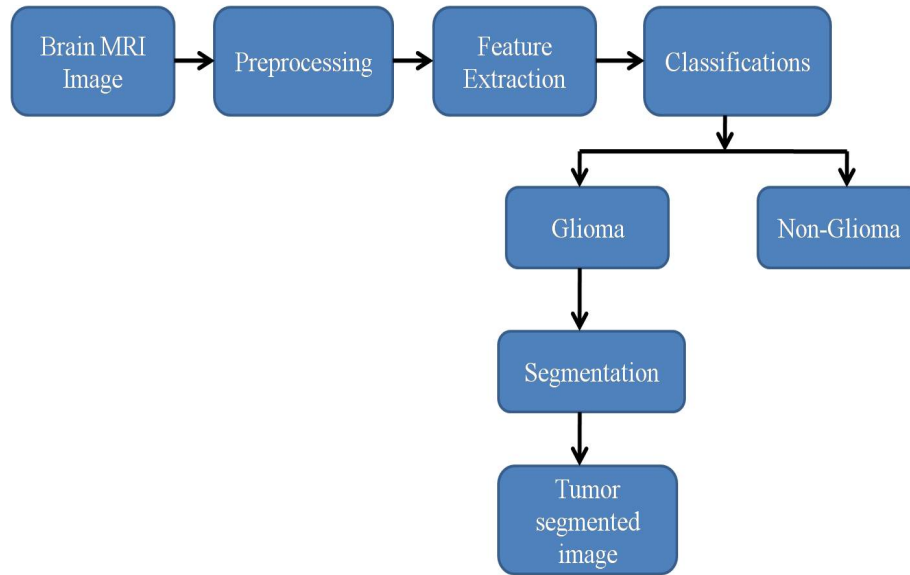
Figure 2: Flow of proposed framework for the classification of glioma images

3.3 Display style

The boundaries of the tumor regions are identified by the abnormal edges of the brain. The cost map image construction approach is used to detect and enhance the image edges. The Horizontal gradient of the test image (I (x, y)) is given by,

$$f_1(x,y) = 1 - \frac{I(x,y)}{Max[I(x,y)]} \tag{1}$$

The vertical gradient of the source brain MRI image (I(x, y)) is given by,

$$f_2(x,y) = 1 - \frac{I(x,y)}{Min[I(x,y)]} \tag{2}$$

The horizontal and vertical cost map images, computed using horizontal and vertical gradients, are used to identify the edges in MR image.

The Horizontal cost map image is determined using the following equation,

$$I_1(x,y) = p_1 * f_1(x,y) + (1 - p_1) * f_2(x,y) \tag{3}$$

where, p_1 is the empirical horizontal scaling function which ranges from 0 to 0.5.

The empirical horizontal scaling function (p_1) can be computed using the following equation,

$$p_1 = Min\{I(x,y)\} \tag{4}$$

The Vertical cost map image is obtained from the following equation,

$$I_2(x,y) = p_2 * f_1(x,y) + (1 - p_2) * f_2(x,y) \tag{5}$$

where, p_2 is the empirical vertical scaling function which ranges from 0.6 to 1.

The empirical horizontal scaling function (p_2) can be computed using the following equation,

$$p_2 = Max\{I(x,y)\} \tag{6}$$

The cost map image (CMI (x, y)) is given by,

$$CMI\ (x, y) = I1(x, y) + I2(x, y) \tag{7}$$

The edge enhanced image is obtained by multiplying the source brain MRI image with the cost map image as follows,

$$Enhanced\ Image = I\ (x, y) * CMI\ (x, y) \tag{8}$$

Open access dataset of the brain MRI images are shown in Fig. 3(a). The enhanced image by using the cost map image construction method is shown in Fig. 3 (b).
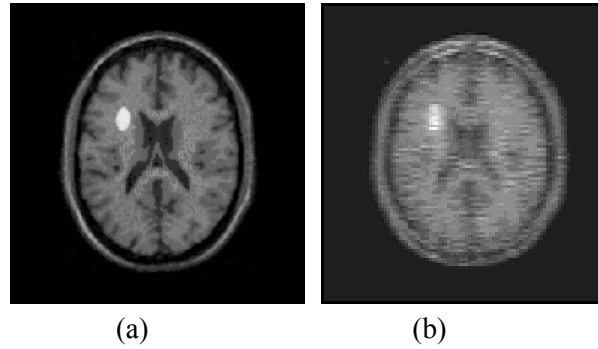

(a) (b)

Figure 3: (a) MR image from dataset (test image) (b) Edge enhanced image

3.4 Feature extraction

Highlights associate the behaviour of every pixel in a picture for separating the non-glioma cerebrum picture from glioma mind MRI picture. Features values from brain MR image is shown in Tab. 1. Linear features used for deriving the features are the following:

$$Mean = \frac{1}{N}\sum_{i=0}^{N-1}\sum_{j=0}^{N-1}P(i,j) \tag{9}$$

$$Std = \sqrt{\frac{1}{N}\sum_{i=0}^{N-1}\sum_{j=0}^{N-1}[P(i,j) - \bar{P}]^2} \tag{10}$$

$$Variance = \frac{1}{N}\sum_{i=0}^{N-1}\sum_{j=0}^{N-1}[P(i,j) - \bar{P}]^2 \tag{11}$$

$$Skewness = \frac{\frac{1}{N}\sum_{i=0}^{N-1}\sum_{j=0}^{N-1}[P(i,j) - \bar{P}]^3}{\frac{1}{N}\left\{\sum_{i=0}^{N-1}\sum_{j=0}^{N-1}[P(i,j) - \bar{P}]^2\right\}^{3/2}} \tag{12}$$

$$Kurtosis = \frac{\frac{1}{N}\sum_{i=0}^{N-1}\sum_{j=0}^{N-1}[P(i,j) - \bar{P}]^4}{\frac{1}{N}\left\{\sum_{i=0}^{N-1}\sum_{j=0}^{N-1}[P(i,j) - \bar{P}]^2\right\}^2} - 3 \tag{13}$$

$$Dissimilarity = \sum_{i=0}^{N-1}\sum_{j=0}^{N-1}P(i,j) * |i - j| \tag{14}$$

$$Homogeneity = \sum_{i=0}^{N-1}\sum_{j=0}^{N-1}\frac{P(i,j)}{1+|i-j|^2} \tag{15}$$

$$Angular\ Second\ Moment = \sum_{i=0}^{N-1}\sum_{j=0}^{N-1}P(i,j)^2 \tag{16}$$

$$Long\ Runs\ Emphasis = \sum_{i=0}^{N-1}\sum_{j=0}^{N-1}j^2 * P(i,j) \tag{17}$$

$$Low\ Grey\ Level\ Run\ Emphasis\ (LGRE) = \sum_{i=0}^{N-1}\sum_{j=0}^{N-1}\frac{P(i,j)}{i^2} \tag{18}$$

$$High\ Grey\ Level\ Run\ Emphasis\ (HGRE) = \sum_{i=0}^{N-1}\sum_{j=0}^{N-1} i^2 * P(i,j) \tag{19}$$

$$Speckle\ Index = \frac{Mean}{\sqrt{Variance}} \tag{20}$$

Table 1: Features values from brain MR image

Extracted features	Non-glioma case	Glioma case
Mean	1254.2	764.97
Std	829.9	128.1
Variance	678.1	1873.2
Skewness	$1.7\times10\text{-}2$	$1.7\times10\text{-}4$
Kurtosis	$1.5\times10\text{-}3$	$2.9\times10\text{-}5$
Dissimilarity	0.01837	6.297
Homogeneity	0.92686	8.193
Angular second moment	$3.29\times10\text{-}18$	$1.29\times10\text{-}2$
Coarse textures	0.2937	12.293
Low grey level run emphasis	1.9862	89.293
High grey level run emphasis	2.1938	128.91
Speckle index	0.8	4.5

3.5 Deep learning algorithm

The proposed CNN Classification framework classifies the brain MRI images into glioma and non-glioma brain images. Keras deep learning with tensor flow model is used to determine the design parameters for the construction of the CNN architecture. This basic architecture for CNN has five convolution blocks, three full connection layers and one softmax layer as illustrated in Fig. 4.
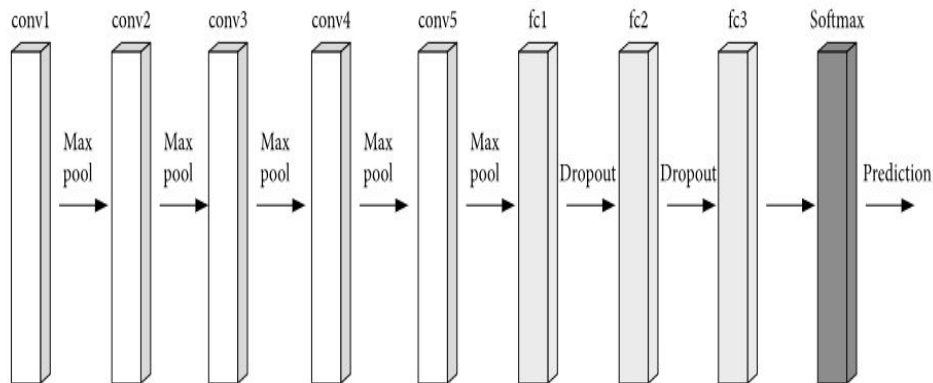
Figure 4: CNN architecture used in this paper

This CNN architecture for the classification of brain image consists of five convolution blocks with three fully connected layers and one softmax layer as output nodule. The convolution block of this architecture contains three internal convolutional layers with pooling function which produces the output for the next layer based on its computational weights in each internal layer. In this paper, average pooling algorithm is used, it takes average value of the pixels in each convolutional layers. The Tab. 2 shows the CNN design parameters.

Table 2: CNN design parameters

Parameters	Value
Filters	32
Kernel size	(5,5)
Convolution step size	4
Activation function	adam
Pool size	2
Drop_out	0.25
Epochs	100

The softmax layer produces either binary value 0 and 1. The low binary value indicates glioma brain image and high binary value indicates the normal brain image.

3.6 Segmentation

The segmentation of abnormal boundary in the MRI images is performed by K-means clustering algorithm. The procedure for K-means clustering algorithm is given as,

Step 1: Initially, 'C' numbers of clusters are randomly selected from the classified brain MRI image;

Step 2: The Euclidean distances between each cluster center to its own pixel are determined and stored in an array;

Step 3: The minimum Euclidean distance for each cluster is determined and the steps restart;

Step 4: The segmented abnormal regions are obtained after the execution of C number of clusters in cluster centers.

Fig. 5(a) Depicts the segmented tumor pixels and Fig. 5(b) Depicts the proposed work simulation results.
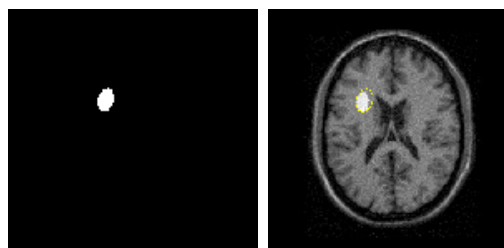

Figure 5: (a) Abnormal tumor pixels segmentation (b) Simulation result for tumor pixels segmentation

Fig. 6(a) Open access dataset brain MRI images Fig. 6(b) Manually detected tumor images, Fig. 6(c) Illustrates the proposed method results and Fig. 6(d) shows the simulation response of conventional method [Josephine (2018)].
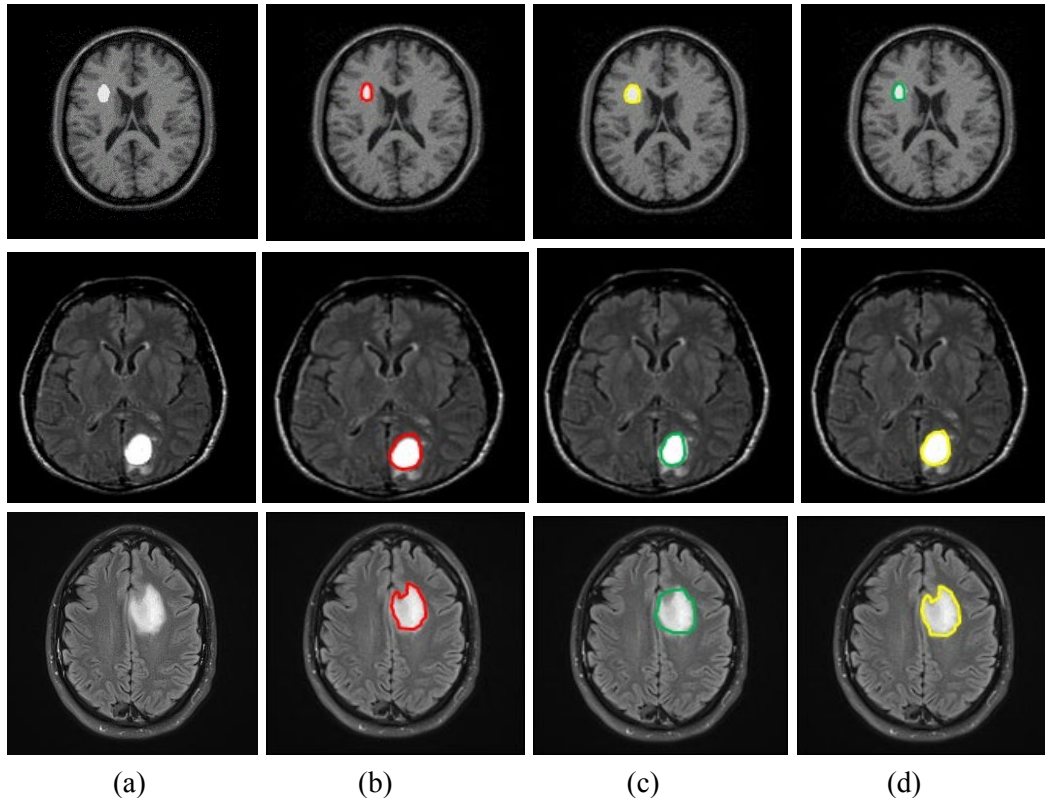

(a)   (b)   (c)   (d)

Figure 6: (a) Open access brain MRI images dataset (b) Radiologist manually tumor detected images (by radiologist) (c) Simulation response of this paper (d) Simulation result of Josephine [Josephine (2018)]

4 Results and discussions

The proposed CNN classification approach differentiates the glioma tumor brain from the non-glioma tumor brain images. The new glioma brain tumor detection technique has been tested on BRATS 2015 open access dataset to analyse its performance. MATLAB R2014 b was used as simulation tool for this research work. In this paper, 176 brain MRI images (glioma images: 78; Non-glioma images: 98) are obtained from this open access dataset and categorized into training and testing phases. The training phase dataset consists of 57 brain images (glioma images: 22; Non-glioma images: 35) and the data set of 119 brain images used in the testing phase. The Classification Rate (CR) as defined in Eq. (21),

$$CR = \frac{\text{Total count of correctly classified images in dataset}}{\text{Total count of images in dataset}} * 100\% \qquad (21)$$

The following parameters were used for the detection of glioma brain tumor images.

$$Sensitivity\ (Se) = \frac{TrPo}{TrPo+FaNe} \tag{22}$$

$$Specificity\ (Sp) = \frac{TrNe}{TrNe+FaPo} \tag{23}$$

$$Accuracy\ (Acc) = \frac{TrPo+TrNe}{TrPo+TrNe+FaPo+FaNe} \tag{24}$$

where, the correct count of tumor pixel is represented as True Positive (TrPo) and the correct count of non-tumor pixels True Negative (TrNe), the non-correct count of tumor pixel is represented as False Positive (FaPo) and the non-correct count of non-tumor pixels False Negative (FaNe). The proposed framework performance evaluation is shown in Tab. 3.

Table 3: Proposed framework performance evaluation

Performance parameters	Experimental results (%)
Sensitivity (Se)	97.1
Specificity (Sp)	98.7
Accuracy (Acc)	99.1

The comparisons of proposed framework with other conventional methods for glioma detection and classification are depicted in Tab. 4. The proposed glioma identification framework proposed in this paper using CNN classification approach achieves 97.1% of sensitivity, 92.7 % of specificity and 99.1% of accuracy. The proposed method surpasses all the current reference methods used in the classification metrics except in sensitivity where it is slightly surpassed by the method proposed by Nilesh et al. [Nilesh, Arun and Har (2017)]. The comparisons of proposed framework with conventional methods is given in Tab. 4.

Table 4: Comparisons of proposed framework with conventional methods

Approaches	Sensitivity (%)	Specificity (%)	Accuracy (%)
Proposed model	97.1	98.7	99.1
[Josephine (2018)]	91.9	92.7	90.5
[Shil, Polly, Hossain et al. (2017]	91.7	95.1	89.6
[Nilesh, Arun and Har (2017)]	97.5	94.2	90.5
[Isselmou, Zhang and Xu (2016)]	95	96.1	92.3

5 Conclusions

This paper proposes a deep learning algorithm for differentiating the normal brain MRI images from glioma cases. The cost map image construction method is developed to enhance the contrast of the abnormal patterns. Further, features are extracted and classified using CNN classification approach. The tumor pixels in the brain image are determined using K-means algorithm. The proposed glioma identification framework is analyzed using performance metrics.

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