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Development of the Tumor Diagnostic Application for Medical Practitioners using Transfer Learning

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Abstract

A brain tumor is the growth of abnormal cells in the tissues of brain. It affects a large number of people of different ages, worldwide. Magnetic Resonance Imaging (MRI) is the most operative and widely used technique for brain tumor detection because it provides better contrast images of the brain. However, the complexity of the problem, manual classification process, requirement of skilled medical practitioners, and a huge amount of MRI scan data are the major factors thwarting the timely classification of tumor vs. non-tumor. Early detection of brain tumors is possible by accurately applying machine learning with the aim to save time, cost, and human life. Recently, deep machine learning via transfer learning techniques was found to be highly effective for classification tasks. A tumor diagnosis application is presented with a VGG-19-based deep learning model by applying transfer learning of knowledge. Five-fold cross-validation of the model demonstrated 88% accuracy along with a 0.881 F1 score. The application could be utilized as a successful tool aid for oncologists and radiologists in the clinical diagnostics process.

1. Introduction

A brain tumor is an unusual growth of cells in the brain. It can be cancerous (malignant) or non-cancerous (benign). When a benign or malignant tumor appears, it increases the weight of the brain. This leads to brain damage and it can be life-threatening. The prevalence of brain tumors is increasing rapidly. Pakistan is the 7th most populous country in the world with an estimated 148,000 cases diagnosed with cancerous tumors, annually. Over 100,000 cancer-related deaths and a prevalence of 350,000 living cancer patients have been reported during the last 5 years [1]. The first major challenge in this regard is the correct and timely diagnosis of a brain tumor due to the diverse shapes, locations, sizes, and appearances of tumors in the brain. The second major challenge is its accurate measurement. However, once a tumor is identified in the initial stage, then proper treatment and medicines can be effective against it. As of now, visual portrayal of the inside of the body is based on the clinical imaging methods designed for clinical examination and investigation [2]. Magnetic Resonance Imaging (MRI) is the most beneficial and broadly used method for brain tumor detection since it offers better contrast images of the brain and

diseased tissues, compared with the other medical imaging methods [2].

The current clinical diagnosis methods are based on manual judgment, increasing the chances of false recognition or delayed detection. Machine learning-based methods can be used to label brain tumors as malignant or benign [2]. Initially, image processing-based methods were proposed in computing to find brain tumors using MRI images. However, these methods were not generalized for some medical cases. Later, a number of machine learning-based approaches were proposed for the classification of brain tumors. Some of these techniques proved to be accurate and were generalized, such as SVM-based classifier, Neural Network (NN), and Convolutional Neural Network (CNN). However, the need of the hour is to provide an application or software system benefiting from machine learning algorithms, since most of the existing applications rely on image processing-based techniques. They require heavy processing and a team of professionals to produce accurate results. Manual intervention by experts is required because these applications focus on image enhancement and segmentation. They don't offer a machine learning-based classification model to aid the clinical diagnosis process. They only provide an enhanced image of a brain tumor for an already diagnosed case, such as CaPTk software. Although there are many medical imaging tools available yet the number of diagnostic tools is very limited.

The diagnosis of brain tumor at an early stage is crucial. Oncologists usually conduct the diagnosis based on the manual investigation of the MRI images of the brain, which is not only cumbersome but also requires extensive skill, experience, and time. Occasionally, it is prone to human errors due to a lack of expertise or experience. Secondly, very often patients or doctors contact senior doctors for a second opinion which also adds to the time and cost of diagnosis. A computer-aided facility for fast, timely, and automated detection of tumors can save time, effort, and cost. Furthermore, it can be a useful support for doctors to save a life. The contribution and objectives of this study are as follows:

i. To facilitate oncologists in cancer diagnosis through the automated aid of machine learning-based software.
ii. To save the time spent by doctors in identifying brain tumors in contrast to the manual process.
iii. To eliminate any possibility of false detection when identifying brain tumors.

The rest of the paper is organized as follows. Section 2 describes related work in the cancer diagnosis domain. Section 3 explains the proposed approach and diagnostic tool. Section 4 presents the results, while Section 5 concludes the current study.

2. Related Work

Numerous methods have been recommended by researchers to detect brain tumors and other anomalies in human brain using MRI images. In [3], the authors proposed an approach using segmentation, histogram, and thresholding to detect a tumor in the brain. In [4], Meyer's flooding watershed algorithm was used along with a fuzzy classifier. In [5, 6], a segmented morphological approach was used to detect tumors in brain images.The Fuzzy Inference System (FIS) was proposed in [7] for brain tumor segmentation. Membership functions of the fuzzy controller were created using supervised classification. The difference of the MRI image was improved using adaptive histogram equalization. Then, tumor was separated from the whole brain image using the Fuzzy C-Means (FCM) based segmentation and the fuzzy logic-based KNN classifier. This system proved

to be complex with a low-performance accuracy. In another study, a CNN-based technique for brain tumor classification was presented [8], combining different segmentation algorithms. The complexity of this system was high [9].

Similarly, various segmentation-based methods exist such as Fuzzy C-Means segmentation, geometric deformable model, Margo Random Field (MRF), threshold-based segmentation, deformable model, region-based segmentation, and atlas-based segmentation [10]. In [11], Local Independent Projection-based Classification (LIPC) was used to classify the voxel of the brain. Another model was proposed by researchers for analyzing the step-by-step growth of tumors in patients. Tumor growth was modeled by combining the discrete and continuous methods. The proposed approach used atlas-based registration to tacitly segment tumor-bearing images. However, all these image processing techniques require a high computation time [12].

Damodharan et al. proposed a neural network-based method for detecting and classifying brain tumors. They predicted tumor regions with 83% accuracy [13]. Alfonse et al. proposed an approach using SVM-based classifier and Fast Fourier Transform (FFT). Features were reduced with the help of the Minimal Redundancy Maximal Relevance (MRMR) technique to improve the performance of the classifier [14]. Kumar et al. proposed an approach using Radial Basis Function (RBF), kernel-based SVM and Principal Component Analysis (PCA) [15]. Chaddad proposed a method known as the Gaussian Mixture Model (GMM) to study MRI images. The performance of GMM feature mining was enhanced through PCA and wavelet-based features. In this regard, 97.05% correctness was obtained using this method for T1- and T2-weighted and 94.11% for FLAIR-weighted MRI images [16]. Deepa et al. suggested a neural network technique for the classification of brain tumors based on 3D MRI images using an extreme learning machine with an accuracy of 93% [17]. ANN-based techniques were presented in [18, 19]. These techniques used PCA for feature selection with 91% accuracy.

Brain tumor identification in its initial phases is mostly based on the knowledge of the radiologist [20]. The detection of tumor remains incomplete without its classification as either benign or malignant [21]. In order to correctly diagnose the tumor and evade an unnecessary medical procedure and subjectivity, it is essential to build up a viable diagnostic tool for tumor characterization [20]. The Brain Tumor Segmentation Challenge (BRATS) [22] is still in progress, as reported in the literature [23–32].

In conclusion, segmentation-based methods of tumor detection are not automated to the extent that makes them generalizable, so that they may applied to new cases. Similarly, machine learning-based approaches described above achieved up to 90% accuracy. However, all of these approaches are based on a manual feature extraction process which has its own limitations, such as skill requirement and time-consumption, which make it a tedious task. Recently, deep learning-based approaches have achieved tremendous success in tumor classification. The only limitation is that deep learning requires huge datasets to unleash its potential. However, small size datasets [33, 34] can also be used for training deep learning models by applying transfer learning. CNN-based deep learning models such as VGG-19 [35-39] can be trained for brain tumor classification using a transfer machine learning approach.

3. Proposed Work

Cancer diagnostic model is presented with a desktop application to identify brain tumors and characterize their types. The methodology is depicted in Figure 1 and explained further in subsections. The following methodological steps are proposed.

- Dataset acquisition
- Data pre-processing
- VGG-19 model training (automated feature extraction and selection using Deep CNN)
- Validation testing for classification.

A. Dataset Description

Figshare dataset [33, 34] was used for training and testing the model in this study. This brain tumor dataset incorporates 3064 T1-weighted contrast-enhanced images from 233 patients. Image samples from the dataset are shown in Figure 2. The data is organized in MATLAB data format (.mat file). The structure of the file is presented in Table 1. The dataset contains images of three different types of tumors including meningioma, glioma, and pituitary tumors, as shown in Table 2. In Figure 2, the tumor is highlighted with a red boundary [35].

B. Data Pre-Processing

MRI image samples in the target dataset are of the dimension 512 x 512 and provided in int16 format. VGG-19 model receives data on its input layer as 224 X 224 X 3. Therefore, input images were normalized and resized to 224 X 224.

C. Network Architecture

Although deep machine learning is very popular due to its impressive performance; however, it requires huge datasets to train with precision. Moreover, it also requires considerable computing resources and time. Furthermore, the utilization of a large number of parameters to train a big dataset using a large network merely increases the complexity of the problem. Therefore, the concept of *transfer learning* or *knowledge transfer* is utilized in the proposed application. This concept employs a complex deep learning architecture already trained on a huge amount of data. This pre-trained model can be used further to train either all layers or partial layers of the proposed model using the new and compact dataset of another similar problem. It also has a strong capability to simplify images outside the ImageNet dataset via *transfer learning*, such as feature mining and fine-tuning.

Table 1. Dataset Detail

Number of Classes	Number of Samples
Meningioma Tumor	708
Pituitary Tumor	930
Glioma Tumor	1426
Sample Size	3064

Table 2. Dataset Structure

Field	Data
Label	1 for meningioma 2 used for glioma 3 for pituitary tumor
PID	Patient ID
Image	(512x512) INT16 image data
TumorBorder	A vector to store the discrete coordinates of tumor's borders

Tumor Mask Binary image

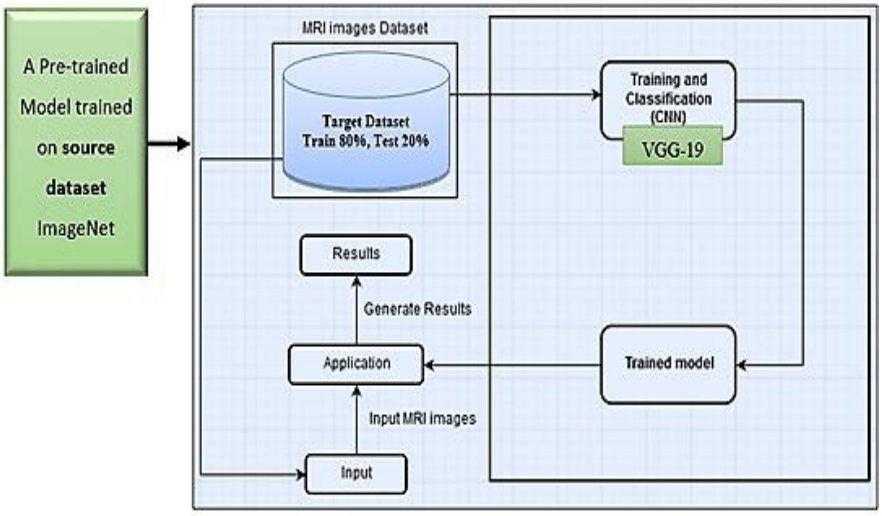

Figure 1.Top Level Methodology

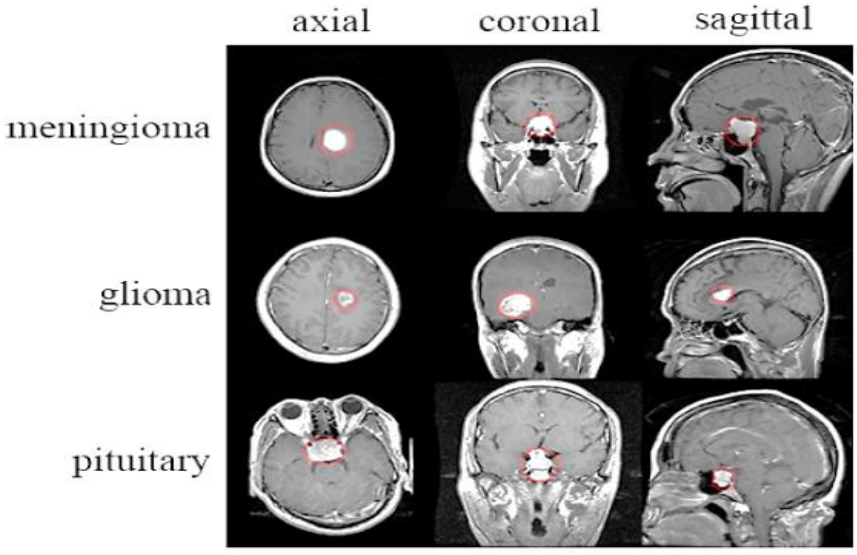

Figure 2. Formalized MRI shows different types of tumors in various planes

VGG-19 [35] is a pre-trained deep learning model based on the Convolutional Neural Network (CNN) which is popular for image-based and video-based data learning. The topology of CNN offers multiple learning stages. It consists of a combination

of different layers, such as the convolutional layer, non-linear processing units, and subsampling layers.

The outer layers of CNN capture low-level features of the input, whereas the advanced layers learn high-level fine-grain features of the images. This automated feature engineering is the major advantage of CNN as it removes the need for manual or hand-crafted feature extraction and feature selection. Convolutional layers learn features tailored by pooling layers, which reduces the dimensionality of the feature map learned in the previous layer. Max pooling operation also decreases the noise in the image.After creating a series of combinations of different convolutional and pooling layers, a flatten layer converts the feature map into a one-dimensional vector of features, that is, 1 x 4096, as shown in Figure 3 and Figure 4. This flatten layer is further followed by dense, fully connected layers which are similar to standard neural networks and used for further weight learning and classification. The last layer is a classification layer based on the SoftMax function and used to classify the final output.

We applied the concept of knowledge transfer to enjoy the benefits of a pre-trained model, as demonstrated in Figure 3. Vgg-19 [36] pre-trained model was used to apply the concept of knowledge transfer or transfer learning. It was pre-trained on millions of images from the ImageNet database [21]. It can classify images into 1000 object groups from our daily life, such as pencil, ball, keyboard, animals, and several other objects. Training for tumor classification was performed using the KERAS library of VGG-19 in MATLAB R2018a [35]. Its weights were pre-trained on ImageNet.

The detail of the layer structure of CNN in VGG-19 is depicted in Figure 4. The default size of an input image for VGG-19 is 224 x 224 x 3. It has a total of 47 layers. Among these layers, 19 layers exist with learnable weights, out of which 16 are convolutional layers and 3 are fully linked layers. Hence, it comprises 19 deep layers to train weights. Two dropout layers with 50% weights dropped are also used in VGG-19. The convolutional stride size used is 1, whereas pooling step size 2 and image padding size 1 are used in the model. CNN architecture of VGG-19 is depicted in Figure 4 and Figure 4. It shows the reduction in the dimensionality of the feature map.

D. Training and Testing

VGG-19 was further trained on the brain MRI dataset Figshare to classify a brain tumor. A k-fold cross-validation strategy was used. We used five folds. The dataset was divided into 5 sets, each set having the same number of images. Four sets were used for training the model and one set was used for testing purposes. Also, 80% of the dataset was used for training and the remaining 20% was used for testing the trained model. A total of 20 epochs were used in each fold and 630 iterations were executed in each epoch. The learning rate was kept as 0.01. We used k-fold cross-validation approach to check network execution [39, 40]. The accuracy of the five-fold cross-validation is shown in Figure 5. It was used to arbitrarily partition the information into 5 general subsets, so that every tumor class was present in each set, insinuated as record-wise cross-validation. This strategy also prevented training from over fitting.

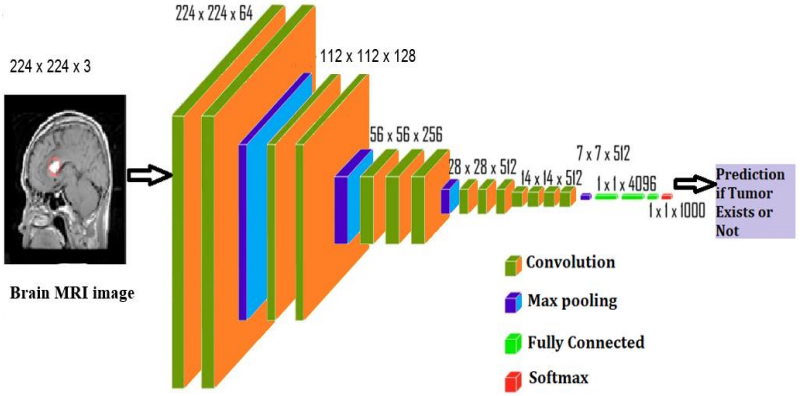

Figure 3.VGG-19 CNN Architecture

1	'input'	Image Input	224x224x3 images with 'zerocenter' normalization
2	'conv1_1'	Convolution	64 3x3x3 convolutions with stride [1 1] and padding [1 1 1 1]
3	'relu1_1'	ReLU	ReLU
4	'conv1_2'	Convolution	64 3x3x64 convolutions with stride [1 1] and padding [1 1 1 1]
5	'relu1_2'	ReLU	ReLU
6	'pool1'	Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
7	'conv2_1'	Convolution	128 3x3x64 convolutions with stride [1 1] and padding [1 1 1 1]
8	'relu2_1'	ReLU	ReLU
9	'conv2_2'	Convolution	128 3x3x128 convolutions with stride [1 1] and padding [1 1 1 1]
10	'relu2_2'	ReLU	ReLU
11	'pool2'	Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
12	'conv3_1'	Convolution	256 3x3x128 convolutions with stride [1 1] and padding [1 1 1 1]
13	'relu3_1'	ReLU	ReLU
14	'conv3_2'	Convolution	256 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
15	'relu3_2'	ReLU	ReLU
16	'conv3_3'	Convolution	256 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
17	'relu3_3'	ReLU	ReLU
18	'conv3_4'	Convolution	256 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
19	'relu3_4'	ReLU	ReLU
20	'pool3'	Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
21	'conv4_1'	Convolution	512 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
22	'relu4_1'	ReLU	ReLU
23	'conv4_2'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
24	'relu4_2'	ReLU	ReLU
25	'conv4_3'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
26	'relu4_3'	ReLU	ReLU
27	'conv4_4'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
28	'relu4_4'	ReLU	ReLU
29	'pool4'	Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
30	'conv5_1'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
31	'relu5_1'	ReLU	ReLU
32	'conv5_2'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
33	'relu5_2'	ReLU	ReLU
34	'conv5_3'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
35	'relu5_3'	ReLU	ReLU
36	'conv5_4'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
37	'relu5_4'	ReLU	ReLU
38	'pool5'	Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
39	'fc6'	Fully Connected	4096 fully connected layer
40	'relu6'	ReLU	ReLU
41	'drop6'	Dropout	50% dropout
42	'fc7'	Fully Connected	4096 fully connected layer
43	'relu7'	ReLU	ReLU
44	'drop7'	Dropout	50% dropout
45	'fc8'	Fully Connected	1000 fully connected layer
46	'prob'	Softmax	softmax
47	'output'	Classification Output	crossentropyex with 'tench' and 999 other classes

Figure 4. Layered description of the architecture of VGG-19 [36]

Figure 5. Five-Fold Training Progress

4. Results and Discussion

E. Performance Metrics

This section describes the performance metrics and notions used for the standardized evaluation of the trained machine learning model. Accuracy, in classification, is explained as the ratio of the number of fittingly classified samples to the total number of data samples. However, accuracy is neither the only nor the true representative of a model's performance. Other performance metrics such as precision, recall, and F1 score are also used to validate the model. These are described as follows.

True Positive (TP): A *true positive* assessment result identifies the condition when the condition is present.

False Positive (FP): A *false positive* test result incorrectly indicates that a specific condition or attribute is present.

True Negative (TN): A *true negative* is a test result in which the model correctly predicts the *negative* class.

False Negative (FN): A *false negative* is a test result that indicates a person does not have a particular infection or symptom when the person does have it.

Accuracy: Classification *accuracy* is defined as the number of correctly classified patterns to the total number of patterns, as shown in equation 1.

$$Accuracy = \frac{(TP+TN)}{(TP+FP+TN+FN)} \qquad (1)$$

Precision*: Precision* is the fraction of the relevant instances among the retrieved instances, as shown in equation 2.

$$Precision = \frac{TP}{(TP+FP+TN+FN)} \quad (2)$$

Recall:

Recall is the fraction of the total number of relevant instances that were retrieved, as shown in equation 3.

$$Recall = \frac{TP}{(TP+FN)} \quad (3)$$

F1-Score: It is the harmonic mean (average) of precision and recall, as shown in equation 4**.**

$$F1 = 2 * \frac{(Recall * Precision)}{(Recall + Precision)} \quad (4)$$

Confusion Matrix*:*

It defines the accuracy of a classification model on a set of test data for which the true values are known. Various measures such as accuracy, recall, and precision are derived from the confusion matrix.

This matrix involves the projection of a classification model on a group of test information for which the right qualities are known. It permits the visualization of the performance of an algorithm. The confusion matrix is depicted via a three-by-three table that contains nine outcomes produced by a multiclass classifier, as shown in Figure 6. The validation score for classification accuracy in this study is 88%.

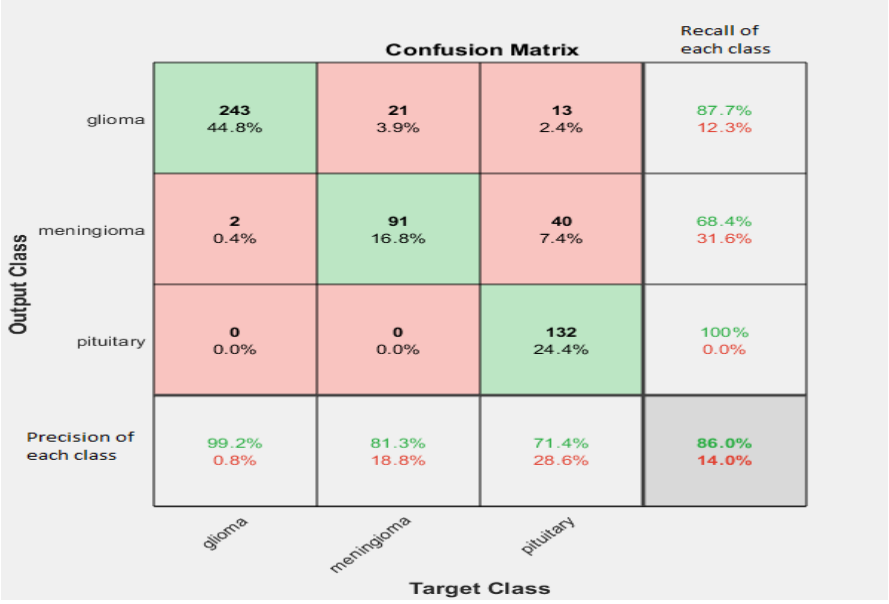

Figure 6. Confusion Matrix of the Trained Model

F. **Comparisons**

Several researchers have used a similar dataset for the classification of brain tumor. To compare the results of the proposed approach, we selected the neural network based studies only, as demonstrated in Table 3. The proposed approach demonstrated 88.5% accuracy, which is

appropriate as per the project's objectives. The model was trained using the k-fold technique. It implies that training contained a total of six folds and with each fold the accuracy of the model increased, up to the fifth fold. After the fifth fold, accuracy started decreasing. So, the model trained till the fifth fold with 88.5% accuracy, which was determined to be adequate for final results.

The trained model was integrated with the application designed to be used by a medical practitioner. Matlab App Designer was used to create a GUI interface and the model was integrated with it. Accuracy and effectiveness can be improved by enhancing the data set. After training, VGG-19 was used to pre-train the neural network with a bigger data set using the fold technique to achieve greater accuracy diagnostic functions by uploading the MRI images of patients in the tool and can also save the generated results. The application interface is shown in Figure 7 and Figure 8.

A GUI interface was built using MATLAB version R2018a. MATLAB provides a feature known as MATLAB App Designer which was used to create a GUI interface and the trained model was integrated with it. This application provides users with an easy and effective way to upload and classify MRI images using the trained model depicted in Figure 8

.

Table 3. Comparison of Results with Different Approaches Trained on the same brain

References	Approach used	Accuracy [%]	Precision [%]	Recall [%]	F1-Score [%]
Gamage [2]	Neural Network	85.03	X	X	X
Karuna and Joshi [5]	Nero Fuzzy Classifier and NN	83.10	X	X	X
Parameshwarappa and Nandish [6]	segmented morphological approach	81.98	X	X	X
P.Meena [8]	KNN	84.30	85.6	84.75	85.09
Menze et al. [9]	CNN	85.03	X	X	X
Huang et al [11]	Local independent projection-based classification	84.30	85.6	84.75	85.09
Damodharan and Raghavan [13]	Neural Network	84.30	X	84.75	85.09
Proposed work	VGG-19 based method	87.07	88.03	87.17	88.10

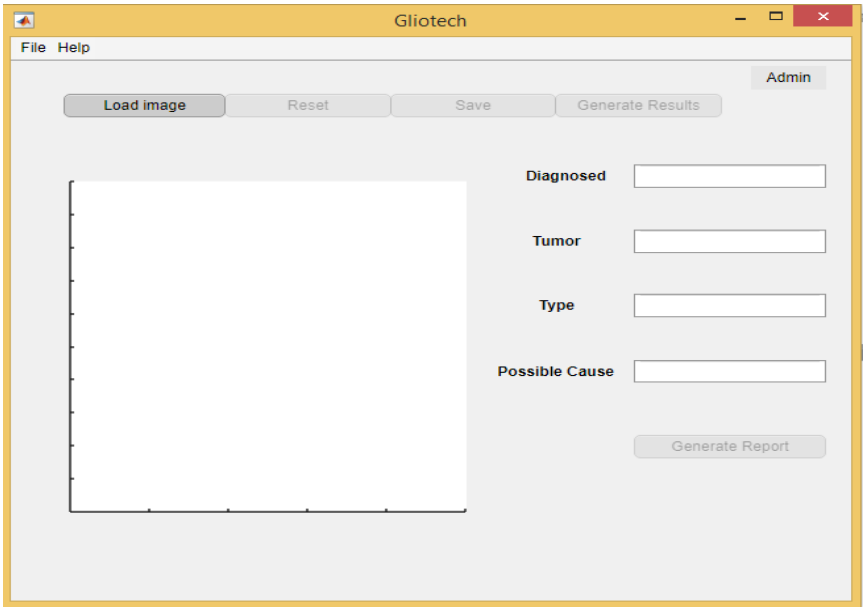

Figure 7.Application Home Screen

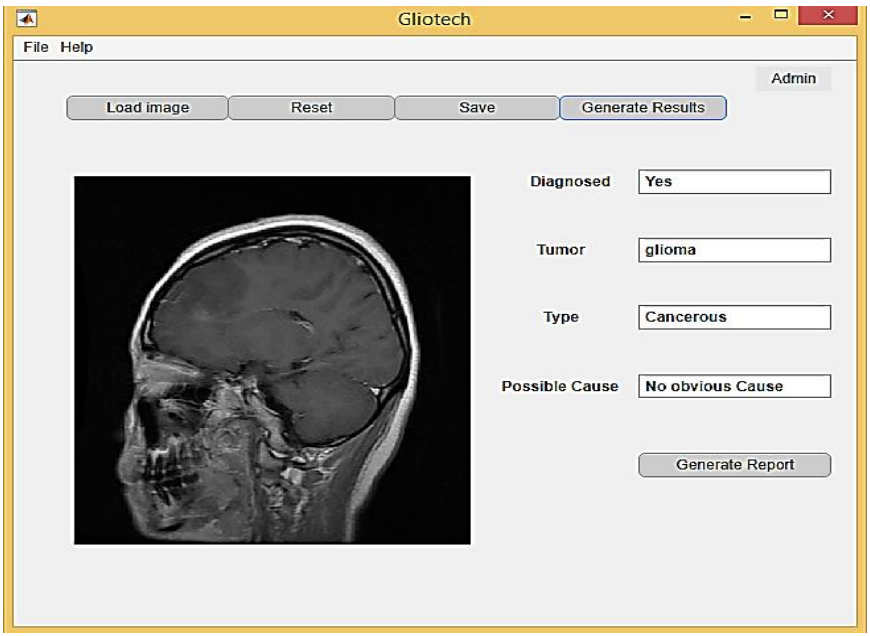

Figure 8. Home Screen After Diagnosis

G.Application Interface

A cancer diagnostic desktop application tool was developed for doctors and medical staff to diagnose patients. Application users can perform

4. Conclusion and Recommendations

In the current study, we developed a tumor diagnosis application with a demonstrated 88.5% accuracy. For this purpose, a machine learning model using VGG-19 for the identification of tumors in brain MRI images was used. A five-fold cross-validation technique was used during model training. The trained model was deployed with a MATLAB App Designer to provide a user-friendly interface for medical practitioners or oncologists. Future work may strive to improve the accuracy of the model and the inclusion of more categories of brain tumors.

Author Contribution

Conceptualization, IN; Methodology, IN, NS.; Software, IN, NS. Validation, IN, Writing, original draft, NS. Writing, review, and editing, IN and NS. All authors have read and agreed to the published version of the manuscript.

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Conflicts of Interest

The authors declare no conflict of interest.

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