

Synergistic deep learning ensemble of DenseNet, ResNet, and Xception for accurate brain tumor diagnosis

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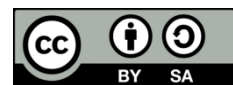
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ABSTRACT

Brain tumor classification plays a pivotal role in medical diagnostics, treatment planning, and patient care. Currently, the biomedical domain has experienced surge in demand of automated computer-aided diagnosis (CAD) systems for efficient diagnosis. Recently, deep learning (DL) architectures have experienced tremendous growth as prevailing tools for automated classification tasks. This study explores the synergistic potential of combining three state-of-the-art DL architectures i.e. densely connected convolutional network (DenseNet), residual network (ResNet), and extreme Inception (Xception) for brain tumor classification. Each architecture brings unique strengths, including feature reuse, skip connections, and depth-wise separable convolutions, respectively. This study proposes an ensemble methodology that capitalizes on the distinctive strengths of each architecture. DenseNet excels in feature reuse, ResNet employs skip connections to mitigate gradient issues, Inception captures multi-scale features, and Xception employs depth-wise separable convolutions for efficiency. By integrating predictions from these diverse models, our ensemble approach aims to achieve enhanced classification accuracy and robustness. After feature extraction, an improved feature selection method is introduced and finally, an ensemble classifier is introduced which uses majority voting method to achieve the classification task. The proposed approach has reported the average score as 0.99, 0.98, 0.99, 0.98, and 0.98 for precision, recall, specificity, sensitivity, and accuracy, respectively.

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1. INTRODUCTION

With recent improvements in biomedical technology, new and efficient ways to diagnose patients have been developed. Cancer is a serious health concern that medical professionals find challenging and can seriously threaten people in many parts of the world [1]. Because lung cancer, leukemia, breast cancer, melanoma, and brain cancer are so common, effective methods must be established to prevent, detect, and address these diseases [2]–[4]. Among all documented cancers, brain tumors are classified as one of the most

life-threatening malignancies. All of our bodily activities are regulated by the important role of the brain in our nervous system. Fortunately, cells in animals can reproduce normally, though without such system human brains are prone to deadly problems such as brain tumors that develop from the growth of abnormal cells. Untreated brain tumors, caused by cancerous cells, can lead to brain injury and disability and may seriously threaten life. World Health Organization (WHO) has recently shown that brain cancer caused around 10 million deaths around the world in 2020 which is the second most common cause of death worldwide. In their study, the WHO predicts that brain tumor patients will increase by 5% per year globally [5]. So, accurately and quickly identifying the tumor can help the patient live healthier and longer. WHO uses both molecular features and how the tumor appears under a microscope to arrange it into four groups (I, II, III, and IV) [6]. As the disease progresses, patients with brain cancer die sooner.

Reviewing tumors directly takes a lot of time and is sometimes not reliable due to human mistakes. Consequently, automated identification of brain tumors is now a main focus for biomedical scientists. Computer-aided diagnosis (CAD) has developed as a solution in biomedical image processing, providing accurate automatic examination of brain tumor images. But, because tumors can be found anywhere in the body and may be any size or shape, it is challenging to identify them early. Before, doctors would use images and carefully find the tumor's location in the brain to identify it. Capturing medical images makes use of magnetic resonance imaging (MRI), computed tomography (CT), and positron emission tomography (PET) [7]. Because MRI scans can produce fine images of inside the brain, radiologists widely use them. Even so, examining for tumors by eye is not easy due to borders obscured by nearby healthy tissue. Spotting tumors by hand takes a long time and often leads to mistakes. In addition, having multiple ways to get medical images often results in noisy pictures which can cause confusion in identification. Biopsies are normally done to find out if tissue is malignant or benign, but they are also quite slow and unpleasant. As a consequence, automated methods are being used more often because they work faster than traditional systems.

Besides taking a lot of time, manual delineation of brain tumors is tricky and depends on the abilities of each operator. For this reason, computerized solutions that operate primarily through automated processes rather than human intervention must be developed. A variety of image processing and machine learning (ML) techniques have been created by computer vision experts. In the current era, numerous automated CAD systems for breast cancer [8], melanoma [9], lung cancer [10], and other cancers are developed using computer vision and ML or deep learning (DL) technology [11], [12]. Applications of image processing are used to improve the data before classification, while ML focuses on placing the images into owned categories. Computer vision methods are generally classified as classical ML and DL. First, a classical approach pre-processes an image and uses handcrafted shape, texture and color features to generate the feature vector which is then classified by supervised learning [13]. Still, using these traditional approaches that need someone to handpick features does not always catch tumors in difficult images, resulting in decreased accuracy. Unlike ML, DL features get taken from the raw image itself. The structures of DL consist of different layers, for instance convolution, pooling and activation functions. As we covered before, a range of classification tasks have adopted these techniques in great numbers. A leading example of DL models is the convolutional neural network (CNN) which stands out with its special features and effective use [14]–[16]. What has interested the research community is this type of architecture's natural ability to spot features, whether they are high-level or low-level, from the data it learns on. The problem statement of this work includes several aspects as follows: manual process consumes excessive time and relies on the skills of individual. Moreover, traditional ML based methods rely on the handcrafted features such as shape, texture, and color however these features vary due to several conditions therefore generalization remains a challenging issue in these models. DL facilitates better performance but suffers from computational complexity, training time, and overfitting related issues.

The motivation behind utilizing DL for brain tumor classification stems from the pressing need to enhance medical diagnostics and planning of the treatment in the realm of neurology. Traditional methods of tumor classification can be time-consuming, subjective, and error prone. DL procedures, predominantly CNNs, and other advanced architectures offer the potential to automate and increase accuracy. By analyzing medical imaging data such as MRI scans, these DL models can learn intricate patterns and features that are often challenging for human experts to discern. This can lead to earlier and more accurate detection of tumors, enabling timely intervention and treatment. DL can also adjust and recognize different kinds of brain tumors which supports the distinction between these different subtypes and their features. DL in brain tumor classification aims to boost patient care by giving doctors important tools for diagnosis, planning treatment and checking on patients afterward. This technology hopes to lessen subjectivity, speed up results and increase the accuracy of classifying brain tumors which can favorably affect those who have these diseases.

A new approach to classifying brain tumor images using DL is the key goal of this study. More specifically, the method uses pre-trained DL models to identify the important features from the images.

The features are then chosen from among many choices and then they are classified using a variety of models. It aims to assess how well this new DL architecture increases the precision of detecting brain tumors in images.

The next area covers the different ways brain tumors are currently classified. Section 2 covers the application of RDXI_{Netdeep} and ensemble learning to brain MRI classification. Section 3 details the results of the RDXI_{Netdeep} and compares it to existing mechanisms; and section 4 concludes and looks ahead to upcoming work.

2. METHOD

RDXI_{Netdeep} hybrid ensemble is explained in this section as a new technique for brain tumor classification. The study of previous work reveals that ensemble learning is crucial in machine vision classification tasks. Feature extraction and increasing classification accuracy are partly the job of pre-trained models used in this area. Brain tumor classification has seen great success thanks to pre-trained DL designs. Because these architectures have already learned from extensive data, they can be adjusted to accurately spot and sort brain tumors in medical images. These models which were trained on the ImageNet dataset, can be adjusted for use in brain tumor classification. If these architectures are applied to medical images, they are able to pick out useful information and patterns revealing the different types and qualities of tumors in the images. It helps a lot when training time is short because data is restricted. Transfer learning lets us skip learning the basic features from the ground and improve the parts of the architecture that need to be customized. By using pre-trained knowledge, this approach manages to achieve strong convergence and good classification performance from a poorly populated dataset. On average, using DL architecture that has been pre-trained makes it easier to classify brain tumors. It allows clinicians to draw meaningful features from images and raise the performance of disease diagnosis and treatment. Figure 1 illustrates the overall arrangement of RDXI_{Netdeep} model.

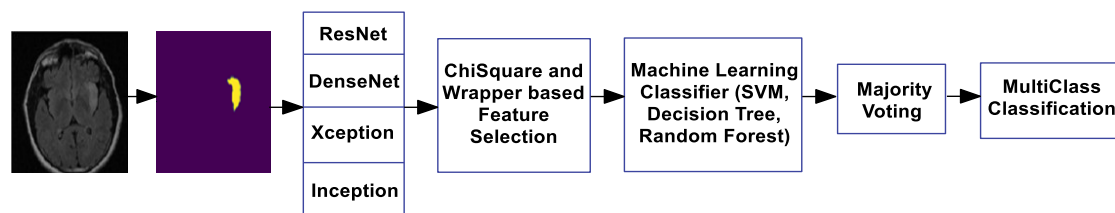


Figure 1. Architecture of the proposed brain tumor classification

The important steps involved in this mechanism are the following:

- i) Step 1: this step includes a data collection step where publicly available brain MRI datasets are considered. These datasets are stored and arranged in specified directories corresponding to their classes' labels.
- ii) Step 2: this step involves performing the image task, and for this purpose, an UNet-based has been adopted for brain tumor segmentation (BTS).
- iii) Step 3: in this step, the segmented region is processed through the DL-based architectures for extracting the deep features.
- iv) Step 4: the obtained deep features will be input to the feature selection module where employ RDXI_{Net} feature selection approach for dimension reduction.
- v) Step 5: finally, an ensemble classification approach is employed by using a traditional ML classifier along with the majority voting system to attain the classification result against the hybrid brain tumor classification approach that uses segmented regions to extract the co-occurrence vector, run-length vector, and gradient features. Some of the important work is reducing the misclassification of brain tumors. The remaining section describes the DL architecture for feature extraction, feature selection, and ensemble classification approach.

2.1. Deep feature extraction

Here, it is shown that how a pre-trained DL model serves as a feature extractor. Densely connected convolutional network (DenseNet), residual network 50 layers (ResNet-50), Inception V3, extreme Inception (Xception), ML-based model and mobile network (MobileNet) were all used for segmentation in this work.

DenseNet [17]: DenseNet121 was built as a solution to the issue of vanishing gradients plaguing some neural networks. In addition, feature reuse and distribution across the network help the network discover and understand various patterns. Traditional CNNs have convolutional and pooling layers in sequence which generates a representation of features in a unified structure. Yet, when the network has many layers, the gradient can become smaller during backpropagation, preventing us from training such models properly. DenseNet tries to deal with this problem by adding links to every layer. All of the DenseNet model's layers are directly linked to every layer that follows. Since each layer is so close to its neighbors, it helps the network access features from before and share information with other layers. Here's how the architecture is designed:

- Dense blocks: it is constructed of dense blocks wherein each block comprises of multiple convolutional layers with densely connected skip connections. These connections enable each layer to receive feature maps from all previous layers in the block, fostering strong feature reuse and information flow.
- Bottleneck layers: before each dense block, there's a bottleneck layer that reduces the number of input feature maps. This helps control the model's computational complexity while maintaining its ability to learn complex features.
- Transition layers: these layers are utilized to limit the spatial dimensions of feature maps and the growth of the network. These layers comprise of a combination of 1×1 convolutional filters and average pooling, followed by concatenation of feature maps.

Figure 2 depicts the architecture of DenseNet-121, which contains convolutional and pooling layers, dense blocks, transition layers, global average pooling, a fully connected layer, and dense layers. The dense blocks facilitate feature reuse through direct connections between layers, while the transition layers help reduce the spatial dimensions of the feature maps. This architecture enables DenseNet-121 to effectively extract and propagate features across the network.

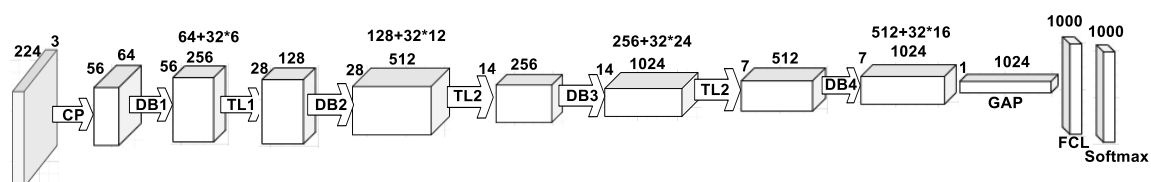


Figure 2. DenseNet-121 architecture

ResNet-50 [18]: it contains 50 different layers out of which convolutional, pooling, fully connected layers and shortcut connections (residual blocks) are included. Compared to previous models, it applies residual learning to the ResNet structure which makes learning in a deep neural network possible. Traditional convolutional layers appear at the first stage and this is followed by four sets of residual blocks. Every set has numerous residual blocks with progressively larger numbers of filters so the network becomes able to find more difficult features as it advances. The bottleneck architecture is applied, combining 1×1 , 3×3 , and 1×1 convolutional layer. With this design, the cost of calculations is greatly reduced, but its expressiveness is not affected. In addition, it uses skip connections between layers to make backpropagated gradients easier to follow and helps prevent gradient disappearance which means very deep networks can be successfully trained. At the final part of the network, ResNet-50 swaps out fully connected layers for global average pooling. By doing so, fewer parameters are needed, so the model has improved generalization. The network speed and stability are improved through the batch normalization technique integrated into ResNet-50. Figure 3 shows how the ResNet architecture is built.

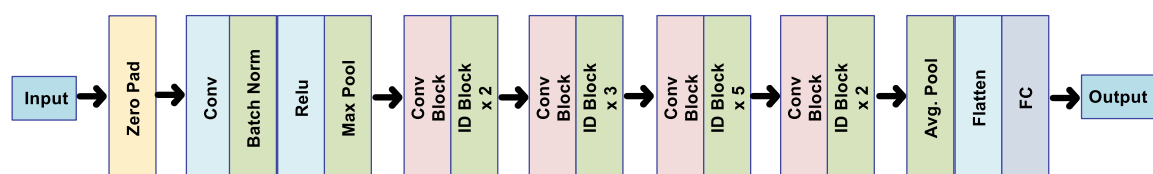


Figure 3. ResNet architecture

Inception V3 [19]: Inception V3 includes many inception modules which help find different parts of an image at different magnifications. To feature extract features of different levels, each Inception module mixes filters and pooling operations with various kernel sizes. This architecture helps the network identify small and large shapes in what is fed into it. The main components of this architecture are as follows:

- Bottleneck layers: similar to DenseNet, Inception V3 uses 1×1 convolutional layer, known as “bottleneck layers”. The bottleneck layers work as dimension reduction step to minimize the computational complexity resulting in improving the computational efficiency of the system.
- Factorization into smaller convolutions: to further reduce the computational cost, some larger convolutions are factorized into smaller convolutions. This makes the network more efficient in terms of both memory and computation.
- Auxiliary classifiers: during the training process, this architecture considers auxiliary classifiers at the intermediate stage to facilitate the additional gradients that help mitigate the vanishing gradient problem.
- Global average pooling: instead of fully connected layers at the end of the network, Inception V3 uses global average pooling. This reduces the risk of overfitting and simplifies the model, as well as eliminating the need for many parameters.

Xception: it is a variation of the inception architecture that places a strong emphasis on the concept of “depth-wise separable convolutions.” This approach aims to increase the efficiency of the network by reducing the number of parameters. The main component of this architecture as follows:

- Depthwise separable convolutions: in traditional convolutional layers, each filter convolves across all input channels, which can be computationally expensive. Depthwise separable convolutions split the convolution into two separate operations: depthwise convolutions, where each input channel is convolved separately, and pointwise convolutions, which perform 1×1 convolutions to combine the depthwise outputs. This approach significantly decreases the number of computations and parameters.
- Entry and exit flow: Xception consist of an “entry flow” that processes the given image and an “exit flow” that produces the classification output. The entry flow performs initial feature extraction using stacked depthwise separable convolutions, and the exit flow uses GAP and connected layers to generate predictions.
- Skip connections: Xception employs skip connections like ResNet which helps to tackle the gradient vanishing problem.
- Batch normalization: like many modern CNN architectures, Xception uses batch normalization to accelerate training and improve convergence.

2.2. Feature fusion and selection

The obtained feature vectors are fused to formulate the final feature vector. The final feature vector is later processed through the feature selection phase where we present an improved wrapper-based feature selection process that considers the chi-square test score to estimate the significant feature. The chi-square test can be characterized as in (1).

$$Chi - square = \frac{N(AD - CB)^2}{(A+C)(B+D)(A+B)(C+D)} \quad (1)$$

Where N represents the number of input samples, A represents the number of samples in class C_i that contains features t_k , B denotes the sample count that consist of feature t_k in other class, C denotes the samples in class C_i , and D denotes the number of samples that do not contains features in other class.

This approach is initiated by evaluating the deep features which are obtained from different pre-trained architectures. During the feature selection phase, these features undergo processing through the chi-square test. The obtained feature ranking score from chi-square measurement, is directly employed to feature search method in wrapper-based feature selection process. The feature search method includes forward backward, and bi-directional approaches. The initial strategy involves starting with all features in the feature space and gradually excluding those with lower ranks. Conversely, the forward strategy initiates with the highest-ranked feature and progressively incorporates subsequent features. The bidirectional strategy oscillates between the forward and backward techniques.

2.3. Ensemble classification

The features are processed through traditional ML models like support vector machine (SVM), decision tree (DT), and random forest (RF). A majority voting mechanism is used in this study to obtain the concluding results. Ensemble learning uses majority voting, as it is simple and works well when you combine the predictions of several models. This study can represent majority voting classification as follows: suppose that we have N total classifiers, written as $C_1, C_2, \dots, C_N$. All classifiers are taught using the same values

produced by blending handmade and DL features. In addition, every classifier is able to place the patterns in K into various classes. The procedure for any input sample is to use majority voting as explained as follows.

- For the input X , the classifiers give their predictions as $P_1, P_2, \dots$, and so on. Their labels corresponding to $C_1, C_2, \dots, C_N$ are $P_1, P_2, \dots, P_N$.
- Make a list of all the class labels and count each occurrence in $\{P_1, P_2, \dots, P_N\}$.
- Look for the one among class labels that occurs most frequently. Should the scores be equal, a plan for breaking a tie such as selecting the class with the lowest index, might be set in advance.
- Out of the labels, give the majority class label as the final output for X . It is possible to explain it in (2).

$$\text{Final Classification} = \arg \max_k \sum_{i=1}^N 1(P_i = k) \quad (2)$$

3. RESULTS AND DISCUSSION

The results from the RDXI_{Net} approach are included and how they compare to ML and DL-based approaches are shown. The first section talks about the dataset, the next discusses the evaluation scheme and the last presents close analysis to confirm the reliability of the RDXI_{Net} method.

3.1. Dataset details

For this work, the T1-weighted MRI dataset uploaded by Cheng in 2017 was downloaded [20]. Within this dataset, glioma, meningioma, and pituitary tumors acquired from coronal, sagittal, and axial planes are included. All the images in this dataset are 512×512 pixels, while each pixel is 49×49 mm in size. Table 1 shows the dataset details. Figure 4 shows the sample images of each type including glioma, pituitary, and meningioma along with their corresponding planes.

Table 1. Dataset details

Tumor type	Image count	Patients count
Glioma	1,426	91
Pituitary	930	60
Meningioma	708	82
Total	3,064	233

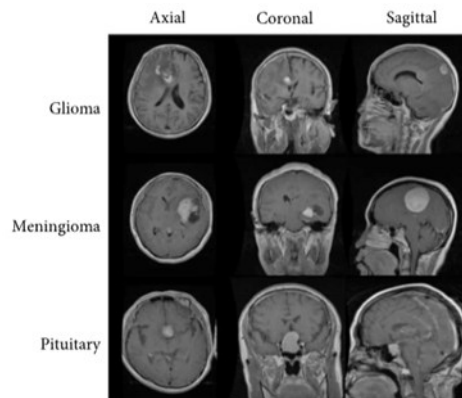


Figure 4. Sample image of each category

3.2. Experimental setup

First, the method relies on pre-trained deep feature extractors and afterward, these features are fed into common classifiers including SVM, DT, and RF. All experiments were carried out on an Intel Core i5 processor equipped with 8 GB of memory, using Python 3.8 on a windows system. Details about the simulation settings used for these CNNs are found in Table 2.

In this experiment have trained the DL architectures for 30 epochs, each epoch runs the data through from start to finish and back again. Learning from the input samples is done by dividing them into batches with a learning rate of $1e-4$. Each epoch uses batch size of and stochastic gradient descent with momentum (SGDM) is considered as the training optimizer.

Table 2. Hyper-parameters of deep feature extraction method

Hyper-parameters	Considered values
Training epoch	50
Batch size	5
Optimizer	SGDM
Learning rate	1e-4

3.3. Performance evaluation parameters

The main parameters that help evaluate the proposed model are described in this section. To check a model's performance, the total true positive (TP), false positive (FP), true negative (TN) and false negative (FN) samples are shown in a confusion matrix. It shows correct predicted counts and misclassified counts in the model. Table 3 presents an illustrative selection of three class confusion matrix.

Table 3. Confusion matrix

	Predicted lesion class			
	Lesion class 1	Lesion class 2	Lesion class 3	FN
Actual lesion class	T_{11}	T_{12}	T_{13}	$(T_{12} + T_{11})$
	T_{21}	T_{22}	T_{23}	$(T_{21} + T_{23})$
	T_{31}	T_{32}	T_{33}	$(T_{31} + T_{32})$
FP	$(T_{21} + T_{31})$	$(T_{21} + T_{32})$	$(T_{13} + T_{33})$	
TP	T_{11}	T_{22}	T_{33}	

TP: see a TP when the classifier identifies a positive case from the set of test cases. TN: means the classifier predicts the given positive examples as negative. The classifier is shown to be accurate by its TN and TP values. But these groups must reflect the true numbers of TP and TN measurements. FP: when a classifier incorrectly guesses something positive, it is known as a false positive. FN: when the classifier says the class is negative but it should have been positive, it's called a false negative. The various points considered for evaluating the performance of the proposed work are given in Table 4.

Table 4. Performance parameters

Parameter	Computation formula
Accuracy	$\frac{TP + TN}{TP + TN + FP + FN}$
Recall	$\frac{TP}{TP + FN}$
Precision	$\frac{TP}{TP + FP}$
F-measure	$\frac{2 \times P \times Sensitivity}{P + Sensitivity}$

3.4. Comparative analysis

Here, this study examines the comparison of the performance of the proposed system against the performance of existing methods. This study assesses the performance starting with individual DL architectures. Table 5 represents the comparison of the results. The proposed method is reported to perform on average with precision of 0.99, recall of 0.98, specificity of 0.99, sensitivity of 0.98 and accuracy of 0.98. This is achieved because of combined deep feature extraction mechanism which also tackles the vanishing gradient problem.

Table 5. Comparative performance for individual pre-trained model

Classifier	Precision	Recall	Specificity	Sensitivity	Accuracy
DenseNet	0.87	0.88	0.87	0.88	0.89
ResNet	0.88	0.87	0.88	0.87	0.91
Xception	0.89	0.91	0.89	0.90	0.92
Inception	0.89	0.93	0.89	0.92	0.92
GoogLeNet	0.91	0.94	0.91	0.95	0.94
ResNet18	0.93	0.95	0.93	0.96	0.96
AlexNet	0.95	0.96	0.95	0.97	0.97
Proposed RDXI _{Net}	0.99	0.98	0.99	0.98	0.98

The performance of DenseNet is reduced due to its high resource utilization and densely connected layers whereas the ResNet model suffer from the issue of vanishing gradient. On the other hand, the Xception suffer from the computational complexity issue because of depth-wise separable kernel whereas ResNet-18 presents poor representation when compared with other deeper architectures. Similarly, this study measured the class-wise performance. Table 6 presents the class-wise precision, recall, and F1-score of the proposed model.

Table 6. Class-wise performance

Tumor class	Precision	Recall	F1-score
Glioma	100	100	100
Meningioma	99	100	99
Pituitary	100	100	100
Average	99	100	99

This study extends the comparative analysis and compared the performance with state-of-art works such as CNN, capsule network (CapsNet), CNN + SVM, DenseNet + Inception + ResNeXt, and AlexNet + visual geometry group 16 (VGG-16). Table 7 shows the proposed approach achieving an overall classification accuracy of 99.85%. This comparative analysis shows that the proposed method obtained the average accuracy as 99.85% whereas the other ensemble of DenseNet169 + Inception V3 + ResNeXt150 reported the accuracy of 98.5%, the combination of AlexNet with VGG-16 reported 96.6% accuracy.

Table 7. Comparative analysis with state-of-art schemes

Method used	Accuracy
CNN [21]	94.2
CapsNet [22]	90.8
CNN+SVM [23]	97.1
DenseNet169 + Inception V3 + ResNeXt150 [24]	98.5
AlexNet + VGG16 [25]	96.6
DenseNet + ResNet + Xception + ensemble [proposed]	99.85

4. CONCLUSION

Brain tumor has profound impact on a person's life and if left untreated then it can lead to death of patient. Therefore, early detection of brain tumor plays important role. The current advancement in ML and DL have paved the development of DL architecture for efficient classification. Therefore, presented an integrated network by combining DenseNet, ResNet, and Xception architectures with an ensemble classification framework. Each of these DL architectures brings distinct advantages, and their combined utilization showcases a powerful synergy that enhances the accuracy and robustness of tumor classification models. DenseNet's dense connectivity adopts feature reuse, allowing for the extraction of intricate patterns from medical images. ResNet's skip connections mitigate the vanishing gradient problem, facilitating the training of deeper networks and improving the model's ability to capture complex features. Xception's innovative depthwise separable convolutions reduce computational demands without compromising feature representation quality. By adopting an ensembling strategy allows for the exploitation of diverse feature representations, leading to a more comprehensive understanding of brain tumor features and resulting in improved overall classification performance. In essence, the fusion of DenseNet, ResNet, and Xception within an ensemble framework showcases the substantial benefits of collaboration in DL. This advancement highlights the significance of leveraging diverse architectural innovations to address complex medical challenges, ultimately contributing to more accurate and reliable brain tumor classification methods that hold immense promise for advancing the field of medical imaging and diagnosis. However, the proposed approach uses pre-trained models which can lead ambiguity in complex image scenarios therefore additional deep feature extraction models can be incorporated to improve the performance of the model.

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CONFLICT OF INTEREST STATEMENT

The author declares that there are no known conflicts of interest associated with this publication. There are no financial or personal relationships that could inappropriately influence or bias the content of this work.

DATA AVAILABILITY

The data that support the findings of this study are available from the corresponding author, [SG], upon reasonable request.

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