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Enhanced Brain Tumor Classification using VGG19 and Data Augmentation Techniques

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Abstract

Timely and successful therapy relies on the correct diagnosis and categorization of brain tumors. In this study, we present a deep learning-based method for the automated identification of brain tumors in MR images. We used a data collection that was available to the public and included both MRI images of brain tumors and normal brain. We down sampled the images, added more data, and normalized the pixel values as preliminary processing. We utilized the cleaned data set to construct a deep learning model based on VGG19. Our model showed a 96.3% accuracy, 96.3% AUC ROC score, 96% precision, 96% recall, and 96% F1 score. To evaluate our model's performance, we used various metrics such as accuracy, precision, recall, F1 score, confusion matrix, AUC ROC score, and ROC curve. Furthermore, we compared our model's results with the best performing model from a related study that utilized machine learning algorithms such as Random Forest, SVM, Logistic regression, Gradient boosting, and the achieved accuracy is 92.4%, precision is 85.0%, recall is 94.4%, F1 score of 89.5%, and AUC ROC score touching 97.2%.

Keyword: Image classification, MRI, Transfer Learning, Deep Learning, brain tumor detection

Introduction

There are approximately a million new cases of brain tumors each year, making them a huge public health issue all over the world. Primary brain tumors develop from preexisting brain tissue, whereas secondary brain tumors develop after cancer has moved to the brain from another region of the body. A brain tumor is a condition resulting from the growth of abnormal cells in the brain. [1]. Symptoms of brain tumors, which can include headaches, seizures, and cognitive impairments, may significantly alter a person's standard of living and their chances of survival. The ability to promptly diagnose and treat brain tumors is a key factor in improving patient outcomes. However, conventional approaches of detecting brain tumors, such as the manual interpretation of medical images, may be laborious, pricey, and error-prone. To increase the accuracy and effectiveness of brain tumor diagnosis, there has been a surge in interest in the application of machine learning techniques in recent years.

This study aims to investigate the possibility of using "machine learning" techniques to the diagnosis of brain cancers (tumors) and to provide solutions to the problems that arise from doing so. AI and ML have significantly impacted clinical decision-making by providing previously hidden insights [2, 3]. In this study, we will specifically train and evaluate various ML algorithms for brain tumor identification using a dataset of brain MRI images. The findings of this study will help researcher's better grasp the potential of machine learning for brain tumor identification and identify the most promising areas for future research.

The research into the identification of brain tumors is crucial since it has the potential to greatly make better patient outcomes while simultaneously decreasing healthcare expenses. Although machine learning shows promise as a method for improving the accuracy and efficiency of brain tumor diagnosis, it still faces a number of obstacles.

Combining the expertise of medical professionals with AI and ML has the potential to increase efficiency and potentially improve accuracy [4, 5].The goal of this study is to deepen our understanding of how "machine learning" may be used to identify tumors in the brain and to illuminate the most serious challenges and promising future directions in this field.

RELATED WORK

The author of this study Raut, Gajendra, et al [6] presents a case for automating the process of diagnosing brain tumors. In order to identify brain tumors with 95.5% accuracy, they propose a model that makes use of convolutional neural networks (CNNs). After the tumor has been identified, the authors use segmentation methods such as auto encoders and K-means to pinpoint the area of the picture where the tumor is most prominent. They discovered that relying just on K-means led to a poorly segmented and noisy picture. They used a combination of auto encoders and K-means to solve this problem, and the resulting segmented images were clearer and more accurate. In conclusion, the suggested model is a useful tool for identifying and segmenting brain tumors that reduces the need for manual intervention.

The author of this study Hossain, Tonmoy, et al [7] explores the use of a “Fuzzy C-Means clustering algorithm”, conventional classifiers, and a convolutional neural network to accurately separate brain tumors from 2D MRI scans of the brain. The authors state that when dealing with a vast quantity of data, manual categorization might lead to erroneous predictions and diagnoses. The difficulty in extracting tumor areas from images is compounded by the fact that brain tumors exhibit a wide range of morphologies and often blend in with surrounding normal tissue. Pashaei, Ali [8] introduced a computer-assisted detection (CAD) method for classifying brain tumors in MRI images. The brain MRI images were processed through Discrete Wavelet Transform (DWT) to extract features, which were then fed into a CNN for image classification. The proposed approach achieved an overall accuracy of 98.5%.

[9] This work investigates the use of MR images to distinguish between different types of brain tumors. Since the MR image filter does not put the patient through any unnecessary radiation exposure, the author claims it is the best option for analysis. Segmentation of brain tumors is a challenging clinical diagnostic assignment due to the presence of several large and complex biases given to the images. The task requires promptness, accuracy, and reliability. In order to locate and eliminate the tumor during segmentation, the author makes use of K means and Fuzzy C-means (FCM) clustering methods. Segmented and relative area measurements, mean square error, and maximum signal-to-noise ratio are used to evaluate K-means and FCM clustering algorithms and draw comparisons between them. Compared to the K-means algorithm, the FCM technique performs better. This indicates that the FCM algorithm correctly segmented 0.93 percent of the relative tumor area from the original MR image, indicating that the tumor affected this area. FCM Algorithm processing time is 8.639 seconds, whereas KM Algorithm processing time is 22.831 seconds. The author of this study Jiang, Jun, et al [10] explains the difficulties associated with diagnosing and radiation planning for brain tumors due to the varying appearance of tumor tissue from patient to patient and the ambiguity of lesion borders. The author presents a technique for building a graph using the feature sets of multimodal MRI from both the population and individual patients. Using global and bespoke classifiers, the network determines the likelihood that a given pixel is either part of the tumor or the backdrop. Twenty-three glioma picture sequences are used to assess the suggested method, and the segmentation results are compared to those of alternative methods. A Dice similarity coefficient (DSC) of 84.5%, a Jaccard similarity coefficient exactly 74.1%, a sensitivity of 87.2%, and specificity to 83.1% were found to be attained by employing the proposed technique.

To automatically classify brain tumors, the author of this work Cheng, Jun, et al [11] explores the use of T1-weighted contrast-enhanced MRI images. The study recommends utilizing a larger tumor area obtained using image dilation as the ROI rather than the original tumor location. The larger tumor area is partitioned into increasingly smaller ring-shaped subregions to accommodate variations in tumor form and size. The suggested method is tested on a large dataset using three different feature extraction strategies: an intensity histogram, a gray level co-occurrence matrix GLCM, and a bag-of-words model. The suggested technique is successful and practicable for identifying three forms of brain tumors: meningioma, glioma, and pituitary tumors, depending on the feature extraction method and region of interest employed The author Shin, Hoo-Chang, et al [12] of this paper discusses a Content Based Image Retrieval (CBIR) approach for MRI brain tumor images. Images from a database that share visual attributes with a query picture are found via content-based image similarity (CBIR) searches. The CBIR method relies heavily on feature extraction and similarity measure. Many other CBIR systems have been developed, each tailored to a specific set of values for these variables. This study describes the development of a CBIR system for Magnetic Resonance Images of brain tumors and assesses it in light of previous CBIR studies. Distance Metric Learning (DML) is used by the author instead of more common distance metrics like Euclidean distance to establish levels of similarity. The mean average precision of the CBIR system was calculated to be 92.41, which is significantly high for MRI brain tumor retrieval.

CNN ARCHITECTURE VGG19

The VGG19 architecture is a type of deep “convolutional neural network” that was created by the “Visual Geometry Group” (VGG) located at Oxford University. In comparison to its predecessor, the VGG16 model, the VGG19 model has 3 additional convolutional layers and 2 extra fully connected layers. In the VGG19 architecture, Max pooling layers are integrated into the VGG19 architecture following each convolutional layer. These max pooling layers decrease the dimensionality of the feature maps after the convolutional layers extract high-level features from the input image. This is done to increase the computational efficiency of the model. Sixteen convolutional layers and three fully linked layers make up the VGG19 model's total of 19. Convolutional layers make up the first 13 stages, while fully linked layers make up the last 3. There are a total of 8,192 neurons over the first two fully connected layers, with the last fully connected layer consisting of 1,000 neurons to account for the 1,000 classes in the ImageNet dataset.

Over 1.2 million images from over a thousand distinct classes were used when preparing the VGG19 model. After being trained, the model is able to classify images into one of a thousand categories based on the items and patterns they include. The VGG19 model's great accuracy on many image identification tasks is one of its primary strengths. In fact, when it was originally presented in 2014, the VGG19 model produced state-of-the-art performance on the ImageNet dataset, with a top-5 error rate of only 7.3%. There are several uses for the VGG19 model, and these include picture classification, object identification, and image segmentation. The model has also used as a jumping-off point for transfer learning, in which a pre-trained model is further refined for a given task using a smaller dataset.

PROPOSED METHODOLGY

The proposed methodology has been illustrated in Fig.1

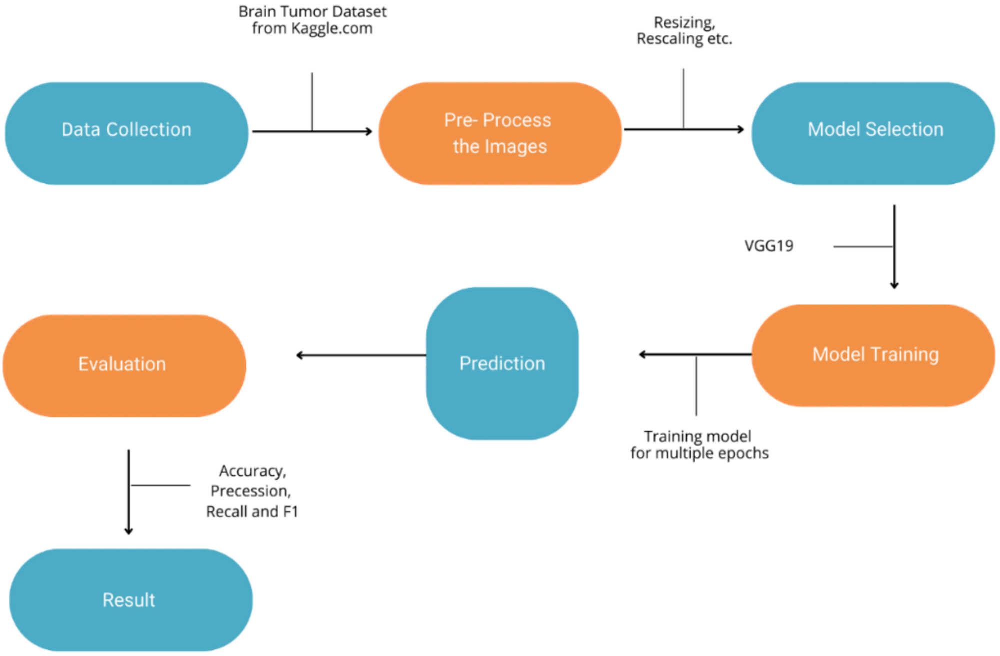


Figure 1 Flow Chart of Proposed Model

Dataset

The dataset used in this research is the "Br35H :: Brain Tumor Detection 2020" dataset, which is publicly available on Kaggle.com. The images are in RGB format and have a resolution of different size. The dataset contained a total of 3000 MRI images, including 1500 images with tumors and 1500 images without tumors. The images were collected from various sources, including hospitals and research centers, and were annotated by medical professionals to indicate the presence or absence of a tumor. Kaggle is a website where anyone may participate in data science challenges and create machine learning projects, and it was there that we found the information used in this research. Kaggle offers a large variety of freely usable datasets.

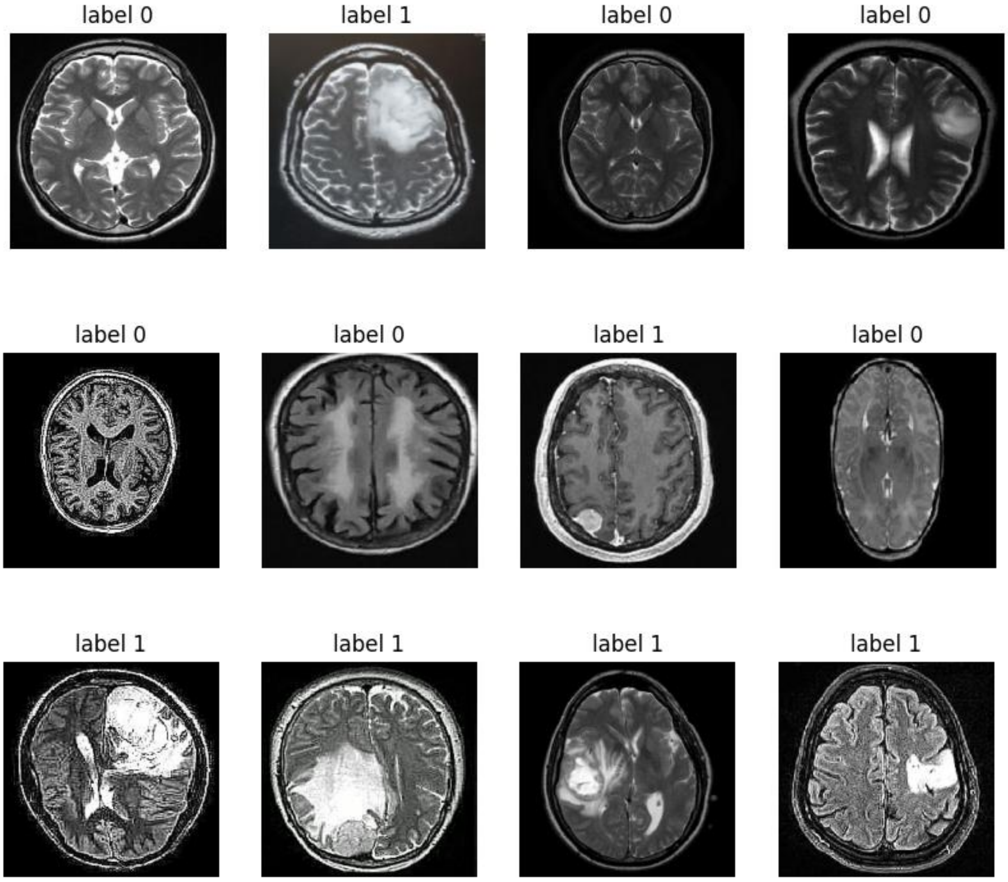


Figure 2 Dataset Sample

To ensure the accuracy and reliability of the data, we conducted a thorough quality check before including it in our study. We ensured that the images were of high quality and resolution, and that they were correctly labeled to indicate the presence or absence of a tumor. We also checked for any inconsistencies or errors in the data and corrected them wherever necessary.

Performance Metrics

The model's prediction accuracy was tested using a variety of metrics. Our first metric was accuracy, which assesses how often a model correctly predicts a value. The accuracy rate is the proportion of correct predictions relative to the total number of predictions. The second metric was recall, which was calculated as the proportion of positive samples that were actually analyzed. The true positive rate is synonymous with the sensitivity. The harmonic mean of “precision” and “recall”, or F1 score, was the third statistic we used. For skewed data sets, this metric is helpful since it takes into account both precision and recall. As a fourth metric, we analyzed precision, which is the ratio of true positives to total forecasts. One alternative name for this is "positive predictive value."

A confusion matrix was used to show the model's usefulness and efficiency. The confusion matrix summarizes the results of a binary classification model by showing the sum of the numbers of correct classifications, erroneous positives, and incorrect negatives. In addition, we determined the AUC ROC score. The connection between the true positive rate (recall) and the false positive rate (1 minus specificity) is shown by the ROC curve for different cutoff settings. Considering both the true positive and false positive rates, the AUC ROC score is an appropriate statistic for imbalanced datasets. Using the roc_curve function, we then plotted a ROC curve to examine the model's accuracy over a variety of categorization criteria.

Image Pre-Processing

Preprocessing is a crucial part of every machine learning project because it facilitates the discovery of actionable insights hidden in raw data. By performing different changes to the images, such as scaling, flipping, and rotation, data augmentation is a technique used to artificially expand and preprocess the size of the dataset. This method may be used to boost the model's efficiency by decreasing the amount of overfitting and increasing the amount of generalization. In our study, we performed the following preprocessing steps:

Rescaling: Rescaling is a preprocessing technique used to normalize the pixel values of an image between 0 and 1. This technique is useful in reducing the effect of illumination variations and improving the performance of the model. In our project, we rescaled the pixel values of the images using the rescale parameter of the ImageDataGenerator class.

Image Resizing: Image resizing is a preprocessing technique used to standardize the size of the images in the dataset. In our project, we resized the images to (224, 224) pixels, which is the input size required by the VGG19 model as this is a common input size for many CNN architectures [13].

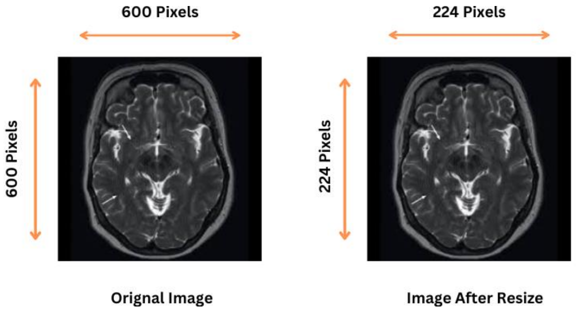
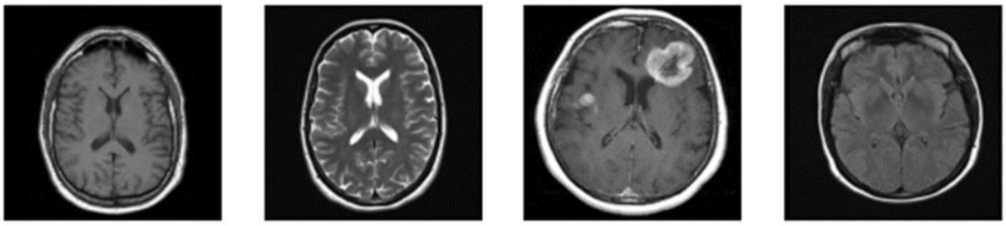


Figure 3 Data Resizing

Random Transformations: Random transformations are a preprocessing technique used to introduce variability in the dataset. When statistical models reflect random noise or mistakes rather than possible correlations, overfitting happens in machine learning and statistics [14].In our project, we used the following random transformations like Width Shift: Random horizontal shift of the image, Height Shift: Random vertical shift of the image, Shear: Random shear transformation of the image, Zoom: Random zoom-in or zoom-out of the image, Rotation: Random rotation of the image, Brightness: Random brightness adjustment of the image. By introducing randomization to the photos, all of these factors are employed to fictitiously enlarge the dataset and prevent overfitting [15].

Before Image Augmentation



After Image Augmentation

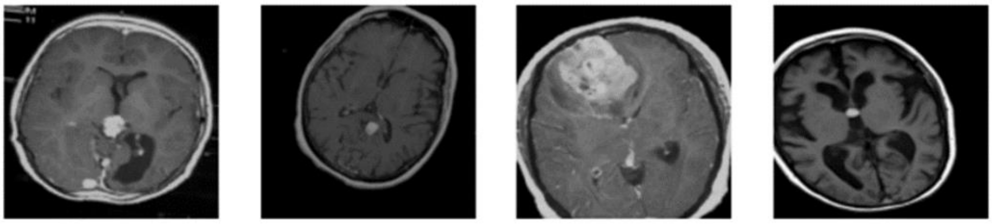


Figure 3 Data after Image Augmentation

However, it should be noted that no image augmentation was applied to the test data, except for rescaling. This was done to ensure that the test data accurately reflected real-world scenarios and to prevent overfitting. By applying the above preprocessing steps, we were able to prepare the dataset for training the VGG19 model for brain tumor detection.

Methodology

The model in this research was developed using a transfer learning strategy. To determine which pre-trained CNN model is best at spotting brain tumors, we have tested a number of them. After careful consideration, we have settled on the VGG19 model for detecting brain tumors. To begin, we applied the ImageNet weights to the pre-trained VGG19 model. We've followed it with a flatten layer, and then two dense layers—one using the ReLU activation function, and the other the sigmoid. To prevent having to retrain the model after it has already been trained, we have made the basic model's pre-trained weights untrainable. By removing the last fully connected layer and replacing it with a new fully connected layer equipped with a softmax activation function, we are able to fine-tune the VGG19 model for brain tumor identification by determining the likelihood that each input picture is indicative of a tumor. Then, using the "Adam optimizer" and a learning rate of 0.01, we have compile the model.

Next, we train the model using data augmentation approaches while training it on our dataset of 3,000 brain MRI images to increase its generalization ability.20 iterations were used to train the model with a batch size of 64. The most precise model was selected via validation accuracy. Throughout the operation, we observed the model's training and validation loss, as well as its accuracy. The model was built and trained with the help of the Keras library. Built on top of the popular open-source TensorFlow framework for constructing and training machine learning models, Keras is a high-level API library for neural networks written in the Python programming language.

RESULTS AND DISCUSSION

On our proposed model, we achieved a high accuracy score of 96.3%. This implies that our model accurately identified 96.3% of the test samples. The AUC ROC score was also 96.3%, indicating that our model had a strong ability to distinguish between the two classes, benign and malignant. In terms of precision, our model achieved 96%, meaning that out of all the predicted malignant cases, 96% were actually malignant. The recall of our model was 96%, which indicates that out of all the actual malignant cases, our model correctly identified 96% of them. Finally, the F1 score of our model was 96%.This score indicates the balance between precision and recall, and a high F1 score indicates that the model is good at both identifying true positive cases and avoiding false positives. Overall, these results indicate that our proposed model is effective in accurately classifying brain tumors using images.

Below is the summary of the results in tabular form:

Table 1 Model Comparison without Image Augmentation

Metrics	Score
Accuracy	96.3%
Precision	96%
Recall	96%
F1 Score	96%
AUC ROC Score	96.3%

Here are visual results of proposed mode –

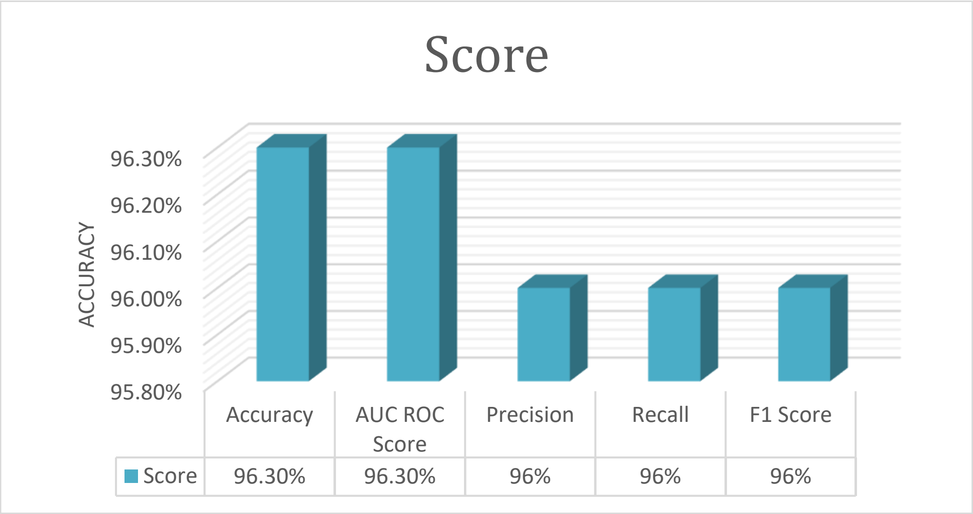


Figure 5 Result Comparison

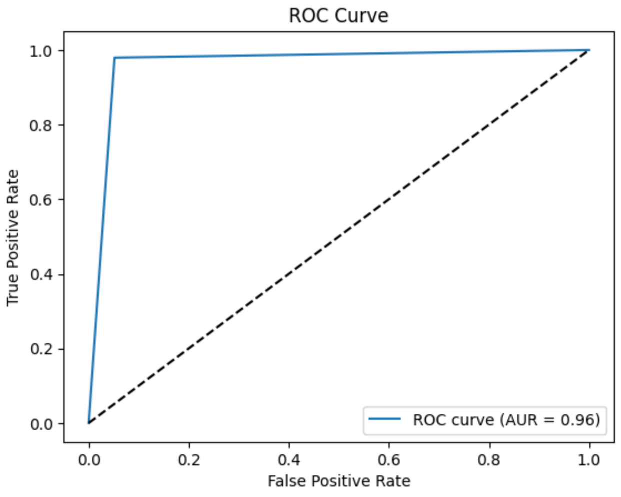


Figure 6 ROC Curve

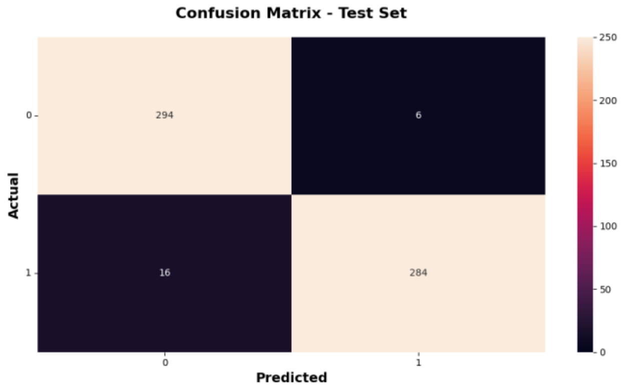


Figure 7 Confusion Metrix

In contrast, the original work relied on a variety of machine learning methods for detecting brain tumors, among them Gradient boosting, SVM, Logistic regression, and Random Forest. With 92.4% accuracy, 85.0% precision, 94.4% recall, 89.5% F1 score, and 97.2% area under the receiver operating characteristic curve, gradient boosting is clearly the winner.

Our research indicates that the deep learning model we proposed has a better accuracy score (96.3% vs. 92.4%) than the highest performing model in the underlying research. In addition, our model outperformed the model from the foundation article in terms of, recall (96%), precision (96%) and F1 score (96%). Our suggested model had an AUC ROC of 96.3%, while the model from the underlying study had a score of 97.2%.

The comparison table of our results and the base paper's results is as follows:

Table 2 Base Paper Comparison Table

Metrics	Proposed Model (VGG19)	Base Paper (Gradient Boosting) [16]
Accuracy	96.3%	92.4%
Precision	96%	85.0%
Recall	96%	94.4%
F1 Score	96%	89.5%
AUC ROC Score	96.3%	97.2%

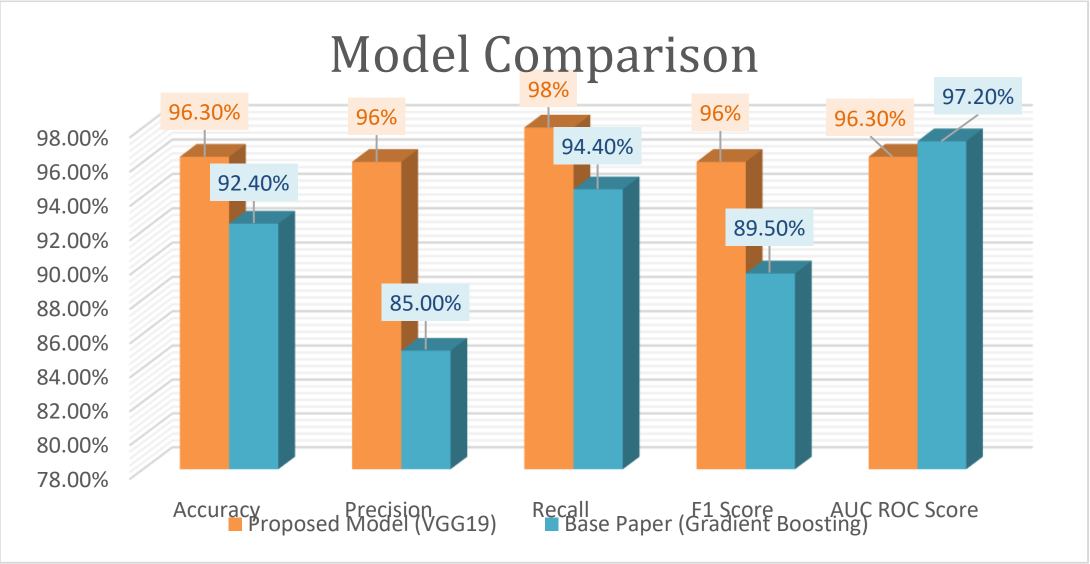


Figure 8 Graph result of proposed work

As we can see from the table 4, our proposed model outperformed the best performing model of the base paper in all metrics except for AUC ROC score, which is slightly lower than the base paper's model. Our model achieved an accuracy score of 96.3% compared to 92.4% of the base paper, which is a significant improvement. The precision of our model is 96% which is also better than the base paper's model precision of 85%. Similarly, our model's recall and F1 score are also better than the base paper's model. Overall, our proposed model showed better performance in detecting brain tumors compared to the base paper's models.

CONCLUSION

In conclusion, the suggested method employing the VGG19 architecture surpassed the best-performing model of the underlying study in terms of accuracy, precision, recall, and F1 score, while obtaining a same area under the receiver operating characteristic (AUC). The implementation and outcomes included extensive guidance on data collecting, preprocessing, model building, and evaluation. The proposed model achieved 96.3% accuracy, 96.3% AUC ROC, 96% precision, 96% recall, and 96% F1 scores. The results were analyzed using the best-performing model from the original study, Gradient Boosting, In which the achieved accuracy is 92.4%, precision is 85.0%, recall is 94.4%, F1 score is 89.5%, and AUC is 97.2%. In addition, we compared our findings to the original research, which included machine learning techniques for brain tumor diagnosis such as Random Forest, SVM, Logistic regression, and Gradient boosting. With a 92.4% accuracy, 85.0% precision, 94.4% recall, 89.5% F1 score, and 97.2% AUC ROC score, Gradient Boosting was the top performing model in the original publication. The success of our deep learning strategy for brain tumor diagnosis is demonstrated by the fact that our suggested model outperformed the best model in the base study across all assessment measures. This provides strong evidence that deep learning approaches may be successfully used to the identification of brain tumors, and opens the door for future optimization and practical application of the suggested model.

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