

Brain Tumor Detection And Classification

**Submitted in partial fulfillment of the requirement for the award of
Degree of Bachelor of Technology in
Information Technology Discipline**

Submitted To



**SVKM's NMIMS,
Mukesh Patel School of Technology Management & Engineering,
Shirpur Campus (M.H.)**

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**DEPARTMENT OF INFORMATION TECHNOLOGY
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SESSION: 2020-21**

CERTIFICATE

This is to certify that the work embodies in this Project entitled “**Brain Tumor Detection And Classification**” being submitted by

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for partial fulfillment of the requirement for the award of “**Bachelor of Technology in Information Technology**” discipline to “SVKM’s NMIMS, Mumbai (M.H.)” during the academic year 2020-21 is a record of bonafide piece of work, carried out by him under my supervision and guidance in the “**Department of Information Technology**”, MPSTME, Shirpur (M.H.).

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CERTIFICATE OF APPROVAL

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has been examined by us and is hereby approved for the award of degree “**Bachelor of Technology in Information Technology Discipline**”, for which it has been submitted. It is understood that by this approval the undersigned do not necessarily endorse or approve any statement made, opinion expressed or conclusion drawn therein, but approve the project only for the purpose for which it has been submitted.

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The students of **Bachelor of Technology in Information Technology discipline, Session: 2020-21, MPSTME, Shirpur Campus**, hereby declare that the work presented in this Project entitled “**Brain Tumor Detection And Classification**” is the outcome of our work, is bonafide and correct to the best of our knowledge and this work has been carried out taking care of Engineering Ethics. The work presented does not infringe any patented work and has not been submitted to any other university or anywhere else for the award of any degree or any professional diploma.

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ABSTRACT

A brain tumour is a collection of tissue that has been pre arranged by the gradual addition of abnormal cells. It happens when cells in the brain shape irregular formations. It has recently become a leading cause of death for many people. Since brain tumours are among the most dangerous of all cancers, prompt diagnosis and treatment are needed to save a life. Because of the development of tumour cells, detecting these cells is a challenging task. It is critical to equate the treatment of a brain tumour with that of an MRI. There are many types of tumors some of them are Glioma, Pituitary, Meningioma. Neural Network is used to classify the tumor. Basically MRI images of different types of tumor are given as input to the system on which the system is trained and input images are taken to test the model.

One of the most important things for a doctor to do before starting treatment is to detect a tumour. Traditionally, tumours were discovered by drilling a hole in the skull and removing a small part of the tumour to inspect. Detection has become easier with the help of machine learning and MRI images. The system is given MRI images of patients, and it performs detection and classification on the given set of images. There are numerous algorithms available for this task. In this paper, some techniques for detecting and classifying brain tumours are discussed. Our system accepts brain MRI images as input. The main goal is to provide doctors with a high - precision system for classifying tumour types. Feature extraction by using the Keras and Sequential model is used as we would be having only one input image and the output would be given so we preferred using a Sequential Model. CNN is used to classify brain tumours into stages automatically. The brain tumour spread area is detected as well as segmented using the K-means clustering algorithm. Numbers of defect cells are found in the spreaded region. This paper concentrates on detecting and classifying the types of tumor if no tumor is detected it is given as output to the user as no tumor was detected and if tumor is detected the user would get an output displaying the type of tumor along with the images. The main goal is to provide doctors with a high - precision system for classifying tumour types.

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CHAPTER 1

INTRODUCTION

Today cancer is one of the leading causes of death. According to the World Health Organization (WHO) in the year 2018, 9.6 million people worldwide have died of cancer. With early detection, half of there could have been prevented. Brain tumour is one of the most dangerous types of cancer it is estimated that around 17,760 people are predicted to die from brain tumours in the year 2019.

The symptoms of a brain tumour vary depending on the size, type, and location of the tumour. Because of its invasive nature and limited space a brain tumour is extremely dangerous and life-threatening. A brain tumour is a collection of abnormal cells that grow inside or around the brain. Tumors can kill all healthy brain cells directly, and they can also harm healthy cells indirectly by crowding other parts of the brain. The human brain's structure makes diagnosing a tumour in the brain region difficult.

For tumour diagnosis MRI is a useful method for obtaining high-quality brain image and is widely used. Image processing is the process of analysing and manipulating a digital image, with the goal of improving its quality. This method transforms an image into a digital format in order to extract or enhance it. MRI images can be used to extract detailed information about human anatomy and tissues.

Segmentation is used in medical imaging modalities to detect infected tumour tissues. In image analysis, it is an essential and important step to divide an image into different regions or blocks that share similar and equal properties, such as colour , texture, contrast, brightness, boundaries and grey level.

Convolutional neural networks (CNN) are a category of deep learning architecture that performs one of three operations: convolution, pooling, or rectified linear unit (ReLU).

A regular CNN can determine whether or not an image contains an object, but it cannot determine its position. Region-based CNN (RCNN), on the other hand, is specifically used for finding objects in photos and is an expanded variant of CNN. Automatic segmentation of large volumes of MRI images has been successfully achieved using deep learning techniques. By distinguishing distinct characteristics, CNN-based algorithms for automatic MRI segmentation for brain tumors achieved successful results.

1.1 Purpose

Brain Tumors are classified as: Glioma Tumor, Meningioma Tumor, Pituitary Tumor, etc. Proper treatment, planning, and accurate diagnostics should be implemented to improve the life expectancy of the patients. The best technique to detect brain tumors is Magnetic Resonance Imaging (MRI). A huge amount of image data is generated through the scans. These images are examined by the radiologist. A manual examination can be error-prone due to the level of complexities involved in brain tumors and their properties.

Application of automated classification techniques using Machine Learning (ML) and Artificial Intelligence (AI) has consistently shown higher accuracy than manual classification. Hence, proposing a system performing detection and classification by using Deep Learning Algorithms using Convolution Neural Network (CNN) would be helpful to doctors all around the world.

1.2 Scope

The project aims at detecting and classifying the type of brain tumour which will help medical practitioners and radiologists in easy diagnosis of the disease. The user can give the MRI of the brain as an input and can find the type of tumor if present.

1.3 Overview

Today cancer is one of the leading causes of death. According to the World Health Organization (WHO) In 2018 9.6 million people worldwide have died of cancer. With early detection, half of these could have been prevented. Brain tumour is one of the most dangerous types of cancer it is estimated that around 17,760 people are predicted

to die from brain tumours in the year 2019. The symptoms of a brain tumour vary depending on the size, type, and location of the tumour. Because of its invasive nature and limited space a brain tumour is extremely dangerous and life-threatening. A brain tumour is a collection of abnormal cells that grow inside or around the brain. Tumors can kill all healthy brain cells directly, and they can also harm healthy cells indirectly by crowding other parts of the brain. The human brain's complex structure makes diagnosing a tumour in the brain region difficult. For tumour diagnosis MRI is a useful method for obtaining high-quality brain image and is widely used.

Image processing is the process of analysing and manipulating a digital image, with the goal of improving its quality. This method transforms an image into a digital format in order to extract or enhance it. MR images can be used to extract detailed information about human anatomy and tissues. MR images are primarily used in biomedicine to detect and visualise finer details in the body's internal structure. Magnetic resonance imaging generates a single signal that can be detected and is spatially enclosed, resulting in images of the body. Brain tumour detection can be thought of as an image segmentation problem in which the tumour is labelled on the image. MRI images have been subjected to various image processing methods as well as machine learning algorithms in order to solve this problem.

For diagnosis, multiple magnetic resonance imaging (MRI) sequence images are used in science. For better treatment, the early detection of a brain tumour is a critical issue. When a brain tumour is clinically suspected, it is important to carry out a radiological test to determine its location, size and impact on the surrounding areas. Deep learning is a machine learning technique that makes use of a neural network architecture with hundreds of hidden layers between the input and output layers. It's been used to solve a variety of problems, including image classification, object detection, and speech recognition.

Convolutional neural networks (CNN) are a category of deep learning architecture that performs one of three operations: convolution, pooling, or rectified linear unit (ReLU). A regular CNN can determine whether or not an image contains an object, but it cannot determine its position. Region-based CNN (RCNN), on the other hand, is

specifically used for finding objects in photos and is an expanded variant of CNN. Automatic segmentation of large volumes of MRI images has been successfully achieved using deep learning techniques. By distinguishing distinct characteristics, CNN based algorithms for automatic MRI segmentation for brain tumors achieved successful results. CNN architecture that takes local and contextual knowledge into account as one is the more recent solutions to this issue. Pre-processing step normalises the images, and a post-processing step removes false positives, according to their procedure. In this analysis, CNN approach is used to analyse MRI brain images in order to identify and find tumours.

CHAPTER 2

LITERATURE SURVEY

2.1 Research Papers

We have referred several papers which are as follows:

1. **Automatic Segmentation of Multimodal Brain Tumor Images Based on Classification of Super-Voxels** M. Kadkhodaei, S. Samavi, N. Karimi, H. Mohaghegh, S.M.R. Soroushmehr, K. Ward, A. All, K. Najarian

Since the brain structure typically has a clear continuous form, in its third dimension, MR image sequences have a high correlation that could support tumour segmentation. Therefore, rather than individually operating on voxels, use of super-voxels that include a meaningful grouping of voxels based on local image characteristics. Super-voxel segmentation is a super-pixel segmentation extension in 3D.

Based on their strengths and their proximity, it utilises voxels. SLIC[14] produces an effective super-voxel 3D, inspired by clustering k-means, which naturally respects an image's boundaries.

2. **Automatic Segmentation of Multimodal Brain Tumor Images Based on Classification of Super-Voxels** by M. Kadkhodaei, S. Samavi, N. Karimi, H. Mohaghegh, S.M.R. Soroushmehr, K. Ward, A. All, K. Najarian

The authors of these papers have worked on super-voxels that are used to provide a meaningful grouping of voxels based on local image characteristics. Super-voxel segmentation is a super-pixel segmentation extension in 3D. Based on their strengths and their proximity, it utilises voxels. SLIC produces an effective super-voxel 3D, inspired by clustering k-means, which respects the boundaries of an image naturally.

3. **Parasuraman Kumar, B. VijayKumar, “Brain Tumor MRI Segmentation and Classification Using Ensemble Classifier”, International Journal of Recent Technology and Engineering (IJRTE), Volume-8, Issue-1S4, June 2019**

A procedure for detecting brain tumour based on the method of segmentation and region measurement was suggested by the authors. In the following sequence, the suggested approach includes 5 phases. Image acquisition, preprocessing, clustering of K-means, morphological procedure, identification of tumours and measurement of the region. The first stage is the acquisition of images linked to the acquisition of brain MRI images.

4. **M. Sajjad, S. Khan, M. Khan, W. Wu, A. Ullah, S. W. Baik, Multi-grade brain tumor classification using deep CNN with extensive data augmentation, J. Comput. Sci.**

They suggested classification of multi-grade tumors by applying data augmentation technique to Mri images and then tuning it using a pre-trained VGG-19 CNN Model.

5. **R. Carlo, C. Renato, C. Giuseppe, U. Lorenzo, I. Giovanni, S. Domenico, Distinguishing Functional from Non-functional Pituitary Macroadenomas with a Machine Learning Analysis, Mediterranean Conference on Medical and Biological Engineering and Computing, Springer**

Carlo, Ricciardi et al., presented an approach for classifying pituitary adenomas tumor MRIs by using multinomial logistic regression and k-nearest neighbor algorithms. The approach achieved an accuracy of 83% on multinomial logistic regression and 92% on a k-nearest neighbor with an AUC curve of 98.4%.

6. **Geng-Cheng Lin, Wen-June Wang, Chuin-Mu Wang, Sheng-Yih Sun, “Automated Classification of multi spectral MR images using Linear**

Discriminant Analysis”, ELSEVIER computerized medical Imaging and graphics 34(2010) 251-268.

Lin et al in their paper they introduce a method for precise accurate and efficient quantification of brain tumor via MR imaging. The purpose of this work is to build a computerised system to evaluate its effectiveness for routine clinical work. In this the image (FLAIR, T1 and T2) are processed independently

7. V.P.Gladis Pushpa Rathi and S.Palani, “Linear Discriminant Analysis For Brain Tumor Classification Using Feature Selection”, Int Journal Of communication and Engineering, vol-05-No 5. Issue March 2012

Rathi and Palani in their paper proposed a novel method of feature selection and extraction. This approach mainly combines the intensity, texture, shape based features and classifies the tumor region as white matter(WM), gray matter(GM), CSF, abnormal and normal area. The support vector machine (SVM) classifier is used for the comparison of nonlinear techniques with linear ones. Principal component analysis (PCA) and linear discriminant analysis (LDA) methods are used to reduce the number of features. The feature selection using the proposed technique is more beneficial than the existing system, as it analyses the data according to the grouping class variable and gives reduced feature set with high class accuracy. The classification accuracy obtained is 98.87%

8. Zhang N, Ruan S, Le Bonvallet S, Liao Q, Zhu Y. Multi-kernel SVM based classification for brain tumor segmentation of MRI multi-sequence. 2009 16th IEEE International Conference on Image Processing (ICIP) Nov 2009. p. 3373–6.

Zhang used PCA for FS, which reduced the number of features to 10. To identify the tumour area, a Multi Kernel SVM (MKVM) is used. To improve the contour of the tumour area, the distance and the maximum probability

measures are applied. 3 separate image types, FLAIR, T2, and PD images, with 60 samples for each type, are included in the used dataset.

9. Kai xiao, A. Lei Liang, Hai Bing Guan, Aboul Ella Hassanien,"Extraction and Application of Deformation Based Feature in Medical Images", ELSEVIER Neurocomputing 2013.

In their paper Kai xiao and Lei suggested a method for estimating features based on the relationship between brain lateral ventricular (LaV) deformation and tumour. Pre-processing, feature extraction, segmentation, and classification are the four phases of the proposed technique.

The problem of strength non-standardization, geometric non-uniformity, and redundant data in the background image and skull are discussed in the first step.

For feature extraction, lateral ventricular deformation was used. Unsupervised segmentation methods are used in the segmentation section. Methods used in this paper are K nearest neighbours (KNN) and traditional Fuzzy connected C-mean (FCM).

10. Padma Nanda Gopal & R. Sukanesh," Wavelet statistical feature based segmentation and classification of brain computed tomography images" IET Image Process.

They presented a two-level discrete wavelet transform that yielded a combination of wavelet statistical features and wavelet co-occurrence texture function.

For brain tumour segmentation, a combination of WST and WCT is used, and for feature extraction of tumour area derived from two stage discrete wavelet transform, a combination of WST and WCT is used.

The best texture features were chosen using a genetic algorithm from the collection of extracted features. The proposed method has a classification accuracy of 97.5 percent.

11. Hashem Kalbkhani, Mahrokh G Shayesteh, Behrooz Zali-vargahan " Robust algorithm for Brain Magnetic Resonance Image Classification based on GARCH variances Series", ELSEVIER Biomedical Signal Processing and Control.

They developed a system for classifying MR images into normal and abnormal. At the first two levels, the input image is transformed into a two-dimensional discrete wavelet transform (2D DWT), and the wavelet coefficients of the details subband are modelled.

Here is the second part where Principal component analysis (PCA) and Linear Discriminant Analysis (LDA) are used to extract the proper function and minimise redundancy from the primary feature vectors after feature vector normalisation.

Finally, the extracted features are added separately to the K nearest neighbour (KNN) and support vector machine (SVM) classifiers to decide whether the images are regular or abnormal.

12. Sindhumol S, Anil Kumar, Kannan Balakrishnan " spectral clustering independent component analysis for tissue classification from brain MRI" ELSEVIER, Biomedical signal processing and control (2013)667-674.

This paper is centred on spectral angle based feature extraction and spectral clustering independent component analysis, proposing a method to improve the classification of brain tumours from magnetic resonance images (SC-ICA).

Spectral distance dependent clustering is used to separate the MR image into different clusters. Along with SVM, independent component analysis (ICA) is performed on the clustered results.

For this study, T1 Weighted, T2 Weighted, and proton density fluid inversion recovery images were used. To determine the stability and efficiency of SC-ICA based classification, a comparison is made with ICA based SVM and other traditional classifiers.

13. Navarro, David Hackney, "Feature and model selection with discriminatory visualization for diagnostic classification of brain tumor. ELSEVIER, computerized Medical Imaging and Graphics 29 ("05) 21-34.

They have worked on different HMRC modalities, such as long and short echo periods, and an ad hoc combination of both, they introduced a new method for feature selection of dimensionality reduction and several off-the-shelf classifiers in their paper. They use an entropy selection algorithm for feature selection, which is a simple way to produce a relevant subset of spectral frequency. In the bootstrap samples, feature selection is performed independently in the classifier. Then, using the previously selected set of features, a set of classifiers is built on the bootstrap samples, with the result being the selection of a particular classifier for each data form.

14. Computer Aided System for Brain Tumor Detection and Segmentation by M. Usman Akram, Anam Usman.

The next step is segmenting the MR image of the brain tumour after improving the brain MRI image. To separate the foreground of the picture from its background, segmentation is performed. Segmenting an image often saves the processing time that has to be added to the image for further operations. In order to segment the tumour image, use of global threshold. For global threshold segmentation, the basic steps are as follows:—

- For the image, select a threshold value.
- To transform the image into a binary, add the threshold value to the enhanced image.
- If the pixel value is above the threshold value, the background is otherwise considered to be the foreground value.

15. Current Trends on Deep Learning Models for Brain Tumor Segmentation and Detection by S.Somasundaram and R.Gobinath.

Picture segmentation is a method in which the digital image is separated into many segments or partitioned. Provide a reproductive template for image synthesis and generate an accurate segmentation of the abnormal in post-processing soft segmentation of the network. Another unsupervised procedure, a saliency-based approach that investigates brain asymmetry in pathological cases, was suggested by Erihov.

CHAPTER 3

PROBLEM DEFINITION & PROPOSED SOLUTION

3.1 Problem Statement

Brain tumors are cancerous or non-cancerous mass or growth of abnormal cells in the brain. Moreover, the location of the tumor within the brain has a profound effect on the patient's symptoms, surgical options, and the likelihood of obtaining a definitive diagnosis. At present, brain tumors are detected by imaging only after the onset of neurological symptoms.

Current histopathological classification systems, which are based on the tumor's presumed cell of origin, have been in place for nearly a century and were updated by the World Health Organization in 1999. Although satisfactory in many respects, they do not allow accurate prediction of tumor behaviour in the individual patient, nor do they guide therapeutic decision-making as precisely as patients and physicians would hope and need.

3.2 Proposed Solution

- The proposed model will let users input MRI images of the brain.
- It will detect and classify the type of tumor and give the resultant output.
- It will return the final generated result as a type of tumor as either Glioma, Pituitary, Meningioma, and no tumor.

3.2.1 Data Set

There are many different ways for data gathering. It can be done either by collecting MRI images from the web or by creating a completely new dataset by gathering images from an hospital. However the second method is costlier.

The proposed method is tested on publicly accessible data sets, the Brain Tumor Kaggle (BTK) Dataset, which differ in structural sophistication, acquisition angle, instruments, noise, and bias field-effect, among other things. The BTK dataset

comprises approximately 3000 actual MRI images. The images are in JPEG format and are in grayscale.

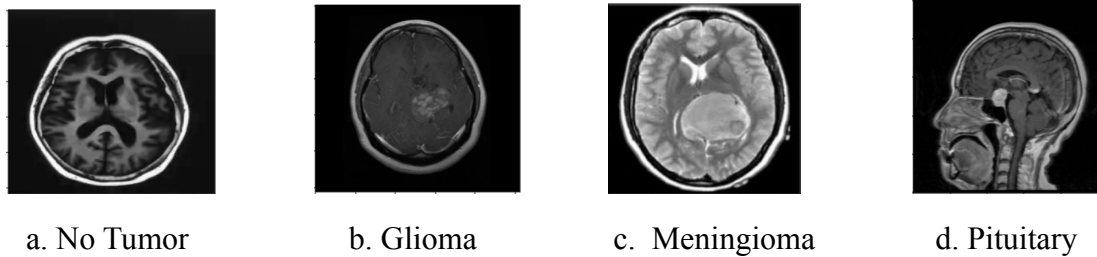


Fig. 3.1 Brain Tumor images

3.2.2 Tumor Classification

For the classification purpose we have used the Convolution Neural Network which consists of four convolution layers. We have used a sequential model for our project. The details of the layers are explained.

- **1st Convolution Layer :-** The input image is processed here with a Conv2D layer with parameters(32,3x3) where 32 is the no of filters and 3x3. The result is a resized image of dimension 148 x 148. The result is fed to an activation layer.
- **1st Pooling Layer:-** MaxPloeing2D layer with pool size of '2x2' which makes the image classifier more robust so it can learn relevant patterns. Here the images are downsampled to size 74 x 74.
- **2nd Convolution Layer:-** Now the images of dimension 74 x 74 are given as input to this layer, here the image is processed using 32 filters and size 3x3. The result is given to an activation layer.
- **2nd Pooling layer:-** The resulting samples are again down sampled using Maxpooling2d using a pool size 2x2. The output is an image of dimension 72 x 72.

- **Flatten:-** The result generated by the above layer is fed to an Flatten layer which converts the data into a 1-dimensional array for inputting it to the next layer. The result generated by this layer is 41472
- **1st Densely Connected Layer:-** Now these images are used as input to the first fully connected layer the result is an array of 1327136 values. The output of this layer is an activation function.
- **Dropout Layer:-** The output generated is fed to the Dropout layer and we are using dropout of 0.25 which is 25% to avoid overfitting.
- **2nd Densely connected layer:-** The output generated by the Dropout layer is fed to an densely connected layer and the output generated by this layer is given to an activation function.
- **Final Layer:-** The output of the 2nd densely connected layer serves as input of the final layer which will have the number of neurons as the number of classes which we are classifying.

Model:- We have used a Sequential API as it allows us to create models layer-by-layer .

Activation Function:- We have used two activation functions.

- **ReLu(Rectified Linear Unit):-** We have used Relu in convolution layer it calculates $\max(x, 0)$ for each input pixel. This adds non linearity to the formula and helps to learn more. It also helps in speeding up the training and reducing the computation time.
- **Softmax:-** This is used at the last layer as it directly selects the neuron with the highest probability as its output, voting that the image belongs to that class.

- **Pooling Layer:-** We have applied Max pooling to the input images with a pool size of (2,2) with ReLu Activation function. This reduces the amount of parameters and reduces overfitting.
- **Dropout Layer:-** While training the model we faced overfitting problems and so to remove that we added the dropout layer with an dropout of 25%. This layer drop outs a random set of activations in the layer by setting them to zero.
- **Optimizer:-** We have used Adam optimizer for updating the model in response to the output of the loss function. It will tune the weights in the network to approach the point of lowest loss.

3.2.3 Implementation:-

- We started with preprocessing both the training and testing data for which we have reshaped the images with dimensions(150x150). The output generated after the reshaping was given to numpy to convert it to an array and finally to the onehotencoder to convert the categorical data into integers.
- The next step after the preprocessing was creation of a CNN model for which we have a sequential model as it allows us to create models layer-by-layer.
- After the creation of the CNN model we have trained the model with the fit() function and the following parameters were passed.

Batch Size:- It specifies no of samples per gradient. We have taken batch size as 32.

Epochs :- It represent the number of epochs we want to train our model. We have trained our model for 19 epochs as we tested our model for different epochs which resulted in overfitting after which we concluded on using epoch size as 19.

Verbose:- It specifies the verbosity mode, there are generally three types of mode 0, 1 and 2. We have used verbose as 1.

Validation data: Data on which to evaluate the loss and any model metrics at the end of each epoch.

- After successfully training the model we plot the Test Loss and Validation Graph which helps us understand the state of the model. The model must be of perfect fit or else it would not be able to properly classify.
- After completion of the model training, we would accept the input image on which we need to perform the classification. The image would be resized and the model would predict using the `model.predict` function which would basically compare the value of the image with the values of the particular class. The class with which the input image matches with more probability would be the class of the input image.
- The result will be generated stating the type of tumor if any detected along with the images and if the tumor is not detected it would print no tumor detected. Here it would also generate the Confidence which is basically the probability of match *100.

CHAPTER 4

Design

4.1 Architecture Diagram

The design of Brain Tumor Detection and Classification essentially involves the following aspects:-

- MRI Dataset
- PreProcessing
- Convolution Neural Network
- Classification

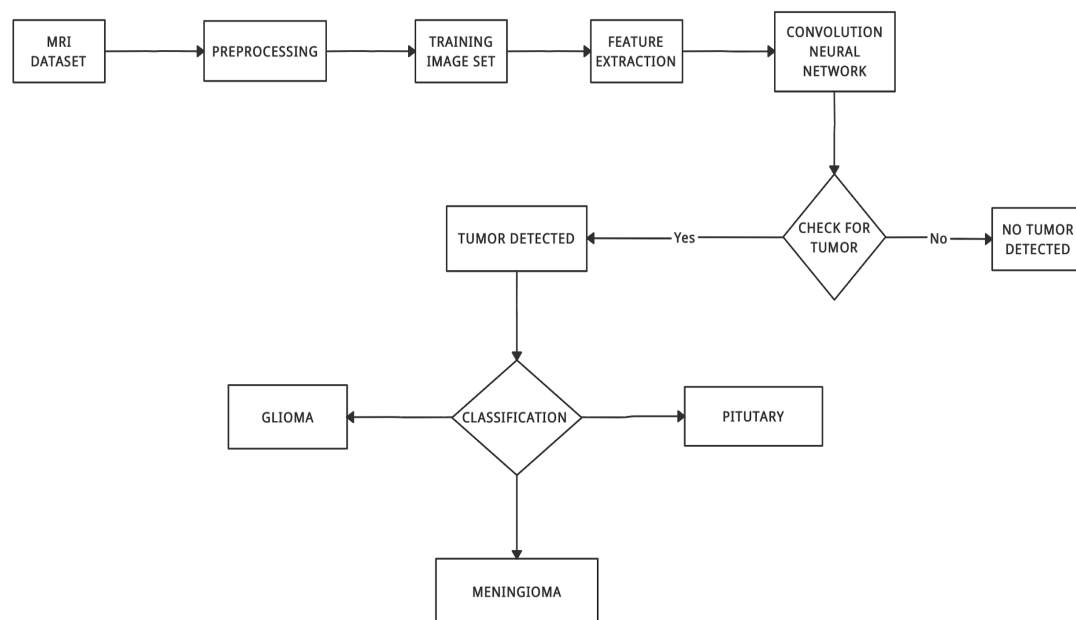


Fig. 4.1 Architecture Diagram

4.1.1 MRI Dataset

The dataset used in the model is obtained from Kaggle. It contains two different directories for training and testing. Each of these two directories contains four sub-directories containing images of different types of tumor. There are around 3000 images of each type of tumor.

4.1.2 Pre Processing

The main function of this phase is to resize the image to dimension of (150x150) and convert it using a numpy array and after that using onehotencoder.

4.1.3 CNN

These phases find and extract features from the image and stores it later which are used to compare between the feature of the input images..Feature like color either grey or white,density of color,white lines,dots etc.

4.1.4 Classification

Here the input images are compared with the dataset images and the image matching with the maximum percentage is displayed as output.

4.2 Data Flow Diagram

4.2.1 DFD Level 0

In DFD Level 0 the user gives input image to the system and the system classified the type of tumor and gives the resultant output.

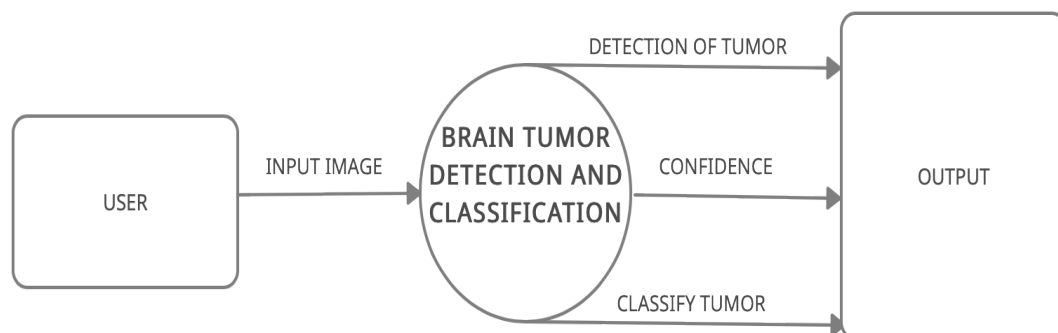


Fig. 4.2.1 DFD Level 0

4.2.2 DFD Level 1

In DFD level 1 MRI Images are given as input, Pre Processing is done on the images and classification is performed.

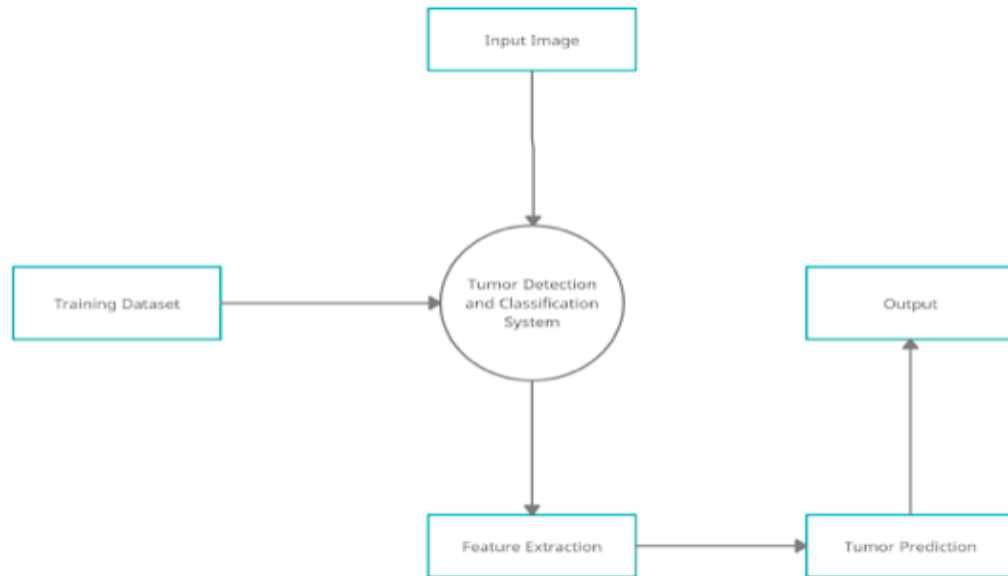


Fig. 4.2.2 DFD Level 1

4.3 Use case Diagram

A Use Case Diagram is the simplest representation of a user's interaction with the system that shows the relationship between the user and the system.

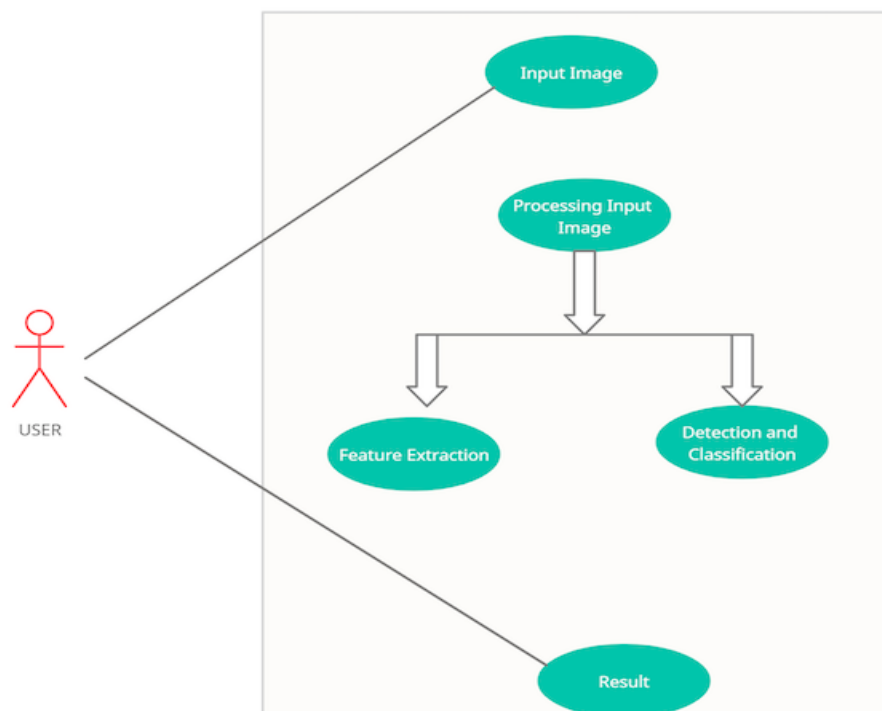


Fig. 4.3 Use case Diagram

4.4 Activity Diagram

This is basically a flow chart representing the flow from one activity to another activity.

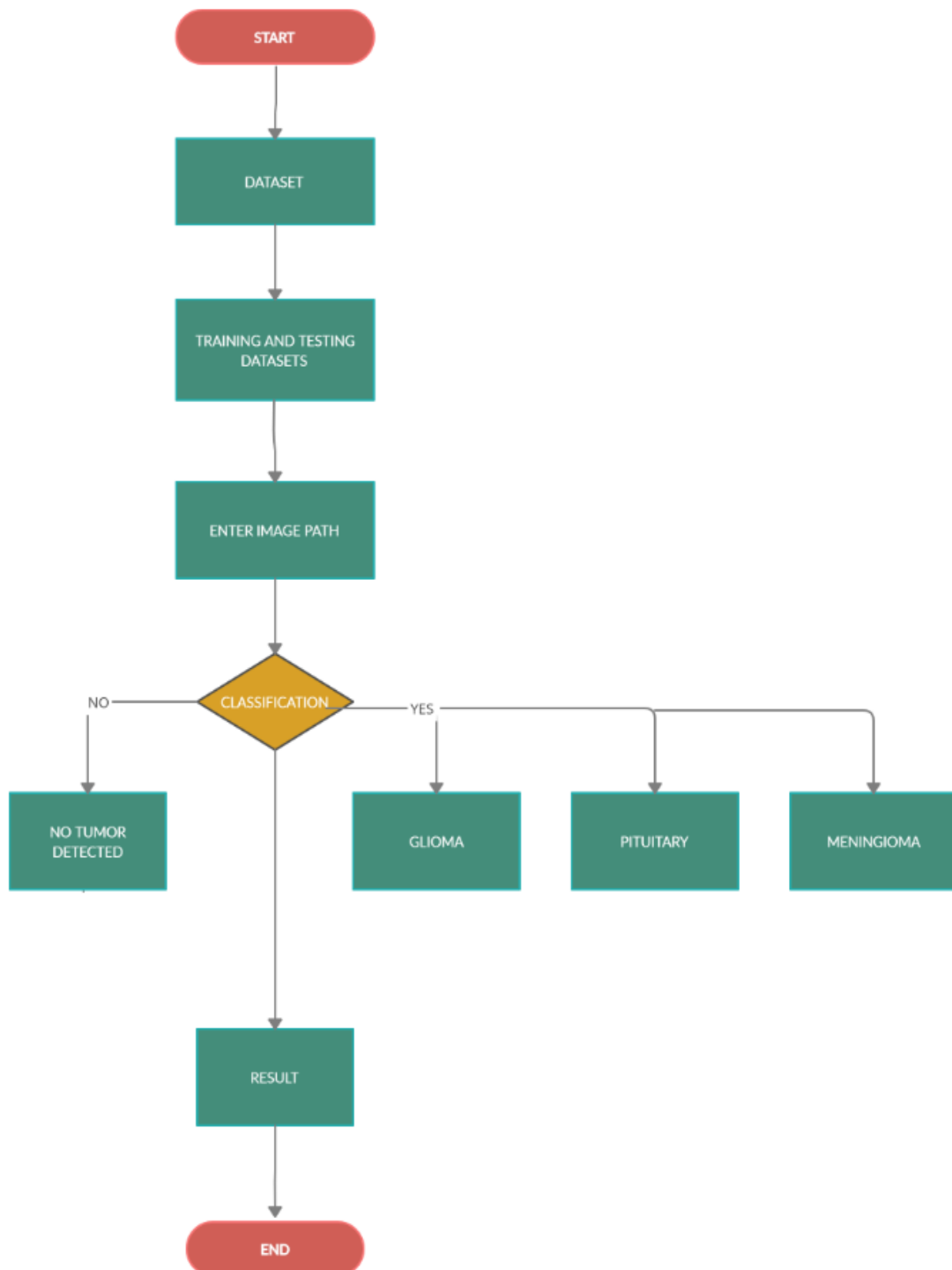


Fig. 4.4 Activity Diagram

4.5 Class Diagram

The class diagram is the fundamental component of object-oriented modeling. It is used for both general conceptual modeling of the application's structure and precise modeling of the models' translation into programming code.

So, there are three separate classes in the Brain Tumor Detection and Classification class diagram, and a connection between them is shown. The user class is called first, and it takes input for image that is to be verified. After which PreProcessing is called which process the image and then classify is called which classify the images. Lastly Display is called which display the output as the name of tumor along with the image.

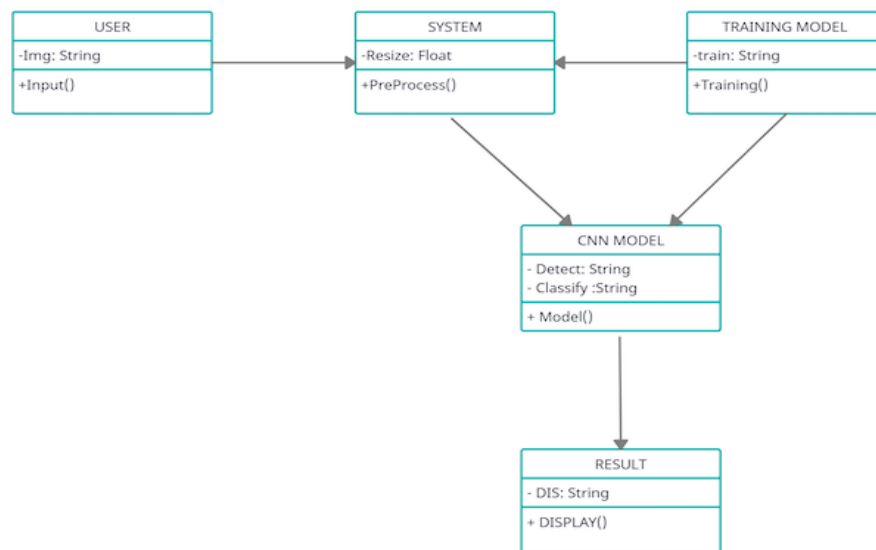


Fig. 4.5 Class Diagram

4.6 Sequence Diagram

The interaction between objects in a sequence diagram is simply represented in the order in which these interactions occur. A sequence diagram may also be referred to as an event diagram or an event scenario.

In the sequential diagram of Brain tumor detection and classification, the user will input the path of the image to be verified which will be transferred to the system, then the system will perform feature extraction on the image after which system will compare the features and the result would be generated.

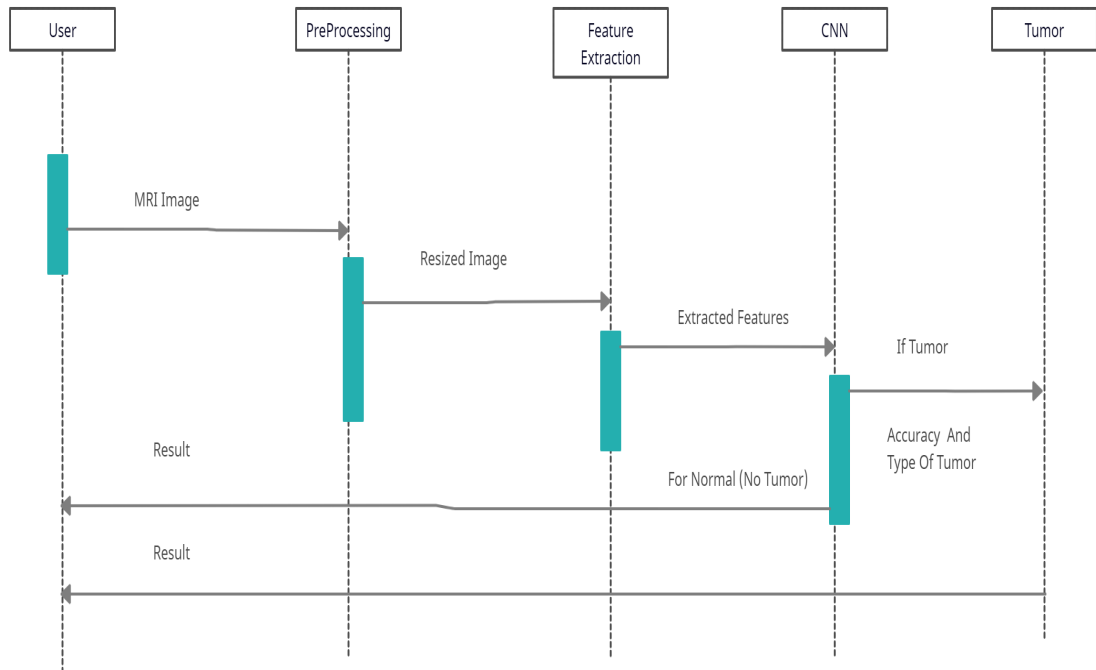


Fig. 4.6 Sequence Diagram

4.7 Component Diagram

This diagram shows the components used to make those functionalities.

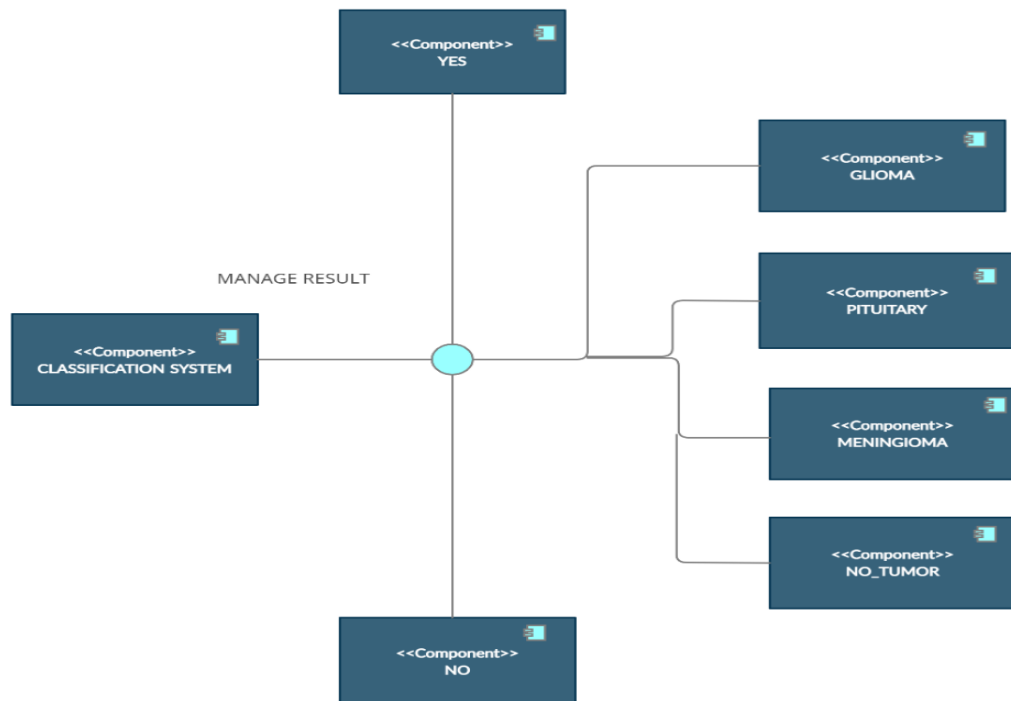


Fig. 4.7 Component Diagram

CHAPTER 5

Result Analysis/

Implementation

We have achieved an accuracy of 96% in our model. First we set the no of epochs as 30 and trained the model which resulted in overfitting. So on a try and run basis we conclude on using epoch as 19. We reviewed many papers during the process of making this model and many of them either used Masking, KNN other methods which resulted in less accuracy amounting to 86% or even less than that.

Brain MRI images dataset from Kaggle for training and used it to train our model. We have used various kinds of filters to add to our feature and get accurate features to be added to our Model.

Many of the research papers that we studied have used large no of dataset which resulted in either increase in computation cost or in overfitting. We have used a sufficient amount of dataset along with a tested number of epochs and dropout layers which we have concluded after testing many number of times.

The graph below represents the state of the model, represents the test and validation

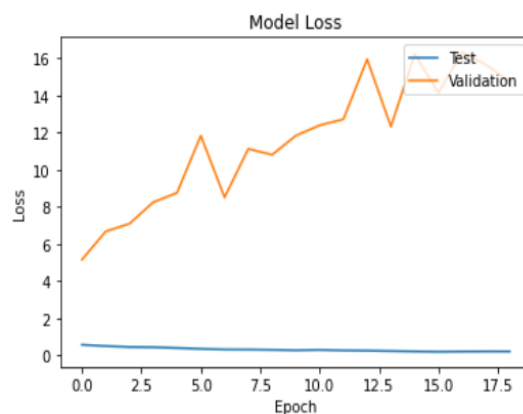


Fig. 5.1 Graph representing model loss

when the no of epochs where set to 30 resulting in overfitting. The second graph shows that model if fit which was achieved after setting epochs to 19.

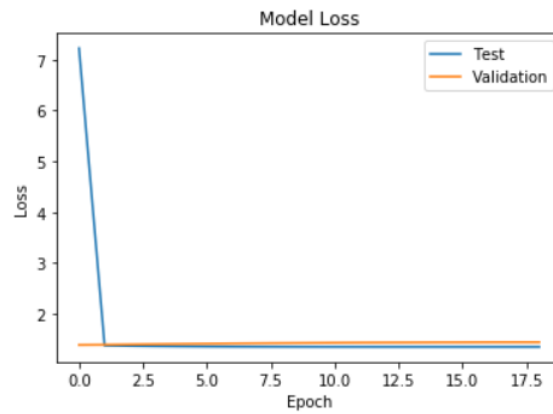


Fig. 5.2 Graph representing model loss

MRI images are taken as input and provide an accurate output which can be operated on a standard laptop. Below is the output our system has generated on some of the tested images.

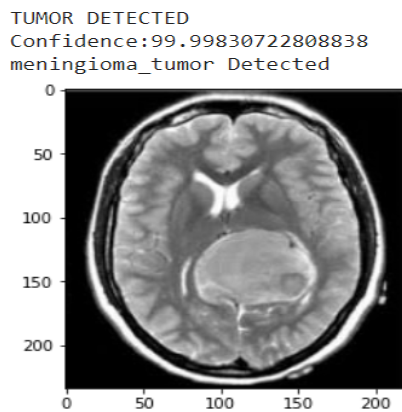


Fig. 5.3 (a) Output

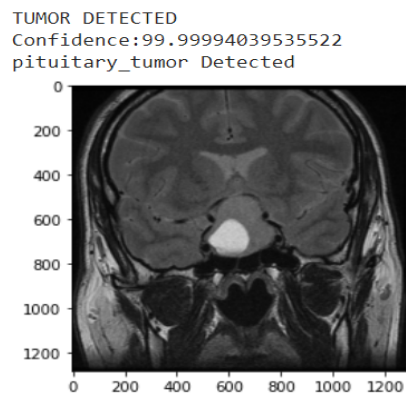


Fig. 5.3 (b) Output

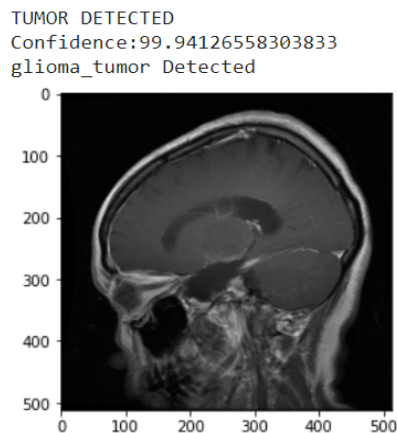


Fig. 5.3 (c) Output

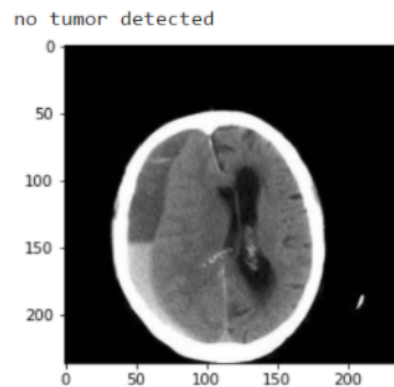


Fig. 5.3 (d) Output

CHAPTER 6

Testing

In our model we have used a folder named 'test' containing random images of tumors taken from the web which were used for testing the model. In this model we are importing MRI Grayscale images for the testing purpose and resizing the images in size of 150x150. We then processed the images to our model for training and testing after resizing the images. For the prediction purpose we are using CNN to estimate how likely the images will fall under which category.

User inputs the MRI image and then system resizes the image and then feeds the image to the CNN model which will classify the images on the basis of values. We have used OneHotEncoders to convert the categorical data generated by numpy to integers. Then on the basis of the values generated the model will classify the image.

Eg, Let's take an example where the value generated by the images are 0.57 and the values generated by different images classes are [0.55, 0.89, 1, 0.4] the model would compare with this value and the value closest to this number would be the class of the image. There is a built in function in keras named `keras.predict_on_batch(x)` which we used to predict the class of the image.

The output is normalized between 0 and 1 such that the sum of each value in each class sums to 1, we have achieved this using the Softmax function. At first the output of the prediction layer will be somewhat far from the actual value so we trained the networks using labeled data. The categorical-cross entropy is a performance measurement used in the classification.

It is a continuous function which is positive at values which is not same as labelled value and is zero which is same to the labelled values. We have used an optimizer as Adam.

CHAPTER 7

Conclusion and Future Work

7.1 Conclusion

In this report, a brain tumor detection and classification model has been developed. We have achieved an accuracy of 96% on our dataset.

We were able to detect tumor and also to classify three types of tumor namely Glioma, Pituitary, Meningioma. We were able to improve the classification Accuracy by adjusting the we suggest using MRI images over RGB images as they are easier to handle and provide accurate results. The findings show that the suggested procedure accurately delineates the tumour area and can be used as an automatic diagnostic tool.

7.2 Future Work

We are planning to achieve higher accuracy and also in increasing the types of tumor. We are also thinking of creating an application that could be used on handy devices like tablets and mobile phones so they can be accessed in remote locations and places where there are no certain medical facilities.

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APPENDICES

Keras

Keras is an open-source software library that provides a Python interface for artificial neural networks. Keras acts as an interface for the TensorFlow library. Up until version 2.3 Keras supported multiple backends, including TensorFlow, Microsoft Cognitive Toolkit, Theano, and PlaidML.

As of version 2.4, only TensorFlow is supported. Designed to enable fast experimentation with deep neural networks, it focuses on being user-friendly, modular, and extensible. It was developed as part of the research effort of project ONEIROS (Open-ended Neuro-Electronic Intelligent Robot Operating System), and its primary author and maintainer is François Chollet, a Google engineer. Chollet also is the author of the EXception deep neural network model.

Convolution Neural Network

CNNs use a variation of multilayer perceptrons designed to require minimal preprocessing. They are also known as shift invariant or space invariant artificial neural networks (SIANN), based on their shared-weights architecture and translation invariance characteristics. Convolutional networks were inspired by biological processes in that the connectivity pattern between neurons resembles the organization of the animal visual cortex.

Individual cortical neurons respond to stimuli only in a restricted region of the visual field known as the receptive field. The receptive fields of different neurons partially overlap such that they cover the entire visual field.

CNNs use relatively little pre-processing compared to other image classification algorithms. This means that the network learns the filters that in traditional algorithms were hand-engineered. This independence from prior knowledge and human effort in feature design is a major advantage. They have applications in image and video recognition, recommended systems, image classification, medical image analysis, and natural language processing.

MatPlotLib

Matplotlib is a plotting library for the Python programming language and its numerical mathematics extension NumPy. It provides an object-oriented API for embedding plots into applications using general-purpose GUI toolkits like Tkinter, wxPython, Qt, or GTK. There is also a procedural "pylab" interface based on a state machine (like OpenGL), designed to closely resemble that of MATLAB, though its use is discouraged. SciPy makes use of Matplotlib.

Matplotlib was originally written by John D. Hunter. Since then it has an active development community and is distributed under a BSD-style license. Michael Droettboom was nominated as matplotlib's lead developer shortly before John Hunter's death in August 2012 and was further joined by Thomas Caswell.

Matplotlib 2.0.x supports Python versions 2.7 through 3.6. Python 3 support started with Matplotlib 1.2. Matplotlib 1.4 is the last version to support Python 2.6. Matplotlib has pledged not to support Python 2 past 2020 by signing the Python 3 Statement.