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RESEARCH ARTICLE

MRI Brain Tumor Prediction using Azure Streamlit Framework and Analysis of CNN Activation Functions

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Abstract

Objective: The present research work is focused on brain tumor classification, prediction and to increase the performance to locate the tumor region. **Methods:** A two-dimensional Convolutional Neural Network (CNN) model is proposed to classify the Magnetic Resonance Images (MRI) into tumor and non-tumor categories. The method is applied on a collected dataset consisting of 2056 MRI images. The model is implemented in Python with hyperparameter tuning and activation functions.**Findings:** In this paper, ReLU and LeakyReLU activation functions are applied with several optimizers. The analysis of the implemented results has been used to gauge performance accuracy. The computed results achieve 99.51% accuracy for predicting the brain tumor using LeakyReLU with Adam optimizer. **Novelty:** The proposed model provides quick, and accurate approach to classify patients by setting hyperparameter tuning parameters which helps to the doctor to detect patients suffering with tumor and the entire process reduces the computation time.

Keywords: Convolutional Neural Network (CNN); Magnetic Resonance Image (MRI); Digital Imaging and Communications in Medicine (DICOM); Brain Tumor; Deep Learning

1 Introduction

The Convolutional Neural Network (CNN) revolution is a harbinger for brain tumor classification which is used to diagnose tumor types with viable accuracy and time. Thus, the CNN approach is helpful to provide the best trained models to improve classification performance using medical image processing and also essential for better treatment planning for radiologists (1). However, as technology improved, radiologists could more effectively provide accurate diagnoses and treatment plans for early detection of brain tumor. The World Health Organisation (WHO) reports that more than 100 different grades of brain tumor have been identified in humans and all of which are not fatal. Meningiomas, which are categorized into three grades, are one of the most prevalent types of brain tumor, according to the report. Grade 1 shows low-grade tumor; Grade 2 shows atypical meningioma and Grade 3 represents anaplastic meningioma (2). So, MRI technology is the more precise way of scanning human body parts to produce patient report for better and early treatment planning as compared to other scanning machines.

The more detailed features were extracted from MRI scans and radiologists examined the patients for further investigations(3). The deep learning scenarios are crucial for determining the tumor's most precise location and producing better outcomes(4). In the present context, the programmers are trying to predict brain tumor more accurately and also developing the web based application based on the constructed trained and also validating the model. The opportunity to diagnose brain tumor is made possible by improving the performance of model.

According to many deep learning experts and advisors, a fully automatic and accurate method will increase the chance of curing diseases. Several research studies are available for brain tumor identification and classification. Ayadi et al.(5) applied the CNN approach to classify the brain tumor into said three categories. The Figshare and Radiopaedia dataset were used i.e., T1-weighted contrast-enhanced MRI brain images consisting of 3064 slices of four grades of tumor. Moreover, with a Figshare dataset, a fivefold cross-validation technique showed accuracy of 94.74% while the Radiopaedia dataset have accuracy of 93.71% after augmentation(5). In another study (2021), CNNs based pre-trained models were used to classify X-ray images; classified into two classes healthy brain and brain tumor; input images were resized into 256*256 pixels; data augmentation were used to increase number of images, and pre-trained models were used for classification. The three pre-trained algorithms are as follows: MobileNetV2, VGG19, and InceptionV3, among which MobileNetV2 had the best performance with 92% of accuracy. The Kaggle dataset was utilised for the brain tumor classification(6). Mzoughi et al.(7) proposed a multi-scale deep 3D CNN model for MRI glioma tumor grading by applying a volumetric T1-Gadolium MR sequence; then, augmenting data using the flipping method. The input is fed to the convolution layers, pooling layers, and fully connected layers; hyperparameter values have been set for better accuracy; then resized the images with cubic B-spline method to 112*112*94 on Brats 2018 database. The proposed model obtained accuracy of 96.49%(7). Saleh et al.(8) employed five CNN architectures to classify the brain tumor such as Xception, Inception v3, ResNet-50, VGG16, and MobileNet models. Firstly, in the pre-processing phase augmentation technique was used to increase the total number of images on Kaggle dataset consists of 4480 images for training and 2880 for validation set; then images were resized to 256*256 pixels; categorized into four classes glioma, meningioma, non-tumor, and pituitary; analysed that Xception model achieved highest accuracy of 98.75%(8). Sarang Sharma et al.(9) also introduced four pre-trained models: VGG16, VGG19, DenseNet121, and DenseNet201 to identify the brain tumor using MRI images; applied to the Kaggle database; classify into two categories brain tumor and non-brain tumor; contains 157 brain tumor images and 100 images of non-brain tumor; flipping, rotation, brightness and zooming techniques were used for augmenting the images; after augmentation, it contains 1100 images for a brain tumor and 700 images for non-tumor; images were resized to 224*224; the model is trained up to 20 epochs; accuracy was obtained with 98% by the VGG19 which is better as compared to other models(9). Amin et al.(10) used the combination of Discrete Wavelet Transform (DWT) with daubechies wavelet kernel for the evaluation of the fusion process; then partial differential diffusion filter is applied to remove noise; a global threshold method was applied to segment the tumor region and a CNN model was applied to categorize into tumor and non-tumor regions. These effective models are used to identify brain tumor. The Brats 2012, Brats 2013, Brats 2015, and Brats 2018 dataset were used for evaluation. The evaluation results showed that the technique proposed in the study obtained an accuracy of 97% on the Brats 2012, 98% on Brats the 2013 challenge, 96% accuracy on Brats 2013 leaderboard, 100% accuracy achieved on the Brats 2015 challenge, and 97% accuracy on Brats 2018 challenge datasets after applying fusion technique(10). Dilated CNN model was used in the study (2020) to broaden the receptive field of filters. It has been concluded that dilated CNN gives better performance with accuracy of 97% but suffers from a gridding problem; the author applied an even number of dilation rates to reduce the gridding problem and also overcome the computational overhead.

Brain tumors are automatically detected using the magnetic resonance images with dilation in combination with a convolutional layer. The objective of this study was to distinguish between normal and tumor images. A comparative study was made among the ANN, Basic CNN, and dilate CNN model and observed that among the three models, dilated CNN had the best performance; increasing the number of epochs in dilated CNN accuracy also improved and at 50 epochs accuracy obtained 97%; but ANN model achieved 85% accuracy; basic CNN achieved 92% accuracy. The localization of the brain tumor was done using synthetic MRI images(11). Dubey et al.(12) proposed deep learning and machine learning models to detect brain tumor from MRI brain images; three different classifier techniques were used: support vector machine, logistic regression, and CNN(12). Additionally, CNN and machine learning were used by Rathod and Khan(13) with various classifiers. The accuracy obtained with CNN SoftMax fully connected layer is 98.67%; with radial basis and decision tree was having accuracy of 97.34% and 94.24%, respectively(13). Wang et al.(14) proposed fuzzy C-Means algorithm with an ARM Linux embedded system for brain tumor prediction using MRI images; discovered that evaluation metrics for optimized fuzzy C-Means are better than the deterministic C-Means clustering algorithm and traditional fuzzy C-Means. An ultra-light deep learning architecture was proposed with a Grey Level Co-occurrence Matrix (GLCM). Furthermore, Qureshi et al.(15) proposed multi-class classification approach with MRI brain tumor datasets that takes very less time, and the Support Vector Machine (SVM) classifier produces the best classification results. A semantic segmentation of brain tumor was produced through U-net model on the datasets of Brats 2018, Brats 2019, and Brats 2020, the suggested model was trained and tested. Further, the author suggested a U-Net model based on 3D large kernel attention for segmenting brain tumors. The training model was applied to the multi-modal brain tumor segmentation of the Brats 2020 dataset(15).

It has been noted from the literature review that the majority of the currently used approaches were implemented over the MRI brain image datasets available online. Machine learning and deep learning techniques have been widely and more frequently used with online available datasets for brain tumor classification. However, most of the schemes have higher computational complexity and are not suitable for small real-data applications. After pre-processing, the 2D CNN model is used with both large and small online available datasets.

The motivation of this work is to develop a web-based application for brain tumor prediction that is also capable for non-technical users to predict brain tumor. It works effectively with small datasets of MRI brain images which requires less computational overhead and high classification of accuracy, which are provided through present work. The schemes employ a 2D CNN model for building a network, LeakyReLU with Adam employed for optimization, SoftMax classifier done classification into tumor and non-tumor, and Azure streamlit framework deploys for tumor prediction. The numerous simulations are performed on real MRI brain images which show that the proposed work achieves higher classification of accuracy than other existing schemes. A straight forward process provides for uploading images and offering predictions based on 2D CNN model with great performance. It is quite capable of analysing images from various sources. The creation of medical diagnostic tools(16) can be helpful for radiologists and patients to speed up diagnosis and treatment planning; thus, addressing the effectiveness of current work.

2 Methodology

The existing 2D CNN model has made an effort to increase the success probability of classification for MRI brain data to predict tumor and non-tumor. The comparison between LeakyReLU and ReLU with several optimizers is performed to check and validate the classification accuracy in terms of reliability and efficiency. Figure 1 defines the methodology for deploying the proposed work like collecting MRI brain images, pre-processing, and trained the model with 2D CNN to predict tumor.

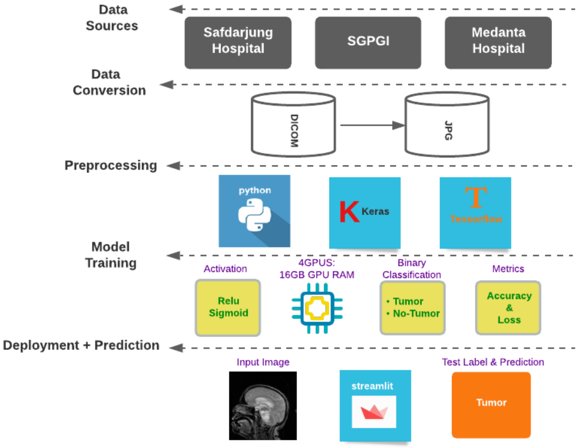


Fig 1. A System Model

2.1 Database

MRI brain tumor and normal images are considered as input for the evaluation of the proposed work. These images are collected from different Hospitals for model training. It consists of three cases of brain tumor which are as follows: Atypical Meningioma, Glioma, and Schwannoma. In Figure 2 MRI multi-modal (T1+C, T2, Flair and T1 MRI sequences) of brain images and expert annotations of three cases are represented. The MRI images were collected in DICOM format which is further converted into JPG format for further evaluation of experiments. These MRI images consists of sagittal, coronal, and axial view and the specifications are given in Table 1.

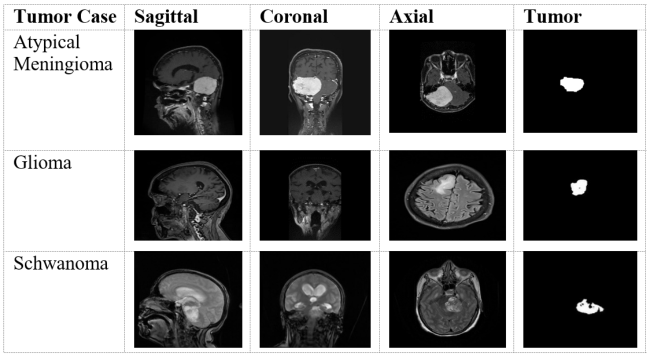


Fig 2. Multimodal MRI Brain Tumor Images

Table 1. A Sample of Collected Dataset

Patient	Hospital	Format	Case	Number of MRI Slices
Patient#1	SGPGI, Lucknow, India	DICOM	Schwannoma	582
Patient#2	Safdarjung, New Delhi, India	DICOM	Atypical meningioma	2165
Patient#3	Medanta, Lucknow, India	DICOM	Glioma	580
Patient#4	SGPGI, Lucknow, India	DICOM	Healthy brain	444

2.2 Pre-processing

In the pre-processing phase, the size of input images is reduced to 150*150 pixels to decrease the computation time of training. For more enhancements, horizontal flipping utilizes for data augmentation to increase the size of data.

2.3 2D CNN

The dataset consists of 2056 multi-modal MRI brain images. The architecture of the 2D CNN model is given in Figure 3. It consists of layers and three basic operations of convolution, max-pooling, and fully connected layers. In the convolution layer, input images are fed into the network and these images are passed through several channels to convolve a filter. Further, the convolved images are transferred into the max-pooling layer to reduce the data dimensionality. The process is repeated until the depth of the CNN layers. After completing the basic CNN operations, it extracts the features and shapes. Then, the flattening layer converts the data from high dimensionality to a 1D vector. In the next step, the SoftMax layer will classify the brain images into tumor and non-tumor classes. In the proposed work, 2D CNN method is chosen due to the sparsity in the system parameters.

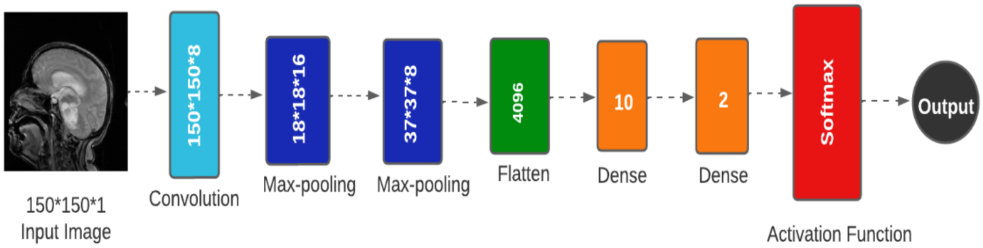


Fig 3. Layering of the CNN

2.4 Data Split

The processed data is divided into two parts i.e. training and validation sets classified into 80:20 ratio. The total of 2056 fragments of data is processed, out of which 80% (1644) is used for training data and 20% (412) is used for testing.

2.5 Hyperparameter tuning

The hyperparameter of the proposed model structure is given in the Table 2. The number of layers, neurons, activation function, optimization, and learning rate are positioned next to each other to fine the tune of model to enhance accuracy. The proposed algorithm related to the performance evaluation of the CNN model is given below:

Algorithm:Perf_Eval_CNN()

```
1. Input-Image (T1, T1+C, T2, Flair);
2. Graysclae_Conversion();
3. Normalize_data();
4. Data_Split(80:20);
5. Build_CNN_Model();
6. Activation_function<ReLU, LeakyReLU>;
7. Optimization= <Adam, RMSprop, SGD, Adagrad, Adadelta>
8. For each epoch in E do
9. For each Batch in B do
10. ⊠ = feature_extract();
11. Loss= crossEntropy(x, ⊠);
12. Optimized(Loss);
13. Calculate_accuracy();
14. Results();
```

Table 2. Representation of Hyperparameters

Stage	Hyperparameters	Value
Initialization	Bias	0
LeakyReLU	A	0.1
Dropout	P	0.5
Training	Learning rate	0.001
	Beta_1	0.9
	Beta_2	0.999
	Epsilon	None
	Epochs	60
	Batch	80

3 Results and Discussion

The experiments are conducted on 2D CNN model using several optimizers to evaluate the performance of proposed work and described the analysis of the results. The basic settings of the experimental environments are shown in Table 3. The performance evaluation is performed by comparing and analysing the experimental results of LeakyReLU and ReLU with several optimizers.

The proposed model is implemented using Python programming in a Google Colab environment with a CPU and 1.17 GB RAM. The proposed model is iterated for 60 epochs with a batch size of 80. The accuracy and loss function are obtained for the data in order to build a model and determine the accuracy for brain tumor prediction. Figure 4 presents the training and validation accuracies obtained for LeakyReLU. The blue line represents the training accuracy, which increases with increase in the number of epochs and approaches achieve of accuracy of 99.51% after 60 epochs. The brown curve shows the validation accuracy, commencing at 81.55% and rising to 98.30% after 60 epochs. The training stopped at 60 epochs because the learning model starts overfitting. The number of training epochs was tuned for the highest training and validation accuracy.

Table 3. Performance Comparison for ReLU and LeakyReLU

Optimizer	Activation function			
	ReLU		LeakyReLU	
	Train accuracy/Train Loss	Val accuracy/Val Loss	Train accuracy/Train Loss	Val accuracy/Val Loss
Adam	0.9840|0.0534	0.9755|0.1508	0.9951|0.0147	0.9830|0.1079
RMSprop	0.9870|0.0344	0.9598|0.2108	0.9885|0.0218	0.9425|0.3381
SGD	0.6349|0.6187	0.6667|0.6434	0.9755|0.1017	0.9655|0.2050
Adagrad	0.8110|0.4043	0.7931|0.4157	0.9755|0.0791	0.9655|0.1768
Adadelta	0.6349|0.6419	0.6667|0.6621	0.9812|0.0619	0.9655|0.1323

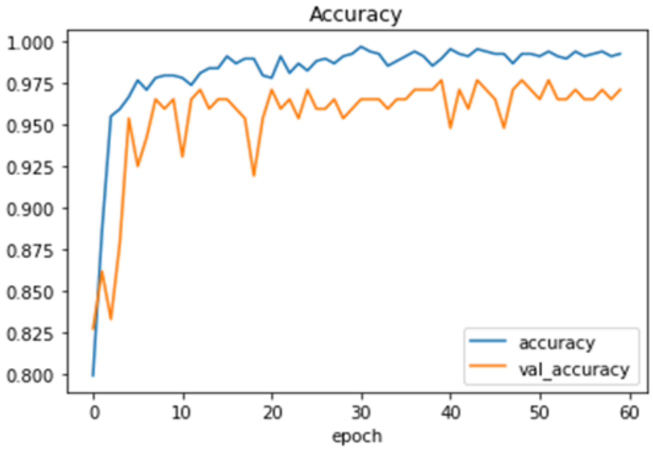


Fig 4. Accuracy for LeakyReLU using Adam Optimizer

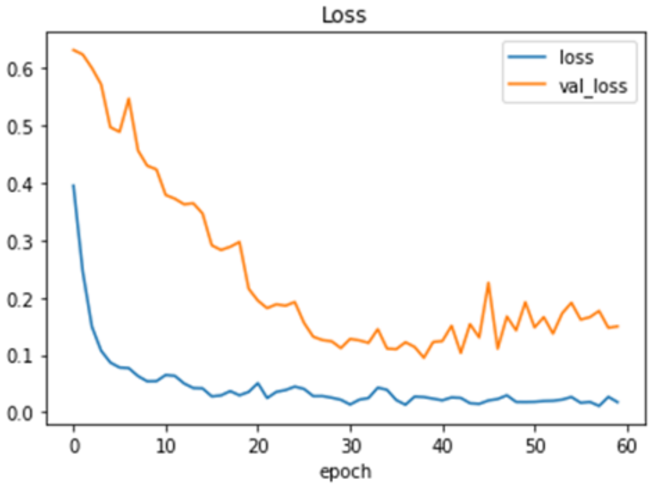


Fig 5. Loss for LeakyReLU

The LeakyReLU model's training and validation loss curves are shown in Figure 5, where a score of 0.0 would represent excellent learning with no errors. The training loss reached 0.0124 after 50 epochs, and the validation loss started at 0.2464. In both the cases, losses continuously decreased due to increase in the number of epochs.

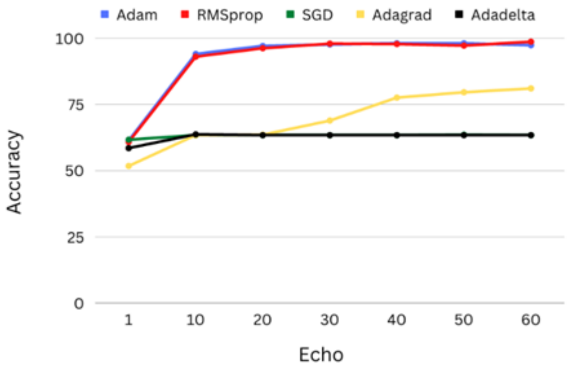


Fig 6. Training Accuracy for ReLU Activation Function

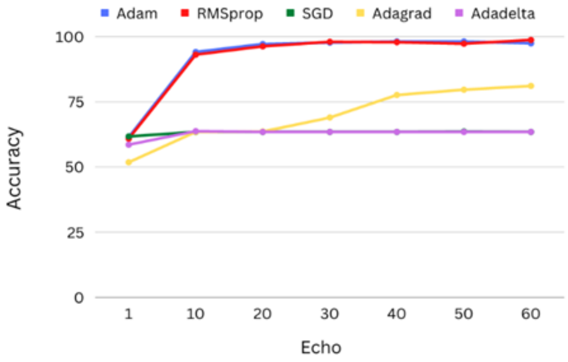


Fig 7. Training Accuracy for LeakyReLU Activation Function

The comparison findings between LeakyReLU and ReLU are presented in Table 3. In the ReLU and LeakyReLU activation function, which is evaluated with different optimizers such as: Adam, RMSprop, SGD, Adagrad, and Adadelta. ReLU with Adam and RMSprop provide better accuracy for training and validation sets. SGD and Adadelta, on the other hand, both produce approximately same training and validation results which is very less. On the other hand, LeakyReLU with adam optimizer presents 99.51% accuracy for training and 98.30% for validation.

In Figures 6 and 7, the training accuracy for LeakyReLU and ReLU activation functions is plotted and experimental analyses are done on each optimizer.

Figure 10 shows the brain tumor prediction for test cases using the proposed approach and after building the model, the saved model is deployed on the Azure Streamlit web app for tumor prediction by uploading images. The patient's MRI brain image is uploaded to the system which will predict that the person has brain tumor or not.

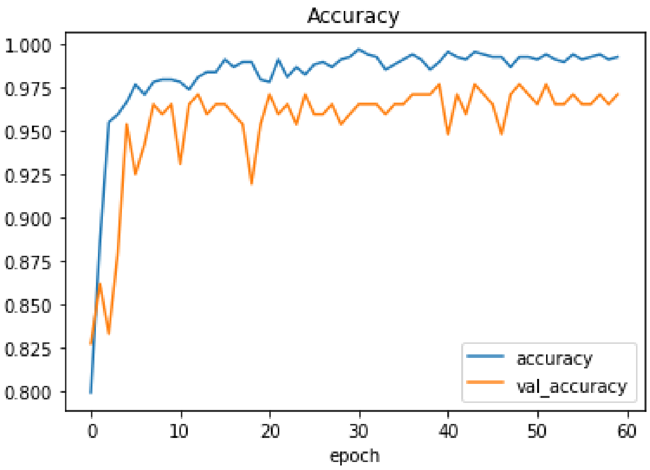


Fig 8. Accuracyfor Leaky ReLU using Adam Optimizer

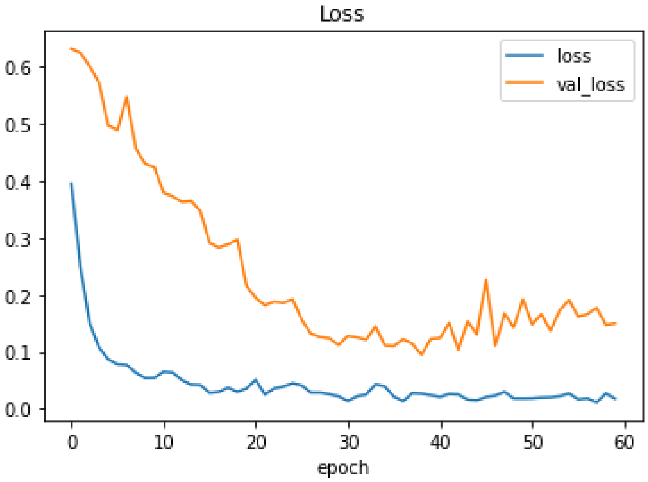
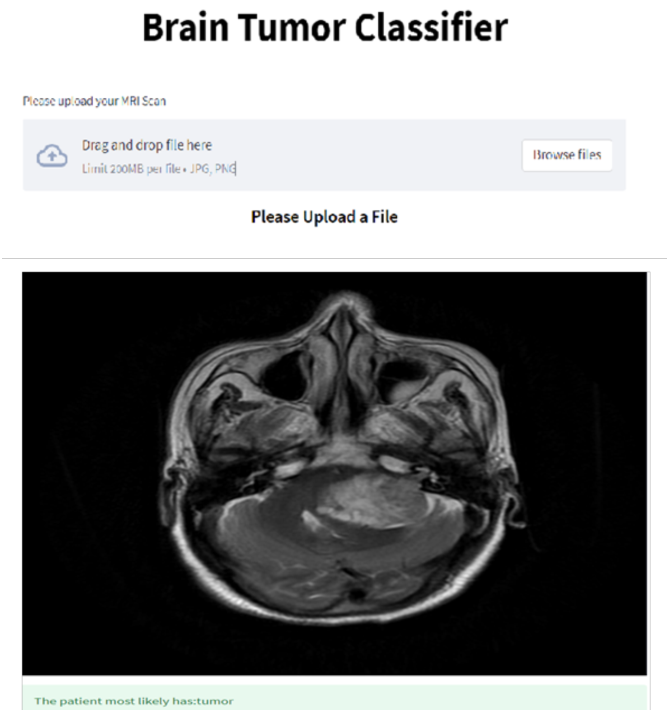


Fig 9. Loss Function for LeakyReLU

Table 4 a comparison of the accuracy achieved by the LeakyReLU and ReLU with previously evaluated results. The testing accuracy of the proposed models are noticeably higher than those achieved by the models listed in the references(17–21).

Table 4. Comparative analysis of proposed approach with previous work

Paper	Method	Classifier	Data	Tools	Accuracy (%)	Data Split
Saeedi S. et. al.(17)	2D CNN, Convolutional auto-encoder	Four	9792	PYTHON	96.47, 95.63	Train- 90 % Test- 10%
Jasmine Paul et. al.(18)	SVM, BOVW	Four	3064	-	95.0%, 96.0%	Train- 80 % Test- 20%
E. Shashikala et. al.(19)	Fuzzy logic	Two	450	-	95.67%	-
Vankdothu et al.(20)	RCNN	Three	264	PYTHON	95.17%	-
Gu et al.(21)	CNN	Three	3064, 1000	PYTHON	97.12%, 97.74%	-
Proposed	2D CNN	Two	864	PYTHON	99.13% 96.55%	Train- 80% Test- 20%



Brain Tumor Classifier

Please upload your MRI Scan

Drag and drop file here

Limit 200MB per file • JPG, PNG

Please Upload a File

The patient most likely has:tumor

Fig 10. Brain Tumor Prediction on Azure Streamlit Web Application

The improved performance is achieved due to the fine-tuning of the model's hyperparameter values, optimizer type, batch and kernel sizes, activation functions, pool size, the number of neurons used in the convolution layers, and the number of training epochs. For LeakyReLU, augmenting data by setting parameters with rotation range = 0, zoom range= 0, width_shift_range = 0, height_shift_range = 0, horizontal_flip = True, and vertical_flip = True, setting the number of training epochs to 60, and batch size to 40, and using a softmax activation function with kernel and pool sizes of the convolutional and max-polling layers adjusted to 5 × 5 and 2 × 2 filters, respectively, LeakyReLU achieved a test accuracy of 97.13%. However, when the batch size was changed to 80 and, the training epochs were reconfigured to 40, augmenting data by setting parameters with rotation range = 0, zoom range= 0, width_shift_range = 0, height_shift_range = 0, horizontal_flip = True, and vertical_flip = True, with a sigmoid activation function, kernel and pool sizes of the convolutional and max-polling layers set to 5 × 5 and 3 × 3 filters, respectively, the LeakyReLU testing accuracy reached only 98.30%. We conclude that the parametric settings can significantly enhance the results.

The primary goal is to compare the ReLU and LeakyReLU activation functions with different optimizers of the 2D CNN model and it is analysed that LeakyReLU with Adam optimizers performed much better and consumed less computational time. Therefore, the limited functionality of hardware and memory can be enough to propose a 2D CNN model with LeakyReLU and also employed that the prediction results for brain tumor are more accurate.

4 Conclusion

Based on experimental investigation, it can be concluded that the 2D CNN model is utilized ReLU and LeakyReLU with optimizers to classify the patients with tumor and non-tumor on MRI brain images. The model was trained and assessed using a dataset of 2056 for each tumor and non-tumor images. Before training, brain images were pre-processed by applying a horizontal flip. Experimental assessment of the accuracy of the ReLU and LeakyReLU by Adam optimizers are 98.40% and 99.51%, respectively, with respective loss rates. The suggested model gives better results due to data pre-processing, setting of optimized hyperparameter values, and applied optimizers on the tumor brain images. In the system, it is also analysed that ReLU with Adam optimizer might give better results using more iterations in comparison to other methods but computationally slower as compared to LeakyReLU. The presented approach is compared with optimizers as well as with existing algorithms. For further improvement, one can choose a deep learning algorithm with more epochs and iterations. The proposed model can be applied to MRI medical images to speed up diagnosis for the benefit of both patients and doctors.

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