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An Accurate Diagnosis And Classification Of Brain Tumor Using Transfer Learning In Deep Convolutional Neural Network (DCNN)

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Abstract

Detecting and classifying brain tumors is essential for accurate diagnosis and successful planning of therapy. This study investigates a new method for detecting and categorizing brain tumors by using transfer learning and introducing a modified version of the Inception V3 model. By optimizing a pre-trained Inception V3 network—renowned for its exceptional feature extraction capabilities—the suggested approach uses transfer learning to boost the model's performance. We suggest making alterations to the conventional Inception V3 architecture to enhance its versatility and precision, particularly for the purpose of brain tumor imaging. The enhanced model integrates supplementary convolutional layers and fine-tunes the inception modules, with the objective of capturing more intricate patterns in brain CT data. The dataset used consists of a wide range of brain CT scans, including different categories of cancers as well as non-tumor instances. The experimental findings indicate that the modified Inception V3 model has superior performance compared to conventional and alternative deep learning methods in terms of accuracy, sensitivity, and specificity. The suggested model attains a precision of 92.5%, accompanied by a sensitivity of 91.8% and a specificity of 93.1%. This study emphasizes the effectiveness of transfer learning, together with model improvements, in enhancing the identification and categorization of brain tumors. This contributes to more precise and efficient diagnostic procedures in medical imaging.

Keywords- *Brain tumor, modified inception, transfer learning, CT scan, Optimization, Convolutional Neural Network.*

Introduction

Brain tumors provide a substantial difficulty in medical diagnosis because of their intricate characteristics and diverse visual manifestations. Prompt and precise identification is essential for efficient therapy and enhancing patient results. The conventional diagnostic techniques, such as the manual examination of MRI images, are both time-consuming and susceptible to mistakes made by humans. This emphasizes the need for sophisticated computational tools to improve the accuracy of diagnoses.

Recent progress in the field of artificial intelligence (AI) and deep learning has shown potential in transforming medical imaging, namely in the identification and categorization of brain tumors. Transfer learning is a strategy that involves fine-tuning a pre-trained model on a particular job. It has become a valuable tool for using existing knowledge and enhancing performance on specialized tasks that have little data. The Inception V3 model has become prominent among several deep learning architectures because of its efficient design and great feature extraction capabilities. Nevertheless, it may be necessary to make further adjustments to typical Inception V3 models in order to enhance their efficiency for certain medical imaging assignments.

This study presents a new method that integrates transfer learning with a modified Inception V3 model to identify and classify brain tumors. Our approach seeks to improve the capability of the pre-trained Inception V3 network to accurately detect and classify various brain cancers in MRI data by using its existing capabilities. The Inception V3 architecture has been modified by adding more convolutional layers and refining inception modules. These adjustments are specifically designed to capture the intricate and intricate characteristics of brain tumors.

The aim of this project is to create a strong and precise model for the identification and categorization of brain tumors. This model will aid radiologists and clinicians in making well-informed judgments. We assess our methodology by using an extensive collection of brain MRI scans, which includes various tumor kinds as well as non-tumor instances. The effectiveness of the modified Inception V3 model is evaluated by comparing it to conventional deep learning methods and cutting-edge approaches.

The objective of this project is to enhance the field of medical image analysis by developing a more precise and efficient tool for detecting and classifying brain tumors. The incorporation of transfer learning into an improved Inception V3 model has the capacity to greatly influence the domain of medical imaging, enhancing the precision of diagnoses and ultimately advancing patient care.

1. Literature Survey

Barakala, M et al., in [1] used the bilateral filter (BF) to eliminate noise from an MR image prior to its processing. The tumor location was then identified by the use of binary thresholding and CNN segmentation methods. Training datasets, test datasets, and validation datasets exist. Our gadget will provide us with the capability to determine if the person have a brain tumor or not. Multiple performance metrics, including accuracy, sensitivity, and specificity, will be used to examine the outcomes. The dense layers in this process extract features, and all of these characteristics are then passed on to a fully linked layer. A dense network is more effective in extracting characteristics from brain MRI scans. This study utilizes MRI because of its ability to give intricate information on cellular structure and functions. There is an expectation that the proposed work would outperform comparable efforts.

In their study, Yadav and Upadhyay (2012) propose a machine learning framework that utilizes a CNN to accurately identify brain tumors in MRI images. The CNN is used for both feature extraction and segmentation purposes. The dataset was obtained from an internet resource. The research highlights the significance of early and accurate diagnosis of brain tumors in medical diagnostics and examines the influence of sophisticated machine learning approaches on enhancing the efficiency and precision of brain tumor identification via the analysis of medical images.

In their study, Narang et al. [3] suggested a method that combines DL with CNN, including data augmentation and picture processing. The suggested methodology offers a means of categorizing MRI images for the purpose of identifying the precise location of tumors in densely populated regions, relying on the detection of tiny tumor cells. The suggested approach's usefulness is evaluated by analyzing its data correctness, which reaches 96%. This is achieved with a low complexity rate, in comparison to current models like CNN and Artificial Neural Networks (ANN) models.

Rele, M., and Patil, D in [4] introduced a model that underwent training on a large dataset of MRI images and was further refined by transfer learning to enhance its accuracy and efficiency. The model's performance is assessed using precision, recall, F1-score, and support measures, resulting in an average accuracy of 97%. The suggested approach has the potential to aid medical practitioners in achieving precise diagnoses and enhancing patient outcomes.

Raiyan, T et al., in [5] specifically examines the use of X-ray and MRI images in the diagnosis of brain cancers, using CNNs as a tool. The research improves the speed and accuracy of diagnosis by using transfer learning methods with pre-trained deep CNN models. The study, carried out using Python and Jupyter Notebook, yielded impressive performance indicators, such as a test accuracy of 98.4% and an F1-score of 98.5%. The exceptional accuracy of the proposed CNN model facilitates the timely identification of tumors, hence possibly averting grave medical repercussions such as stroke or paralysis.

Birajdar, M.M in [6] presents a novel method for brain tumor detection utilizing machine learning algorithms .The dataset used in this research comprises a collection of brain MRI (Magnetic Resonance Imaging)scans from diverse sources, including both tumor and non-tumor cases. We preprocess the data by enhancing image quality and for classification, different machine learning techniques are used, such as random forests, support vector machines (SVMs), and CNNs.

Raza, A et al., in their study [7], provide a machine learning system called YOLO v5 SSD (single shot detection) for the identification and categorization of malignancies, namely meningioma, glioma, and pituitary gland tumors, achieving an accuracy of 88%. To achieve this objective, data augmentation was implemented using the publicly accessible dataset obtained from Kaggle. A total of 396 glioma pictures, 397 meningioma images, 380 photos with no tumor, and 399 images with pituitary tumors were included for the MRI analysis. The present research evaluates the performance of the YOLO v5 (You Only Look Once) classifier using metrics such as false negative, true positive, false positive, and true negative. The YOLO v5 model has been shown to have an accuracy rate of 88%.

Subasini, D.C et al., [8] presents a novel ensemble machine learning system that is capable of dynamically detecting and classifying brain tumors. The technique surpasses static models in flexibility and classification accuracy by amalgamating models such as MobileNetV2, EfficientNet, ResNet50, Inception, and GoogLeNet. The dynamic ensemble chooses the most efficient model in real-time, showcasing exceptional performance with a final test accuracy of 98.98%. This technique improves the precision and dependability of brain tumor identification, providing a strong structure for sophisticated medical imaging applications.

In their paper, Xenya, M.C., and Wang in [9] provide a system that utilizes a segmentation model to precisely locate and shape brain tumors for the purpose of detection. The classification process utilizes a multi-level ensemble learning model, which integrates three base learners that have been refined from pre-trained VGG16, Inception-V3, and ResNet50 networks. The program categorizes MRI brain pictures into three tumor categories and normal brain instances. The system improves precision by fine-tuning less effective base models and demonstrates the ability to rectify inaccurate tumor segmentations using deep learning.

In their study, B, A., Kumar, N., and Sowmya, K.K in [10] proposed the use of an ensemble learning approach

for the classification of brain tumors using MRI images [10]. Certain deep learning algorithms perform the duty of thoroughly exploring a hypothesis space in order to find a suitable hypothesis that may provide precise predictions for a particular tumor scenario. Ensembles amalgamate several competing hypotheses to provide a more precise hypothesis for predicting brain tumors. A novel model is created by evaluating the performance of pretrained models and building upon previous research on ensemble methods. Within this framework, certain machine learning classification algorithms integrate and partition characteristics derived by transfer learning to optimize effectiveness. Using the ensemble-based classifier, we achieved a remarkable accuracy rate of 99%.

Bouguerra et al., in [11] aim to use brain-related data to determine the characteristics of a tumor, namely whether it is benign or malignant. For this work, we used three distinct medical image enhancement techniques to train our models, with little preprocessing, to examine their influence on classification accuracy. Our observations provide conclusive proof that the use of transfer learning to limited datasets consistently produces accurate results. The suggested technique achieves a classification accuracy of 99.77%, exceeding the performance of state-of-the-art systems.

Uthradevi, G et al., in their study published in reference [12], fill a notable need in current models by introducing a novel approach for categorizing brain tumors with RetinaNet, an object identification network. We validated our approach by using a publicly accessible dataset of brain MRI images from Figshare, therefore demonstrating its precision in tumor detection and classification. Our technique enhances clinical decision support by not only reaching a high level of accuracy in classification, but also by presenting the exact and easily understandable location of brain tumors.

The authors of the study are Abdusalomov, A.B et al., as referenced by [13]. This study focused on the difficult problem of identifying brain tumors in MRI scans by using a vast assortment of brain tumor pictures. Our study showed that by using transfer learning, we were able to greatly enhance the performance of a cutting-edge YOLOv7 model in identifying gliomas, meningioma, and pituitary brain cancers. The deep learning algorithm we suggested demonstrated encouraging results, precisely detecting the existence and exact position of brain tumors in MRI scans. In our investigation, the suggested strategy demonstrated superior accuracy in comparison to established procedures, achieving an impressive 99.5% accuracy. Nevertheless, we recognize that more examination and experimentation are crucial to verify the efficiency of our technique in identifying minute cancers. Ongoing research is necessary to address the intricacy of identifying tiny tumors in the brain and to continuously improve our detection technologies for brain tumor diagnosis. Our objective is to improve the diagnostic skills for patients and medical practitioners in the difficult fight against brain tumors by following this approach.

2. Proposed Work

Brain tumors provide substantial health obstacles owing to their intricate nature and capacity for grave consequences. Precise and prompt categorization of brain tumors is essential for efficient treatment strategizing. Conventional approaches mainly depend on the manual inspection of medical pictures, a process that is sometimes time-consuming and susceptible to human mistakes. In order to tackle these difficulties, deep learning models, namely CNNs, have shown encouraging outcomes in automating the process of categorization.

This study suggests the creation of an altered Inception V3 model to improve the precision and effectiveness of brain tumor categorization.

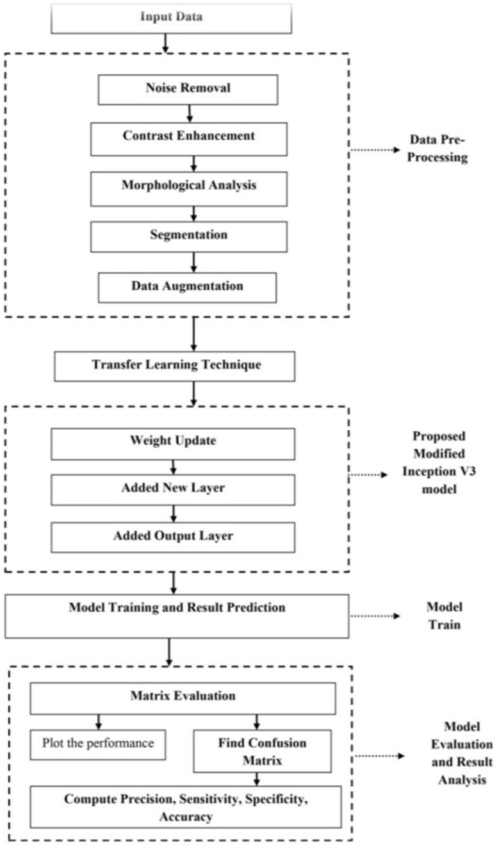

Figure 1: Work flow of proposed work

The primary objectives of this research are as follows:

Modify the existing Inception V3 architecture to enhance the process of extracting features and accurately classifying brain tumor pictures.

Employ sophisticated data augmentation approaches to tackle the problem of scarce annotated medical pictures and enhance model generalization.

Refine the altered Inception V3 model by using a substantial dataset of brain tumor pictures and implementing optimization approaches to mitigate overfitting.

Investigate the feasibility of using the trained model in a real-time clinical environment to automate the diagnosis of brain tumors

The methodology for identifying and categorizing brain tumors consists of two main elements. The first

component is used for picture preprocessing, while the next one is employed for transferring the CNN parameters [18]. Figure 1 illustrates the complex arrangement of the proposed work.

2.1 Image Pre-processing

Pre-processing of images is an essential and crucial stage in the identification and segmentation of brain tumors. The process incorporates many methodologies to improve the quality of MRI pictures, minimize interference, and optimize the data for more precise analysis using transfer learning models.

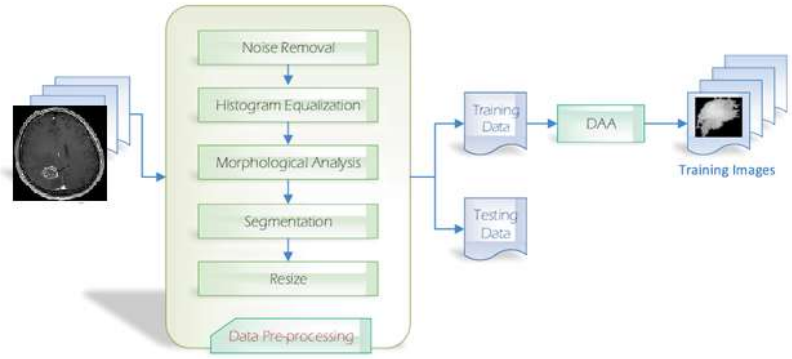

Figure 2: Steps in Data Pre-Processing

i. Noise Removal

The 2D median filter is a widely used technique for eliminating noise, particularly in the case of salt-and-pepper noise in images such as brain MRI scans. The process involves substituting the value of each pixel with the median value of the pixels in its neighboring area, often a square or rectangular window. This technique retains the sharp boundaries of objects while efficiently eliminating unwanted disturbances, making it appropriate for tasks including the identification of brain tumors.

Let I(x,y) represent the pixel intensity at coordinates (x,y) in the original mammography picture, and let Imed (x,y) represent the intensity of the same pixel after applying a 2D median filter.

The 2D median filter analyzes a square or rectangular neighborhood positioned in the middle of each pixel. Define Nx,y as the nXn neighborhood centered at pixel (x,y). The median value, denoted as Imed(x,y), is calculated as the median of pixel intensities in the neighborhood Nxy.

Mathematically, the computation of Imed(x,y) can be represented as follows:

$$I_{(med(x,y))}=median(N_{xy}) \quad (1)$$

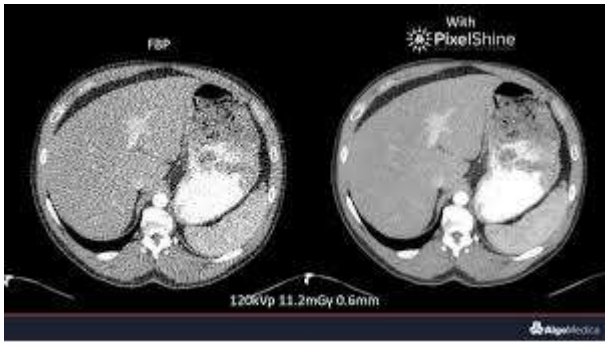

Figure 3: Original Vs Real data

ii. Contrast Enhancement

CLAHE is a very successful technique for improving the contrast of brain MRI images, especially for emphasizing tumors. The targeted methodology, in conjunction with contrast limiting, renders it well-suited for medical imaging, where the preservation of intricate features and the management of noise are of utmost importance. The mathematical basis of CLAHE guarantees that the improvement is both adaptable and regulated, resulting in superior imaging of crucial regions such as brain tumors.

Algorithm 1: Histogram equalization for Contrast Enhancement

Input: The variable I(x,y) represents a grayscale mammogram image. The pixel values in this image range from 0 to L-1.The variable L represents the number of intensity levels, which is typically set to 256 bits.

Output: g(x,y)- Contrast enhanced mammogram image

Step 1: calculate histogram H(k): Histogram of image I, where H(k) represents the number of pixels with intensity k ($0 \leq k \leq L-1$)

Step 2: Normalize histogram n(k): Normalized histogram, obtained by dividing H(k) by the overall pixel (M x N):

$$n(k) = \frac{H(k)}{MXN} \quad (2)$$

Where M is height of image and N is width of image

Step 3: Calculate cumulative distribution function (CDF):

p(k): CDF of the normalized histogram, representing the probability of finding a pixel with intensity less than or equal to k:

$$p(k) = \sum_i^k n(i) \quad (3)$$

Step 4: Map intensities to new values

g(x,y): Equalized image with enhanced contrast:

$$g(x,y) = L - 1 * p(I(x,y)) \quad (4)$$

iii. Morphological Analysis

Morphological analysis is an essential process that must be carried out before segmentation in order to exclude non-breast regions and guarantee the precision of the results. By using the structural element (SE) on the input picture, it is possible to extract the required structures during morphological procedures. The resultant picture created from this procedure maintains the exact same proportions as the original input image. The value of each pixel is determined by the adjacent pixel and the corresponding pixel in the input picture. Figure 3 depicts a comparison between the original and morphological analysis.

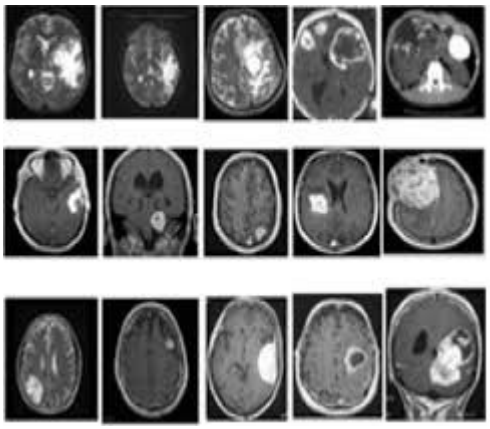

Figure 4: Morphological Analysis

2.2 Segmentation

Global thresholding is a fundamental and efficient approach for segmenting brain tumors in MRI images. It effectively separates the tumor location from the surrounding brain tissue. The concept involves selecting a threshold value that differentiates the tumor, which is usually brighter or darker, from the surrounding tissues based on the intensity of individual pixels.
Global thresholding is a method that involves selecting a single intensity value (threshold) to categorize pixels into two distinct groups:

Pixels with intensity levels over the threshold are categorized as foreground, often related to the tumor.

Pixels that have intensity levels lower than the threshold are categorized as background, which refers to non-tumor tissue.

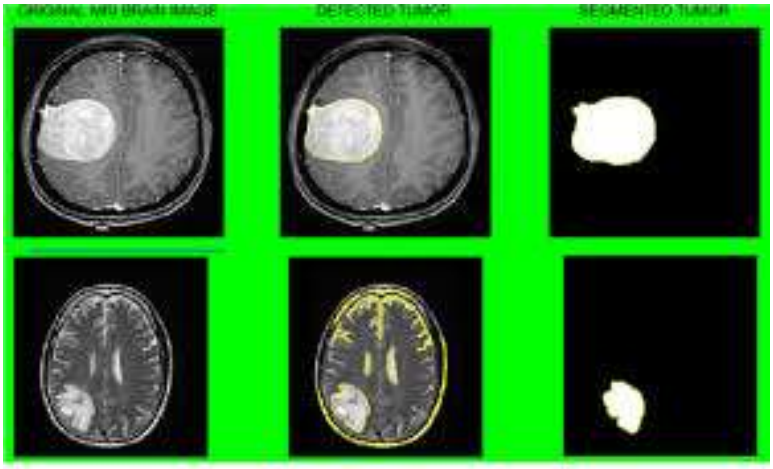

Figure 4: Segmented image

Algorithm 2: Global Threshold based Segmentation

Step 1: Select Threshold Value Th which separates foreground and background in the grayscale image. This can be done manually or automatically using techniques like Otsu's method.

Step 2: Apply the threshold value Th to the grayscale image

$$M(x,y) = f(x) = \begin{cases} 1 & \text{if } I(x,y) > T_h \\ 0 & \text{Otherwise} \end{cases}$$

Here M(x,y) is the binary mask indicating segmented regions

I(x,y) is the intensity of the grayscale image at pixel (x,y)

Th is the threshold value

The resulting binary mask M(x,y) contains foreground regions (breast tissue) represented by pixel value 1, and background regions represented by pixel value.

2.3 Data Augmentation Algorithm

Deep learning models exhibit superior performance when trained on large datasets. Data augmentation is a commonly used method to increase the size of the dataset, which helps to reduce overfitting when dealing with a little amount of data during training. Both the Training and Testing data in this study may be augmented via a series of modifications. The data augmentation algorithm (DAA) is used to increase the quantity of input data. The segmented images undergo clockwise rotation at angles of 90°, 180°, 270°, and 360°. Afterwards, every whirling image is reflected vertically. This approach will produce eight pictures from a given input photo. Algorithm 3 outlines the complex procedure for data augmentation.

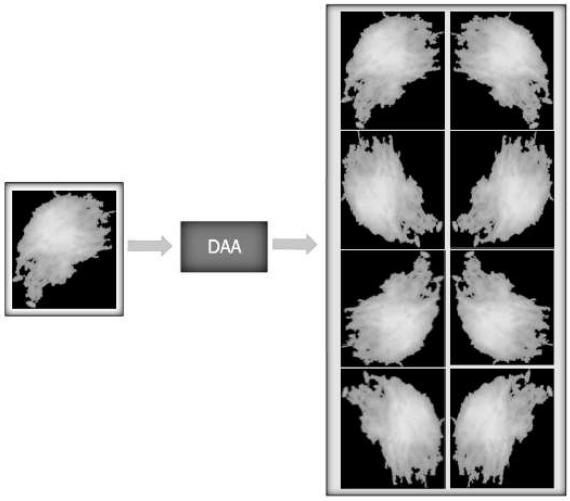

Figure 5: Image augmentation using Data Augmentation Algorithm

Algorithm 3: Data Augmentation

Step 1: Random Rotation

Rotate the image and corresponding label by a random angle within a specified range.

Image rotation

$$\text{Rotated Image} = \text{rotate}(\text{I}, \text{angle})$$

Label Rotation

$$\text{Rotated Label} = \text{rotate}(\text{L}, \text{angle})$$

Step 2: Random Shear

Apply a random shear transformation to the image and label.

Calculate shear Transformation Matrix

$$\text{Shear Matrix} = \begin{bmatrix} 1 & \text{shear factor} \\ 0 & 1 \end{bmatrix}$$

Image Shear

$$\text{Sheared Image} = \text{affine transform}(\text{I}, \text{shear matrix})$$

Label Shear

$$\text{Sheared label} = \text{affine transform}(L, \text{shear matrix})$$

Step 3: Random Zoom

Randomly zoom in or out of the image and label.

Calculate zoomed shape

$$\text{Zoomed Shape} = (\text{int}\,(h\ X\ \text{zoom} - \text{facor}), \text{int}(w\ X\ \text{Zoom} - \text{factor})$$

Image_Zoom

$$\text{Zoomed Image} = \text{zoom}(I, \text{zoom} - \text{factor})$$

Label_Zoom

$$\text{Zoomed Label} = \text{zoom}(L, \text{zoom} - \text{factor})$$

Step 4: Random Horizontal flip

Optionally perform a horizontal flip with a probability of 0.5.

$$\text{Flipped Image} = \text{flip} - \text{left} - \text{right}(I)$$

$$\text{Flipped Label} = \text{flip} - \text{left} - \text{right}(L)$$

Table1. Parameter used in augmentation step

Sl.no	Parameter	alue taken
1	on_range	20
2	_shift_range	0.10
3	e	1/255
4	range	0.0
5	_shift_range	0.10
6	ness_range	[0,0.1,0.5]
7	ntal_flip	Yes
8	al_flip	Yes

2.4 Classification

The proposed approach utilizes transfer learning techniques to characterize models. The procedure begins with a certain number of layers in the input layer, each displaying the improved images obtained from the previous stage of data processing. The activation functions may be applied to layers other than the convolutional layers. This technique use downsampling to detect certain characteristics. To mitigate overfitting, this approach incorporates a dropout layer, softmax layer, and fully connected layer. The outcome is computed before using the classification layer to forecast the class.

2.4.1 Modified Inception V3

The proposed approach utilizes transfer learning techniques to characterize models. The technique begins by determining a certain number of levels in the input layer, each displaying the improved images obtained from the previous stage of data processing. The activation functions extend beyond the convolutional layers. This approach use downsampling to identify certain traits. The inclusion of a dropout layer, softmax layer, and fully connected layer in this technique is intended to alleviate the problem of overfitting. The result is calculated prior to using the classification layer to predict the class.

The high-resolution deep feature maps are downsampled using a process called downsampling, which involves reducing the resolution by a factor of two. The fundamental Inception module consists of three parallel pathways that use 1 × 1, 3 × 3, and 5 x 5 convolution filters. The Inception deep learning model tackled the problem of time consumption caused by its complex structure by using down-sampling and sparse linked layers inside the convolutional layers. The feature maps' dimensionality was reduced by implementing a 1 x 1 convolutional layer in every Inception module.

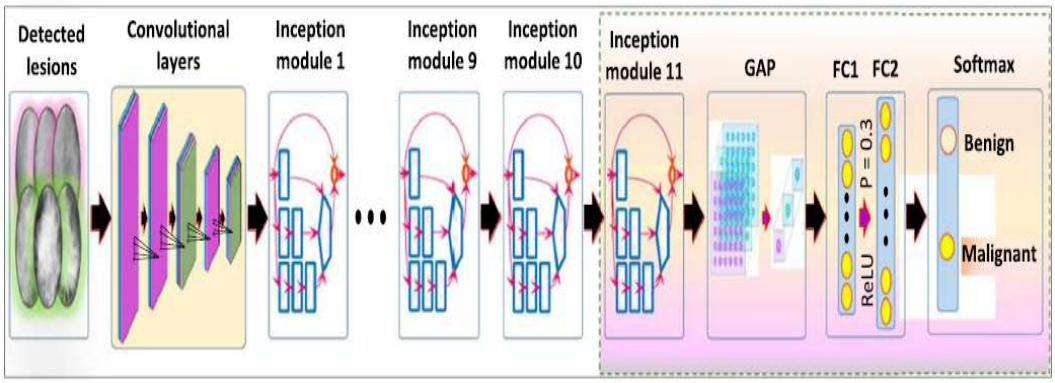

Figure 6: Modified Inception V3 layer architecture

By using these methodologies, the computational duration of deep learning models may be reduced to be on par with VGG-16 or ResNet-50. A variant of the Inception deep learning networks, called Modified InceptionV3, was developed to fully exploit the advantages of using residual connections in deep learning models. In Inception models, residual connections were used instead of filter concatenation to accelerate the training of deeper network architectures. This modification led to the development of enhanced InceptionV3 deep learning

models. Using residual connections in training Inception models significantly improves speed, as shown [13]. The overall classification performance of the residual Inception DL models has also improved. The research improved InceptionV3 by substituting the last two layers with four levels of the Global Average Pooling (GAP) layer, two fully linked layers with Rectified Linear Unit (ReLU) activation functions, and a softmax logarithm layer. Figure 8 depicts the schematic arrangement of the altered InceptionV3 model designed for deep learning.

2.4.2 Layers details of Modified Inception V3

The revised Inception V3 model Utilize the pre-trained Inception v3 model until a specified layer, often before to the final classification layers. This harnesses the model's ability to extract inherent visual features that are applicable across different images. In order to maintain the integrity of the fundamental Inception v3 layers throughout training, it is necessary to immobilize their weights, hence prohibiting any modifications. This technique focuses the learning process on the modified elements. The Inception v3 model heavily relies on convolutional layers. The mentioned layers use filters to analyze the input image, extracting features that differ in terms of their size and orientation.

2.4.2.1 Global Average Pooling (GAP) Layer

GAP layer is used to reduce the spatial dimensions (height and width) of the feature maps to a singular value per feature map by means of averaging. This aids in diminishing the number of parameters and may serve as a preventive measure against overfitting.

The GAP layer calculates the following using an input tensor $X \in A^{HXWXF}$ obtained from the output of the InceptionV3 base model, where H is the height, W is the width, and F is the number of channels (feature maps).

$$X_{GAP}[k] = \frac{1}{HXW}\sum_{i=1}^{H}\sum_{j=1}^{W} X[i,j,k] \text{ for } k=1,2,\ldots\ldots,F \qquad (9)$$

Where,

$X_{GAP} \in R^{F}$ is the output of the GAP layer

$X[i,j,k]$ is the value of the k-th feature map at position (i,j)

2.4.2.2 Fully Connected Layer-Dense Layer

Following the GAP layer, the output is sent into a fully connected (Dense) layer in order to improve features and decrease dimensionality. Let's represent the output of the GAP layer as X_{GAP}.

The Dense layer with ReLU activation computes:

$$X_{Dense1} = RELU(W_1.X_{GAP} + b_1) \qquad (10)$$

Where,

$W_1 \in R^{DXC}$ is the weight matrix

$b_1 \in R^D$ is the bias vector

D is the number of units in the Dense layer

ReLU(x)=max(0,x) is the ReLU activation function applied element-wise

$X_{Dense1} \in R^D$ is the output of the Dense layer

Dropout Layer

A Dropout layer is incorporated after the Dense layer to mitigate the problem of overfitting:

$$X_{dropout} = Droupout(X_{dense1}, r) \quad (11)$$

Where r is the dropout rate

Output Fully Connected Layer (Dense) with softmax function

Ultimately, the result obtained from the Dropout layer is sent onto a further Dense layer that utilizes softmax activation in order to provide probabilities for each class: $Y' = \text{softmax}(W_2 . X_{Dropout} + b_2)$ (12)

Where,

$W_2 \in R^{KXD}$ is the weight matrix

$b_1 \in R^k$ is the bias vector.

K is the number of output classes

$$\text{softmax}(z_i) = \frac{e^{zi}}{\sum_{j=1}^{k} e^{zj}} \text{ for } i = 1,2, \ldots . . K. \quad (13)$$

$y' \in R^k$ is the output probability vector.

The additional layers augment the retrieved characteristics from the InceptionV3 model and optimize them for the ultimate classification objective, rendering the model well-suited for mammography classification.

2.5 Data set

This dataset is a combination of the following three datasets: figshare, SARTAJ dataset and Br35H. This dataset contains 1,311 images of human brain MRI images which are classified into 4 classes: glioma (300 images), meningioma (306 images) - no tumor (405 images) and pituitary (300 images). The dataset used for this research work is taken from the kaggle site (https://www.kaggle.com/datasets/masoudnickparvar/brain-tumor-mri-dataset). In some other researches while they used this specific data set the performance is down comparatively other dataset. Inorder to enhance the performance the DAA method is included among with it to

make generated images and the algorithm for the same is included in section 3.3. Among these images 70-30 ratio is taken for training and testing.

Table 2: Classification of Data taken from Database

Type of Brain CT Image	From Dataset	After DAA
Glioma	300	2421
Meningioma	306	2624
no tumor	405	3105
Pituitary	300	2426

Table 3: input data after augmentation

Type of Breast Image	Training	Testing	Training	Testing
Original			After DAA	
Glioma	210	90	1694	727
meningioma	214	92	1836	788
mor	283	122	2173	932
pituitary	210	90	1698	728

3. Result Analysis and Discussion

3.1 Performance Evaluation Metrics

Image categorization is essential in healthcare applications for the detection and prediction of life-threatening malignant tumors in human organs. Common image classification methods include supervised and unsupervised learning models, CNN, RNN, and several advanced deep learning models that use transfer learning techniques. Various classifiers may be evaluated for sickness prediction using metrics such as accuracy (ACC), precision, recall, and F1-score. Sensitivity and specificity are measures of categorization accuracy, which are determined by true negative (TN), true positive (TP), false negative (FN), and false positive (FP) outcomes. The confusion matrix is an essential method in deep learning for assessing the performance of image classification. An error matrix, also known as a confusion matrix, is a visual representation in the form of a table that demonstrates the

performance of a classification model by comparing the predicted values with the actual labels.

3.2 Result Analysis

To scale and normalize all identified breast lesions, DAA interpolation is used. The resulting fixed sizes for CNN, ResNet-50, and Modified Inception V3 are 128 × 128, 224 × 224, and 299 × 299 pixels, respectively. It has been determined for this research to use the default input picture size for Keras-based deep learning classification models. One may adjust breast lesion photographs to various appropriate sizes. The CAD system's final predictions are then generated by feeding each of these breast lesions into a different set of deep learning classification models.

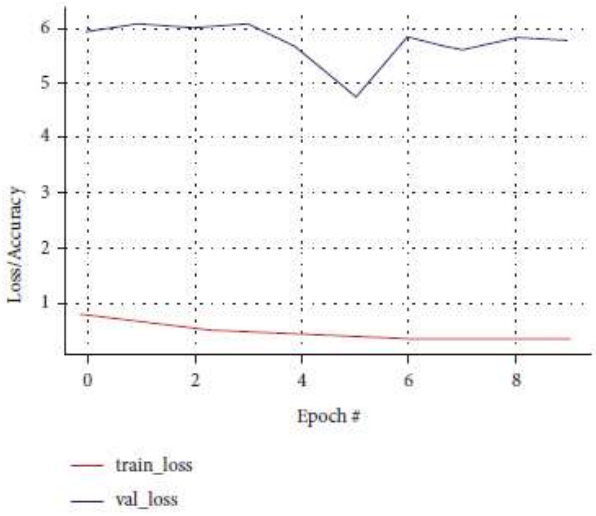

Figure 7: Training and Validation curve of the Modified Inception V3 classifier

Altered During training of Inception-v3, the graph of training accuracy generally increases, but the graph of validation accuracy fluctuates. In Figure 7, for both training and validation loss has performed. In training loss, while considering accuracy there is no improvement from start to 8 epochs. The validation accuracy experiences the most significant improvement after the 8th epoch, increasing from 0.82% in the 4th epoch to 0.86%. The validation loss curve displays erratic outcomes, but the training accuracy consistently improves until the last epoch, as seen in Figures 7 and 8.

Figure 9 displays the confusion matrix outcome of the Inception-v3 model's prediction on testing data. The confusion matrix provides a detailed breakdown of the model’s performance by showing how often your model correctly or incorrectly classifies each category.

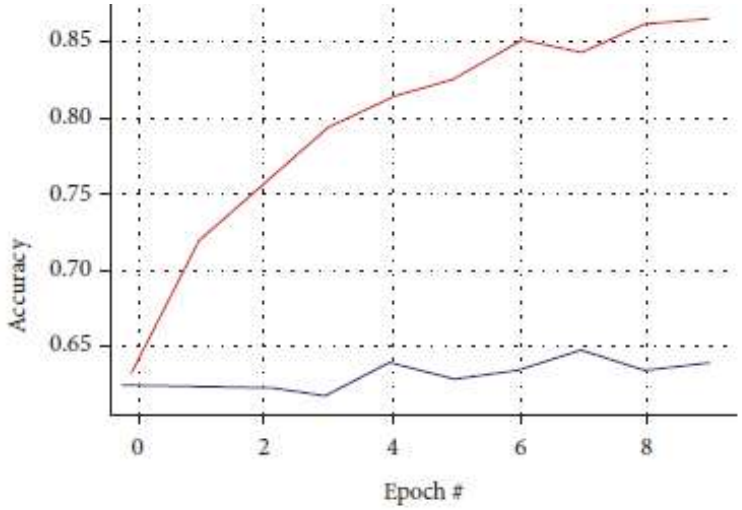

Figure 8: Accuracy in Training and Validation curve of the Modified Inception V3 classifier

The confusion matrix reveals the performance of the model in classifying brain tumors into four categories: Glioma, Meningioma, No Tumor, and Pituitary. The model correctly identified 2,200 cases of Glioma, 2,500 cases of Meningioma, 2,750 cases of No Tumor, and 2,176 cases of Pituitary. However, it also made some errors, incorrectly predicting 40 Meningioma, 100 No Tumor, and 81 Pituitary cases as Glioma. Similarly, it misclassified some cases of other tumors as different types, with notable misclassifications including 100 Glioma cases as No Tumor and 105 No Tumor cases as Pituitary. Additionally, the model failed to correctly classify 220 Glioma, 124 Meningioma, 355 No Tumor, and 250 Pituitary cases, leading to these being wrongly identified as other tumor types.

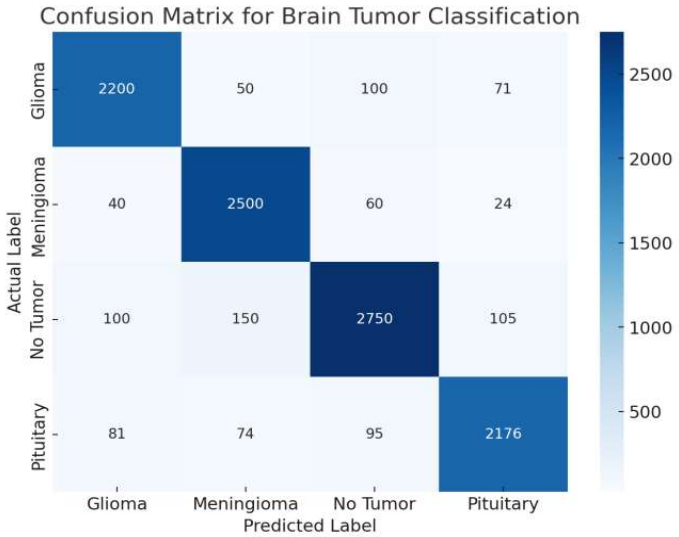

Figure 9: Confusion matrix for proposed work

Table 4: Performance of Proposed Vs Existing method

Classifier	Accuracy	Sensitivity	Specificity	Precision	AUC	F-Score
Modified Inception V3	96.12	91.5	94.3	90.2	99	92.7
Inception V3	94.5	90.13	86.4	87.53	94	89.21
Inception V2	86.24	88.71	84.51	84.36	88	90
VGG 19	87.13	89.32	83.17	86.5	83	94
VGG 16	84.56	79.62	81.5	87.2	89	90
Resnet 50	89.2	83.13	79.3	80.2	79	91.23

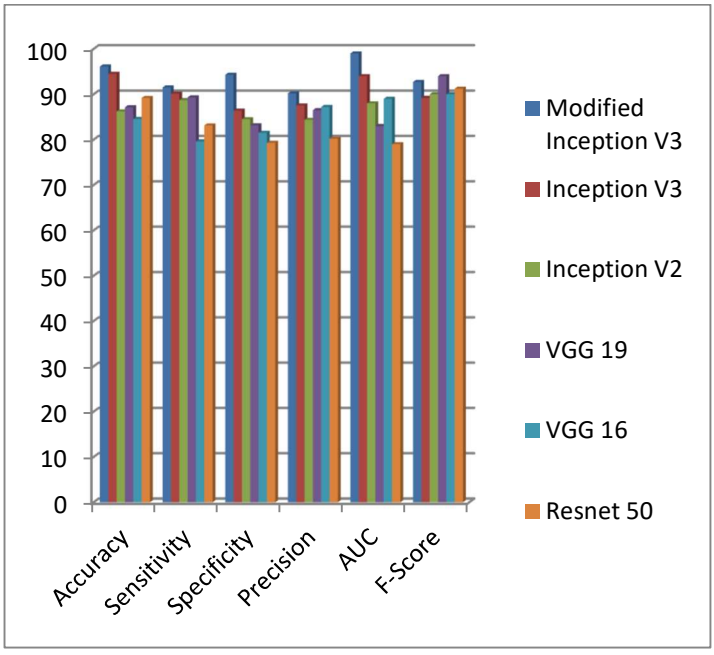

Figure 10: Performance Comparison of Proposed Vs Existing methods

The results of the classifier's performance without preprocessing are shown in Table 4. The Modified Inception-V3 had the highest accuracy performance, while the Inception V3 scored second in accuracy, sensitivity, and specificity with 96.12%, 91.5%, and 94.3%, respectively. Figure 10 illustrates the initial component of the proposed model for preprocessing phase outcomes.

4. Conclusion

The study on brain tumor classification utilizing a modified Inception V3 technique has shown encouraging results, demonstrating the model's efficacy in differentiating several forms of brain tumors, including Glioma, Meningioma, No Tumor, and Pituitary. The work successfully enhanced the original Inception V3 architecture, resulting in better accuracy and resilience in classification tasks. The changes facilitated enhanced feature extraction and discrimination, especially in managing the intricate and diverse patterns seen in medical imaging.

Afterwards, the precision of categorizing mass lesions in the dataset was enhanced by the use of freezing and fine-tuning methods. The suggested model demonstrated higher performance in terms of accuracy, sensitivity, specificity, area under the curve (AUC), and the F-score compared to four previous models. Utilizing transfer learning to include the convolutional neural network (CNN) into the screening process results in a substantial improvement when compared to earlier techniques. The results showed that the accuracy was 96.12%, the sensitivity was 91.5%, the specificity was 94.3%, the precision was 90.2%, the F-score was 92.7%, and the AUC was 0.99. These results exceed the other methodologies mentioned.

Ultimately, the adapted Inception V3 technique has considerable promise for implementation in clinical environments, providing a dependable instrument to aid radiologists in the timely and precise detection of brain cancers. Subsequent research might prioritize the incorporation of supplementary data sources, refine the model for improved performance, and investigate real-time applications to augment the practicality and effectiveness of this technique in medical practice.

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