Brain Tumor Detection in MRI Images using Input Cascaded CNN with Wavelet Features

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ABSTRACT

The automated detection of infected tumor from brain Magnetic Resonance Image (MRI) is important for clinical assessments and treatment planning. In this research, automated tumor identification based on Input cascaded Convolutional Neural Network (CNN) with Discrete Wavelet Transformation (DWT) features is proposed. The significant tumoral features from all input images are extracted using DWT. The extracted features are then processed with input cascaded CNN to identify the tumor images. The evaluated results of this proposed method have been compared with original truth results for performance evaluation. The proposed system is tested with BRATS 2018 dataset and achieved an average of 97% accuracy, 99% F1-score, 99% Recall or sensitivity, 99% precision, and 98% specificity. Thus, our method achieves 5.29 % higher accuracy for identifying normal and abnormal MRI images than the currently available methods.

Keyworks: Brain Tumor, Diagnosis, Input Cascaded Convolutional Neural Network, Discrete Wavelet Transform, Magnetic Resonance Imaging

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1. INTRODUCTION

The tumor is an aggregation of abnormal cells within the brain. Accurate and automated tumor detection from MRI helps us to take an appropriate decision for medical analysis, clinical assessments and treatment [15]. The tumor has categorized into malignant and benign. Malignant being cancerous is treated high infected tumor and benign is non-cancerous having very less infected tumor area. High-Grade Gliomas (HGG) and Low-Grade Gliomas (LGG) are the most common category of tumor present within the brain [20]. Each grade contains four MRI sequences: FLAIR, T1-Weighted image, T1c-T1 Weighted with contrast-enhanced and T2-Weighted

contrast image [10]. Now a day, the brain tumor is generally diagnosed by experienced radiologists. Once the tumor is suspected, radiologists have to evaluate and determine the size, location and shape of the tumor in brain MRI images [14].

The computer-based diagnosis system is necessary for avoiding human-based missing diagnostic errors [4]. For this purpose, a fully-automated tumor identification method based on Input cascaded CNN with DWT features is implemented for identifying tumoral features automatically from brain MRI images. In this method, all images from BRATS 2018 dataset are processed using Haar DWT transformation to extract significant tumoral features [1]. The extracted image features are processed using input cascaded CNN for detecting tumor [12]. Here, each extracted features are processed with 7 x 7 and 3 x 3 kernels to yield the output. The outcome is cascaded with input image and processed by upcoming three convolutional layers and three max pooling layers to give the final extracted feature outcome. These feature outcomes are converted into a single dimensional array in the Fully Connected (FC) layer for predicting class labels probabilities. Further, softmax technique has been applied for identifying two class labels of tumor and non-tumor tissue types. These identified classes are compared with original classes for performing evaluation.

The proposed system is tested with BRATS 2018 dataset and achieved an average of 97% accuracy, 99% F1-score, 99% Recall or sensitivity, 99% precision, and 98% specificity. This research article has been structured as follows: The various related tumor detection methods are reviewed in Sec. 2; experimental methods of internal fused CNN has detailed in Sec. 3; results and discussions of the proposed method are explained in Sec. 4; finally, the conclusion leads in Sec. 5.

2. RELATED WORKS

The tumor detection plays a vital role for clinical assessments, diagnosis and treatment planning [6]. Initially, some conventional semi-automatic segmentation methods have used for identifying brain tumors in MRI images [21]. Some conventional semi-automatic segmentation methods like Fuzzy-C-Means, Support Vector Machine (SVM) [5], K-Nearest Neighbor (KNN) and some Ensemble Classifier (EC) and Extreme Learning Machine are mostly used for identifying tumor images. These techniques are having the drawbacks of very low accuracy and higher time-consuming. To avoid, an automated detection method is essential for clinical assessments and treatment planning [7]. Parveen et al implemented a novel method using FCM algorithm, which needs programmer interaction for initializing parameters in the cluster number selection [19].

The Gray Level Occurrence Matrix (GLCM) is extracted for identifying tumors in brain images [9]. Sometimes DWT methods are used for extracting features. Detailed information from brain images may lose while using these two GLCM and DWT [8]. Marco et al have used Support Vector Machine (SVM) for identifying tumor images [5]. Anitha et al proposed KNN for brain tumor detection [13]. SVM and KNN are semi-automatic and it needs interaction from the detector for initializing some parameters [14]. Then, Ensemble Classifier (EC) [11] and Extreme Learning Machine [16] are used for tumor diagnosis. But these methods contain very lesser accuracy than other methods.

For these reasons automated methods have been used to identify tumor images. Feed-Forward Artificial Neural Network (FFANN) and Feed-Forward Backpropagation Network (FFBN) have used for identifying tumor images [17] [18]. These methods are having a limited performance on real images. To avoid this, an automated input cascaded CNN with DWT features has been proposed. Thus, our proposed method achieves 5.29 % higher accuracy for identifying normal and abnormal MRI images than the currently available tumor detection methods.

3. PROPOSED METHODOLOGY

This proposed network is based on Deep Neural Network (DNN) learning architecture for detecting brain tumors in MRI images. This method having four main phases: DWT feature extraction; input cascaded CNN based feature classification; calculating loss function; training and performance evaluation using Benchmark metrics. The block diagram of this proposed automated technique is visualized in Figure 1 and explained by upcoming following subsections

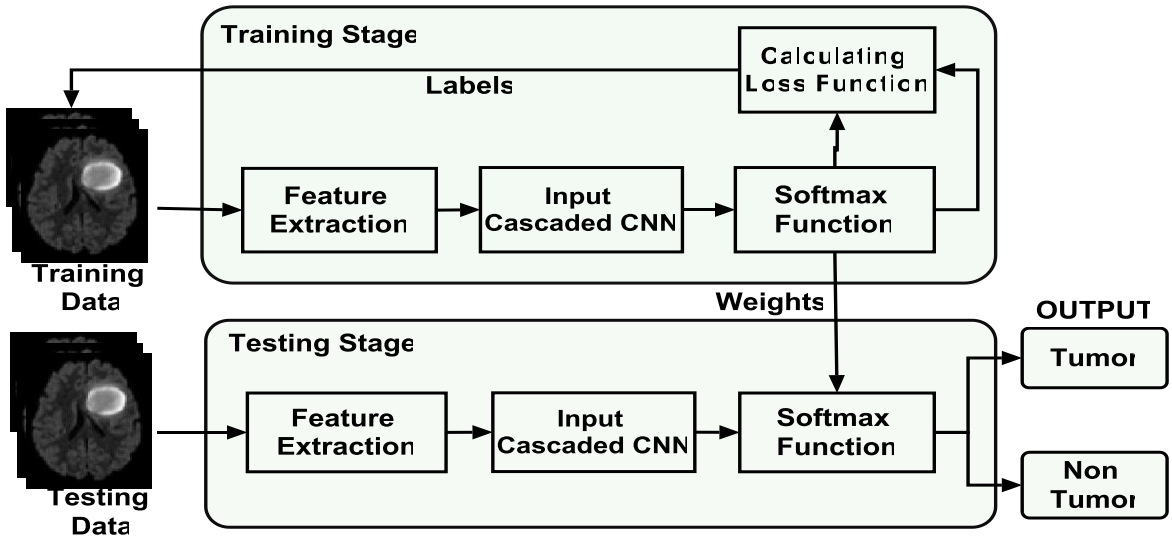

Figure 1: The proposed architecture

3.1. Feature Extraction using DWT

All images from BRATS 2018 dataset are processed using Haar DWT transformation [3] to extract frequency sub-band features. In this, each input image is fed into filters like high and low pass to yield two frequencies like high and low frequencies [2]. These two frequencies are further again with high and low pass to produce four types of frequencies like High-Low (HL), High-High (HH), Low-Low (LL) and Low-High (LH). The LL sub-band is approximation co-efficient and HH, LH and HL sub-bands are detailed co-efficient. The brain image feature extraction using Haar DWT is visualized in Figure 2.

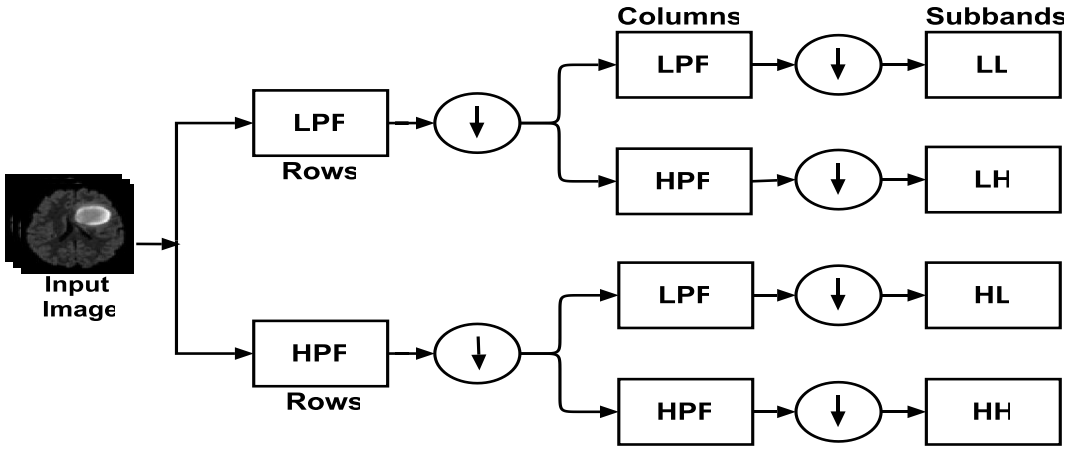

Figure 2: The feature extraction using Haar DWT

3.2. Classification using Input Cascaded CNN

The ultimate aim of the input cascaded CNN is to learn features automatically from MRI brain images. The extracted LL sub-band feature images are processed using processed with input cascaded CNN to identify the tumor images. First, the LL image features are processed with 7 x 7 and 3 x 3 kernels to yield the output feature maps in layer 1 and layer 2. F_{7x7} and F_{3x3} are the two feature maps produced by the convolution of weight W with input X and addition of bios B have been defined in equations (1) & (2).

$$F_{7x7} = f\left(\sum_{i=1}^{n}\left[X_i * W_i\right] + B\right) \quad \ldots (1)$$

$$F_{3x3} = f\left(\sum_{j=1}^{n}\left[X_j * W_j\right] + B\right) \quad \ldots (2)$$

Where, j = 1,2,3… and i=1,2,3… n and n are the pixel intensity value of an image and the non-linear activation function f is used to transform the convolution process. Here, Rectifier Linear Unit (ReLU) activation function is used to transform input to output. The formula for ReLU activation function is defined in equation 3.

$$f(i,j) = max(0,(X)) \quad \ldots (3)$$

$$f(i,j) = \begin{cases} 0 & If\ (X) < 0 \\ X & otherwise \end{cases}$$

The two average feature maps F_{7x7} and F_{3x3} are calculated by the following equation 4.

$$Y = Mean\left(F_{7x7}, F_{7x7}\right) \quad \ldots (4)$$

The mean output Y is cascaded with the input X to yield Y_{out} is mentioned in equation 5.

$$Y_{out} = Y + X \quad \ldots (5)$$

The outcome Y has been processed in the upcoming two hierarchy of three convolutions and three max pooling layers to give final extracted feature outcome. These feature outcomes are converted as a single dimension in Fully Connected (FC) layer. This layer takes an input features from the existing layer and “flattens” them as a single vector to predict the pixel-wise probabilities of class labels using the softmax function. The detailed configuration of input cascaded CNN layers used in this proposed architecture is defined in Ta ble 1.

Table 1: Detailed Configuration of Proposed Architecture

Layers	Type	Stride value	Filter Size	Normalization	Filters	FC units	Activation	Input

I Layer	Conv1	1 x 1	3 x 3	B-N	64	-	ReLU	1 x 128 x 128
II Layer	Conv2	1 x 1	7 x 7	B-N	64	-	ReLU	64 x 128 x128
Input image cascaded with the average feature map of Layer 1 and Layer 2								
III Layer	Conv3	1 x 1	3 x 3	B-N	64	-	ReLU	65 x 128 x 128
IV Layer	Max-pool1	2 x 2	3 x 3	B-N	-	-	-	64 x 128 x 128
V Layer	Conv4	1 x 1	3 x 3	B-N	64	-	ReLU	64 x 64 x 64
VI Layer	Max-pool2	2 x 2	3 x 3	B-N	-	-	-	64 x 64 x 64
VII Layer	Conv5	1 x 1	3 x 3	B-N	64	-	ReLU	64 x 32 x 32
VIII Layer	Max-pool3	2 x 2	3 x 3	B-N	-	-	-	64 x 32 x 32
IX Layer	-	-	-	-	-	2	-	16384 (64x16x16)

3.3. Loss Function

This Loss function has been used to predict errors between identified and targeted labels. Errors between identified distribution $r(x_j)$ and predicted distribution $s(x_j)$ are calculated using Categorical Cross Entropy is defined in equation (6) and (7).

$$H(r,s) = -\sum_{j=1}^{n} r(x_j)\log(s(x_j)) \quad \text{... (6)}$$

$$H(r,s) = -(r(x_1)\log(s(x_1)) + (r(x_1)\log(s(x_1)) \ldots r(x_n)\log(s(x_n)) \quad \text{... (7)}$$

3.4. Training and Evaluation

The whole architecture is trained to extract image features from BRATS 2018 database and identify class labels at the final softmax layer. These predicted class labels performance is evaluated by comparison of ground truth using benchmark metrics namely; Accuracy value, F1-score value, Recall value, Precision value, specificity value and Sensitivity value are illustrated in equation (8) - (13).

$$Accuracy = (TN + TP) / (TN+TP+FN+FP) \quad \text{... (8)}$$

$$F1\text{-}score = (2TP) / (FN+FP+2TP) \quad \text{... (9)}$$

$$Recall = (TP) / (FN+TP) \quad \text{... (10)}$$

$$Precision = (TP) / (FP+TP) \quad \text{... (11)}$$

$$Specificity = (TN) / (FP+TN) \quad \text{... (12)}$$

$$Sensitivity = (TP) / (FN+TP) \quad \text{... (13)}$$

where, TN (True Negative) and TP (True Positive) are the total number of correctly predicted negative pixels and positive pixels respectively, FN (False Negative) and FP (False Positive) are the wrongly determined negative pixels and positive pixels.

4. RESULTS AND DISCUSSION

4.1. Workstation and Database

The proposed work has been implemented and tested with BRATS 2018 dataset, which contains 75 LGG and 210 HGG images. Each patient image comprised four MRI sequences, namely FLAIR, T1, T1c, and T2. These are annotated by experienced radiologists and scanned by different vendors from various centers, namely Center for Neuroimaging in Psychiatry (CNIP), Massachusetts General Hospital, Bern University, Heidelberg University, Computational Biomarker Imaging Group (CBIG), Wang lab and Debrecen University. The images from BRATS 2018 dataset have been visualized in Figure 3.

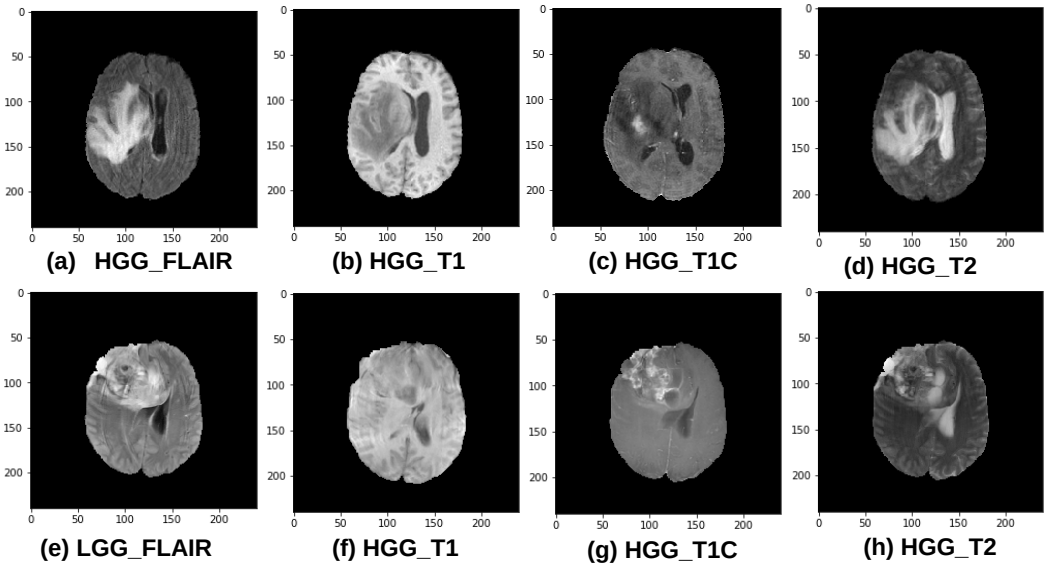

Figure 3: The HGG and LGG images from BRATS 2018 dataset.

4.2 Effectiveness of the Proposed Method

The performance of this proposed system is tested with the imaging data provided by the BRATS 2018 dataset. This work is to extract and train image features automatically from input brain data. This extracted output has been converted as a single dimensional array in the Fully Connected (FC) layer for class label prediction. Further, the softmax technique has been applied for identifying two

class labels of the tumor and non-tumor tissue types. These identified class labels are compared with original classes for performing evaluation using benchmark metrics namely; Accuracy, F1-score, Recall, Precision, specificity and Sensitivity. The results of tumor identification using BRATS 2018 dataset have been detailed in Table 2.

Table 2 Performance of Input cascaded CNN

Gliomas Type	Sequence Name	Accuracy	F1-Score	Recall or Sensitivity	Precision	Specificity
HGG	Flair	0.97	0.99	0.99	0.99	0.97
	T1	0.95	0.99	0.99	0.99	0.97
	T1C	0.97	0.98	0.98	0.98	0.99
	T2	0.98	1.00	1.00	1.00	1.00
LGG	Flair	0.96	1.00	1.00	1.00	1.00
	T1	0.96	0.99	0.99	0.99	0.98
	T1C	0.97	0.99	0.99	0.99	0.97
	T2	0.98	0.99	0.99	0.99	0.97
Average (HGG, LGG)		0.97	0.99	0.99	0.99	0.98

4.3. Performance Comparison

The proposed performance of input cascaded CNN architecture is evaluated by comparing state-of-art detection methods like FFANN [17], ELM [16], SVM and EC [11]. Accuracy, F1-score, Sensitivity and Precision values of existing methods are compared with proposed methods. These methods are able to extract tumoral image features automatically from input data. The evaluated results of existing and proposed methods have mentioned in Table 3.

Table 3: Comparing Accuracy, F1-score, Precision and Sensitivity values of Proposed Input cascaded CNN with existing detection methods.

Technique	Accuracy (%)	F1-Score (%)	Precision (%)	Sensitivity (%)
FFANN	84.33	90.66	89.41	91.94
ELM	86.00	91.63	90.20	93.12
SVM	89.67	93.90	92.99	94.83
EC	91.17	94.81	94.17	95.47

Proposed Method	**97.00**	**99.00**	**99.00**	**99.00**

ELM and SVM are the semi-automatic brain tumor detection method, which requires interactions from the user in every step for initializing parameters. Feed Forward Artificial Neural Network and ensemble classifier are the automatic brain tumor detection method [18]. It has very low performance on high-intensity variated images. Contrasting these methods, our proposed algorithm is having higher accuracy, F1-score, precision and sensitivity values than existing methods. This performance comparison is detailed in Figure 4. The results of detection show that the accuracy values of our method are 5.29 % higher than existing methods.

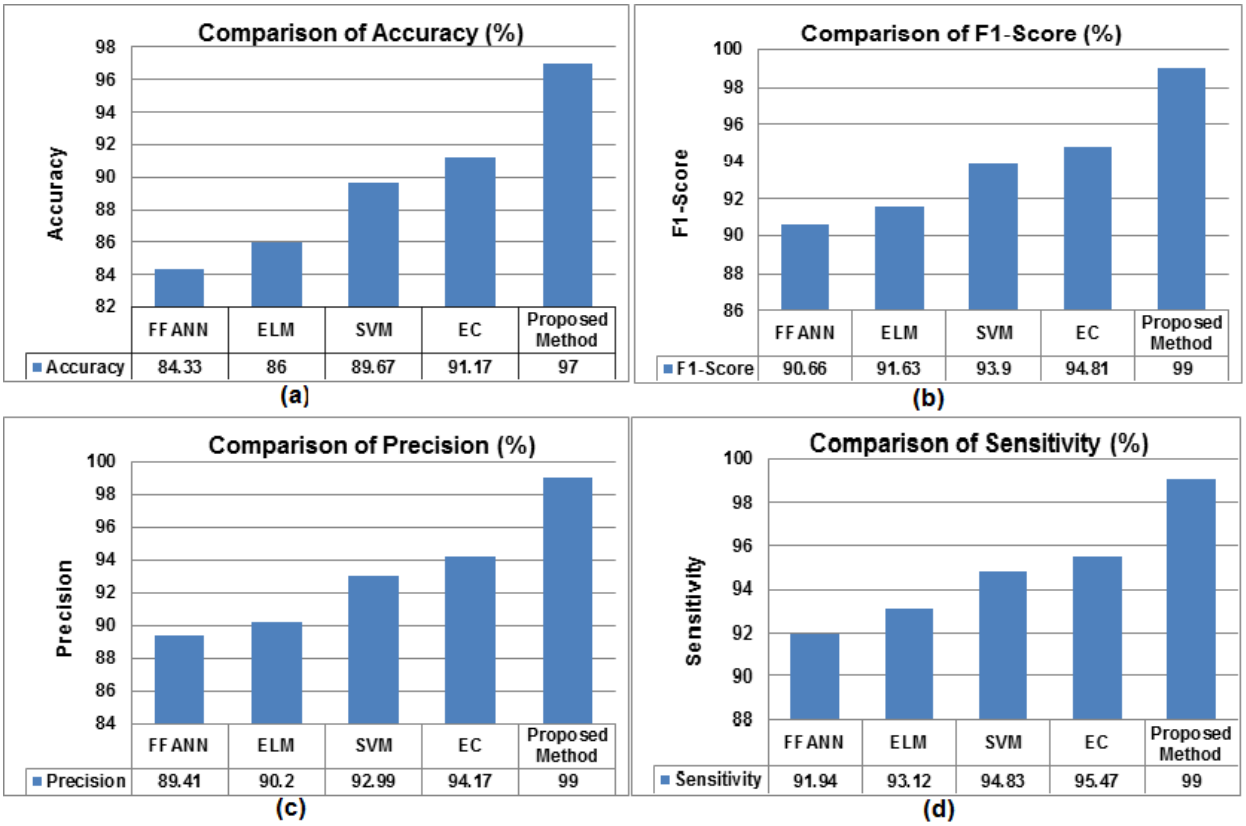

Figure 4: Comparing Accuracy, F1-score, Precision and Sensitivity values of Proposed Input cascaded CNN with existing detection methods.

5. CONCLUSION

Accurate and automated tumor detection from MRI helps us to take an appropriate decision for medical analysis, clinical assessments and treatment. In this research, automated tumor identification based on Input cascaded

Convolutional Neural Network (CNN) with Discrete Wavelet Transformation (DWT) features is proposed. In this, all images from BRATS 2018 dataset are processed using Haar DWT transformation to extract significant tumoral features. The extracted features are fed into input cascaded CNN for identifying class labels of the tumor and non-tumor tissue types. The evaluated results of this proposed method have been compared with original truth results for performance evaluation. Thus, our method achieves 5.29 % higher accuracy for identifying normal and abnormal MRI images than the currently available tumor detection methods.

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