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Brain Tumor Classification Using ResNet-101 Based Squeeze and Excitation Deep Neural Network

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***Abstract*—The brain tumor is one of the leading and most alarming cause of death with a high socio-economic impact in Occidental as well as eastern countries. Differential diagnosis and classification of tumor types (Gliomas, Meningioma, and Pituitary tumor) from MRI data are required to assist radiologists as well as to avoid the dangerous histological biopsies. In the meantime, improving the accuracy and stability of diagnosis is also one challenging task. Many methods have been proposed for this purpose till now. In this work, an automatic tool for classification of brain tumor from MRI data is presented where the image slice samples are passed into a Squeeze and Excitation ResNet model based on Convolutional Neural Network (CNN). The use of zero-centering and normalization of intensity for smooth variation of the intensity over the tissues was also investigated as a pre-processing step which together with data augmentation proved to be very effective. A relative study had been done to prove the efficacy of the proposed CNN model in free tumor database. Experimental evaluation shows that the proposed CNN archives an overall accuracy rate of 89.93% without data augmentation. Addition of data augmentation has further improved the accuracies up to 98.67%, 91.81% and 91.03% for Glioma, Meningioma and Pituitary tumor respectively with an overall accuracy of 93.83%. Promising improvement with reference to sensitivity and specificity compared with some of the state-of-the-art methods was also observed.**

***Index Terms*—ResNet, Convolutional Neural Network, Classification, Brain Tumor**

I. Introduction

Among various diseases, the brain tumor has become a pressing health concern in our country today. For many of the cases, treatment options are extremely limited due to late detection and wrong diagnosis. Brain tumors are diagnosed with 40,000 to 50,000 new people living in India every year according to a recent hospital-based study that was carried out in the country, out of which 20% are children which amounts to over 2,500 children each year [1]–[3]. Due to the lack of adequate doctors, many districts and rural parts of India is covered by a single specialist. As a result of this disparity, only a small proportion of the patients with the different socio-economic background can find their way to the specialists. It is also anticipated that it will take a long time before the neurology workforce in clinical sciences is adequate to deal with this kind of problems faced by the Indian population. Human assessment is one of the typical ways for brain tumor detection and classification from MR images and it highly depends on the experience of radiologists who evaluate the characteristics of image slices thoroughly and makes it time-consuming and prone to error. The heavy workload in a densely populated country like India may cause fatigue and distraction for the physicians which may pose a constant threat to patient safety. Consequently, a demand has been raised up from the neuroradiologists for the new approach of Computer-Aided Diagnosis (CAD). In view of this, there is a good scope of developing a computerized diagnostic tool which will automatically detect and classify the brain tumors from the MR images and thus assist the medical practitioners.

Magnetic Resonance Imaging (MRI) is a non-invasive, based on non-ionizing radiation imaging procedure and treated as the most popular techniques to diagnose and treatment of brain tumor than the Computer Tomography (CT) or Ultrasound image [4], [5]. Recognizing patterns or texture for classification from highly variable images is time-consuming and needs a lot of human effort especially if the data is very large. Various techniques have been proposed to help radiologists to increase their diagnostic accuracy. Convolutional Neural Network (CNN) which automatically learns a hierarchy of increasingly complex features directly from data have recently achieved impressive results by raising the accuracy of medical diagnosis and disease classification [6]–[9].

In this work, a fully automatic methodology which can

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categorize brain tumors from a limited amount of data into different pathological types is proposed by using convolutional neural networks, which may release some workload of the doctors. The squeeze and excitation [10] CNN model using Residual network architecture [11] was used for the classification of tumors. The remaining paper is structured as follows: The dataset, preprocessing, data augmentation are described in Section II. Section III delivers an analysis of the proposed model. The experimental setup and results are shown in Section IV. Finally, some conclusion is drawn in Section V.

II. Description of Dataset

A. Data Acquisition

The proposed method was tested and evaluated on the Brain tumor database which has been collected in the year from 2005 to 2010, from Nanfang Hospital, Guangzhou, China, and General Hospital, Tianjin Medical University, China [12], [13]. The brain tumor dataset contained 3064 T1-weighted contrast-enhanced images from 233 patients with three kinds of brain tumor: meningioma (708 slices), glioma (1426 slices), and pituitary tumor (930 slices). The dimension of each MR slice was 512×512 pixels with a thickness and slice gap of 6 mm and 1 mm respectively. Only 3049 out of 3064 images were used here because remaining 15 images were of lesser resolution of 256×256 pixels. The dataset also contained the tumor masks which was manually delineated and validated by three experienced radiologists from Medical College and Hospital Kolkata, India. One sample from each class of tumor is displayed in Fig.1 where the red line indicates tumor boundary. Fig.2 shows the Preprocessed images for the same.

B. Pre-processing

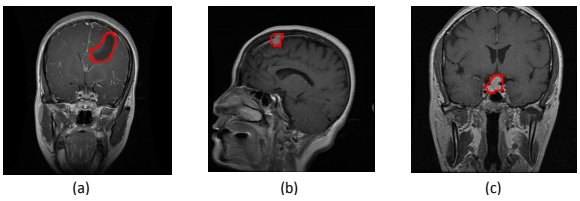

Fig. 1. Brain MRI dataset sample of Glioma(a), Meningioma (b), Pituitary tumor (c)

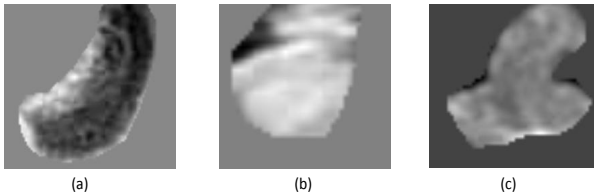

Fig. 2. Preprocessed image of Glioma(a), Meningioma (b), Pituitary tumor (c)

1) ROI segmentation: A region of interest (ROI) is a subset of an image or a dataset identified from the original samples for a specific purpose. The boundary of a brain tumor in T1 weighted MRI slices is the ROI in this case. The annotated masks of the tumors, which contained labels '1' for tumor region and '0' for everything else, were provided in the brain tumor database. The exact tumors were extracted from the brain MRI samples by multiplying them pixelwise with the corresponding masks. Due to the variability of tumor sizes in the samples, tumor ROI images were resized and added zero padding to fit into the particular input shape for the proposed model. The dimension of each of the image after ROI segmentation was 256×256 pixels.

2) Intensity Zero-centering: Intensity zero-centering(or mean-centering) [14] is a transformation of the data linearly which shifts the data so that it is centered at the origin. Generally, because of zero-centering, non-linear operations and analysis perform well. Zero-centering to each of the ROI segmented dataset images was performed because it is much easier to understand variation when you are centered at the origin. This process was done by subtracting the mean of all the pixels of an image from all the pixels of that image.

3) Intensity Normalization: Generally, MRI intensities are acquired in arbitrary units; thus, it becomes difficult to compare images across scanners, subjects, and visits, even if the same procedure is used. Intensity normalization brings the intensities to a common scale across people. This affected the model's performance, prediction, and inference. It is an important step in any image analysis with more than one subject or time point to ensure comparability across images. Division of all pixel values of one image by their standard deviation was performed to get the normalized images.

4) Data Augmentation: Data augmentation [15] is another way of Regularization which is used to reduce overfitting of models by an increase in the amount of training data using the present original information only. The idea of data augmentation is very old, and in fact, various data augmentation techniques have been applied to numerous problems. In this case, several combinations of transformations on the zero-centered, normalized, ROI segmented images of Glioma, Meningioma, and Pituitary tumor data were applied. The transformations were Flip, Rotate, Elastic transform [16] and Shear with variable degrees of transformations, for example, 25 to 40 degrees of rotation, left-right, and top-bottom flip etc. TensorLayer [17], a python library, is used as a framework for this purpose.

TABLE I
AUGMENTED DATA AFTER APPLYING DATA AUGMENTATION ON ORIGINAL DATASET

Class	Training data before augmentation	Total data after augmentation
Glioma	1426	2852
Meningioma	780	2124
Pituitary Tumor	915	2745
Total	3049[a]	7721[a]

[a]Randomly Shuffled Data

After applying all these preprocessing techniques, dataset was increased to 2850 Glioma, 2124 Meningioma, and 2745 Pituitary tumor samples (Table I). Further, it was divided into training and testing data randomly at a ratio of 9:1. Testing data contains 10% of the total data.

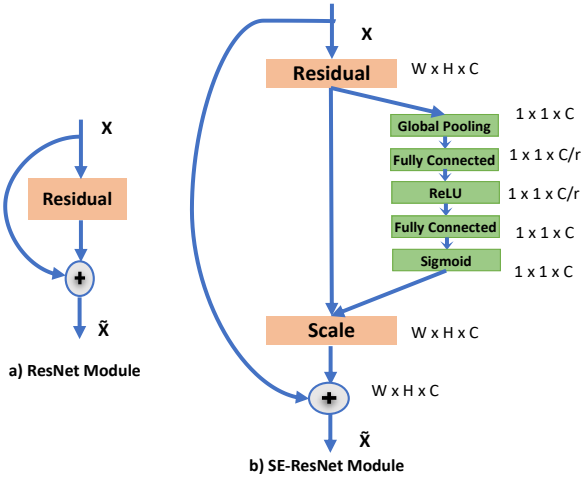

Fig. 3. Block Diagram of a) Residual Module b) SE-ResNet module

III. Proposed Method

A. Deep CNN Architecture

Following are the architectural design details and training of the model used. The proposed methodology is shown in Fig.4.

1) ResNet-101: The design of ResNets [11] was inspired by VGG-19 [18] model. It is one of the deepest proposed architectures for ImageNet (Object detection and Image classification Challenge). Usually, in a CNN, several layers are connected to each other and are trained to perform various tasks. The network learns several levels of features at the end of its layers. The size of convolutional layers in this model have mostly 33 filters. In ResNet, the layers have the same number of filters for same output feature map size and the number of filters is doubled if the feature map size is halved so as to maintain the time complexity for every layer. It executes downsampling directly by convolving layers with a stride of two. This ResNet terminates with a global average pooling layer and a SoftMax activated fully connected layer. ResNet Module is illustrated in Fig.3(a). Residual learning can be easily interpreted as subtraction of input features learned from that layer. This is done by ResNet using shortcut connections to each pair of 33 filters, directly connecting the input of k^{th} layer to $(k+x)^{th}$ layer. The motive behind bypassing layers is to keep away the problem of vanishing gradients by re-utilizing activations from the preceding layer till the layer next to the present one has learned its weights. While training the network, weights will amplify the layer next to the present one and will also adjust to mute the preceding layer. It has been observed that it is easier to train this network than training simple deep convolutional neural networks. It also resolves the problem of accuracy degradation. ResNet-101 is 101-layer Residual Network and is a modified version of the 50-layer ResNet.

2) Squeeze and Excitation block with ResNet: It was found that Squeeze and Excitation (SE) blocks [10] combined with ResNet architecture, has performed outstandingly good in classifying the brain tumors. By stacking the SE blocks one after the other, SE-ResNet-101 [10] architecture is constructed that generalise extremely well across our brain tumor dataset. For given transformation of a convolution or a set of convolutions, equation (1) is as follows:

$$Z_{tr} : X \rightarrow Y,\ X \epsilon R^{W_0 \times H_0 \times C_0},\ Y \epsilon R^{W \times H \times C} \qquad (1)$$

Here width, height, and the number of channels are represented by W, H, and C respectively after taking X and Y as input and output feature maps and r signifies the reduction ratio [10]. The input features X are first passed through a squeeze operation, which is used to average the feature maps in a spatial plane. After this, two fully connected layers with ReLU and Sigmoid activations are used separately for excitation operation. The Squeeze and Excitation block with ResNet-101 which performs feature recalibration is shown in Fig.3(b) [10].

B. Training of Model

SE-ResNet-101 model was trained from scratch and finely tuned to just fit training data, first without data augmentation containing 3064 samples in total, and then using data augmentation which increased the data size to 7771. The proposed method for classification of brain tumor used the SE-ResNet-101 architecture with single channel SE block. The original dataset contained images of size $512 \times 512 \times 1$ which were then pre-processed using the above-described methods to generate images of dimension $256 \times 256 \times 1$ which focused only on the segmented tumors or ROI. The optimizer used for training purpose was **Adam** [20] with a learning rate of 0.005 at first and then reduced by a factor of 0.2 up to 0.001 after every 3^{rd} epoch when the validation loss was not improved. EarlyStopping, a Keras library module, was used to stop the training of model if validation loss didnt improve during 5 epochs consecutively. These regularization methods were used to prevent overfitting of our model. At first, the network was trained without data augmentation till 12,196 iterations and then with data augmentation, the pre-trained model was again trained for 13,898 iterations. The preprocessed dataset was divided into training and testing parts as described. The test dataset was used for evaluating the performance of the model. The total duration of training was 7 hours with a batch size of 5 for 26,094 iterations. The model got automatically updated weights while training on the suitable features.

C. Validation of proposed Model

We validated our model in 2 phases. The 1^{st} phase consisted of evaluating the model on the left-out 10 percent testing data

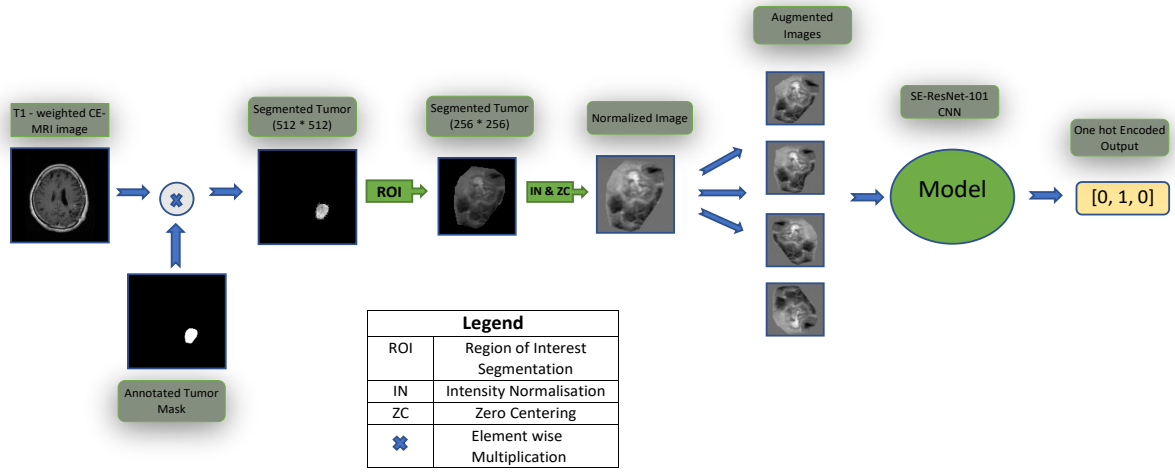

Fig. 4. Block diagram of the proposed methodology

consisting of all 3 classes of the tumor to get the overall result of the model. The 2^{nd} phase was about evaluating the model on 3 separate classes of tumors to get the accuracy on the particular type of tumor.

IV. Experimental Setup and Results

A. Implementation

The whole setup was implemented and trained in Linux environment using NVIDIA GTX 1060 8GB GPU on a system of 16 GB RAM and core-i7 7^{th} generation @4.0GHz processor. Keras, a python module, was used as a framework for all the networks.

B. Performance metrics

1) Categorical Accuracy i.e Accuracy: Categorical Accuracy calculates the mean accuracy rate which calculates the proportion of true positive and true negative across all predictions for multi-class classification problems.

$$\text{Accuracy} = \frac{\text{No. of correct predictions}}{\text{Total No. of predictions}} \tag{2}$$

2) Specificity: Specificity [19] (True negative rate) measures the proportion of actual negatives that are correctly identified.

$$\text{Specificity} = \frac{\text{No. of true negatives}}{\text{No. of true negatives + No. of false positives}} \tag{3}$$

3) Sensitivity: Sensitivity [19] (True positive rate or recall) measures the proportion of actual positives that are correctly identified.

$$\text{Sensitivity} = \frac{\text{No. of true positives}}{\text{No. of true positives + No. of false negatives}} \tag{4}$$

4) Cross-entropy loss: Cross-entropy loss [21], sometimes known as log loss, computes the performance of a multi-class classification model whose output value lies in between 0 and 1. Cross-entropy loss increases as the predicted probability deviate from the actual value.

C. Results

After the training of the proposed neural network for 29 epochs, training and validations plots of accuracy and cross-entropy loss are shown in Fig.6 and Fig.5. This model was trained on the original dataset for 20 epochs and after that, it was trained on the augmented dataset with pre-trained weights. This gives slightly low accuracy and high loss in 21^{st} epoch, which becomes much better at around 29^{th} epoch. During testing the trained model on the testing data, the accuracy was 88.18%. The accuracy of the model on testing data, when model got further trained on augmented data, was improved to 94.70%.

The performance of the proposed model can be evaluated from the tables and plots provided. Table II shows the confusion matrix along with the Specificity [19], Sensitivity [19] and Accuracy (Categorical accuracy) obtained for each of the 3 classes. It was observed that classification of Glioma gave the best result as Glioma is having largest training data in comparison with other two tumor classes.

The presented model had the overall accuracy of 93.83%, specificity of 0.9715 and sensitivity of 0.9384 respectively,

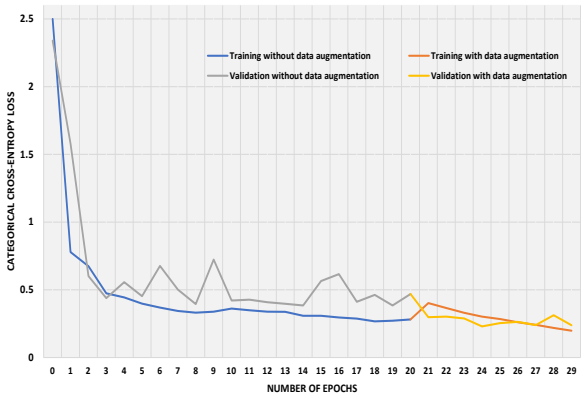

Fig. 5. Plot of categorial cross-entropy during Training of Neural network model

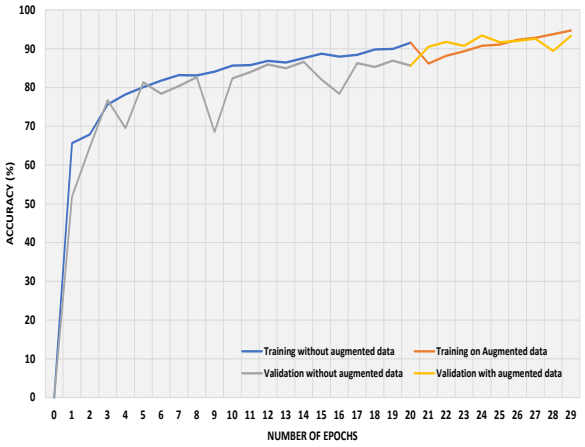

Fig. 6. Plot of Accuracy during Training of Neural network model

TABLE II
CONFUSION MATRIX AND RESULTS

Type of Tumor	Glioma	Meningioma	Pituitary Tumor	Specificity	Sensitivity	Accuracy
Glioma	1407	9	10	0.9564	0.9867	98.67
Meningioma	16	650	42	0.9829	0.9181	91.81
Pituitary Tumor	52	30	833	0.9753	0.9104	91.03
Average				0.9715	0.9384	93.83

which shows that state-of-the-art results can be obtained from our proposed method. We also tested this model with original MRI samples which were provided by Kolkata Medical College, West Bengal and got up to the mark results.

D. Comparison of proposed classification method

We compared our results with two other models on tumor classification. One was Support Vector Machine (SVM) based model by JunCheng et. al [13] and other was Deep Convolution Network based model by Justin S. Paul et. al [22]. Three feature extraction methods namely Bag-of-Words (BoW), Gray Level Co-occurrence Matrix (GLCM)and Intensity Histogram model based on SVM [13] was used by JunCheng et. al for classification of tumors. The overall accuracy of the SVM model [13] is 91.14%. Justin S. Paul et. al used two types of neural networks - fully connected and convolutional neural networks. This Deep Neural Network(DNN) [22] model achieved the overall accuracy of 91.43% for the classification on the same dataset. As shown in Table III and Fig.7, SE-ResNet-101 shows the best performance for classification of Tumor on the same dataset.

TABLE III
COMPARISON OF SPECIFICITY AND SENSITIVITY WITH SVM MODEL

Performance Metrics	Glioma		Meningioma		Pituitary Tumor	
	SVM model	SE-ResNet-101	SVM model	SE-ResNet-101	SVM model	SE-ResNet-101
Specificity	95.5%	95.64%	96.3%	98.29%	95.3%	97.53%
Sensitivity	86.0%	98.67%	94.4%	91.81%	87.3%	91.04%

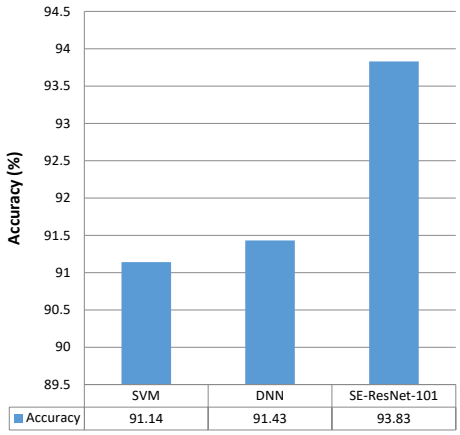

Fig. 7. Comparison of previous methods and proposed method

V. CONCLUSION

A deep CNN based SE-ResNet-101 architecture is proposed for the automatic classification of brain tumor MR images into 3 classes: Gliomas, Meningioma, and Pituitary tumor. Furthermore, experimental outcomes show that the proposed technique can provide a significant improvement in terms of overall accuracy, sensitivity, and specificity which significantly outperformed the other two recent competitive brain tumor classification techniques. We believe that this proposed method may be used as a handy tool to doctors for brain tumor classification. It may also be applicable to the other usages, such as liver lesion classification, breast tumor classification, etc. The proposed model's future extension may include enhancement of the CNN based architecture to three-dimensional data provided by MRI outputs as well as covering a greater number of classes.

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