# A SHARROW CNN DEEP LEARNING MODEL TO DETECT BRAIN TUMORS FROM MAGNETIC RESONANCE IMAGE

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**Abstract -** Brain tumor is among the deadliest disease worldwide. Once the patient is diagnosed with the disease, The tumor damage brain' health tissues otherwise its intensified intra cranial pressure(ICP).Most death occurs from above causes or related adverse events. The earlier the tumor is diagnosed the luckier curing and survival probability increases. In this article, we presented a coherent techniques for detecting brain tumors in magnetic resonance images. Input gray-scale image are loaded inside our proposed method. A zero pading layer with a pool size of (2,2) is being considered and a double-convolutional layer with 32 neurons and a filter size of (9,9) with one unit stridal is applied, with two batch normalization layer. The normalizing pixel values speed up the computational process with a RelU activation function. Two max pooling layer with a filter size and stridal value four (4)has being used. Finally we applied a flatten layer to flatten our 3-dimensional matrix into a one-dimensional vector, this is then propelled into a Dense block (output Unit), which is a fully connected layer with one neuron using a sigmoid activation function . The classification task take place, where brain with tumor cells are being detected and classified as tumorous MR brain images and those without tumor cells are Non-tumorous brain MR images. Our method exhibits a higher Testing accuracy compared with the existing model Referring Tab.4

**Keywords** - Brain Tumor MRI(Magnetic Resonance Images), Convolution Neural Network, Tumor Classification Detection

## I. INTRODUCTION

An anomalous mass of tissue that forms when cells grow up and divide more than they should or do not die when they should. They exhibit uncontrolled growth rate which create pathological cells known as cancerous cells[pei2021machine] .Tumors are subdivided into two main parts benign and malignant for non-cancerous and cancerous cells [fayed2020differences].

We used MRI data-sets based on its smooth tissue, contrast normalization characteristics, this enhance a soft analysis of the tumorous region.

Medical Researchers Fan et al.(2020) showed that, Deep learning can analyze image much better than medical professional. Rating a good Deep learning algorithms bellow functions must be considered to accurately detect and classify tumorous region: the model has to be robust in its performing classification task , efficient filters, possessing a precised feature extractors and finally adapting faultless classifiers. Our proposed model discussed in Sec.3 has carefully map and employed above listed functions.

Existing Machine learning and Deep learning models have done tremendous work in-terms of classification[amin2020use,deepa2019efficient,patil2021automated] etc.. Although they show good results and promising robust Models, we can still notice numerous Weakness , to wit: Expensive computational resources, very large feature vectors etc...Our proposed model discussed in Sec.3 highlights how we addressed above drawbacks and achieve a better classification accuracy compared to existing models.

## II. LITERATURE REVIEW

Deep learning models have displayed an important role in brain tumor classifications.[?] used ResNet-50 with global average pooling to resolve the vanishing gradient and over fitting issues. [5] adopted a fusion-based brain tumor detections through fusing the input images adopting a discrete wavelet transform, To categorize the brain images as either tumorous or non-tumorous here an optimal Deep Neural Network techniques was adapted, a mean accruacy of 99.3% was reported.

Sethy and Behera (2021) proposed a deep classification technics which employ deep features to shows tumorous brain MR images. An AlexNet,vgg16 & vgg19 per-trained models were put in place. To reduce the feature vector dimensions, a principal component analysis(PCA) was applied.vgg16 with the fused features of fc6 and fc7 combine with linear SVM achieve a maximum classification accuracy of 97.89%. Deb and Roy (2021) exploited an adaptive fuzzy deep neural network using frog leap optimization, detecting tumorous and nontumorous images, the mean classification accuracy was reported with 99.6%.

Kumar et al.(2021) proposed a deep neural network model which utulize ResNet-50 and global average pooling to address the vanishing gradient and overfitting problems.This were resolved and he reported a classifications mean accuracy of 97.4% .

Sethy and Behera (2021) Harness the use of deep classfication methods detecting tumorous and non-tumorous region inside brain'MRI, an alexnet, VGG16 and VGG19 was put in place with an

outsanting accuracy of a 97.89%
Ahmed et al.(2021) employed a hybrib system based on an integration of Gray Wolf Optimizer and support vector machine combined with Radial Basis Function kernel to detect and classify MR images as benign or malignant, 5-fold cross validations boosting generalization, a hybrid system 80 images was utilized, an outstanding mean accuracy of 98.78% was reported.

## III. PROPOSED METHOD

In this Sect.3, the proposed framework for brain tumor detection using convolution neural network in tensor flow and keras [sajid2019brain,ari2018deep]is discussed. There are five main steps in our algorithm: the first one is to insert the input gray-scale image inside our proposed method[sadad2021brain] ;secondly, A zero pading layer with a pool size of (2,2) is being considered [hashemi2019enlarging] and a double-convolutional layer with 32 neurons and a filter size of (9,9) with a stridal value of one [sharma2012application] is applied with two batch normalization layer, normalizing pixel values and speed up the computational process with a RelU activation function. Thirdly two max pooling layer [abiwinanda2019brain]with a filter size and stridal value four (4), Finally we applied a flatten layer to flatten our 3-dimensional matrix into a one-dimensional vector, this is then propelled into a Dense block (output Unit), which is fully connected layer with one neuron using a sigmoid activation function [sun2019drrnet].The classification task take place, where brain with tumor cells will be detected and classified as tumorous MR brain images and those without tumor cells will be Non-tumorous brain MR images
The Fig. 1 shows the details of the proposed method.

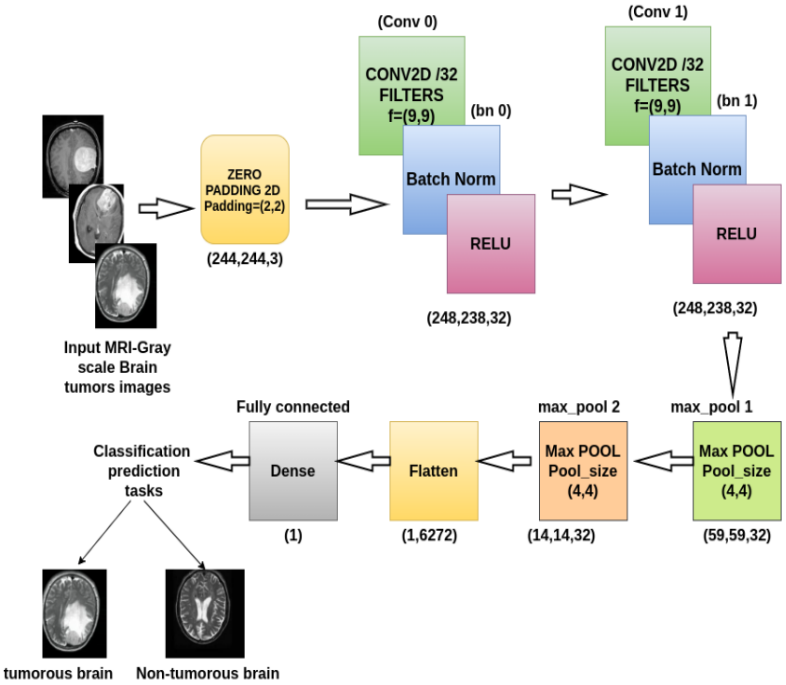



**Figure 1: Flowchart for the proposed method**

### 3.1 Zero padding 2D

In Artificial intelligent and especially in deep learning, The padding process refer to the amount of pixels added to an certain images when the kernel of a convolutional neural network is being used. Padding is being used and added to the frame of our gray scale image to allow more space, so that our kernel may cover the whole image.in our proposed method we set our padding to zero, to obtain a pixel value that is added but with zero value. This allowed our kernel to process our brain tumor grayscale image properly and being accurate to analyze our image.
Fig. 2 Illustrates an MR input grayscale image taken from kaggle, a public standard datasets [MohamedAliHabib2021]. Whereas Fig. 3 Highlights details of a Non-tumorous and tumorous brain respectively.

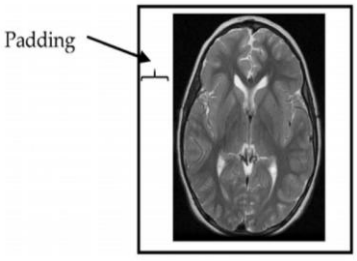



**Figure 2: Input grayscale image from Kaggle MR brain Images datasets [MohamedAliHabib2021], which has undergone a padding process**

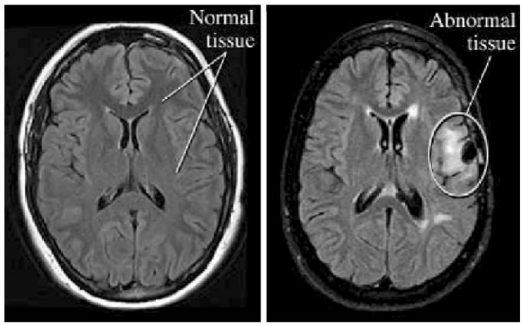



**Figure 3: Input grayscale image from a public datasets [MohamedAliHabib2021] the left image is normal brain without any tumorous tissue whereas the left one has tumorours tissues**

### 3.2 Two-Dimensional Convolution layer

In deep learning the convolution process is a simple application of a filter to a given input data that usually results in an activation.A repetion application of the same used filter results in a map of activations also known as feauture map.which show the location and the strenght of the detected feautures. In this manuscript we used a two-dimensional convolutional neural network (CNN), this is a linear operation which involves multiplications of weights and with input images. The multiplication is being performed by filters or kernel size of (9,9).

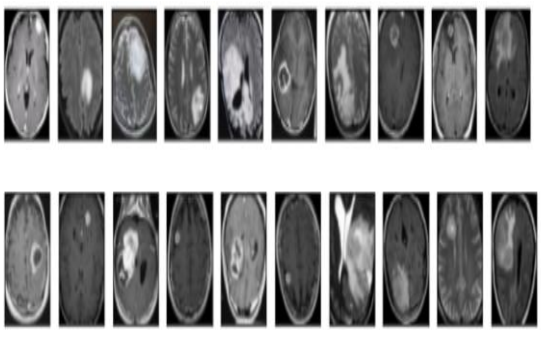
### 3.3 Max-pooling layer

Based on our discussion in Sub.3.2, Here the Max-pooling layers provide an approach to down sampling feauture maps and summarize feautures into patches of the feauture map. We adopted the max pooling to calculates the maximum or the largest, value in each patch of each feauture map, here a max filter was applied.

Max pooling was also used, to avoid over-fitting and to provide an abstracted form of the brain tumor representation.this process assists us to reduce the computational cost and the number of parameters to learn.

Based on the proposed model in Sub.1 the first pooling layer has filter of (4,4) and (59,59,32) whereas the second pooling layer reduced to (14,14,32) with (4,4) kernel size.

Fig. 4 Display the input grayscale MR image, after being preprocessed as explain in Sect.3



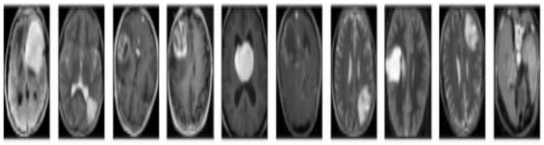


**Figure 4: Input grayscale image from Kaggle MR brain Images datasets [MohamedAliHabib2021], with brain Tumors**

Fig. 5 Display the input grayscale MR image, after being preprocessed as explain in Sect.3

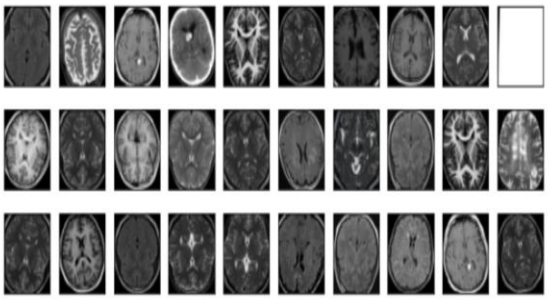


**Figure 5: Input grayscale image from Kaggle MR brain Images datasets [MohamedAliHabib2021], without brain Tumors**

### 3.4 Flattern and Dense layers

Taking into account of our brain tumor classification problem domain, we used the flattern layer to convert our data into a 1-dimensional array for inputing the the next layer this created a single long feature vector which linked us to the Dense layer.

The Dense layer, does the classification task. To detect tumorous regions of the brain and separate Images with tumor and non-tumor. Bellow are the dense layer formuolar.

Y = activation(*(X,kernel) +bias ). Here X represent the input MR Image, Kernel represent the weight data, * represents numpy of dot product of given input and corresponding weights, Bias highlights value used to optimize the model and the activation represents the used activation function.

## IV. EXPERIMENTS AND RESULTS

In this section, datasets used are discussed in Sect.4.1. Evaluation metrics are given in Sect.4.2. Whereas analysis of running time and platforms are described in Sect.4.3. Finally, the experiment details are given in Sect.4.4 and comparative results are discussed in Sect.4.5.

### 4.1 Used datasets

We considered a public standard dataset [MohamedAliHabib2021] obtained from Kaggle repository.It had $253$ tumorous and $155$ non-tumorous brain MRI images. This was a small dataset we adopted a data augmentation and tackling with imbalanced datas. After this augmentaton process, Non-tumorous and tumurous images become $980$ and $1085$ respectively. The summations of all

images of this dataset turned into $2065$.

### 4.2 Evaluation Metrics

Our model was evaluated based on Train and validation Loss, Train and validaton accuracy and the Test accuracy.

### 4.3 Analysis of running time and platforms

Experiments are done using $2065$ images from the standard dataset. non-tumorous images are $980$ and tumorous are $1085$. The sizes (width, height) of these images varie from $372 \times 364$.
The platforms used include a laptop with Intel(R) Core(TM) i7-3540M CPU @ 3.00GHz x 4. 64-bit with 8GB RAM. Python 3.7.6, Sklearn 0.23.1 and Ubuntu 18.04.3 LTS OS. Tab. ?? reports the running time in minutes. Training size = $60\%$ and test size = $40\%$

### 4.4 Experiments

Experiments are performed both on a standard public datasets for brain-tumour detection and BRATS 2015 as discussed in Sect.4.1. Our model was first tested on [MohamedAliHabib2021] datasets with Different CNN models as discussed in sect.3 The detection results T-L,T-A,V-L,V-A,T-A; Training Loss,Training Accuracy,Validation loss,Validation Accuracy,and Testing Accuracy respectively) are reported.
Tab. 1 reports the Tesing accuracy of the model when the we consider only one convolutional layer with kernel size of (3,3),Number of trainning parameters are 8,225 and the Fig. 10, 11 are the Loss and training metrics curve respectively.

| CNN model description | T-L | T-A | V-L | V-A | T-A |
|---|---|---|---|---|---|
| One-ConvLayer & Filter size = (3,3)<br>Epochs = 46<br>Number of parameters = 8,225 | 0.39 | 83.49% | 0.34 | 86.17% | 86.17% |

**Table 1: Evaluations metrics of CNN, considering One convolutional Input layer; Kernel or filter size of (3,3) and 8,225 parameters.**




**Figure 6: Trainning and validation loss metrics**

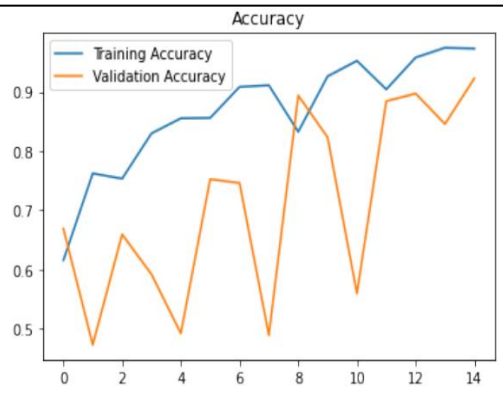



**Figure 7: training and validation accuracy metrics**

The results from Tab. 1 shows the performance of our model with one input layer and zero Padding, one convolutional 2D layer with kernel-size 3,3 two max pooling layers with kernel size of (4,4) each, a flattern layer and a dense layer of sigmoid as the activation function is presented. As the table highlights this model presents a Testing-Accuracy of 86.17%.

We retrain our datasets, to improve the Testing - Accuracy, this time we add an additional convolutional layer and remain with other properties exhibited by the Tab. 1

Tab. 2 reports the Tesing accuracy of the model when the we consider TWO convolutional layer with kernel size of (9,9). The number of parameters are 97,313 and the Fig. 10, 11 are the Loss and training metrics curve.

| CNN model description | T-L | T-A | V-L | V-A | T-A |
|---|---|---|---|---|---|
| One-ConvLayer & Filter size = (3,3)<br>Epochs = 46<br>Number of parameters = 8,225 | 0.091 | 97.31% | 0.3102 | 86.17% | 90.03% |

**Table 2: Evaluations metrics of CNN, considering Two convolutional Input layer; Kernel or filter size of (9,9) and 97,313 parameters.**




**Figure 8: Trainning and validation loss metrics**

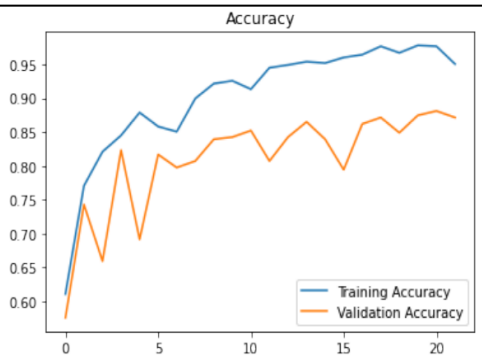



**Figure 9: training and validation accuracy metrics**

The optained results were not satisfactory yet, we retrain our data sets [MohamedAliHabib2021] using the proposed model as discussed in Section 3 to improve the testing accuracy. This time we considered same results from the table 2, but we reduced the number of convolution layer to One and the kernel size and decrease this to a filter size of (3,3). this model exhibits an increase interms of Testing accuracy.

Tab. 2 reports the Tesing accuracy of the model, we consider TWO convolutional layer with kernel size of (9,9). The total number of parameters are 97,313 and the Fig. 10, 11 are the Loss and training metrics curve.

| CNN model description | T-L | T-A | V-L | V-A | T-A |
|---|---|---|---|---|---|
| One-ConvLayer & Filter size = (3,3)<br>Epochs = 46<br>Number of parameters = 8,225 | 0.0807 | 98.21.791% | 0.3076 | 89.07% | 92.00% |

**Table 3: Evaluations metrics of CNN, considering Two convolutional Input layer; Kernel or filter size of (9,9) and 97,313 parameters.**




**Figure 10: Trainning and validation loss metrics**

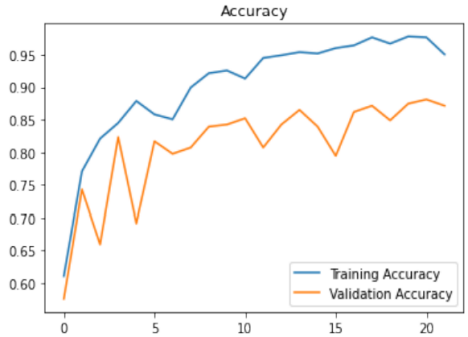



**Figure 11: training and validation accuracy metrics**

### 4.5 Comparative results

| CNN model comparisons | T-A (Testing Accuracy) |
|---|---|
| CNN [13] | 89% |
| Our MODEL | **92%** |

**Table 4: This table highligts the comparative results of our model and [Mohamed(2019]**

From the above comparative table, it is visible that our model outperform [Mohamed(2019] interms of accuracy. Our model exhibits as well a better trainning and validation accuracy and loss metrics. The proposed model is robus, flexible and cost effective in terms of performance as compared to other sharrow CNN methods.

## V. CONCLUSION

In this article,we presented a coherent techniques for detecting brain tumors in magnetic resonance images.Input grayscale image are loaded inside our proposed method.A zero pading layer with a pool size of (2,2) is being considered and a double-convolutional layer with 32 neurons and a filter size of (9,9) with one unit stridal is applied, with two batch normalization layer. The normalizing pixel values speed up the computational process with a RelU activation function.Two max pooling layer with a filter size and stridal value four (4)has being used. Finaly we applied a flatten layer to flatten our 3-dimensional matrix into a one-dimensional vector, this is then propelled into a Dense block (output Unit), which is a fully connected layer with one neuron using a sigmoid activation function . The classification task take place, where brain with tumor cells are being detected and classified as tumorous MR brain images and those without tumor cells are Non-tumourous brain MR images. Our method exhibits a higher Testing accuracy compared with the existing model discussed in Sect.4

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