Convolutional Neural Network based MRI Brain Tumor Identification

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Abstract—**In this paper, two different Convolutional Neural Network (CNN) models are presented for identifying the different classes of brain tumors in MR image modality. The first model consists of sixteen layers that give validation accuracy of 85% and testing accuracy of 79.7%. The second model consists of twenty-five layers having validation accuracy of 87.7% and testing accuracy of 84.3% is obtained. Two different optimizers Sgdm (Stochastic Gradient Descent with Momentum) and Adam are used for training the network.**

Index Terms— **Sgdm optimizer, Adam optimizer, CNN, MRI.**

I. INTRODUCTION

The collection or mass of abnormal cells in the brain is referred to as a brain tumor. People affected due to brain tumors are increasing day by day. Magnetic Resonance (MR) imaging is used for brain tumor detection because it is a non-invasive and painless procedure. It also does not use any harmful ionizing radiation. There are cancerous and non-cancerous tumors. In 2014, the World Health Organisation (WHO), reported that less than 2% of human cancers are brain cancers [1]. These tumors must be identified in the early stage else they may be harmful. Therefore tumor detection and classification are important as they can be treated easily in the early stage. The process to identify the different types of tumors is a challenging task and it takes a lot of time. To overcome this problem, classification using neural networks is used which is fast and accurate compared to that of done manually. The CNN model is used to classify 3 types of brain tumors as meningioma, glioma, and pituitary. Meningioma is formed from the meninges that surround the brain and the spinal cord. Glioma tumor is formed around the glial cells in the brain and spine. Glioma tumor almost comprises one-third of the brain tumors and pituitary type tumor is formed around the pituitary glands in the brain.

In these CNN architectures, source images are passed through various layers like the convolution layer, max-pooling layer, ReLU layer, etc. In this process, the images are passed forward through the layer network and their weights get updated. These weights are further used in classification. Once the images are processed forward, backward propagation is done and this is used for the calculation of minimum loss. The gradient descent algorithm updates the weights and biases to minimize the loss by taking a small number of steps in every iteration in the direction of the negative gradient of loss. The stochastic gradient descent algorithm oscillates along the path of steepest descent for optimization. So, adding momentum to the parameter reduces

the oscillation. Stochastic gradient descent is used to maintain a constant learning rate for updating the weights and it does not change during the training procedure. Whereas, 'Adam' optimizer uses individual learning rates that are adaptive for various parameters from the estimates of first and second moments of gradients.

In 2019, Sultan et al. [2] proposed a classification method for MRI tumor images using deep neural network The CNN model used consists of sixteen layers and they achieved 96.13% accuracy. In 2017, Kumar et al. [3] proposed an approach which classifies MRI tumor images into a benign tumor and malignant tumor. This approach reduces the time taken for classification and avoids human error. Anjali et al. [4] proposed a system which is used in the diagnosis of brain tumor from MRI brain tumor images. In this system, there are many phases to detect the tumor part from the brain image. Segmentation is used for extracting tumor portion. A median filter is used for noise removal. Textural feature extraction is also used. In 2018, Williams et al. [5] proposed a network which uses wavelet pooling for classification. Their experimental results show that the accuracy increases for certain datasets like MNIST when wavelet pooling is used instead of max pooling or average pooling.

Moreover, Lavanyadevi et al. [6] presented a segmentation and classification approach using PNN (Probabilistic Neural Network) for MRI images and showed that PNN has more advantages when compared to CNN and stated that PNN can adapt easily in real-time. Zacharaki et al. [7] classified glioma tumors into different grades using SVM and an accuracy of 85% are obtained. Litjens et al. [8] stated the use of deep learning in medical imaging and provide methods that help to overcome medical problems. In 2015, Machhale et al. [9] proposed the classification of brain cancer using SVM (Support Vector Machine). In this context, two different CNN based classification models are presented for identifying the brain tumors in MR images. The simple framework is shown in Fig.1. Firstly, the images extracted from the dataset are divided into training data, validation data, and testing data. The training data and validation data are used to train the network which helps in providing certain coefficients and these are called training coefficients. Now, validation data is used to test the network which again tunes the trained network further. These obtained training coefficients are passed through the testing classifier along with the test data. Now the network is used for classification of test data into their respective classes. The computation accuracy like validation accuracy and testing accuracy are calculated based on the predicted classes and the classified labels from the network. The accuracy of the obtained classes is calculated based on the predicted classes and testing labels.
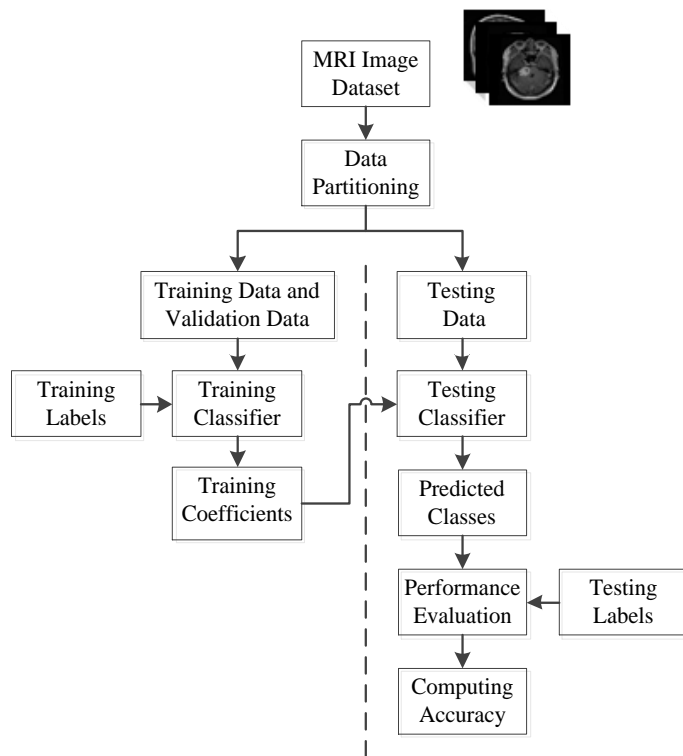

Fig. 1. The framework of the proposed study

II. METHODOLOGY

Deep Learning is a part of machine learning which helps in data representations and learning of hierarchical features. The algorithms in deep learning arrange various layers in a hierarchical manner in which the output of one layer is the input to the next layer and they are used for extraction of features [10]. Different layers used in CNN are convolution layer, pooling layer, ReLU layer, fully connected layer, dropout layer. In the convolution layer, a predefined kernel is passed over the image with a specific stride and the center pixel of impression caused by the kernel is replaced by adding all the results which are obtained by multiplying the corresponding image pixels with the kernel. In the pooling layer, a filter is passed over the image and the maximum value of the impression caused by the filter is used to replace the whole impression. It is a process of down-sampling. ReLU layer is used to remove the negative weights which are passed from the previous layers. A fully connected layer is used for connecting the neurons of one layer with other layer neurons. The dropout layer drops the specific probability neurons to overcome overfitting [11].

III. CLASSIFICATION MODELS

CNN based two models are presented to classify the three classes of brain tumors in MR images. One model consists of 16 layers and the other consists of 25 layers. The complete details of the presented framework are given as follows.

A. Model 1 (16 layers)

This model consists of 16 layers. The images for this model are augmented to $128 \times 128 \times 1$. In this model, the images are passed through various layers like the convolutional layer, ReLU (Rectified Linear Unit) layer, max-pooling layer, dropout layer, norm (normalization layer) and fully connected layers. In model-1, the parameters for convolution layer Conv1 are the number of filters (K)=64, padding P=0, filter size 10×10 and Stride S=1. Similarly, for Conv2, K=128, P=2, S=1, filter size 3×3 and for Conv3, K=128, P=2, S=1and filter size 2×2. The max-pooling layers pooling1, pooling2, and pooling3 have filter size 2×2 and S=2. The probabilities used for dropout layer dropout1 are 0.1 and for dropout2 is 0.2. The output size for fully connected layer FC is 3.

B. Model 2 (25 layers)

This model consists of 25 layers. The images for this model are augmented to $227 \times 227 \times 1$. The two models are shown in Fig. 2. In model-2, the parameters for convolution layer Conv1 are K=96, padding P=0, filter size 11×11 and Stride S=4. For Conv2, K=128, P=2, S=1 and filter size 5×5. For Conv3, K=384, P=1, S=1 and filter size 3×3. For Conv4, K=192, P=1, S=1 and filter size 3×3. For Conv5, K=128, P=1, S=1 and filter size 3×3. The max-pooling layers pooling1, pooling2, and pooling3 have filter sizes 3×3 and S=2. The probabilities used for dropout layer dropout1 is 0.5 and for dropout2 is 0.5. The output size for fully connected layers FC1, FC2, FC3 are 4096, 4096 and 3 respectively.

IV. EXPERIMENTAL RESULTS AND DISCUSSIONS

A. Dataset

Our database consists of T1-weighted images obtained from 233 patients. The dataset is classified into 3 types of brain tumors. They are meningioma tumor, glioma tumor, and pituitary tumor as shown in Table I [12]. Figshare dataset is modified into two different datasets out of which one dataset contains 12,256 MRI images and the other contains 15,320 MRI images. 12,256 images are obtained by flipping the images up-down, mirroring the images right-left, flipping the mirrored image and the original image. Whereas, 15,320 images are obtained by flipping the images up-down, mirroring the images right-left, rotating the image by 45 degrees, adding salt-noise to the image and the original image.

TABLE I. THE NUMBER OF IMAGES AND PATIENTS FOR EACH TUMOR

Brain tumor Class	#Patients	#Slices
Meningioma	82	708
Glioma	91	1426
Pituitary	60	930
Total	233	3064

B. Results and Discussions

In the presented models, the complete dataset is divided by two ways, first is 70% of the data for training the network, 15% for validation and 15% for testing. Fig. 3 and Fig. 4 show the confusion matrix of validation and testing accuracy for 15,320 MRI images, respectively where class 1 represents meningioma. Class 2 represents glioma and class 3 represents pituitary.

Input → Conv1 → ReLU1 → Norm1 → Pooling1 → Conv2 → ReLU2 → Pooling2 → Dropout1 → Conv3 → ReLU3 → Pooling3 → Dropout2 → FC → Softmax → Classify

B

Input → Conv1 → ReLU1 → Norm1 → Pooling1 → Conv2 → ReLU2 → Norm2 → Pooling2 → Conv3 → ReLU3 → Conv4 → ReLU4 → Conv5 → ReLU5 → Pooling3 → FC1 → ReLU6 → Dropout1 → FC2 → ReLU7 → Dropout2 → FC3 → Softmax → Classify
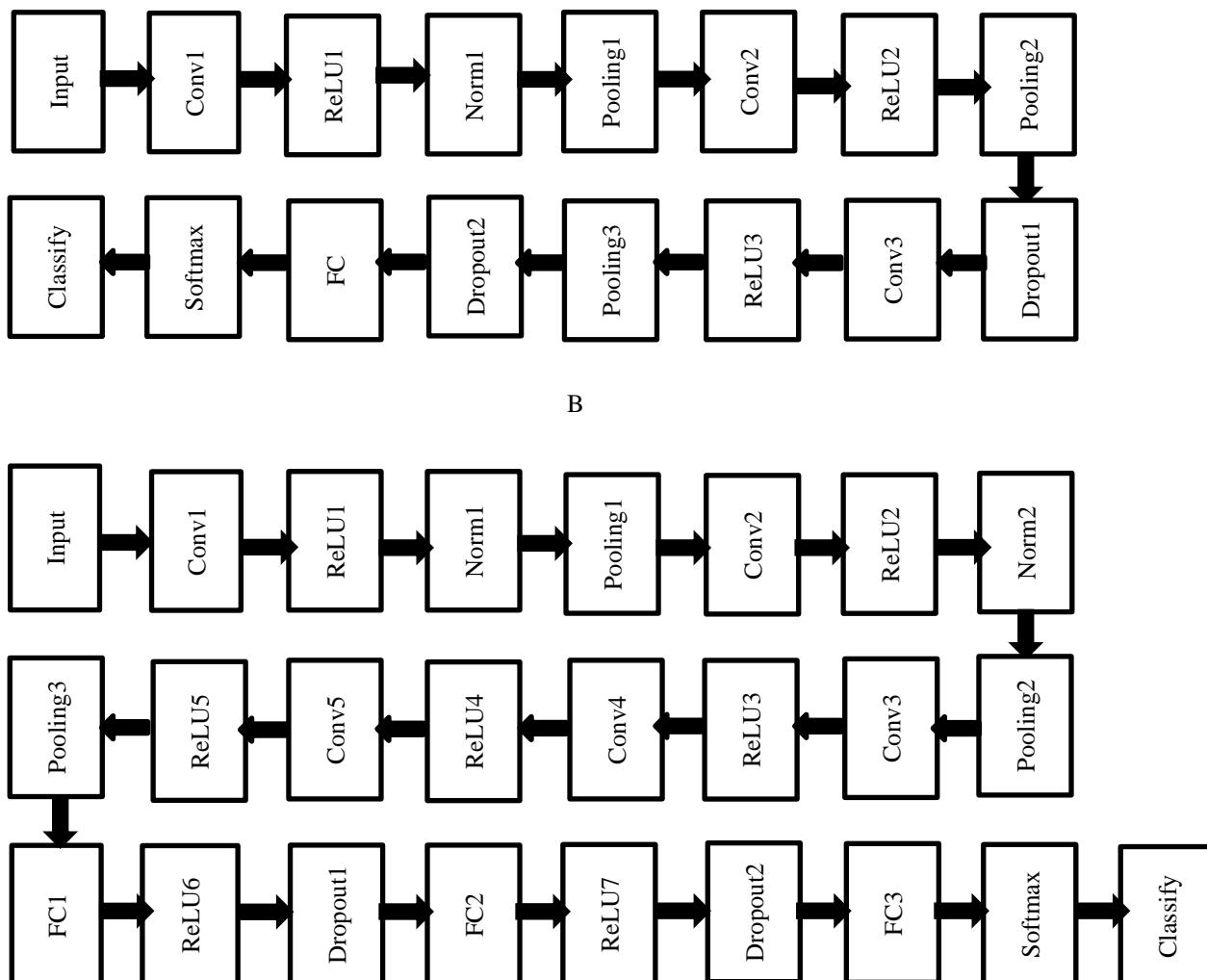
Fig. 2. Flow chart of A) Model 1 containing 16 layers,
B) Model 2 containing 25 layers.

The other trail consists of 60% of data for training the network, 20% for validation and 20% for testing. Fig. 5 and Fig. 6 show the confusion matrix for validation and testing accuracy of 12,256 MRI images, respectively.

For both the CNN based classification models, during the training process, the learning rate is 0.0001. For model-1, the images are augmented to $128 \times 128 \times 1$ whereas for model-2 the images are augmented to $227 \times 227 \times 1$. The mini-batch size used in the training process is 64. For the dataset containing 15,320 MRI images, validation accuracy for class 1 is 73.2%, class 2 is 88.3% and class 3 is 97.7% whereas testing accuracies for class 1, class 2 and class 3 are 66.4%, 85.1% and 96.5% respectively. For the dataset containing 12,256 MRI images, validation accuracy for class 1 is 76.4%, class 2 is 81.3% and class 3 is 97.1% whereas testing accuracies for class 1, class 2 and class 3 are 70.8%, 73.8%, and 95.7% respectively.

Validation Confusion Matrix

Fig. 3. Confusion matrix for Validation data (15,320 MRI images)

Test Confusion Matrix

Fig. 4. Confusion matrix for Testing data (15,320 MRI images)

Validation Confusion Matrix

Fig. 5. Confusion matrix for Validation data (12,256 MRI images)

Test Confusion Matrix

Fig. 6. Confusion matrix for Testing data (12,256 MRI images)

V. CONCLUSIONS

For the dataset containing 15,320 MRI images, the maximum validation accuracy (Valid acc.) and testing accuracy (Test acc.) obtained are 87.7% and 84.3% respectively as shown in Table II. For the second dataset containing 12,256 MRI images, the maximum validation accuracy and testing accuracy obtained are 85% and 79.7% respectively as shown in Table III. For both the cases, the maximum validation and testing accuracies are achieved using model 2, with Adam optimizer, whereas the complete dataset is divided into 70% training data, 15% validation data and 15% testing data. From the obtained experimental results, it is observed that Adam optimizer gives better results compared to that of the Sgdm optimizer and this is because of the adaptive nature of the Adam optimizer.

TABLE II. ACCURACY FOR THE DATASET CONTAINING 15,320 MRI IMAGES

Data Partition[*]	Model	Optimizer	Epochs	Valid Acc.[&]	Test Acc.[$]
70-15-15	2	Sgdm	50	80.7	77.3
70-15-15	2	Adam	30	**87.7**	**84.3**
70-15-15	1	Sgdm	50	74.4	60.9
70-15-15	1	Adam	50	74.4	63.1
60-20-20	2	Sgdm	50	77.8	71.9
60-20-20	2	Adam	30	80.6	75.4
60-20-20	1	Sgdm	50	72.4	60.4
60-20-20	1	Adam	50	72.2	62.3

TABLE III. ACCURACY FOR THE DATASET CONTAINING 12,256 MRI IMAGES

Data Partition[*]	Model	Optimizer	Epochs	Valid Acc.[&]	Test Acc.[$]
70-15-15	2	Sgdm	40	78.3	76.1
70-15-15	2	Adam	50	**85**	**79.7**
70-15-15	1	Sgdm	50	73.4	63.8
70-15-15	1	Adam	50	74.8	63.8
60-20-20	2	Sgdm	50	78.3	72.6
60-20-20	2	Adam	50	80.3	73.3
60-20-20	1	Sgdm	50	72.2	64.5
60-20-20	1	Adam	50	73.7	62.2

*represents data partitioning in %.
& represents validation accuracy in %.
$ represents testing accuracy in %.

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