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Efficient deep learning approach for brain tumor detection and segmentation based on advanced CNN and U-Net

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ABSTRACT

In this paper, we propose an innovative deep learning methodology dedicated to tumor detection and segmentation in medical images using convolutional neural networks (CNNs) and the U-Net architecture. The study emphasizes the importance of improving the quality and relevance of these features by employing advanced preprocessing methods. The subsequent development involves training a CNN model to achieve accurate tumor classification within the medical images. Among the various deep learning techniques proposed for medical image analysis, U-net-based models have gained significant popularity for multimodal medical image segmentation. However, due to the diverse shapes, sizes, and appearances of brain tumors, simple block architectures commonly used in segmentation tasks may not adequately capture the complexity of tumor boundaries and internal structures. The experimental results provide compelling evidence of the proposed approach's efficacy in accurately detecting and segmenting brain tumors. The results highlight the successful performance of the approach and its ability to achieve accurate tumor identification and segmentation.

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1. INTRODUCTION

In recent years, numerous techniques have emerged to segment brain tumors from magnetic resonance imaging (MRI) datasets, with a significant proportion of these approaches being based on deep learning [1]-[5]. Initially, studies focused on using MRI images alone to segment and detect brain cancers. These initial methods relied heavily on manually developed features that exploited texture and intensity information. These features were carefully crafted by experts to capture relevant patterns and characteristics indicative of the presence of a tumor. However, with the advent of deep learning, the field has undergone a paradigm shift. Deep learning-based approaches have enjoyed remarkable success in automatically learning discriminative features directly from data, reducing reliance on manual feature engineering. These models can efficiently analyze complex relationships within MRI images, capturing subtle and complex tumor features that were previously difficult to extract with traditional methods. The integration of deep learning techniques has dramatically improved The precision and efficiency of segmenting brain tumor, paving the way for more accurate and reliable diagnosis and treatment planning in clinical applications [6]-[9]. Convolutional neural network (CNN) techniques, which have been developed recently, are heavily utilized in more modern segmentation frameworks, which provide superior results [10]. Recent advances in brain tumor segmentation from MRI images follow a similar trend. In particular, U-shaped systems constructed using the U-Net deep learning technique have been the most successful strategy for dense semantic segmentation [11]-[18]. Recent developments in this design include the incorporation of long and short residual skip connections, either by increasing their length or adding them to the architecture for three-dimensional (3D) volumetric segmentation. Subsequent versions of U-Net variants, such as M-Net, Dense U-Net, U-Net++, and U-Net3+, have further improved feature utilization. These improvements in U-Net and its variants have made significant contributions to the field of brain tumor segmentation, enabling more accurate and comprehensive analysis of MRI data [19]-[25]. This paper presents a new and innovative deep learning technique for brain tumor detection and segmentation using multiple imaging modalities. The main contribution of this study is the development of a hybrid approach that combines a modified CNN architecture, leading to improved accuracy in brain tumor detection. In addition, we propose a separate model for brain tumor segmentation based on the U-Net framework, which offres a more stable and adaptive solution with significant potential [26]-[30].

Khan *et al.* [31] address the difficult task of brain tumor classification using deep learning techniques. Specifically, they focus on developing CNNs capable of performing binary and multi-class categorization of brain tumors. The methodology employed by the authors demonstrates the immense potential of deep learning to simplify the diagnostic process by eliminating the need for manual feature extraction. This significant advancement in automation paves the way for more efficient and accurate tumor detection methods.

Irmak [32] presents an extensively optimized CNN framework specifically designed for multi-classification tasks, which achieves outstanding levels of accuracy. This research not only demonstrates the effectiveness of CNNs, but also pioneers the algorithmic fine-tuning of hyperparameters. By enhancing the diagnostic capabilities available to the medical community, this work makes a significant contribution to enhanced precision and reliability of brain tumor detection. Soumik and Hossain [33] contribute to the advancement of the area by using learning by transfer techniques with the InceptionV3 model. This approach proves to be particularly valuable in mitigating the challenge of limited availability of brain MRI images. The remarkable accuracy achieved by their method highlights the effectiveness of transfer learning in optimizing deep learning models when faced with constraints in the dataset.

Dheepak *et al.* [34] present a pioneering approach to brain tumor classification using a multi-kernel support vector machine (SVM). Their method is characterized by the integration of different kernel functions, which significantly improves the robustness of the model. This innovative approach not only advances the field of brain tumor classification, but also opens novel avenues for improving diagnostic accuracy beyond the limitations of conventional SVM architectures. A study by Montoya *et al.* [35] provides a comprehensive evaluation of the performance of shallow and deep neural networks. Their results show that the ResNet50 architecture outperforms shallow networks in terms of classification capabilities.

Vu [3] introduces a deep learning concept to CNNs for tumor identification in medical imaging. The research emphasizes the use of tumor-detection-related image enhancement pre-processing techniques. The proposed method involves training a CNN model for accurate classification, with preprocessing steps such as gaussian blending, two-way filtering, and K-means grouping applied to highlight tumor regions in the input images.

In view of the above shortcomings,In this paper, a novel deep learning approach for multimodal brain tumor segmentation and detection is proposed. In summary, this study introduces a hybrid strategy that incorporates modified CNN architecture to further the research on improved accuracy brain tumor identification. Furthermore, we suggested an additional brain tumor segmentation model based on the U-Net framework, which offers a more reliable and broadly applicable solution with considerable promise.

The remainder of this paper is structured as follows: the content and methods, which comprise the suggested strategy and the modules utilized, are presented in section 2. In section 3, the simulations are presented and the outcomes are discussed. In section 4, we conclude this work.

2. METHOD

An overview is provided in this section about the dataset used for the experiments. Next, the training specifics employed in this study are described. Finally, detailed information on the proposed methods is presented. This approach offers a novel framework based on deep learning that is intended to divide and categorize brain tumors. To improve the input's quality of photos, our method makes advantage of publically accessible datasets and pre-processing methods including image resizing and contrast improvement. Utilizing the UNet-based segmentation model in the pre-processing pipeline helps to reduce the impact of retinal biomarkers on the classification of brain tumours. Once pre-processing and segmentation are completed, this method yields an enhanced brain tumor image.

2.1. Dataset description

In this work, a dataset of brain MRI pictures was used, divided into two parts: images containing tumors (1,500 slices) and images without tumors (1,500 slices). This division of the dataset was intended to facilitate the analysis and classification of brain tumors. To ensure efficient evaluation, the dataset has been further split, with 70% of the pictures allocated to model training and the remaining 30% used for testing and validation. Each image was normalized, resized to a uniform resolution of 256×256 pixels. This standardized resolution enables consistent evaluation and comparison of images across all samples, guaranteeing reliable and accurate evaluation of tumor detection and classification algorithms.

2.2. Training details

The proposed tumor detection model is designed as a fully convolutional network, and the tumor segmentation model uses a U-Net that enables it to procedure pictures of any size during the training and test phases. However, to ensure a consistent and generic learning process, the training images were resized to a fixed size of 256×256. The model is able to learn and generalize patterns thanks to this scaling step across different images while maintaining computational efficiency. The model was then tested on images in their original dimensions. The network was optimized using an Adam optimizer [34], with the classification model trained for 32 epochs and the segmentation model trained for 90 epochs. All experiments were performed on a hardware setup consisting of an AMD Ryzen 5600 H central processing unit (CPU) running at a clock speed of 3.3 GHz, 16 GB of random-access memory, and an AMD Radeon RX 6500M (4 GB) graphical processing unit (GPU).

The suggested CNN was formed with a mixture of cross-entropy loss and Dice coefficient loss. The entropy is calculated by (1).

$$Entropy = \sum_{y=i} yi \times \log\big(f(x)\big)i \tag{1}$$

Function of the cross entropy loss quantifies the discrepancy between the predicted probability distribution f(x) and the actual distribution (y). On the other hand, the dice coefficient is calculated as (2) and (3):

$$Dice\ Coefficient = \frac{1-2\times\sum_{yi}\times f(x)+\mathcal{E}}{\sum_{yi}+\sum_{ji}\times f(x)+\mathcal{E}} \tag{2}$$

$$Loss = Entropy + (1 - Dice\ Coefficient) \tag{3}$$

During the training process of tumor detection and segmentation, the training data set is divided into a number of mini-lots. The weights of the model are in sync with the Adam optimization algorithm. The first part of Table 1 provides an overview of the main hyperparameters used in the tumor detection training process. Similarly, the second part shows the key hyperparameters specific to the tumor segmentation training process.

Table 1. Training hyperparameters

Tumor detection		Tumor segmentation	
Hyperparameters	Value	Hyperparameters	Value
Epochs	32	Epochs	90
Batch size	32	Batch size	16
Learning rate	0.001	Learning rate	0.001
Optimizer	Adam	Optimizer	Adam
Activation function	ReLU	Activation function	ReLU
Trainable parameters	3730881	Trainable parameters	31042369
Non-trainable parameters	0	Non-trainable parameters	11776

2.3. The proposed architecture

2.3.1. Optimizing MRI image preprocessing

The pre-processing stage is of paramount importance as it enhances the features within the MRI images and enables efficient tumor detection. This stage involves a series of carefully designed steps that focus on optimizing the images for subsequent analysis [36].

- Resize image: resize the image to the desired dimensions specified by image size. The resized image is stored back in the image variable.
- Image normalization: to ensure consistent pixel value ranges, each pixel value in the image is divided by 255.0. This step normalizes the pixel values of the image.

- Data type conversion: the datatype of the image is converted to np.float32. This step allows more precise calculations and compatibility with other operations.
- Append image: the preprocessed image is added to the all-images list.
- Read mask image: similar to the image read step, the code reads the corresponding mask image from the specified mask path in grayscale mode. The resulting mask image is stored in the variable image_1.
- Resize mask image: resizes image_1 to the specified image size. The resized mask image is stored back in the image_1 variable.
- Mask image normalization: similar to the image normalization step, each pixel value in image_1 is divided by 255.0 to ensure consistent pixel value ranges.
- Mask data type conversion: the datatype of image_1 is converted to np.float32 using the.
- Mask appending: the preprocessed mask image_1 is appended to the all-mask list.

2.3.2. Tumor detection architecture

We proposed an approach for brain tumor detection that comprises three steps: preprocessing, feature extraction and tumor prediction. First, the input data, consisting of images, undergoes preprocessing. Next, relevant features such as images, labels, borders and masks are extracted from the pre-processed data. Finally, the tumor detection step uses these extracted attributes as input, which is implemented using a CNN optimized with Adam's algorithm. The parameters of the CNN and Adam algorithm are fine-tuned for optimum performance, along with other fixed parameters. The synopsis of the suggested technique is described in the Figure 1, this visual representations provides a concise illustration of the proposed approach, highlighting its key components and workflow. The proposed CNN architecture aims to efficiently classify and separate brain tumors. Details of the specific architecture of the suggested CNN are shown in the Table 2, where the different layers, filters and connections are specified.

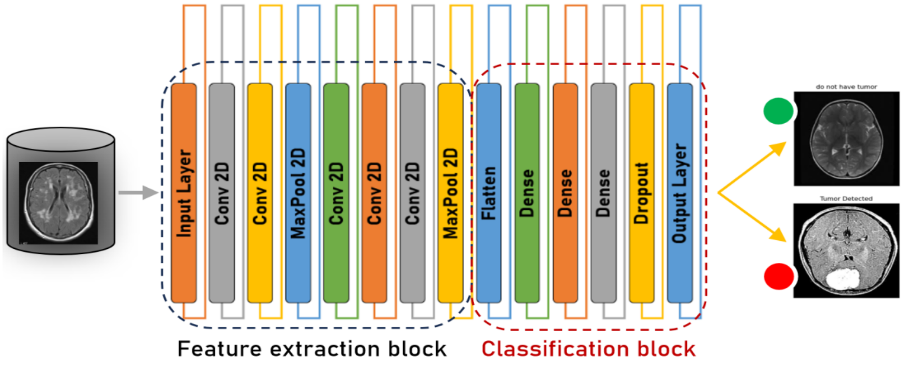


Figure 1. Proposed 14-layers 2D CNN architecture

Table 2. The proposed CNN model

Layer type	Output size	Activation function
Convolution	254×254×64	ReLU
Convolution	252×252×32	ReLU
Max pooling	126×126×32	-
Convolution	124×124×32	ReLU
Convolution	122×122×32	ReLU
Convolution	120×120×64	ReLU
Max pooling	30×30×64	-
Flatten	57600	-
Dense	64	ReLU
Dense	32	ReLU
Dense	16	ReLU
Dropout	16	-
Dense	1	Sigmoid

2.3.3. Tumor segmentation architecture

The segmentation approach employed is based on the combination of on advanced U-Net based on retaining the dataset, which follows an encoder-decoder design. In this architecture, the encoder is asymmetrically larger to efficiently extract relevant characteristics from the image, while the decoder is relatively smaller to reconstruct the segmentation mask. This design enables efficient feature extraction and accurate reconstruction of the segmentation mask, improving segmentation performance. The proposed technique is outlined in Figure 2, which gives a summary of its key elements and processes.

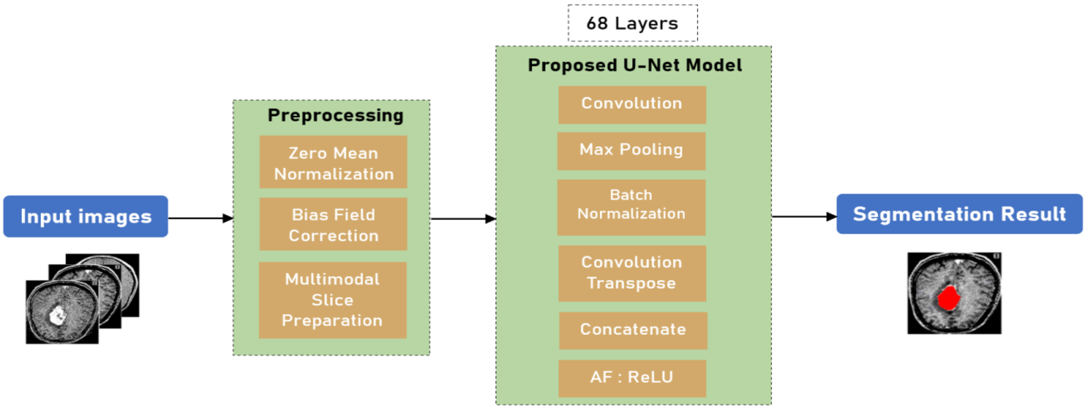


Figure 2. The architecture of the proposed method based on U-Net

The two paths that make up the suggested U-Net architecture for brain tumor segmentation are the encoding and decoding paths. The encoding path captures contextual information by reducing the spatial dimensions of the input data. The decoding path, enables precise localization by increasing the spatial dimensions. These components work together to efficiently separate brain tumors by combining contextual information and precise localization. Table 3 gives a detailed overview of the proposed U-Net architecture. Figure 3 illustrates the modified convolutional module designed to improve the extraction of feature information in image segmentation networks. This architectural modification aims to address the problem of incomplete feature extraction that is often encountered in such networks.

Table 3. The proposed advanced U-Net architecture

Layer no	Layer type	Output size	Layer no	Layer type	Output size
1	Input	256×256×64	37	Concat	32×32×1024
2,3,4	Conv, BN, AF	256×256×64	38,39,40	Conv, BN, AF	32×32×512
5,6,7	Conv, BN, AF	256×256×64	41,42,43	Conv, BN, AF	32×32×512
8	MP	128×128×64	44	ConvTrans	64×64×256
9,10,11	Conv, BN, AF	128×128×128	45	Concat	64×64×512
12,13,14	Conv, BN, AF	128×128×128	46,47,48	Conv, BN, AF	64×64×256
15	MP	64×64×128	49,50,51	Conv, BN, AF	64×64×256
16,17,18	Conv, BN, AF	64×64×256	52	ConvTrans	128×128×128
19,20,21	Conv, BN, AF	64×64×256	53	Concat	128×128×256
22	MP	32×32×256	54,55,56	Conv, BN, AF	128×128×128
23,24,25	Conv, BN, AF	32×32×512	57,58,59	Conv, BN, AF	128×128×128
26,27,28	Conv, BN, AF	32×32×512	60	ConvTrans	256×256×64
29	MP	16×16×512	61	Concat	256×256×128
30,31,32	Conv, BN, AF	16×16×1024	62,63,64	Conv, BN, AF	256×256×64
33,34,35	Conv, BN, AF	16×16×1024	65,66,67	Conv, BN, AF	256×256×64
36	ConvTrans	32×32×512	68	Conv	256×256×1

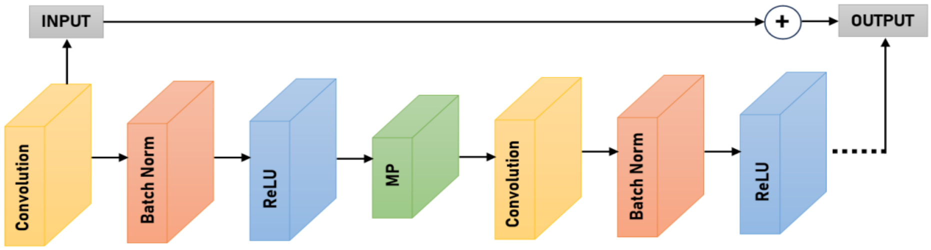


Figure 3. The modified convolutional module

3. RESULTS AND DISCUSSIONS

The outcomes of the recommended approach are displayed. in this part along with a performance comparison with other available segmentation and classification techniques. The experimental conditions used in this investigation are described in detail in the first subsection, and the tumor categorization outcome is presented in the second subsection. Subsequently, we elucidate the tumor segmentation outcomes, and ultimately, we offer a comparison analysis for discourse.

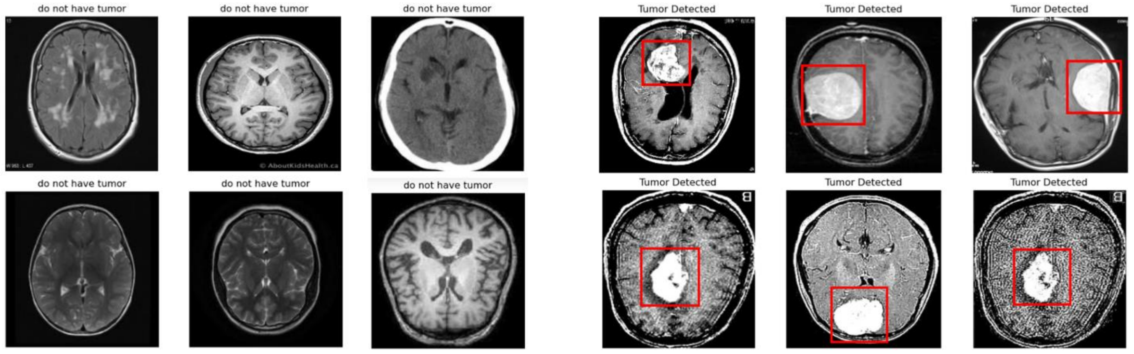
3.1. Assessment measures

Several evaluation techniques are used to evaluate how this study performed, including precision in segmentation, dice score, and model loss. These measures comprehensively assess segmentation performance, taking into account factors like as overlap, false positives, and false negatives. Segmenting precision is a commonly used measure in image segmentating that quantifies the effectiveness of the method by determining the percentage of correctly identified pixels. It provides a direct assessment of the accuracy with which the method assigns correct labels to individual pixels. The dice score, which ranges from 0 to 1, measures the agreement between the predicted and actual segmentation masks. It takes into account false positives and false negatives, and is less affected by class imbalance than segmentation accuracy, making it valuable for medical image segmentation.

3.1.1. Tumor classification results

We used the suggested advanced CNN model for brain tumor classification, picking MRI pictures at random. The results of the brain tumor classification are displayed in Figure 4. The figure offers a visual display of the result and shows the execution of classification model. In Figure 4(a), no tumor detected and Figure 4(b) tumor detected. It provides thorough insights into the model's efficacy and accuracy in correctly categorizing brain cancers.

Figure 5 shows the outcomes for training loss, validation loss, training accuracy, and validation accuracy. In Figure 5(a), the number of epochs on the x-axis, while the accuracy value on the y-axis that changes with each epoch. Figure 5(b) illustrates the relationship between the number of epochs and the loss value. The model loss graph shows a consistent decrease in loss for both the training and test sets, indicating the model's improvement in minimizing errors. Although there is a noticeable increase in test loss in the middle of the training phase, the overall trend of decreasing loss suggests that the model is successfully learning and refining its ability to predict and approximate the desired outcome. Despite occasional fluctuations, the general downward pattern confirms the effectiveness of the training process.

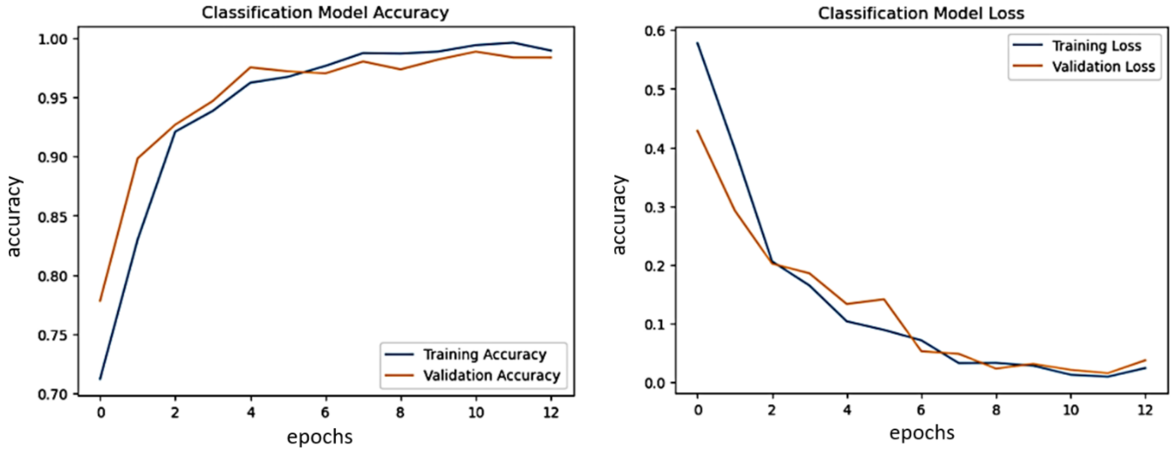


(b) (b)

Figure 4. Classification of brain tumor results (a) no tumor detected and (b) tumor detected

3.1.2. Tumor segmentation results

For the segmentation task in this work, a UNet-based architecture was used a CNN created especially for segmenting images, particularly in the area of analysis of medical images, is the UNet model. It is now widely used as a popular framework for many image segmentation tasks. Its two paths, a contraction path and an expansion path, allow this comprehensive architecture to capture fine specifics while maintaining geographical data. By randomly selecting MRI images, we applied the proposed U-Net-based approach for segmenting brain tumors. The qualitative results, shown in Figure 6, clearly illustrate that this approach performs better than other approaches currently in use for precise tumor segmentation. The visual evidence presented in the figure emphasizes the superior performance of our approach in precisely delineating tumor boundaries and accurately capturing the tumor region. The findings for training precision, validation accuracy, training loss, and validation accuracy are shown in Figure 7. The accuracy value, which varies with each epoch, is shown by the y-axis in Figure 7(a), while the x-axis shows the number of epochs. The connection between the number of epochs and the associated loss value is displayed in Figure 7(b).



(a) (b)

Figure 5. Accuracy of classification model performance (a) number of epochs on the (x, y) axis and (b) relationship between number of epochs and loss value

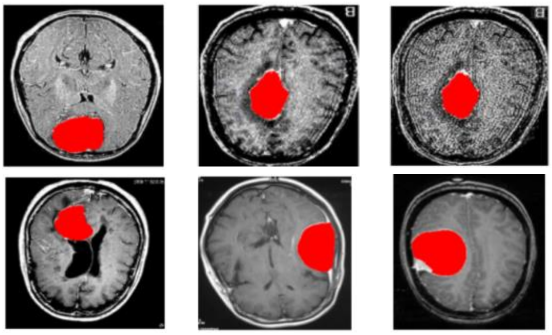
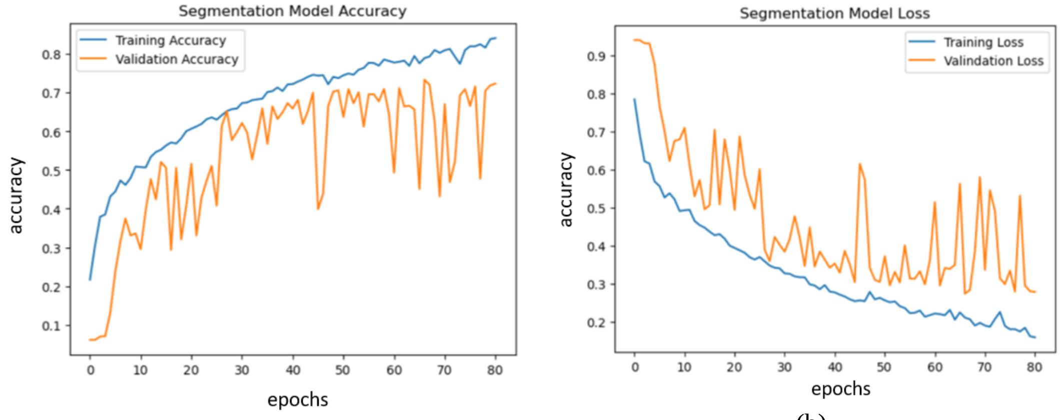


Figure 6. Results of brain tumors predicted segmentation



(a) (b)

Figure 7. Accuracy of segmentation model performance (a) epoch accuracy value and (b) relationship between the number of epochs and the loss value

3.2. Discussions

In this part, a detailed comparative evaluation is conducted between the development methodologies in this aproach and those explored in other research studies. To facilitate a meaningful comparison, a comprehensive table is provided, which includes various methods, including the proposed approach, that have undergone rigorous comparative testing and analysis. This approach provides a fair and consistent evaluation platform for all techniques, enabling an objective assessment of their relative performance in classifying brain tumors. The performance of the suggested model is assessed by contrasting it with recent studies in the field, and the summarized results of these comparisons are presented in Table 4. Based on the results of this experiment, the suggested method used the Adam optimizer to get the greatest classification accuracy of 99.50 for learning rate 0.001. Therefore, the Adam optimiser with learning rate 0.001 was adopted in this work. Furthermore, this study's objective is to ascertain the ideal amount of iterations. Consequently, tests with various epoch counts were conducted, along with assessments of the system's overall accuracy for various epoch counts. The resultant performance (accuracy) is visually presented in Figure 8, where the performance of proposed architecture is compared with several existing methods.

Table 4. Comparative evaluation: proposed method vs. other models

Method	Classifier	Accuracy %
Abdullah *et al.* [18]	SVM	97.8
Xu *et al.* [20]	InceptionV3	99
Awasthi *et al.* [19]	3 different CNN	99.33, 92.66, 98.14
Shelatkar and Bansal [21]	SVM	93
LeCun *et al.* [22]	Shallow neural networks (MLP)	86.82
Vu [3]	K-means + ResNet50	75
Proposed method	CNN	99.5

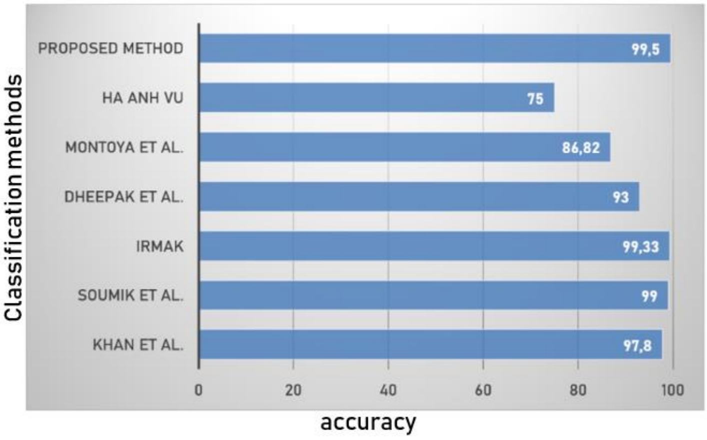


Figure 8. Classification accuracy comparaison

After conducting a quantitative assessment on the training datasets, it was found that The suggested system operated well and achieved satisfactory results. The rendering metrics were achieved at similar heights, indicating the effectiveness of the system. The obtained dice overlap, which evaluate the similarity between the predicted and ground truth masks, reached 70% after applying filtering enhancement steps. In addition, the binary accuracy score, which evaluates the percentage of correctly classified samples, reached an impressive 98% as shown in Table 5. These results indicate the success of the suggested segmentation framework. The improvement presented in the training of MRI scans significantly enhanced the U-net training process, resulting in improved performance and higher accuracy.

Table 5. Performance of U-Net based method

The proposed method based on U-Net		
Dice coefficient	Binary accuracy	Model loss
0.70	0.98	0.30

This comparative analysis shows that the overall accuracy is greatly improved when CNN-based feature extraction is used. Although CNN-based techniques have also been used in state-of-the-art methods, Issues like excessive resource consumption, training loss, and high computational complexity have plagued these methods. In contrast, the suggested approach trains the CNN model and effectively extracts dependable features using transfer learning. The results of this work show that the sophisticated approach for reliable and accurate brain tumor identification and segmentation is feasible. Future studies could look into how different feature fusion methodologies and fine-tuning methods affect the functionality of this model.

4. CONCLUSION

This research focuses on exploring the application of deep learning models, specifically using preprocessing techniques in conjunction with CNNs. The proposed CNN architecture has demonstrated its effectiveness in accurately classifying and detecting brain tumors by analyzing patterns in medical images that indicate the presence of tumors. The model consists of 5 convolutional layers and achieves an average accuracy of 99.5%. This paper offers a fresh perspective to MRI image segmentation for brain tumor detection. The proposed method aims to increase the segmentation accuracy of brain tumors by extending and refining the architecture based on the U-Net framework. This enriched and reliable architecture incorporates multimodal segmentation techniques, enabling more comprehensive and accurate detection of brain tumors. To address the constraints observed in this study, future research can explore several directions. The investigation of various feature fusion methods and fine-tuning approaches is an avenue worth exploring. Increasing the degree of model performance can be achieved by investigating various approaches to the objectives, such as using reinforcement learning techniques. For the greatest results, these can involve applying sophisticated algorithms, building new neural network machines, or adjusting the current model design.

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