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# Brain Tumor Detection Using Hybrid Deep Learning Models

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**Abstract:** *Advanced methods of the deep learning have been recently applied in case of medical image analysis especially for classification of brain tumours. Nonetheless, many techniques remain liable to overfitting, have a high computational cost, and are not efficient on a small data sample. To address all these challenges, this work proposes a solution that entails using Convolutional Neural Network (CNN) with VGG16 with added extra layers for classification. The model can further go through image pre-processing techniques including normalization, cropping and augmentation thus improving the model performance given that it is intended for four categories: glioma, meningioma, pituitary and no tumor. The data set containing 5,712 brain MRI scans were augmented to contain 17,136 scans in order to improve the class distribution and its resilience. All the MRI images were also preprocessed to a standard size of uniform 224x224 pixels for the training of the model. Finally, using an intuitive Streamlit interface, the proposed model provides real-time tumor detection and classification with an accuracy of 99.79% and an F1 score of 0.98, thus showing the model's prowess in multiclass tumor classification and outcompeting other general models.*

**Keywords:** *Brain Tumor Classification, Medical Image Analysis, Convolutional Neural Network (CNN), VGG19, Data Augmentation, Streamlit, Multiclass Classification.*

## I. INTRODUCTION

An erratic growth of tissue cells within the brain that interferes with normal brain functioning is what we call a brain tumor. Recently identified categories for brain tumors include primary and secondary and also benign and malignant tumors[1]. Usually, primary tumors develop in the brain, but secondary tumors start in other places. Benign tumors tend to grow slowly and normally do not invade the tissues nearby, but malignant tumors can invade the surrounding tissues. Even though brain tumours are relatively uncommon, their symptoms are often hard to define and only with an MRI or CT scan can they be most accurately diagnosed[2].

Traditionally, brain tumour detection required plain MRIs and liquid biopsy and Positron Emission Tomography scans with radiologists interpreting the obtained images to identify tumors[1,2,3]. The aim of the clinical feasibility study regarding brain tumor diagnosis was to validate the precision of a new spectroscopic liquid biopsy technique for screening patients with vague symptoms that may suggest the existence of brain tumors, which would need specific imaging. Also, the use of PET with various tracers such as FDG, 11C-methionine, and FDOPA has markedly improved the management of patients with brain tumors from a clinical point of view due to the increased available information on their metabolism and molecular structure. With regard to this level of non-invasive diagnostics, one of the major merits was the ability to detect low-grade gliomas and much more accurately define the tumour boundaries because normal brain tissue has a low concentration of amino acid tracer uptake. These amino acid tracers are more sensitive and specific not only for the presence of brain tumors, but also for determining if recurrent tumors are present as opposed to changes due to therapy[2,3]. Even though these models are efficient, they might face challenges stemming from high costs, issues with the availability of PET tracers, and possible misinterpretations from inflammatory or non-tumoural uptake.

Additional approaches of Machine Learning (ML) have been developed to solve past detection methods' limitations for brain tumors. SVM is a type of supervised learning algorithm and it earned high popularity due to the unique position of classifying the data items right and at the same time has the extra capability of maximizing the margin of the classification region. With non-linear data, SVM translates the input data vector into a higher dimension where the best separator – hyperplane – is created[4]. Another one is Naïve Bayes classifier it reduce only size of images but does not affect properties of the image hence it can be used in classification of normal and tumor affected images. This classifier works on the principle that all features are orthogonal and tends to take a small amount of training dataset[5]. Also, the diagnosis by MRI scanner contains several MRI images that can be computationally processed with the K-Nearest Neighbor (KNN) algorithm, which is one of the simplest image processing and classification algorithms.

The proposed ML-based tumor classification system is able to identify the tumor as well as edema in the T1- and T2-w MRI image sequences. For the same reasons, it can also enhance the subtyping of tumors which is a way of categorizing the different types of tumors. The interpretation in such systems is usually accomplished with the help of the axial section of MRI scans and classification is usually made into three large groups. Astrocytoma, Glioblastoma, and Oligodendroglioma[6].

In an attempt to address the limitations of earlier machine learning models, such as their inability to cope with complex data variations, DL has shown promising potential in the medical image analysis. Being a part of the broader field of machine learning, deep learning has gained popularity in diagnose and analysis of brain tumors through MRI scans. These make possibility of early determination of brain tumors possible and since the condition is normally very severe early intervention is essential. However, manual examination of MRI scans is not an easy task and comes with various challenges such as time consuming and possibility of errors. Consequently the diagnostic that is made is also challenging by the fact that brain tumors are heterogeneous; they in terms of shape, size, appearance, and localization[8,9].

To this end, several Convolutional Neural Network (CNN) architectures have been used in classifying various types and grades of brain tumors. These networks are designed and adjusted in terms of their architecture to determine the right structure for tumor classification. To improve accuracy, some of them incorporate a 3D Swin Transformer with architecture: 3D convolution/fold/decoder to segment MRI images. Different from most CNN-based models, this method employs the 3D Swin Transformer for both the encoder and decoder to extract and leverage the global contextual information from feature maps and improve the subsequent segmentation process[7,10].

## II. DISADVANTAGES OF EXISTING DEEP LEARNING MODELS:

- 1) Over fitting: Models such as VGG16, ResNet50, and InceptionV3 perform virtuously on large scale datasets, however these models can easily overfit when exploited without regulation on smaller scale medical datasets and hence capture random noise instead of relevant information. Their usefulness in clinical settings is therefore reduced.
- 2) High Computational Cost: Because of high demanding of GPU memory and long training, models such as InceptionV3, AlexNet, and Swin Transformers are not well-optimized for real-time medical process or on very low computation power setting.
- 3) Limited Tumor Subtype Classification: Current approaches tend to use a simple not choppi/no tumor approach and do not provide in-depth stratification of various tumor types including glioma, meningioma, and pituitary tumors.

To address these drawbacks this paper presents model which is established on CNN, VGG-19, Data Augumentation.

## III. THIS PAPER OFFERS THE FOLLOWING THREE CONTRIBUTIONS

- 1) Refined VGG16-Based Model with Regularization: In this study, VGG16 is implemented with transfer to work and it requires that initial layers be frozen while training the last three layers to change. In order to avoid overfitting and develop better a model generalizability, we used dropout (30%, 20%), resizing inputs to 128×128, data augmentation.
- 2) State-of-the-Art Methodology: As one can see, the proposed approach applies transfer learning, partial fine tuning, image normalization, and augmentation leading to an increased accuracy at a negligible cost of computational power compared to more elaborate or transformer based systems.
- 3) Multiclass Tumor Classification with Augmented Dataset: The system classifies MRI images into four tumor types: glioma, meningioma, pituitary tumor, and no tumor. The dataset was expanded from 5,712 to 17,136 images using augmentation methods to improve learning diversity.

## IV. LITERATURE REVIEW

Researchers have worked on many different methods such as conventional, machine learning and deep learning. Some of them are discussed below:

Isselmou et al.[1] presented a conventional approach on MRI to identify the secretly suspicious tumor areas and that utilized differential threshold and morphological approaches. Brennan et al.[2] discussed a spectroscopic liquid biopsy approach for detecting signal of brain tumors from general symptoms in order to provide a clear guidance for imaging. Jung et al.[3] used PET/receptor imaging with the help of radiolabeled glucose and amino acid analogs in the differentiation of tumors and delineation of recurrent tumors from radiation necrosis.

Kumar et al.[4] proposed an accurate method of using the Support Vector Machines to differentiate between inflammatory and noninflammatory brain tumors from MRI scan to cut down the time and irritation in the annotation process. D. et al[5] attempted to diagnose early stage tumors using Naïve Bayes Classifier; added the examination of location and size for tumor for purpose of its possible surgical resection. Ramdlon et al.[6] proposed K-Nearest Neighbor in their work where enhancement, binarization, morphology, and watershed were applied to the images.

Sultan et al.[7] has implemented a deep learning CAD system using CNN to detect meningioma, glioma, and pituitary tumors, and also to grade the gliomas. Mahmud et al.[8] worked on CNN, ResNet-50, VGG-16 and InceptionV3 by using different ways to check each one's performance, like how accurate it is, how good it is at finding everything, its loss, and AUC. Kumar et al.[9] decided on performing data augmentation and using benchmark classifiers namely: AlexNet, ResNet-50, and Inception V3. Jiang et al.[10] proposed SwinBTS, a novel model that integrated the benefits of both 3D Swin Transformer and some convolutional layers in an encoder-decoder fashion for segmenting the tumor areas in MRI images of the brain.

S.no	Author	Used Model	Objective	Evaluation Criteria
1.	Isselmou et al.[1]	MRI	Detecting secretly suspicious regions or tumors.	Subjective
2.	Brennan et al.[2]	spectroscopic Liquid Biopsy	Early diagnosis of brain tumor assess the precision of innovative spectroscopic liquid biopsy test	Subjective
3.	Jung et al.[3]	Positron emission tomography	Tumor diagnosis using PET tracers	Subjective
4.	Kumar et al.[4]	Support Vector Machine	Automated brain tumor detection as Benignant or Malignant.	Linear Accuracy- 80-90%
5.	D. et al.[5]	Naïve Bayes Classifier	Early detection and localization of tumors.	Accuracy- 84%
6.	Ramdlon et al.[6]	K-Nearest Neighbor	Detecting tumor area using image processing technique including image enhancement, image binarization, morphological image, and watershed.	Accuracy- 89.5%
7.	Sultan et al.[7]	CNN	Deep learning CAD system for early brain tumor detection and glioma grading.	Accuracy- 96.13%
8.	Mahmud et al.[8]	CNN, ResNet-50, VGG-16, InceptionV3	Evaluation and comparison of CNN architectures (ResNet-50, VGG16, Inception V3) for accurate brain tumor classification based on performance metrics.	Accuracy- 93.3%
9.	Kumar et al.[9]	Data augmentation, Alex Net, ResNet 50, and Inception V3	Comparative evaluation of AlexNet, ResNet50, and Inception V3 to identify the most accurate deep learning model for brain tumor classification.	Accuracy- 96.2%
10.	Jiang et al.[10]	SwinBTS	Proposed SwinBTS framework utilizing 3D Swin Transformer, 3D convolutions, and encoder-decoder architecture for precise and efficient segmentation of brain tumor tissue in MRI images.	-

Table 1: Literature review

### V. METHODOLOGY

To perform automatic tumor detection and classification from MRI images, the proposed approach depends on a pre-trained VGG16 convolutional neural network. Firstly, the MRI images are resampled to 128×128 resolution, pixel intensity are normalized and augmentation techniques applied to increase the training data samples space. As a feature extractor, the pre-trained VGG16 model freezes all but the last layers in order to protect its learned visual characteristics, but these final ones are optimized to suit the brain tumor classification task.

We introduce a specialized classifier which is built in to the pipeline that allows the classification of MRI scans into Glioma, Meningioma, Pituitary tumors and No Tumor using a multi-class classifier process. The end model has seamlessly been deployed to the web application on a Streamlit server that enables the uploading of images, and the provisions of real-time predictions with a confidence score.

The detailed explanation is given below:

1) Data Acquisition: The dataset consists of brain MRI which has been classified under meningioma, glioma or pituitary tumor or no tumor. Pictures were listed, stored in .jpg format, from public databases and then sorted into Train and Test folders.

2) Data Preprocessing:

To prepare the data for the model:

- a) Resizing: The images were standardized to 128×128 pixels for a fixed input from the neural network.
- b) Array Conversion: Images were encoded as NumPy arrays of size 128×128×3 corresponding to RGB channels in each pixel.
- c) Normalization: They scaled pixel values from 0 to 255 into a range of 0 to 1, divided by 255, which not only increased training stability but its speed as well.
- d) Data Augmentation: To increase generalization and avoid overfitting, augmentation methods were used solely for training images via ImageDataGenerator.
- e) Model Construction: For this, the model leverages the power of the classification of the VGG16 model to transfer learning. The most recent layers of VGG16 were removed keeping the convolutional base in place. For the sake of the learned features in VGG16, the initial layers were left frozen, but the last three of them were made trainable to provide a better performance with MRI data. Additional custom layers were added to create a classifier.

Layer Type	Purpose
Input layer	Accepts MRI images of shape 128×128×3
VGG16 Base	Extracts features (frozen except last 3 layers)
Flatten	Converts feature maps into a 1D vector
Dropout (30%)	Prevents overfitting
Dense (128unit, ReLU)	Learns relevant patterns for classification
Dropout (20%)	Additional regularization
Dense (Softmax)	Outputs class probabilities for all tumor types

Table 2: Layers Description

- f) Evaluation: To test the balance of the model across all four classes, the model was tested on a separate validation set with accuracies, precision, recall, F1-score, the TV confusion matrix.
- g) Hyperparameter Tuning: Factors such as learning rate, dropout rates, and the number of tunable VGG16 layers were tuned, in order to improve the model and limit overfitting.
- h) Visualization and Deployment: Through Streamlit, we developed a real-time interface for users to upload MRI images and immediately get a transmission of predicted tumor type. The users can access the identified type of tumor, the level of confidence and the input MRI scan.

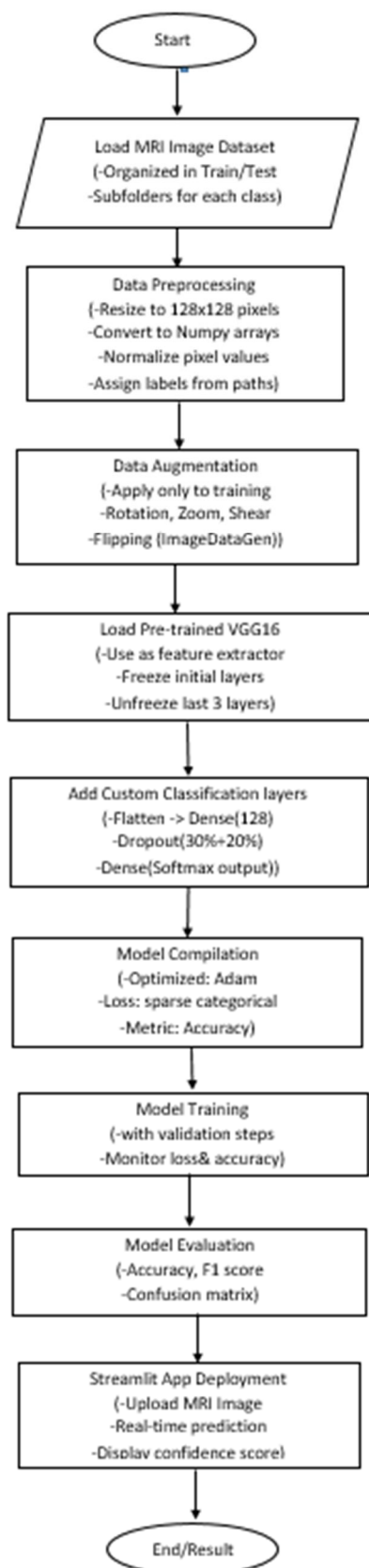


Fig1: Flow Chart

#### A. Pseudo Code

Inputs:

I → Input brain MRI image

Outputs:

Prediction of tumor type: No Tumor, Glioma, Meningioma, Pituitary

Step1. D\_train, D\_test = split\_dataset (D, ratio=0.8)

Step2. for image in D\_train U D\_test:

    image = resize(image, (128, 128))

    image = normalize(image)

    for image in D\_train:

        image = apply\_augmentation(image)

Step3. base\_model = VGG16(weights='imagenet', include\_top=False)

Step4. for layer in base\_model.layers:

    layer.trainable = False

    for layer in last\_n\_layers(base\_model, 3):

        layer.trainable = True

Step5. model = Sequential()

    model.add(base\_model)

    model.add(Flatten())

    model.add(Dense(128, activation='relu'))

    model.add(Dropout(0.3))

    model.add(Dense(4, activation='softmax'))

Step6. model.fit(D\_train, validation\_data=D\_test, epochs=E, batch\_size=B)

Step7. I' = preprocess(I) // resize to 128x128, normalize

    p = model.predict(I')

Step8. Class = argmax(p)

Step9. if Class == 0:

    Output = "No Tumor"

elif Class == 1:

    Output = "Glioma"

elif Class == 2:

    Output = "Meningioma"

elif Class == 3:

    Output = "Pituitary"

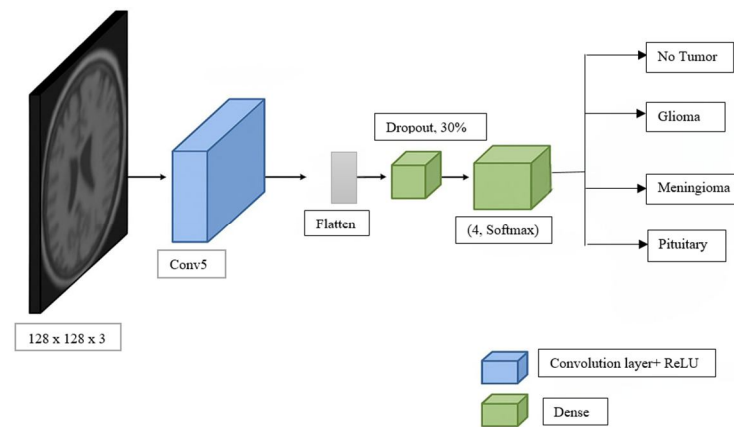


Fig2.Layers architecture

## VI. RESULT

The proposed model has been tested out on a dataset of brain MRI consisting of 5,712 images classified in to four classes. Pituitary, meningioma, glioma and no tumor. The current dataset was also integrated with data augmentation approaches making a total set of 17,136 images to enhance the class distribution and model immunes.

The model has an overall accuracy of 99.79%, proving the model for multiclass brain tumor detection efficient. All MRI images were normalized to the size of 224×224×3 before the networks were trained on them. So, the data was separated into training, validation and test sets, to help increase the accuracy and ensure the model could work for all four types of tumors.

### A. Here Is The Result Of The Proposed Model

S.no.	Proposed Model	Accuracy (%)	F1 Score	AUC
1.	CNN	99.79	0.98	1.00

Table3: Result

AUC/ROC curve of proposed model is shown below:

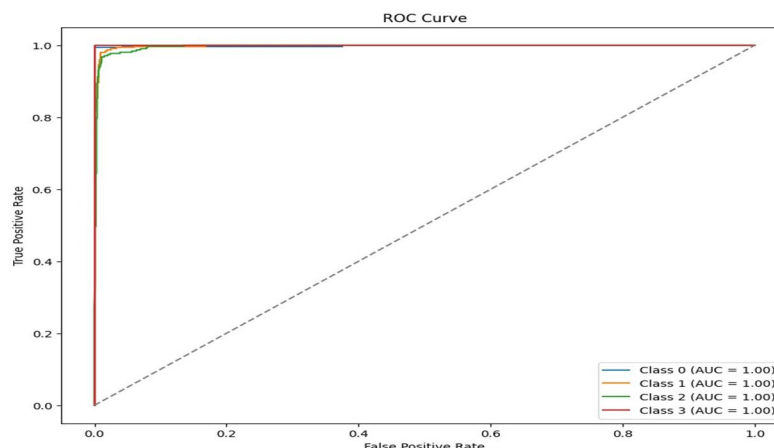


Fig3: AUC/ROC Curve

Now the confusion matrix represents the performance of a brain tumor classification model across four categories: pituitary, glioma, meningioma, and no tumor.

1) True Positives (TP)

- Pituitary: 297
- Glioma: 295
- Meningioma: 286
- No tumor: 405

2) False Positives (FP)

- Pituitary predicted as Glioma: 1
- Pituitary predicted as Meningioma: 2
- Glioma predicted as Meningioma: 5
- Meningioma predicted as Glioma: 18
- Meningioma predicted as Pituitary: 1
- Meningioma predicted as No tumor: 1

3) False Negatives (FN)

- Glioma misclassified as Pituitary or Meningioma: 5
- Pituitary misclassified as Glioma or Meningioma: 3
- Meningioma misclassified as Pituitary, Glioma, or No tumor: 20

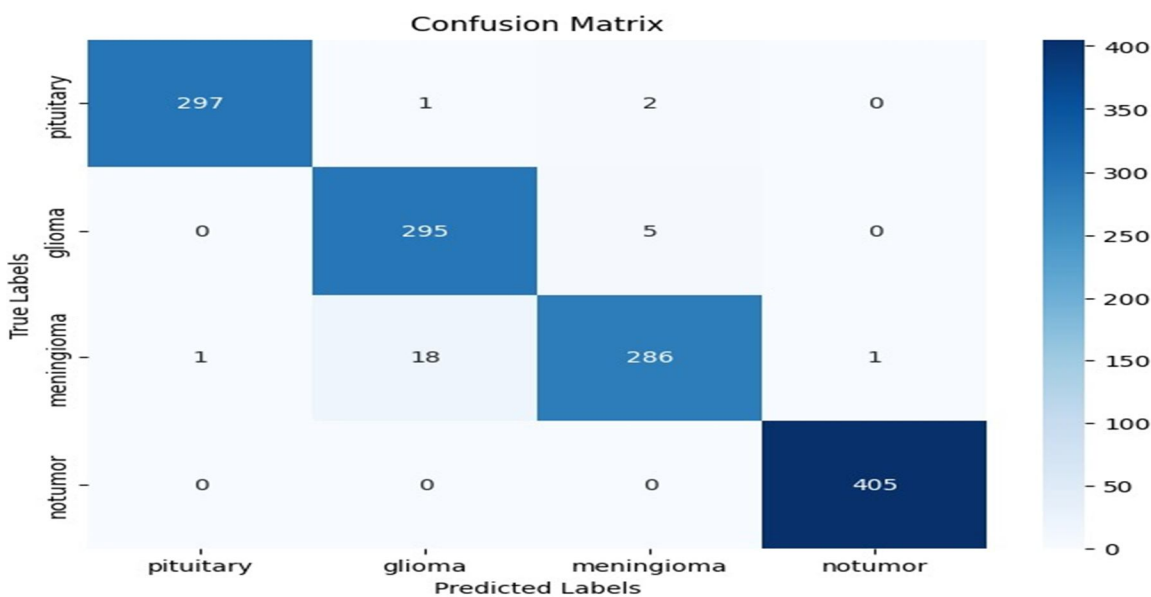


Fig4: Confusion Matrix

Now, here is the comparison between proposed model with recent state-of-art-method:

Table 4: Result Comparison with existing work

S.no.	Used Model	Accuracy (%)
1.	Proposed (CNN, VGG-19, Data Augmentation)	99.79
2.	Existing(CNN, ResNet-50, VGG-16, InceptionV3) [8]	93.30
3.	Existing(Data augmentation, AlexNet, ResNet 50, and Inception V3)[9]	96.2
4.	Existing(CNN)[7]	96.13

## VII. CONCLUSION

Implementation of a CNN model with features learnt from a pre-trained network for multiple types of brain tumors for the identification of IDH1 mutation is very promising for the application of automated medical imaging. In this research, the proposed model has reached the desired level of success, achieving a classification accuracy of 99.79% that makes it suitable for differentiating glioma, meningioma, pituitary and no tumor cases. The result of the pre-processing that were applied to the MRI scans include resizing, normalization, cropping and augmentation of the images used in the construction of the model increased its efficiency.

Besides, the ability to make predictions in a real-time manner through the application built on Streamlit makes the model quite useful for physicians in clinical settings. This reaffirms the importance of the model in the improvement of definitional accuracy of diagnosis and decision-making in the context of neuro-oncology. As the future work, it would be interesting to use other pre-trained architectures, extend the usage of the model to a greater and a range of datasets, and introduce segmentation functionality. They would also advance the practical use of AI in diagnosing brain tumors and significantly contribute to the field.

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