

Brain Tumor Analysis Using Deep Neural Network

BY

Iftekhar Khan
ID: 171-15-9174

Kuheli Ahsan
ID: 171-15-8680

This Report Presented in Partial Fulfillment of the Requirements for
The Degree of Bachelor of Science in Computer Science and Engineering

Supervised By

Abdus Sattar

Assistant Professor

Department of CSE

Daffodil International University



DAFFODIL INTERNATIONAL UNIVERSITY

DHAKA, BANGLADESH

MAY 2021

APPROVAL

This Project titled “**Brain Tumor Analysis Using Deep Neural Network**”, submitted by **Iftekhhar Khan**, ID No: **171-15-9174** and **Kuheli Ahsan**, ID No: **171-15-8680** to the Department of Computer Science and Engineering, Daffodil International University, has been accepted as satisfactory for the partial fulfillment of the requirements for the degree of B.Sc. in Computer Science and Engineering (BSc) and approved as to its style and contents. The presentation has been held on 2 June, 2021.

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Professor and Head

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Faculty of Science & Information Technology
Daffodil International University

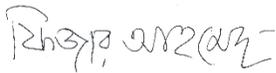
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Faculty of Science & Information Technology
Daffodil International University

Internal Examiner



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Assistant Professor

Department of Computer Science and Engineering
Faculty of Science & Information Technology
Daffodil International University

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Professor

Department of Computer Science and Engineering
East West University

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We hereby declare that, this thesis has been done by us under the supervision of **Abdus Sattar, Assistant Professor, Department of CSE** Daffodil International University. We also declare that neither this thesis nor any part of this thesis has been submitted elsewhere for award of any degree or diploma.

Supervised by:

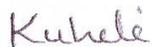


Abdus Sattar
Assistant Professor
Department of CSE
Daffodil International University

Submitted by:



Iftekhar Khan
ID: 171-15-9174
Department of CSE
Daffodil International University



Kuheli Ahsan
ID: 171-15-8680
Department of CSE
Daffodil International University

ACKNOWLEDGEMENT

First we express our heartiest thanks and gratefulness to almighty God for His divine blessing makes us possible to complete the final thesis successfully.

We really grateful and wish our profound our indebtedness to **Abdus Sattar**, Assistant Professor, Department of CSE Daffodil International University, Dhaka. Deep Knowledge & keen interest of our supervisor in the field of “Human Computer Interaction in Education” to carry out this thesis. His endless patience ,scholarly guidance ,continual encouragement , constant and energetic supervision, constructive criticism , valuable advice ,reading many inferior draft and correcting them at all stage have made it possible to complete this thesis.

We would like to express our heartiest gratitude to **Pro. Dr. Touhid Bhuiyan, Professor, and Head**, Department of CSE, for his kind help to finish our thesis and also to other faculty members and the staff of CSE department of Daffodil International University.

We would like to thank our entire course mate in Daffodil International University, who took part in this discuss while completing the course work.

Finally, we must acknowledge with due respect the constant support and passion of our parents.

ABSTRACT

The identification of tumors is one of the most tenacious and emerging fields in medical image processing. A tumor means the unrestricted existence of a bunch of cells in a precise area of the human body which destroys the normal body cells and keeps increasing. In human body, brain tumor is measured as the most common tumor which affects the nervous system, memory functional cells, glands, and membranes that surround the brain and can conduct to a high mortality rate if the affected one is unsuccessful to reach proper medical treatment. For effective treatment, precise and early recognition of the tumors is critical work and also a vital step in diagnosis and treatment preparation for affected one which not only benefits to arise with improved medications but also saves the affected life in due time. In this work, we use Magnetic Resonance Imaging (MRI) which is a prominent imaging procedure in terms of brain tumor recognitions. For features extraction, segmentation and classification, we proposed a work that contains the deep neural network integrated method Convolutional Neural Network (CNN) to classify the MRI images and we achieved an accuracy of 97.92%.

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CHAPTER 1

INTRODUCTION

1.1 Introduction

In the human body, old cells die and their place is taken by new cells. It's a usual procedure but sometimes this procedure goes incorrect, the body creates new cells when it doesn't require by the body because early cells didn't expire yet. This process is called abnormal growth of cells which is also called a tumor. A tumor can be grown at several points of our body, the brain tumor is one of them. Brain tumors can be benign or malignant like other tumors of the human body. If the tumors grow slowly in only one place and don't spread out to other points of the brain then it's called benign which is a non-cancerous tumor. On the other side, malignant which is a cancerous tumor, grow much more rapidly and spread frequently surrounding the brain. For effective treatment and saving patient life, early detection of tumors inside the brain is the key.

Medical image diagnosis plays a vital role in tumor detection. Medical images can be obtained from several diagnosis systems like Computed Tomography (CT), Magnetic Resonance Imaging (MRI), and Positron Emission Tomography (PET) [1]. We chose an MRI for our work among them. MRI produces images of the brain which can be used to identify the different sizes of the tumors and their location. The doctor can get a proper idea of a benign or malignant tumor before involves in surgery. Reducing diagnosis time and human eye error for tumor detection and classification is the main concern of our work. We used an automatic procedure for that work.

In this study, reducing errors of prediction, we work on a Convolutional Neural Network (CNN) created tumor prediction model using a large number of brain images. For performing image classification, we need to preprocess the images first because there is a lot of noise in the MRI images. We resize the images and rescale the MRI images 0 to 1. To identify the region of interest and leaving other reasons untouched feature extraction played an important role. Our CNN model contains 3 convolutional layers where we use

ReLU as an activation function. In the first convolutional layer, we use 16 3x3 filters for feature extraction. Similarly, we use 32 and 64 3x3 filters for the next 2 convolutional layers, and MaxPool2D (2,2) is used in our model which considers ReLU created feature map as an input and making a slice of 2x2matrix on the top-left of the import feature map and finds the max value. After that, we flatten the feature maps and create the dense layer. The sigmoid activation function is used to predict that there has a tumor or not in the images of MRI. Using this large amount of data, our model can predict tumorous or non-tumorous brain images with elevated accuracy. The model is trained with the training and validation dataset and then we use the test dataset on that model to predict as 0 (no tumor) or 1 (have tumor). Comparing the predicting data with the actual test data, we find the test accuracy of our model. Our model achieves 99.76% of training accuracy, 99.36% of validation accuracy, and 97.9% of test accuracy. Considering f1 scores, our model performs 98 for predicting both tumorous or non-tumorous brain images.

1.2 Motivation

In the human body, old cells die and their place is taken by new cells. It's a usual procedure but sometimes this procedure goes incorrect, the body creates new cells when it doesn't require by the body because early cells didn't expire yet. This process is called abnormal growth of cells which is also called a tumor. A tumor can be grown at several points of our body, the brain tumor is one of them. Brain tumor is measured as the most common tumor which affects the nervous system, memory functional cells, glands, and membranes that surround the brain and can conduct to a high mortality rate if the affected one is unsuccessful to reach proper medical treatment. For effective treatment, precise and early recognition of the tumors is critical work and also a vital step in diagnosis and treatment preparation for affected one which not only benefits to arise with improved medications but also saves the affected life in due time.

1.3 Problem Definition

Recently, tumors have become a more common and dangerous threat to humanity because of many mortality and disabilities rate around the world. The brain tumor is the most adventurous of them which directly affects the nervous procedure, blood circulation, organs functionalities. Several approaches are applied to identify the tumors among them we use the classification of MRIs. A faster involuntary brain tumor recognition and classification procedure are described in this study using Convolutional Neural Networks (CNN).

1.4 Research Questions

Here are the main questions those are focuses in this thesis are given below:

- What kind of affects Brain Tumor has in human life?
- How Convolutional Neural Networks helps us to identify the brain tumor?
- How MRI images are implemented in this prediction model?

1.5 Research Methodology

In this section of our research paper, we reveal the Experiment Data Set, Data Pre-processing, Architecture of the Model, Learning Rate and Optimizer of the Model, Data Augmentation process and Training the Model. At the end of this chapter performance of the proposed model will be described.

1.6 Research Objectives

There are some benefits of using Convolutional Neural Networks to predict the brain tumor. Some objectives are given below:

- Develop an efficient model to detect brain tumor.
- Describe the importance of early identification of tumor and provide medical support
- Using better algorithm for tumor detection

- To inspire the software developers to work with AI using the model.
- Integrate the model in mobile apps and websites.

1.7 Research Layout

Chapter 1: will discuss about introduction, motivation, problem definition, research question, and research methodology.

Chapter 2: will discuss about background of this research and the related.

Chapter 3: will describe experiment Data Set, Data Pre-Processing, Image Segmentation, Feature Extraction, Tumor Classification.

Chapter 4: will discuss about Training, Testing and the Validation of the model.

Chapter 5: it is focus to the result comparison and analysis.

Chapter 6: It describes the Conclusion and Future work..

Chapter 7: here all the references we used for this research.

CHAPTER 2

BACKGROUND

2.1 Introduction

In Bangladesh there are no similar work or research was done which can detect brain tumor perfectly. So the background describe the current situation of this research field and the use of deep learning for tumor prediction.

2.2 Related Works

A faster deep learning algorithm R-CNN is proposed and classified the MR images into normal Glioma, Meningioma, and Pituitary. To make the area of the tumor they used Region Proposal Network (RPN). For the equal region identification procedure proposed in the classifier system, they used VGG-16 architecture, and the mean average precision for the algorithm was 77.60% [1]. The proposed a CNN-based system where extracting features through CNN and Categorizing with a fully linked network. The model achieved 96.08% accuracy and 97.3 f-score by having 3 layers and 35 epochs of CNN [2].

They introduce a high permit filter image to protruding the inhomogeneities field outcome of the MRI based on the input portions and a median filter is used to the fused parts. 200 hidden units used in the first layer and 400 unseen units are operated in the second layer and using the softmax layer the testing is performed to identify having tumors and no tumors [3]. For segmentation of brain tumor tissues, they investigate the possibility to directly apply convolutional neural networks (CNN) where they only apply quality intensity of preprocessing to the previously given data but for the output data, no post-processing is applied [4].

A BrainMRNet model is more effective than the pre-trained convolutional neural network models (AlexNet, GoogleNet, VGG-16) which are constructed on attention units and hypercolumn method. In BrainMRNet image is preprocessed then relocated to attention

modules with image augmentation procedures for each image. After choosing significant areas, images are relocated to convolutional layers. The accuracy of the BrainMRNet model was 96.05% [5]. They advanced six CNN models for brain tumor classification such as Model 1, Model 2, Model 3, Model 4, Model 5, and Model 6 which takes more time to execute and then using BraTS2013 dataset trained all the models and verified them with the WBA dataset. After the classification of all the models, they analyzed the accuracies which were mostly 96-99% [6]. A new fully automatic model called CNN-SVM by combining features of the CNN which were applied for features extraction and Support Vector Machine (SVM) which was applied for enhanced performance in the classification of MRI images. The Fivefold cross-validation procedure of the integrated system attained an accuracy of 95.82% [7].

In this paper, they describe the MLBPNN analysis with the support of an infra-red sensor imaging system. This imaging sensor is combined via a wireless infrared imaging sensor and the features are extracted with a fractal dimension algorithm. The sensor is formed to convey the tumor warm data to a professional clinician to screen the wellbeing condition [8]. They discussed the identification of MRI images and segmentation based on a morphological operation (Fuzzy transformation) of brain tumor. They explained four different methods such as pre-processing, image fragmentation, extraction, and classification of images for the identification of brain tumors [9]. Acquiring brain images from patients, they applied noise removal, a morphological operation based on segmentation, feature extraction, Naive Bayes. Accuracy was predicted by using the Naive Bayes classifier [10].

An LIPC based methodology was introduced. This methodology is used for the classification and segmentation of brain tumors. Firstly, preprocessing techniques such as noise removal of the MRI images and the enhancement were performed. Also performed PCA and LDA for feature extraction, reduction, and improvement of classification performance. LIPC performed the main part of the distribution of different classes. The

planned technique achieved a Dice Score of 0.95. [11] A multiblock framework for involuntary segmentation which includes automatic image-guided treatment arrangement, assessment of outcome, development of data-driven analytical models of brain tumor patients using MR images. Anomaly detection using OC-SVM to generate the tumor disguises for each image part was used [12].

In this paper, the use feature extraction algorithm and Convolutional Neural Network(CNN) to detect cancer of brain images. Create two categories of normal and patient classes and trained system with 1666 images and 226 test images. Evaluate the performance by using three classifiers of CNN. Softmax fully connected layer classifier obtained 98.67% accuracy, Radial Basis Function(RBF) classifier obtained 97.37%, and Decision tree 94.24%. For evaluating network performance, used benchmarks of Sensitivity, Specificity, and Precision. [13]

They present a novel CNN architecture which activities both local structures as well as more global contextual structures and varies from those conventionally used in computer vision. A convolutional execution of a fully connected layer is used on the model which permits a 40 fold speed up and also defines a 2-phase to confrontation problems related to the inequity of tumor labels [14]. They compared with existing supervised models, and all the accessible approaches morphological operations were incorporated to eliminate undesirable regions and got an accuracy rate above 96.23% to citemajib2020framework. Brain tumor recognition and segmentation are completed based on transfer learning where brain tumor images are classified into normal, Low-Grade Glioma (LGG), and High-Grade Glioma (HGG). VGG-19 transfer learning model is performed with 6 epochs which gave training accuracy 99.82%, validation accuracy 96.32%, and test accuracy 99.30% [15].

CHAPTER 3

RESEARCH METHODOLOGY

3.1 Introduction

MRI images contain many more defects, for example, noises and distortion which make it problematic for surgeons to examine the tumor and deliver necessary treatment [10]. The noises and distortion sometimes created by the movement of the patients or mechanical defect of MRI which act as tumor, it is very hard to classify the tumor cells and normal cells. Our model can identify brain tumors with good accuracy. In, this part, we will narrate our complete work and the framework is revealed in Figure.

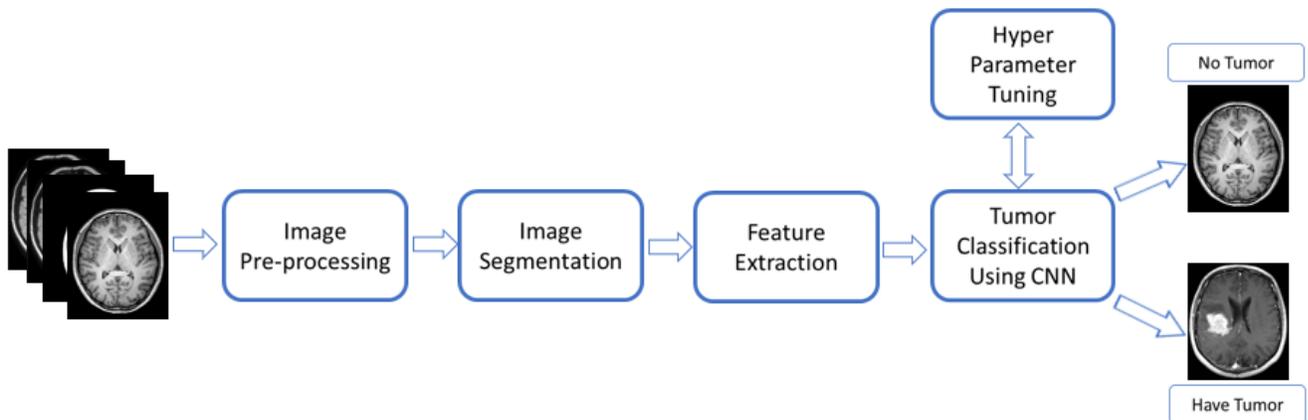


Figure 3.1.1 Complete workflow of Brain Tumor Detection.

3.2 Experiment Data Set

For this study, 8,298 MRI images were collected from Kaggle 123, where 3573 of those MRI images has tumor, and 4725 images has no tumor. Along with these data, we collected 56 MRI images from a public medical college hospital⁴. Among our collected data, 26 MRI images have tumors, and 30 images don't have tumors. Merging all the MRI images, we apply a data augmentation process which usually uses to preciously enlarge the amount

of the data by producing altered versions of images. This operation makes the images resized, rescaled, and flipped, etc.

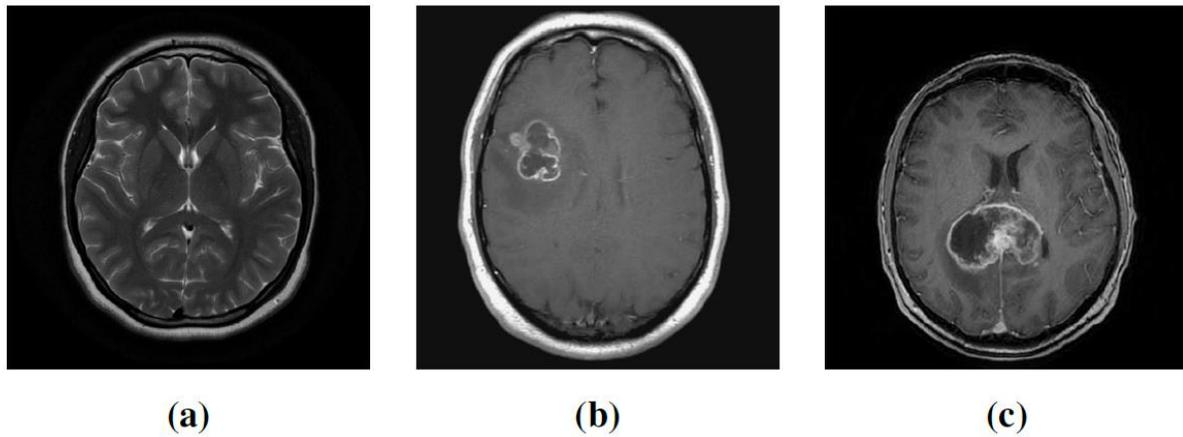


Figure 3.2.1 Collected Dataset

After that, we achieve 33,416 tumorous and non-tumorous images of the brain for classification. For classification and segmentation, we split 33,416 images of MRI in the ratio of 70% images (23,390 images) as the training dataset, 15% images (5014 images) as the test dataset, and 15% images (5012 images) as validation dataset.

3.3 Data Pre-Processing

All For image-based prediction models, pre-processing under-take an important role. During the acquisition of MRI machines, movements made by the subject can be obtained artifacts such as noise, distortion, and motion heterogeneity which also can be obtained by the limitations of MRI machines. False intensity levels of artifacts conduct us a false prediction. N4ITK bias field correction technique is used to deal with artifacts [16]. Gaussian filter which is a linear filter is used widely for the high sensitivity and remove noise from medical images such as MRI [17]. The equation defines by

$$G(x, y) = \frac{1}{2\pi\sigma} e^{-\frac{x^2+y^2}{2\sigma^2}} \quad (1)$$

Here, x and y defines the distance from the sequentially horizontal and vertical axis, and σ means the standard deviation of the equation. The intensity normalization process makes the intensity values in a coherent range of our image dataset. The intensity normalization means intensity value obtains 0 and standard deviation obtains 1 [16]. The equation defines by

$$i_0 = \frac{i - \mu}{\sigma} \quad (2)$$

Where i is normalized the terms of mean μ and standard deviation σ to get output i_0 . To improve the exactness of tumor detection, all the MRI picture resized into 200x200 and RGB images are converted into gray scale images.

3.4 Image Segmentation

In image processing, segmentation is a commonly used classification method and the fundamental objectives are, depend on regions splitting the images. On segmentation, images are converting into something more understandable and each pixel is assigned with a label such that each pixel under the same label shares some common characteristics [18]. For ordering pixel values of grayscale images, Morphological processing is performed which is a collection of non-linear procedures using for binary processing of image related to the image shape [10].

$$f(x) = \max(0, x) \quad (3)$$

In image segmentation, threshold-based binary segmentation is mostly incorporated method because of its fast-processing approach and simple mathematical calculation. A region-based segmentation is done by extracting the pixel intensity values of MRI images

considering the regions of the image with identical pixel values which are widely used in medical fields. In this segmentation process, the areas are checked for the adjoining pixel values of intensities if values are similar to the earlier values then apply to the area until all the similar values are matched [19].

3.5 Feature Extraction

In this procedure, we are getting the significant elements of the images while discounting excessive elements which may central to erroneous identification. Recognizing the Region of Interests (ROIs) of specific regions while leaving other regions untouched can be considered into three separate groups which contain shaped, sized, and color counting mean, standard deviation, entropy, energy, and secondary features such as smoothness, IDM, contrast, correlation, and homogeneity [20]. Computer Vision and Machine Learning texture analysis is the decisive feature for utilizing proficiently by selecting projecting features to exploit the precision for the diagnosis of the tumor. By textual observations and analyses, therapy can be enhanced. Based on the grey level histogram, superior-level image details are calculated by extracting parameters with statistics of different degrees, and secondary-level features are applied for more precise analysis [21].

3.6 Tumor Classification

In deep learning, Convolutional Neural Networks (CNN) are mostly used network which contains input, output, and one or more hidden layers that have confirmed very operative in the regions such as image identification and classification. CNN contains numerous nonlinear stages of the process and its layers are arranged in three dimensions such as width, height, and depth. The networks among pixels in the initially giving images are the combination of Convolution Layers, ReLU, Pooling, Normalization, and Fully Connected layers. Simple elements like edge detection are completed in the initial stage, complex features extracted are completed in the other layers and the max-pooling layer improves detection of unusually placed objects. Images are treated as an array of pixels combination of height x width x dimension based on 3D or grayscale. In the convolution operation,

images of MRI are converted into an array based on its size. All the images were not the same size in the initial stage. We resized them and converted them into 200x200x3 pixels.

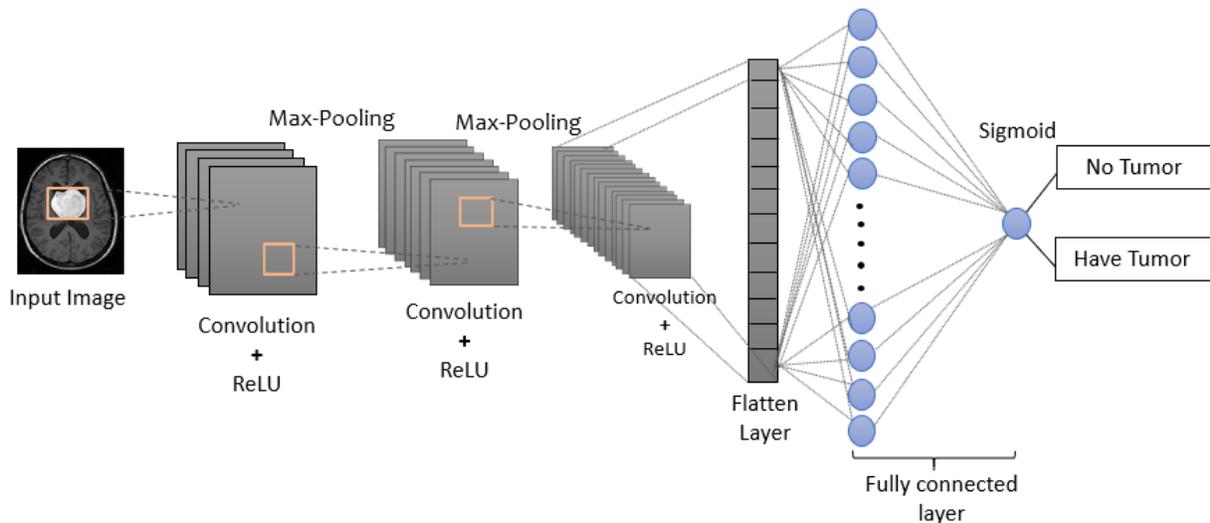


Figure 3.6.1 Convolutional Neural Network (CNN).

To identify a certain area of the images, we use 3x3 filters which are mainly used for detecting the features from the images. In the initial stage of convolution, we used 16 3x3 filters for edge detection. Filters are nothing but the 3x3 matrices. The values of the matrices can be obtained during the training process. Each filter identifies different parts of the image. Filters usually place on the left top of the MRI images and move one stride at a time in the right. During that process summation after matrices multiplication of values filter placed area of the MRI images with the filter's value and placed all the new values in a feature map.

After generating the new feature map, we applied the Rectified Linear Units (ReLU) to make the model non-linear. The slope of the ReLU function isn't constant. ReLU is a commonly used activation function in Convolutional Neural Network. It makes all the negative value to zero and keep all the positive value remain the same that makes the training process faster and as we increase extra layers, the probable complexity of interactions only rises. The equation can be written as, After ReLU, local or global pooling

layers are included in convolutional networks. Max pooling is commonly used in CNN to reduce the size of neuron clusters in the outputs at one layer into a single neuron in the next layer. We used MaxPool2D(2,2) in our model which basically considers ReLU created feature map as an input and making a slice of 2x2 matrix on the top-left of the import feature map and finds the max value.

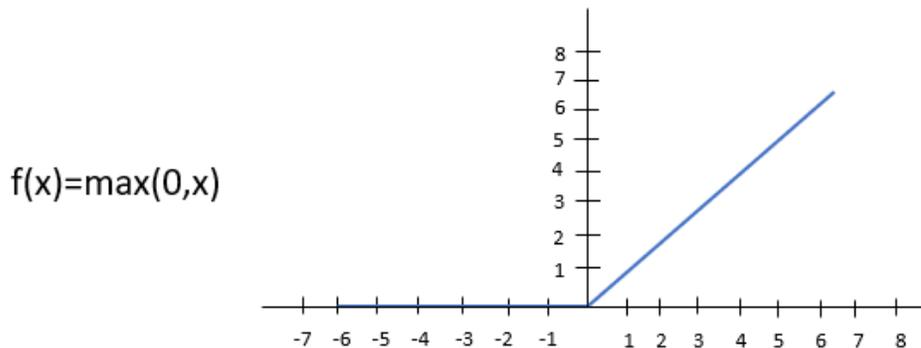


Figure 3.6.2 Rectified Linear Units (ReLU).

The feature map would be comprehending the most protruding features of the prior feature map. A stride of one at a time from left to right reduce the dimensions and computation of the import feature map. In the next convolution layer, we use 32 filters for features extraction and creating feature maps containing the ReLU activation function and 2x2 max-pooling layers. After that, 64 filters are taken place with ReLU and max-pooling layers. The final stage of CNN is called a dense layer, which is a classifier of Artificial Neural Network (ANN). This ANN classifier requires discrete features which is a feature vector as an input. So, the convolutional layer provided output converted into a one-dimensional feature vector and this is called flattening. We flatten all the imports from the convolution layer to create a single long feature vector for the dense layer.

At the end of a CNN, the feature vector as an output of the flatten Layer uses as an input to the fully connected layer which executes classification created by the features extracted of the earlier layers. The 1D data from the flatten layer acts as the input to the neurons of fully connected layers to perform dot product of previously provided data and the Neuron's Weights created output. There can be one or more fully connected layers where each node of the initial layer is connected to every single node in the subsequent layer. We use 512 dense layers which are connected with the flatten layer and this is connected with a single neuron that uses a sigmoid activation function for predicting the output.

$$\sigma(z) = \frac{1}{1 + e^{-z}} \quad (4)$$

The main reason behind using this activation function called the sigmoid function is because it exists between (0 to 1). Therefore, we are specially used for models where we have to predict that there has a tumor or not in the images of MRI.

CHAPTER 4

PERFORMANCE OF THE PROPOSED MODEL

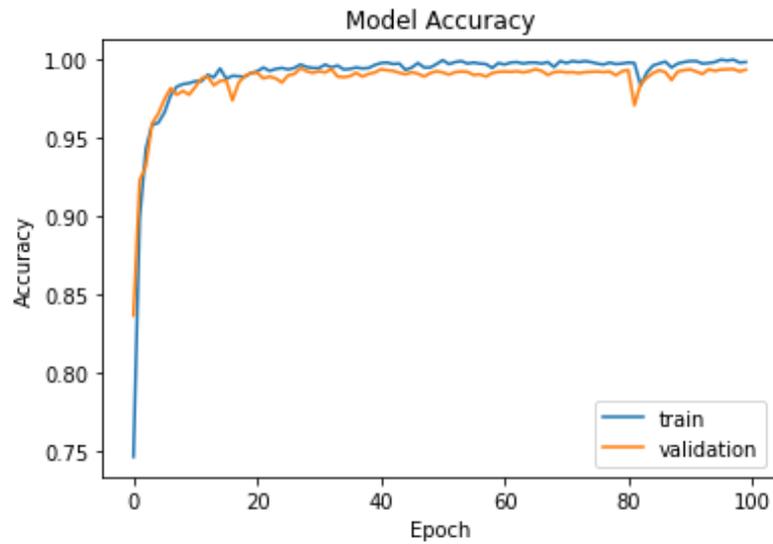
4.1 Training, Testing and the Validation of the model

We split our full dataset of 33416 MRI images into 3 parts using the ratio of 70% of train data, 15% of test data, and 15% of validation data. For training, we use 23390 images where 10663 images have no tumor and 12727 images have a tumor. For validation data, we use 5012 images where 2285 images have no tumor and 2727 images have a tumor.

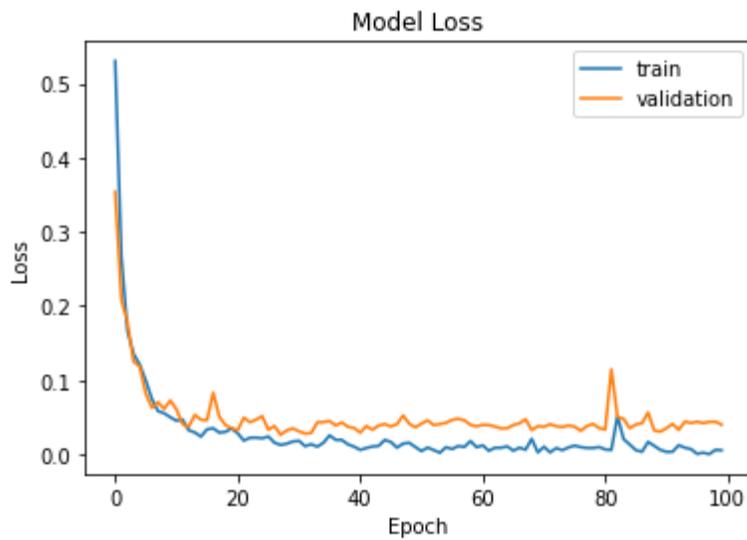
Table 4.1 Accuracy and Loss Function of Dataset

Datasets	Accuracy	Loss
Training	0.9976	0.0024
Validation	0.9936	0.0064
Test	0.9792	0.0208

We use the training dataset and test dataset to fit our model containing 100 epochs and steps per epoch is 50. After fitting our model, we find an excellent train and validation accuracy. For test accuracy, the model is used to predict 5014 MRI images where 2286 images have no tumors and 2728 images have tumors. We save this prediction in a list and converted the actual test data label into another list. Then we use the accuracy matrix to find the test accuracy of our model.



(a)



(b)

Figure 4.1. In figures, (a) shows the accuracy of train and validation datasets. (b) shows the loss of those to datasets.

Then we create a Confusion Matrix, which is a special data table that is frequently applied to define the representation of a classification model based on predicted data and the true values. The confusion matrix helps us to understand the model easily, but the related

functionality can be confusing. It predicts 4 kind of possible data which is true positive, false positive, true negative, and false negative. True positive means model predicts as a tumor that patient has the tumor. False positive means the model predicted yes, but they don't have the tumor. In the true negative, the model predicted no, and the patient doesn't have the tumor and false negatives describe that model predicted no, but they do have the tumor. Based on that explanation, my model performs extremely well on that large amount of data.

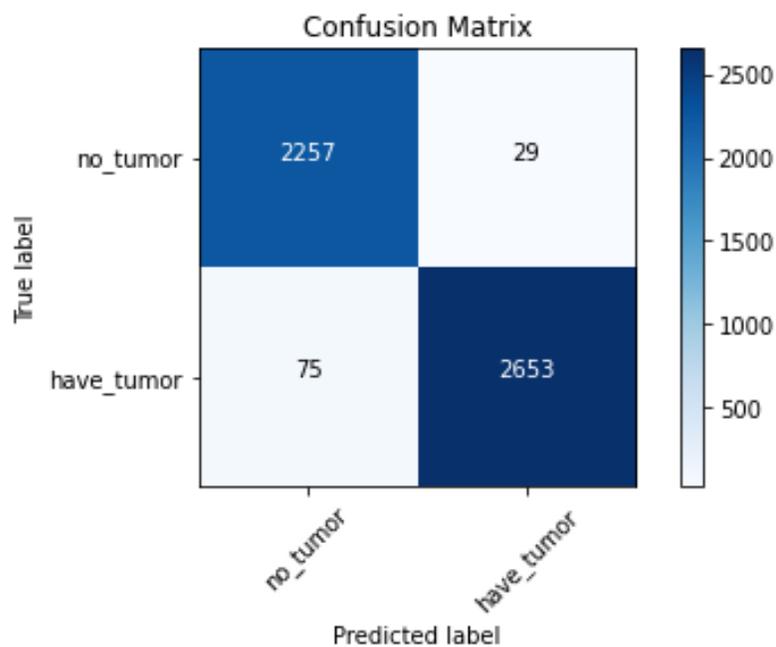


Figure 4.2. Confusion Matrix

	precision	recall	f1-score	support
0	0.97	0.99	0.98	2286
1	0.99	0.97	0.98	2728
accuracy			0.98	5014
macro avg	0.98	0.98	0.98	5014
weighted avg	0.98	0.98	0.98	5014

Figure 4.3. Precision, Recall, and F1 Score.

Then we find precision, recall, and f1 score which indicate how good perform our model to predict tumors. Precision shows the percentage of correctly predicted positive with the entire observations of positive predicted. The precision of our model is high which means a low false prediction rate. Recall shows the percentage of appropriately predicted positive observations with all positive observations. The Precision and Recall created weighted average are revealed by the F1 Score. Sometimes, understanding the accuracy will be difficult if false positives and false negatives have similar costs, so F1 is generally more beneficial than accuracy.

CHAPTER 5

RESULT COMPARISON AND ANALYSIS

This work gives us the highest accuracy and make a comparison with other algorithms. There are some research works which was nearly closed to this work. Table 1 exhibiting some Interrelation between our work and some previous work on several insect detections.

Table 5.1 Comparison with the other model

Algorithms	Accuracy
Gaussian Filtering with MLP (Multi-Layer Perceptron)) [22]	93 %
Naive Bayes [23]	94 %
Clustering Algorithms [24]	94.55 %
SVM [25]	95 %
Decision Tree [26]	96 %
K-Means and support vector machine [27]	96.96 %
Our model	97.92 %

CHAPTER 6

CONCLUSION AND FUTURE WORK

Recently, tumors have become a more common and dangerous threat to humanity because of many mortality and disabilities rate around the world. The brain tumor is the most adventurous of them which directly affects the nervous procedure, blood circulation, organs functionalities. Several approaches are applied to identify the tumors among them we use the classification of MRIs. A faster involuntary brain tumor recognition and classification procedure are described in this study using Convolutional Neural Networks (CNN). The algorithm was selected for the identification of the tumor sections and categorizing them into tumorous or not. Although we use a huge dataset for model prediction, our CNN model benefits us to obtain 97.92% test accuracy with an f1-score of 98. The main objective of this paper is to highlight the importance of early tumor prediction and give the therapist more time to diagnose the patients properly. In the future, we plan to make an application which not only predicts the tumors but also provide us a 3D visualization of the tumor infected area.

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