BRAIN TUMOR DETECTION

Dr G. Prabhakar Raju Ch. Sindhuja, B. Chandana, Obed Emmanuel

[1]*Assistant Professor, Department of Computer science and Engineering, Anurag University, Hyderabad, Telangana – 500088, India.*
[2] *Department of Computer science and Engineering, Anurag University, Hyderabad, Telangana – 500088, India.*
[3]*Department of Computer science and Engineering, Anurag University, Hyderabad, Telangana – 500088, India.*
[4]*Department of Computer science and Engineering, Anurag University, Hyderabad, Telangana – 500088, India.*

[1]*prabhakarrajucse@anurag.edu.in*
[2]*21eg105b11@anurag.edu.in*
[3]*21eg105b09@anurag.edu.in*
[4]*21eg105b38@anuarg.edu.in*

Abstract. In the planning and quantitative assessment of brain tumors, determining the tumor extent is a critical challenge. MRI is a non-invasive technology that has emerged as a first-line diagnostic tool for brain tumors that does not require ionizing radiation. Gliomas are the most aggressive brain tumors, with a life expectancy of only a few months in the most advanced stages. Manual segmentation is a time-consuming procedure in clinical practice, and its success is greatly dependent on the operator's expertise. Hence, our paper aims to develop a system wherein it takes in the MRI scan images as input and classifies if the specific patient has Brain Tumor or not using the VGG-19 architecture of Convolutional Neural Networks.

Keywords. Manual Segmentation, Convolutional Neural Networks

INTRODUCTION

Cancer has evolved into a highly lethal illness that affects people of all ages. In 2020, 308,102 persons worldwide were expected to be identified with a primary spinal cord or brain cord tumor [1]. Brain tumors are the tenth largest cause of mortality [2]. A tissue anomaly brings it on in the central spine or the brain. As a result, it causes problems with brain function. Although the etiology of brain tumors is uncertain, radiation exposure and family history might increase the risk [3].Early diagnosis and identification of brain tumors are critical for successful therapy. According to a WHO assessment [1], [4] brain cancers are divided into many categories, such as glioma, meningioma, metastasis, sarcoma, and so on, as shown in figure 1. Many of the most present investigation initiatives are to divide brain tumor types into four classes. Recent developments in medical image processing, together with the use of computer-assisted diagnosis (CAD) as well as magnetic resonance imaging (MRI), make tumor portion detection much more effortless. Nonetheless, identifying and classifying brain tumor kinds and grades remains a tedious task. In this study, we describe a CAD-based augmentation-based model for brain tumor detection and prediction.

CT scans and MRI diagnosis are used to detect brain tumor. MRI uses magnetic fields, instead of x-rays, to produce detailed images of the body. Accurate detection is very important in brain tumor detection. The rate of accuracy can be increased by using computer aided system. This system can help the radiologist to detect brain tumor more appropriately. Our experiment provides a discussion about a new compute raided method to improve the accuracy rate of the detection of brain tumor along with the calculation of the tumor size and its location. Besides it helps to determine whether the tumor is malignant or not. Moreover, when a neurologist decides to dean operation, tumor’s width, height, area or thickness matters. This paper provides such a way by which we can compute the surface area of the tumor. It is obviously a vital factor in surgery.

LITERATURE SURVEY

TABLE 1. Review Paper 1

Resource Paper Name	**Description**	**Limitations**
"Brain Cancer Diagnosis Using GGD Analysis"	Proposes a GGD (Generalized Gaussian Distribution) analysis technique for bone sarcoma detection using image processing and medical imaging	Does not discuss real-time implementation or large-scale dataset testing

TABLE 2 . Review Paper 2

Resource Paper Name	**Description**	**Limitations**
"Detection & Classification of Tumor Cells from Brain MR Imagery Using Connected Component Analysis & Neural Network"	Uses Connected Component Labelling to detect tumors and trains an Artificial Neural Network (ANN) on MR images for classification. The approach maintains key image edges using Anisotropic Diffusion Filter (ADF).	ANN requires a large dataset for training; may not generalize well to diverse patient populations.

TABLE 3 . Review Paper 3

Resource Paper Name	**Description**	**Limitations**
"Analysis of Brain Cancer and Features for Prediction Using Computer Vision Techniques"	Compares edge-based and region-based segmentation methods for detecting osteosarcoma from X-ray images using MATLAB.	The accuracy depends on image quality; segmentation may struggle with unclear tumor boundaries.

PROPOSED SYSTEM

The data that we used is the BRATS dataset. This dataset contains the segmented images of the brain tissues. After the image has been segmented, there are 3 classes namely Necrotic and Non-Enhancing tumour (NCR/NET), Peritumoral Edema (ED) and GD-Enhancing tumour (ET). There are about 220 images in the training dataset. To segment the brain MRI we use a popular network called The U-Net architecture is built upon the Fully Convolutional Network and modified in a way that it yields better segmentation in medical imaging. Compared to FCN-8, the two main differences are. U-net is symmetric. The skip connections between the down sampling

Advantages over the previous system

- Less time Consumtion
- High accuracy
- Future-Enhancements
- Scalability

operator instead of a sum. These skip connections intend to provide local information to the global information while up sampling. Because of its symmetry, the network has a large number of feature maps in the up-sampling path, which allows transferring information. By comparison, the basic FCN architecture only had number of classes feature maps in its up-sampling path.

Model Implementation

1. System Architecture

Convolutional layers consist of a rectangular grid of neurons, which takes a rectangular region of previous layer as input. Moreover, there may be several grids in each convolutional neural network layer, using potentially different filters. Typically, there is a pooling layer after each convolutional layer, which are subsampled from the previous convolutional layer. This pooling can be carried out in many ways, such as the average, maximum, and so on. Finally, after several convolutional layers and max pooling layers, a fully connected layer (or several layers) will be built using outputs from previous layers (maybe the fully connected, pooling) which is used as a compact feature to describe the whole input image of retina. The network is optimized by back propagation and stochastic gradient descent. Note that the backward and forward propagations may differ depending on the layer types.

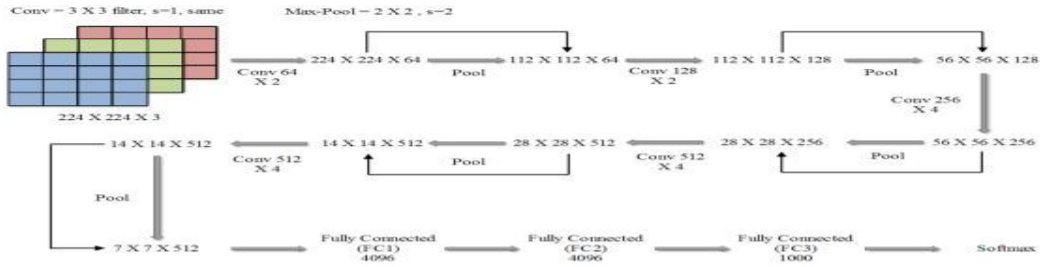
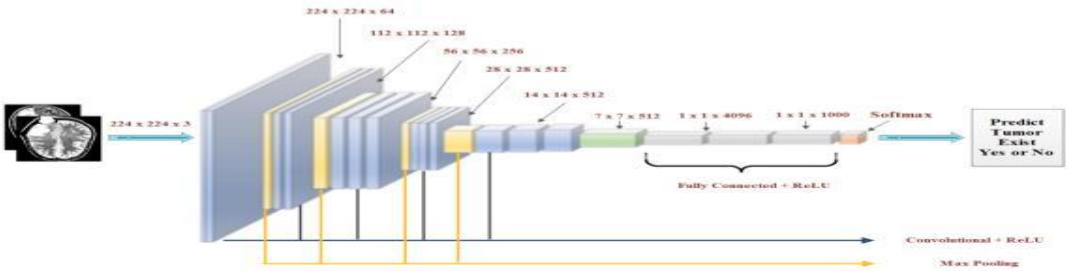


Figure 14. VGG 19 Architecture Walkthrough



2. Dataset Collection

Around 250 MRI images were used in the proposed network 60-70% of the data is used in training, whereas 30-40% in testing The proposed methodology contains two main phases. The first is a training phase which concerns the preparation and augmentation of data followed by a CNN model. The second phase is the test phase in which we pre-process our test image, classify the image to find out if the tumor exists and finally segment the tumor according to the characteristics extracted from our model. We use in this work two different datasets. The first one is acquired from Hospital and others are downloaded from Google Images.

3.Preprocessing Stage

In the windowing procedure, the radiography is cut into smaller square segments (windows), which are here used for training and testing the CNN. Figure 2 shows an example of the windowing procedure applied to the radiography shown in Figure 1. Experiments (not shown here) were performed in order to compare the performance of the system for 50×50 pixels and 100×100 pixels windows. Best results were obtained for 100× 100 windows; this size is used in the experiments presented in Section III. The 50 × 50 windows resulted in incorrectly classifying all examples with osteosarcoma, i.e., the model was unable to learn the relevant characteristics for the classification of tumors. Despite resulting in more examples for training, the 50 × 50 windows have a smaller amount of information relevant for the classification. This can be seen in the example presented in Figure 3, where it is easier to identify relevant characteristics in the window with 100 × 100 pixels. In the labeling procedure, the windows used for training and testing the classifier are automatically labeled into one of two classes. The labels indicate the presence (0) or absence (1) of a tumor in the window. In order to create the dataset for training and testing the CNN, a radiologist manually marked the regions of the radiographs with tumor (osteosarcoma). These regions are represented in green in Figure 2. Using the image marked by the

radiologist and the windowing procedure, the labeling procedure checks the percentage of the green color in the window. If the percentage is higher than a threshold, the window is marked with 0; otherwise it is marked with 1 (Figure 2). The threshold is equal to 19% in the experiments presented in Section III. This threshold was obtained in initial experiments (not shown here), where it was observed that thresholds with higher values resulted, for some radiographs, in the labeling of any window with tumor. The threshold equals to 19% ensures that at least one window is labeled with tumor on each of the images of the dataset.

4. Classification

Python libraries and routines, such as TensorFlow [16] and Keras [17], were used in this work for implementing the CNNs. The open source library Pillow was used for image manipulation [18] and Google Colab [19] for running the CNNs. Google Colab is a free cloud service that offers free access to GPUs and easy sharing of codes. We propose two approaches for generating the CNN in the computer-aided diagnosis system. 1) CNN trained from scratch: The input of the CNN is the 100 × 100 pixels images and one single output indicates the presence or absence of osteosarcoma in the window. Experiments (not shown here) with a single radiography were carried out to select the architecture and hiper-parameters of the CNN trained from scratch. Accuracy was used to evaluate CNNs with different hiper-paramenters and architecture. The model with best results has five convolutional layers with 3 × 3 windows. The first two convolutional layers have 128 filters each, while the

third and fourth layers have 64 filters each and the fifth layer has 32 filters. After the second, fourth and fifth convolutional layers, one MaxPooling layer is applied. MaxPooling layers have 2×2 windows. Finally, three fully connected layers, with respectively 8, 4 and 1 neurons, are added. In all convolutional and dense layers, the ReLu activation function is used, except in the last dense layer, where sigmoid function is used. Batch normalization is applied. The Adam optimizer with default parameters for TensorFlow is employed for adjusting the weights of the CNN

5. Testing and Validation

With the provided images in dataset, the images will be classified into training images and testing images. With respect to the testing images, the model will be validated.

Training Dataset :-
Out of total images in the dataset 80% images are used for training.

Test Dataset :-
The images left in the dataset after training is used for testing.

80% of the data was given for training to the model, with the left 20% testing was done. Each epoch different weights are provided to layers by the model.

Tools Used

The project utilizes several tools and libraries for image processing, deep learning, and model deployment. TensorFlow and Keras are the primary deep learning frameworks used for training the VGG19-based CNN model for brain tumor classification. OpenCV is employed for image preprocessing techniques like noise reduction, histogram equalization, and edge detection. Matplotlib is used for visualizing the training progress and model results. The dataset is processed and trained using Google Colab, which provides GPU acceleration for faster computation. Additionally, Flask is used for deploying the model in a web-based application, with SQLite/MySQL handling database operations for storing patient MRI records and classification results.

Project Specification

Category Details	Details
Framework	Deep Learning (CNN - VGG19 Architecture) for brain tumor classification.
Dataset	Dataset BRATS Dataset – Includes segmented MRI images of brain tumors categorized into three

Image Processing	- Preprocessing Techniques: Noise reduction, histogram equalization, grayscale conversion. - Feature Extraction: Edge detection (Sobel, Prewitt, Laplacian of Gaussian), Texture Analysis..
Deep learning	VGG19 (Transfer Learning-based CNN) – Used for brain tumor classification and segmentation.
Training & Testing	- Training Data: 60-70% of MRI images. - Testing Data: 30-40% of MRI images. - Image Resizing: 224×224 pixels for CNN processing.
Performance Metrics	Accuracy Improvement: Model initially had 16% accuracy (with 1 epoch), improved to 25% (after 50 epochs), and further optimized for higher accuracy.
Libraries & Tools	TensorFlow & Keras – Deep learning framework. OpenCV – Image preprocessing. - Matplotlib – Visualization of results. Google Colab – Model training with GPU support.
Classification Approach	CNN with Convolutional & Pooling Layers to extract relevant tumor features. - Final Prediction: Outputs two probabilities for binary classification (Tumor/No Tumor)
Programming Language	Python – Used for image preprocessing, model training, and testing.
User Interface	Flask-based Web Application (optional). SQLite/MySQL Database for storing user uploads and results.

RESULTS

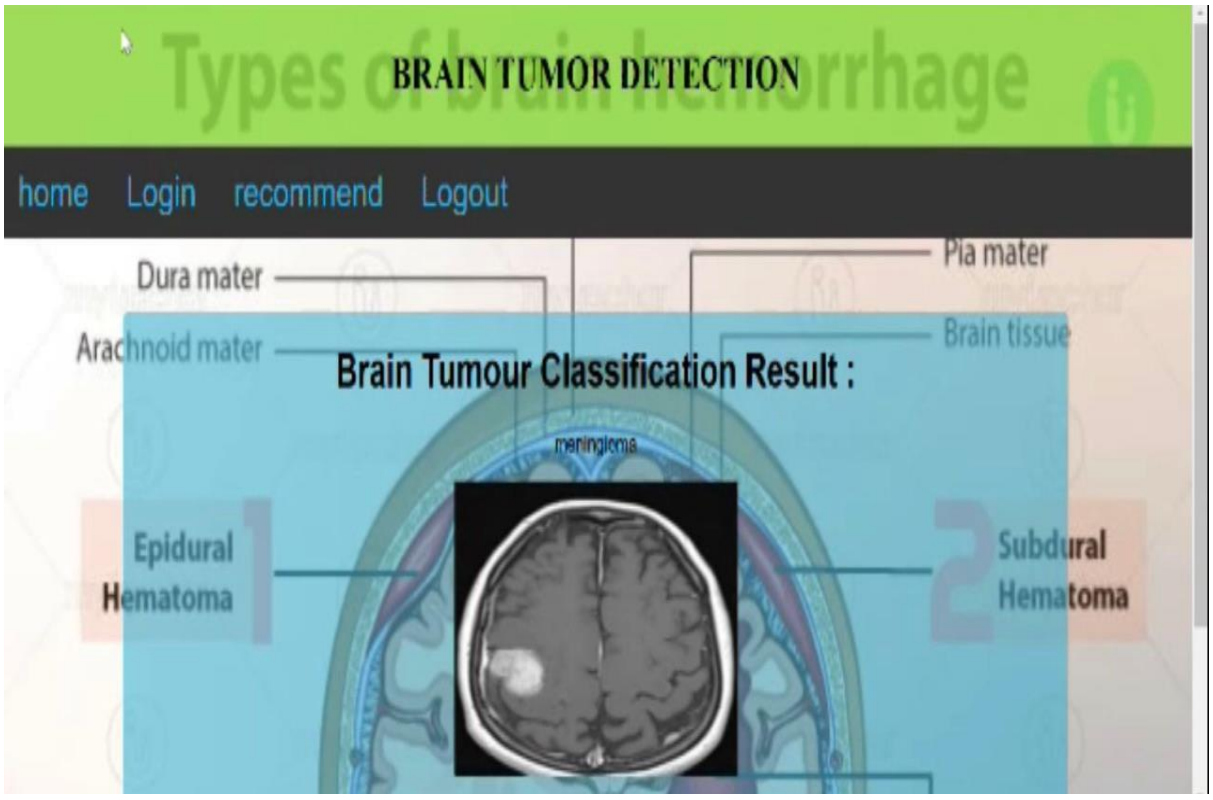


Figure 1

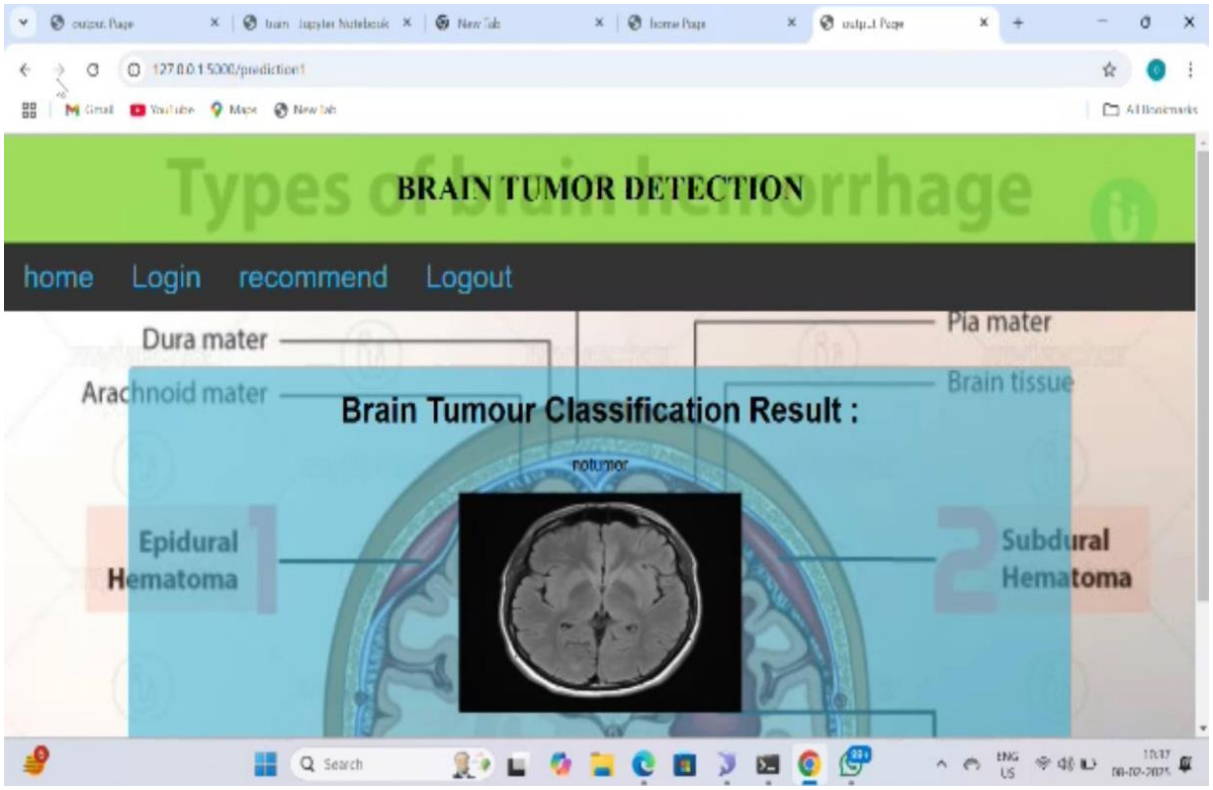


Figure 2

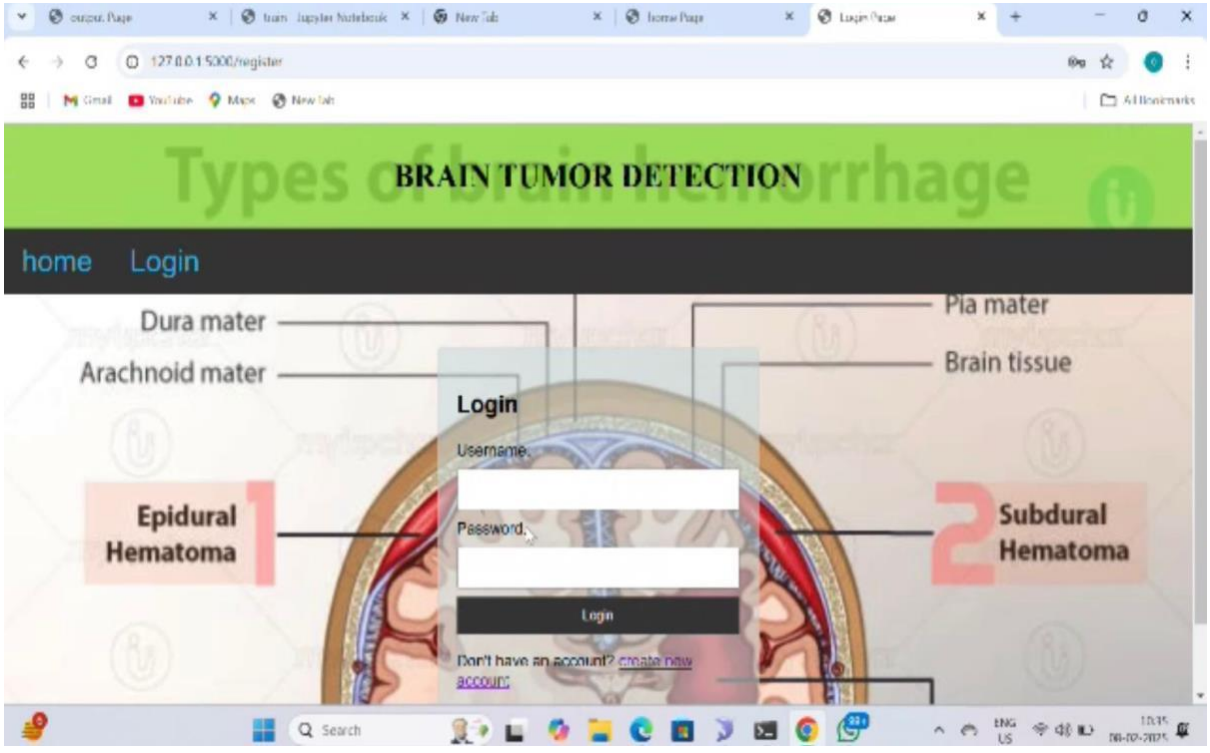


Figure 3

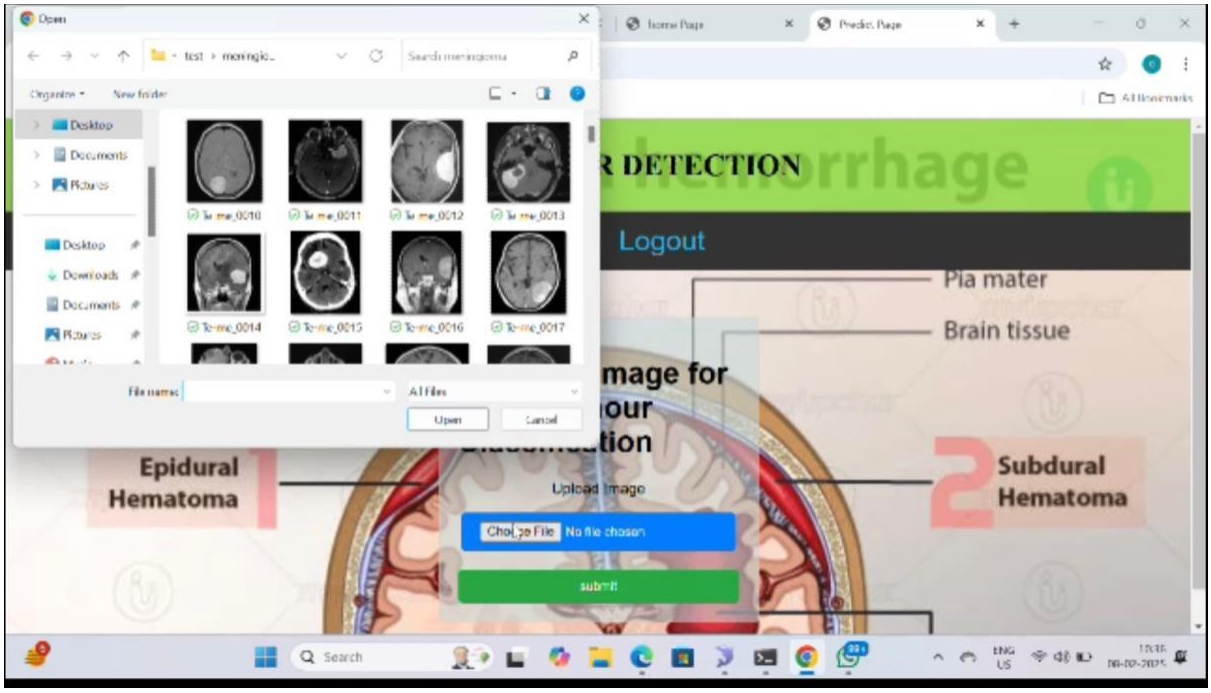


Figure 4

CONCLUSION

The VGG19as a basis layer and data augmentation approach were used to create a brain tumors detection and prediction with classification in this research. The literature component of the study included a comprehensive assessment of several CNN designs and their limitations. Then, using data augmentation, we demonstrated how we may increase performance on restricted brain tumors datasets. The model's capacity and accuracy in identifying images were shown to be extremely motivating in experimental findings. Even in an MRI dataset, our data augmentation-based method demonstrated great detection efficiency and strong assessment metrics value.

FUTURE ENHANCEMENTS

We intend to investigate more complicated architecture, a wider range of datasets, and additional data augmentation approaches in the future.

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