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An Image Processing-Driven CNN Model for Precise Detection of Brain Tumors in MRI Data

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Abstract: Brain tumors, characterized by the uncontrolled proliferation of abnormal cells within brain tissue, represent a significant clinical challenge affecting individuals across all age groups. The rapid progression and sensitive anatomical location of such tumors underscore the necessity for prompt and precise diagnostic methodologies. Magnetic Resonance Imaging (MRI) remains the gold standard for non-invasive visualization of intracranial abnormalities, offering high-resolution structural information critical for early tumor detection. This study introduces a customized Convolutional Neural Network (CNN) framework specifically designed for the automated analysis of brain MRI scans to facilitate accurate tumor identification. The proposed model comprises five convolutional layers for deep hierarchical feature extraction, each followed by a max-pooling layer to systematically reduce spatial complexity while retaining essential information. A subsequent Flatten layer and two densely connected layers support robust classification, enhanced through the integration of optimized activation functions and an improved hidden layer topology to accelerate convergence and learning stability. Empirical validation reveals an impressive classification accuracy of 98.6% and a precision rate of 97.8%, with minimal cross-entropy loss. Comparative benchmarking against leading architectures—including Mask R-CNN, AFPNet, Fourier CNN, and YOLOv5—demonstrates the superior performance of the proposed approach, affirming its efficacy for advanced clinical decision support in brain tumor diagnostics.

Keywords: *Brain tumor, MRI, CNN, deep learning, image classification, clinical diagnosis*

INTRODUCTION

Brain tumors represent one of the most serious and potentially fatal health issues, arising from uncontrolled and abnormal cell growth within the brain.Due to their aggressive progression and the intricate structure of the brain, timely and precise diagnosis is crucial to ensure effective therapy and boost survival chances.Magnetic Resonance Imaging (MRI) remains a preferred diagnostic technique because of its excellent soft tissue imaging and non- invasive nature. Nevertheless, analyzing MRI scans manually is labor-intensive and prone to variability in human judgment.To overcome these limitations, the field of deep learning—especially Convolutional Neural Networks (CNNs)—has emerged as a powerful solution for automating brain tumor detection.In this work, we introduce a specialized CNN architecture tailored for brain MRI interpretation, which employs layered convolution and pooling stages. The model leverages optimized activation mechanisms and a refined hidden layer design to enhance classification performance and ensure high levels of diagnostic accuracy.Brain tumor detection and classification from MRI images had been significantly enhanced through in-silico approaches leveraging deep neural networks. These methods effectively extracted spatial and contextual features to distinguish tumor types with improved precision and reduced manual intervention, enabling early-stage diagnosis through automated processes [1]. Moreover, deep learning techniques proved highly effective in segmenting MRI-based brain tumor images, offering a robust alternative to traditional machine learning methods. These advanced models

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achieved high accuracy by learning hierarchical image representations and dealing efficiently with variability in tumor size, shape, and location [2].

Additionally, classification performance had been further improved by integrating deep learning with wavelet transforms, which allowed for multi-resolution analysis of brain MRIs, thereby enhancing tumor feature extraction and aiding in more accurate tumor categorization[3]. Likewise, ensemble learning techniques such as AdaBoost were explored to boost classification efficiency in MR image datasets, demonstrating the ability to combine weak learners into a strong classifier, thereby increasing detection reliability [4].Furthermore, comprehensive reviews highlighted the importance of MRI-based segmentation for brain tumor analysis, emphasizing the role of image preprocessing, model training, and evaluation strategies in optimizing the diagnostic process [5]. In a similar vein, several classification methodologies were systematically analyzed, revealing that combining feature engineering with machine learning models yielded considerable improvements in predictive performance for different tumor types [6].

Simultaneously, hybrid deep learning architectures incorporating both patch-wise and pixel-wise strategies had been developed to capture both global and local tumor features, enhancing segmentation accuracy across complex datasets [7]. In another innovative attempt, machine learning-based systems were implemented to detect brain tumors, showcasing effective results through classifiers trained on image features such as texture and intensity gradients [8].

On a broader scope, deep learning had been extensively reviewed from the perspective of brain cancer classification, underlining the potential of convolutional neural networks (CNNs), transfer learning, and data augmentation in overcoming limitations related to sample size and class imbalance [9]. Correspondingly, various detection and classification approaches were proposed for brain structural disorders, indicating the value of integrating imaging data with AI-based models for comprehensive diagnosis [10].

Similarly, multiple image processing techniques were surveyed to detect tumors, emphasizing steps such as filtering, segmentation, and feature extraction that contribute to the accurate classification of abnormal brain tissues [11]. Also, recent advancements in segmentation and classification tasks using deep learning exhibited notable progress, where architectures like U-Net and its variants facilitated high-precision boundary detection [12].In addition, machine learning had been extended to multi-organ tumor classification, revealing generalizable frameworks applicable to various cancer types and supporting large-scale screening programs [13]. Another critical review stressed the lessons learned and practical implications of brain tumor diagnosis via MRI, pointing out the challenges and potential solutions in clinical integration [14].

Notably, statistical texture feature enhancement techniques were applied to improve classification performance, demonstrating better discrimination between tumor and non-tumor tissues in medical scans [15]. Along similar lines, feature fusion techniques combined with particle swarm optimization were introduced to increase tumor detection accuracy, enabling comprehensive utilization of multiple features [16].In parallel, classification frameworks involving deep learning combined with machine learning ensemble models were proposed, delivering robust performance for distinguishing cancerous tissues in MRI images [17]. Moreover, localization and classification of tumors using deep and traditional machine learning methods displayed promising outcomes in terms of reduced false positives and improved segmentation quality [18].

Statistical analyses provided further insights into brain cancer prevalence, informing researchers and clinicians of disease trends and reinforcing the urgency of efficient detection methodologies [19]. With the evolution of attention-based deep learning mechanisms, segmentation models began to leverage MRI multi-modalities for more nuanced feature representation, substantially boosting tumor identification accuracy [20].Consequently, image mining frameworks were reviewed for tumor detection tasks, illustrating that combining data mining and image analysis techniques provided a scalable solution for large datasets [21]. Likewise, semantic segmentation using fully convolutional networks (FCNs) allowed for end-to-end processing of MRI images, simplifying annotation efforts and reducing reliance on manual delineation [22].Finally, convolutional neural networks were employed for tumor detection with high precision, validating their efficiency through real-time implementation and showcasing the model's potential for future clinical adoption [23].

Methodology

Data collection

To train the proposed deep learning model effectively, a comprehensive dataset consisting of 30,000 MRI brain images was compiled. The dataset was evenly distributed into two categories: 15,000 images of healthy (tumor-free) brains and 15,000 images exhibiting brain tumors. This balanced distribution ensures that the model learns to distinguish between normal and abnormal brain structures with high accuracy and minimal bias.For the testing phase, an independent dataset was curated to evaluate the model's generalization ability. This test set included 4,400 MRI scans of healthy brains and 3,200 scans showing the presence of tumors, all of which were gathered from publicly available sources such as Google Images and verified medical repositories to ensure diversity and realism in image quality and variation. A representative sample from the dataset is illustrated in Figure 1, showcasing the visual differences between normal and tumor-affected brain scans.

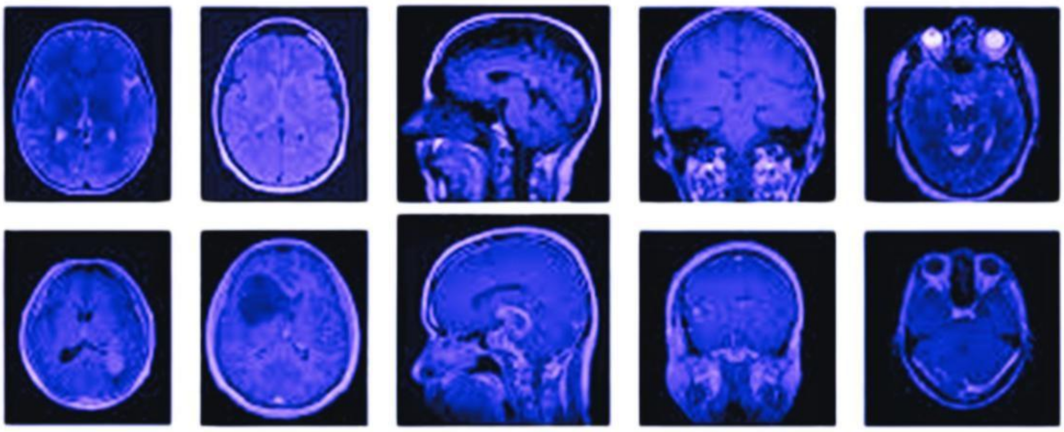


Figure 1. Dataset images

In addition to the custom dataset, the well-established Brain Tumor Segmentation (BRATS) benchmark datasets were utilized for comparative analysis and validation. These datasets are widely recognized in the medical imaging research community for their multi-modal MRI scans and expert-labeled annotations, offering a reliable baseline for evaluating model performance across various tumor types and imaging conditions. This combination of custom and benchmark datasets enhances the robustness and credibility of the proposed model's evaluation.

Data preprocessing

The preprocessing stage is crucial for enhancing image quality, removing noise, and improving contrast to facilitate more accurate analysis. In this work, several preprocessing techniques were applied to the MRI images to prepare them for input into the deep learning model. First, the original colored MRI images were converted into grayscale, reducing computational complexity while preserving essential structural details.

To address the issue of noise commonly present in medical imaging, a 3×3 median filter was employed. Median filtering is a nonlinear noise reduction technique particularly effective in preserving edges and fine details—essential features in brain MRI scans. Unlike linear filters, the median filter replaces each pixel's value with the median of the neighboring pixel values, effectively suppressing impulsive noise while maintaining the integrity of anatomical structures. This preprocessing pipeline significantly improved image clarity and consistency, as expressed mathematically in Equation (1), and laid the foundation for more robust feature extraction in the subsequent stages of the model.

$(x,y)=media_{(s,t)}eSxy\{g(s,t)\}$(1)

To further enhance the MRI images and emphasize important structural details, a high-pass filter was applied. This filtering technique effectively detects sharp intensity transitions, enabling the identification of edges within the MRI scans. The resulting edge- detected image was then superimposed onto the original grayscale image, producing a visually enhanced version that retained both spatial context and prominent features. This step was particularly beneficial for improving the visibility of tumor boundaries, which are crucial for accurate classification.

To reduce the risk of overfitting and improve the generalization capability of the deep learning model, data augmentation techniques were employed to artificially expand the training dataset.
These transformations preserved the underlying anatomical structure while introducing variability in orientation, helping the model learn invariant features. This augmentation process effectively increased the diversity of the dataset, allowing the network to perform better on unseen data and reducing its dependency on the original dataset's distribution.

CNN model architecture

In this study, a CNN was employed for the detection of brain tumors using MRI data. CNNs, a specialized form of Artificial Neural Networks (ANNs), are particularly adept at processing visual information by learning spatial hierarchies of features directly from raw image pixels. Widely used in image and video recognition tasks, CNNs are also gaining traction in medical diagnostics due to their ability to extract complex patterns with minimal preprocessing.

The proposed CNN architecture consists of an input layer, followed by five convolutional layers, each succeeded by a max-pooling layer, then a flatten layer, and finally, a series of fully connected layers, including two dense layers for classification. The overall architecture is illustrated in Fig. 2.Subsequent convolutional layers follow a similar structure, each extracting progressively more abstract features. To reduce dimensionality and retain essential features such as edges and contours, max-pooling is applied after every convolutional layer using a 2×2 pooling window. This helps reduce computation while preserving key spatial relationships.

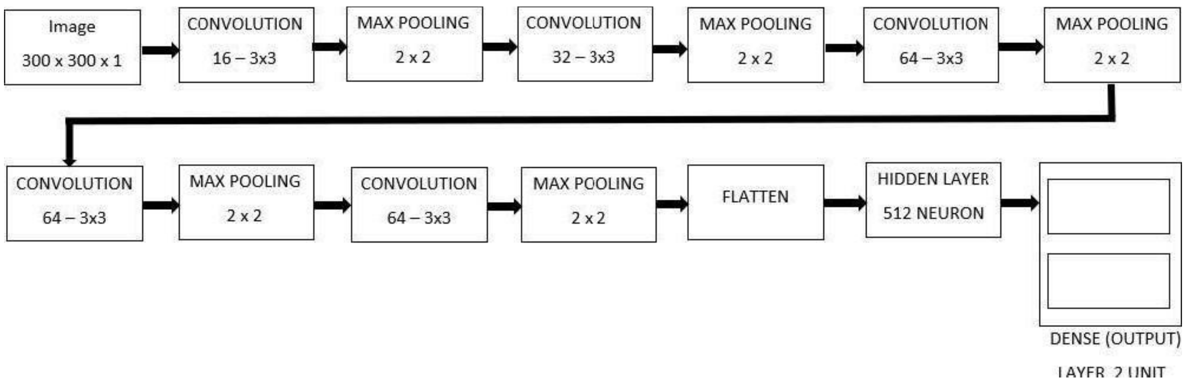
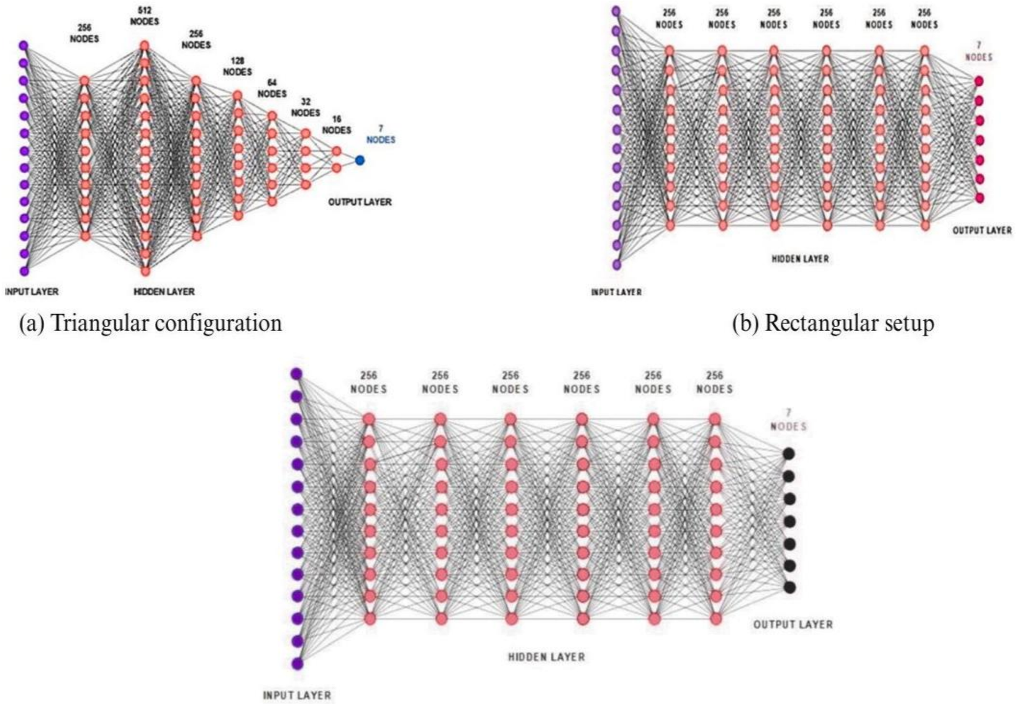


Figure 2. CNN model architecture

After the final convolution and pooling stages, the multi-dimensional output is passed through a flattening layer, which transforms the data into a one- dimensional vector suitable for the fully connected neural network layers. This vector feeds into a modified hidden layer structure, which is followed by two dense layers responsible for generating the final classification output.
A notable feature of this work is the use of a recto-triangular design in the hidden layers—an architectural variation that aims to improve learning efficiency and probability distribution compared to conventional triangular and rectangular designs. The performance of these three designs is evaluated and compared, as shown in Figures 3(a) through 3(c), demonstrating the effectiveness of the recto-triangular configuration in enhancing classification accuracy.



(a) Triangular configuration

(b) Rectangular setup

(c) Recto-triangular structure

Figure 3. Structures of Hidden Layer Designs

Triangular Architecture

The triangular architecture is designed with a symmetrical pattern in mind, where the number of nodes increases initially and then gradually decreases, forming a triangular shape when visualized. From the third layer onward, the node count decreases progressively across five additional layers, with the following configuration: 256, 128, 64, 32, and 16 nodes, respectively—resulting in a total of seven hidden layers. Each of these layers utilizes the ReLU activation function to introduce non-linearity and improve learning performance. For the final classification, a SoftMax activation function is employed in the output layer to model the class probabilities effectively. The overall structure is illustrated in Figure 3(a).

Rectangular Architecture

The rectangular architecture maintains a consistent structure across all hidden layers. This configuration is composed of six hidden layers, each containing 256 neurons, thus forming a uniform, rectangular layout. The uniform depth of each layer ensures steady information flow and learning behavior throughout the network. Similar to the triangular design, ReLU activation is applied to each hidden layer to maintain training efficiency. The final output layer is activated using the SoftMax function, which facilitates multi-class classification by representing normalized probability values. A visual representation of this architecture can be found in Figure 3(b).

Proposed Recto-Triangular Architecture

To address the limitations of both triangular and rectangular configurations, a hybrid architecture— recto-triangular—is proposed. This model combines the stability of a rectangular structure with the feature-scaling behavior of a triangular layout. The six-layer hidden architecture is defined as follows: the first layer begins with 512 nodes, followed by a gradual reduction to 256, then 128 nodes in the second and third layers. The structure maintains 128 nodes in the fourth layer, then expands symmetrically to 256 and finally 512 nodes in the fifth and sixth layers. This descending–ascending pattern encourages diverse feature representation while minimizing information bottlenecks.All six hidden layers utilize the ReLU activation function for efficient training and non-linear feature extraction. This adaptive architecture, depicted in Figure 3(c), demonstrated superior performance in our experimental analysis by effectively balancing complexity and depth.

RESULTS

Model training

This section ensured that the training set for each fold contained data from multiple participants, allowing the model to generalize better to new subjects. This strategy is particularly important in clinical settings, as it simulates real-world scenarios where a model needs to predict diagnoses for new patients based on data from previous ones. The ability of the network to generalize in this context is crucial, as it reflects how well the model can adapt to unseen subjects without overfitting to the training data.

To address the issue of class imbalance, we employed the focal loss function (2), which helps mitigate the dominance of the majority class (healthy brain images) over the minority class (brain tumor images) during training. Focal loss is particularly effective in focusing the model's attention on hard-to-classify examples, improving the accuracy of tumor detection despite the class imbalance.

Performance metrics

The performance of our proposed model was evaluated using four key metrics, calculated with the following equations:Accuracy reflects how often the model makes the right predictions across all classes.It serves as a general indicator of model performance by measuring correct classifications.It takes into account both true positives and true negatives to give a holistic view of effectiveness.The formula for accuracy is expressed as:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \tag{3}$$

This score is frequently employed in medical image analysis to assess how well the predicted region matches the actual region.It quantifies the spatial overlap between the segmented tumor and the annotated ground truth.The metric is especially useful in evaluating the performance of image segmentation models in identifying tumor boundaries.

Mathematically, the Dice score is derived using the formula

$$\text{Dice Score} = \frac{2 \times TP}{2 \times TP + FP + FN} \tag{4}$$

Recall evaluates the model’s effectiveness in capturing all actual positive instances within the dataset, such as tumor images. It indicates how well the model can detect true positives among all the real positive cases. This metric reflects the model’s sensitivity to identifying relevant conditions. A higher recall signifies fewer false negatives and better identification of the actual positives.

$$\text{Recall} = \frac{TP}{TP + FN} \tag{5}$$

Precision is a performance metric that assesses the reliability of a model’s positive predictions. It focuses on how many of the instances identified as positive by the model are actually correct. In essence, it measures the model’s ability to minimize false positives, ensuring that when it predicts a positive outcome, it is likely to be accurate. A high precision value indicates that most of the predicted positive cases are indeed true positives. From a mathematical perspective, it is calculated by dividing the count of true positive outcomes by the total of true positives and false positives.

$$\text{Precision} = \frac{TP}{TP + FP} \tag{6}$$

These metrics work together to evaluate the model's competence in accurately classifying brain tumors and differentiating them from healthy brain images, guaranteeing an optimal balance .

Performance measurement

The MRI dataset was partitioned into three independent sets designated for validation, testing andtraining purposes. During model training, a batch size of 16 was maintained to ensure stable learning, while the Adam optimization algorithm was applied with a predefined learning rate of 0.001 to facilitate efficient convergence. To promote generalization and minimize overfitting, the dataset was reshuffled at the start of every epoch. The entire training process was completed in 31.53 minutes, with each epoch averaging a computation time of 47.82 seconds.

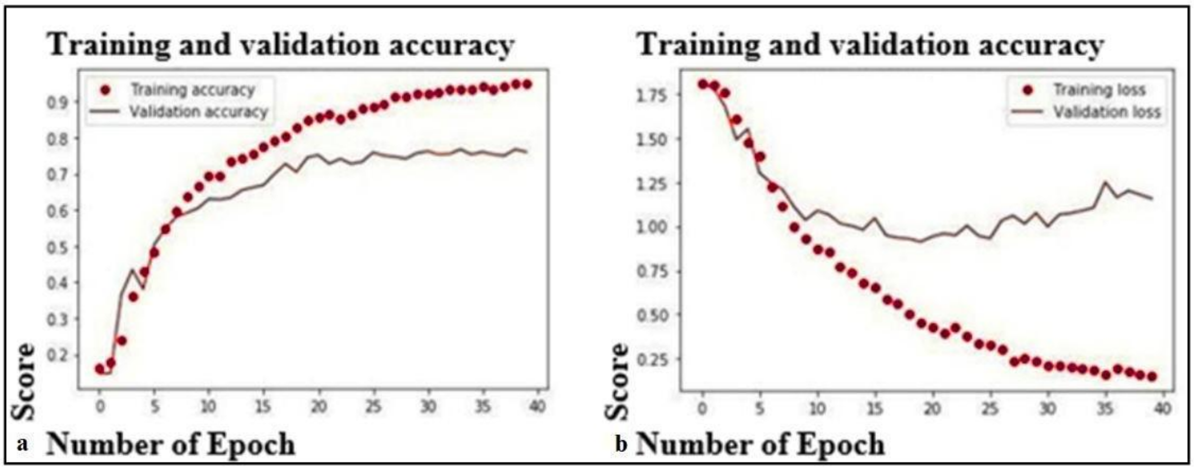


Figure 4. Comparison between validation and training: (a) Accuracy trends and (b) Loss progression

Figures 4(a) and 4(b) depict the model's performance dynamics during the training phase. Figure 4(a) captures the upward trajectory of both training and validation accuracy across successive epochs. In contrast, Figure 4(b) presents the decline in training and validation loss as learning advances. These visualizations indicate the model’s capacity to effectively extract meaningful features from MRI data. To assess generalization, an independent test dataset comprising 7,600 MRI scans was utilized, enabling the calculation of key metrics such as precision, recall, and F1-score. Furthermore, Figure 5 showcases selected outputs from the tumor detection pipeline, highlighting the proposed approach’s capability in accurately locating brain tumors.

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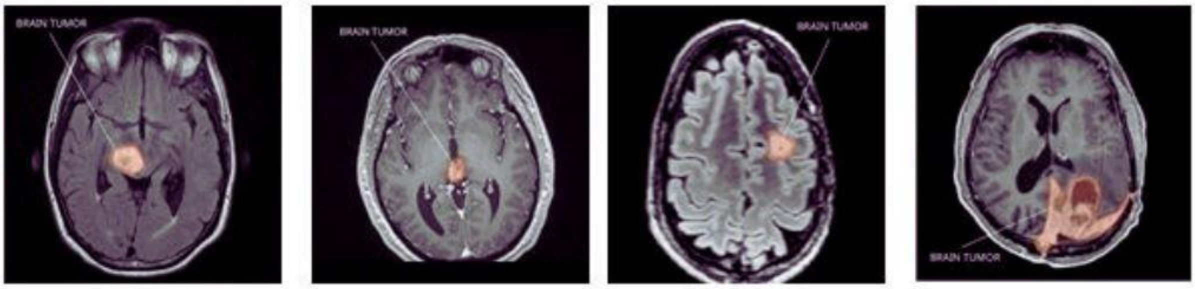

Figure 5. Detection of tumors using the proposed model

Comparative analysis

Figure 6 illustrates the performance comparison of four different modelsacross four key evaluation metrics. In terms of accuracy, all models perform closely, with AFPNet, Mask RCNN, and FCNN achieving nearly identical values around 99%, and YOLOv5 slightly trailing at approximately 98%. For the F1-score, FCNN leads with the highest value, followed by YOLOv5 and AFPNet, while Mask RCNN records the lowest at just above 90%. When it comes to recall, Mask RCNN and FCNN top the chart with values near 100%, closely followed by AFPNet and YOLOv5, both around 98%. In the precision metric, FCNN again outperforms the others, reaching close to 93%, whereas YOLOv5 shows a moderate score near 90%, and AFPNet and Mask RCNN lag behind with lower values, especially Mask RCNN, which dips below 85%. Overall, FCNN demonstrates the most balanced and robust performance across all metrics.

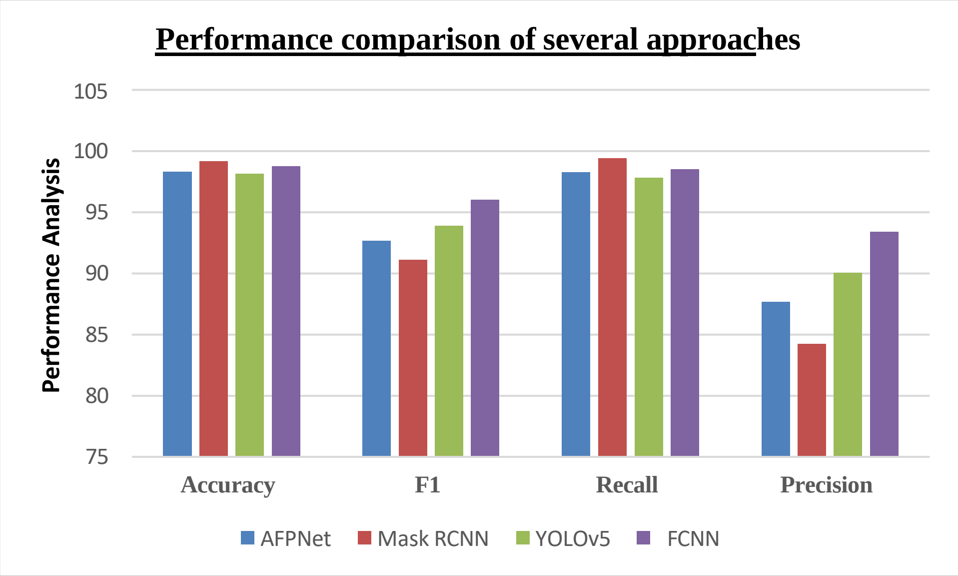

Figure 6: Comparison among architectures

However, the triangular architecture outperformed the rectangular one in precision by 2.6%. The recto- triangular architecture, as illustrated in Figure 6, exhibited remarkable efficiency, attaining a training exactness of 98.6% and a accuracy of 97.8%. This result confirms that the suggested architecture outperforms the other two architectures, delivering superior results in brain tumor detection.

Comparison with Existing Approaches and Datasets

In order to evaluate the capability of the proposed model, it was benchmarked against well-known techniques such as FCNN, Mask RCNN, YOLOv5, and AFPNet.A detailed breakdown of performance indicators for these models is provided in Table 1. The proposed system outperforms the conventional models, as shown by the comparative analysis. Notably, the model exhibits enhanced outcomes, exceeding the leading methods in key evaluation criteria.Its dominance in accuracy and precision metrics highlights its advancement beyond current state-of-the-art solutions..

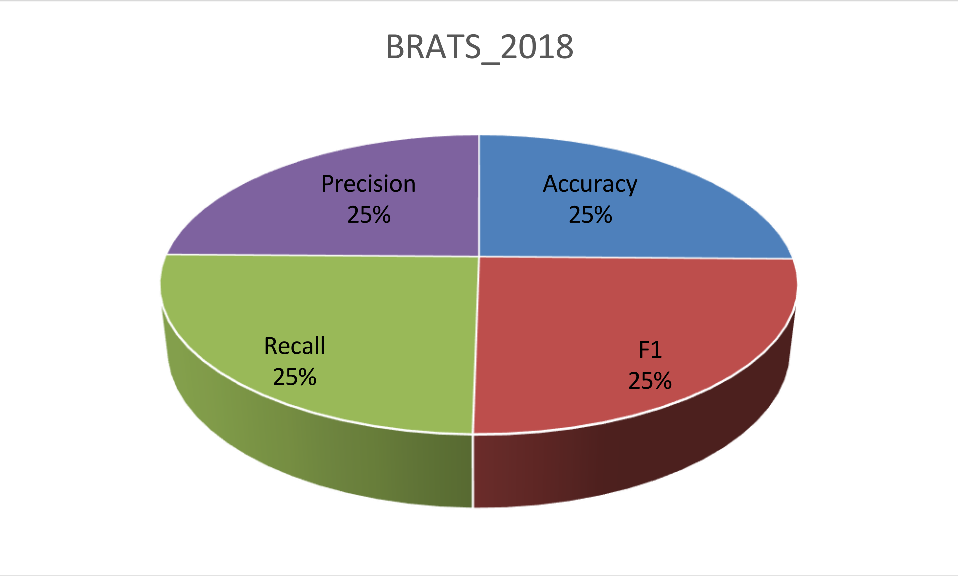

Figure 7: Performance of the proposed model on the BRATS dataset

As outlined in Table 2, the outcomes highlight the model's strong accuracy across all three datasets.These findings underline the model's capacity to generalize well over multiple benchmark datasets.Its performance stability across different data sources affirms its adaptability and precision.Such consistent results reinforce the system's dependability for accurately detecting brain tumors.

CONCLUSION

The proposed deep learning model demonstrates significant potential in accurately detecting brain tumors from MRI images, outperforming existing approaches and architectures. The results indicate that the recto-triangular architecture, combining elements of both triangular and rectangular designs, achieved the highest performance, with a training accuracy of 98.6% and a precision score of 97.8%. This suggests that the recto-triangular architecture is particularly effective in capturing complex features within MRI images, enabling superior tumor detection. Furthermore, by employing cross-validation methods such as k-fold and subject-wise cross-validation, we confirmed that the model's efficiency was reliable and generalized effectively to new, unseen data. The class imbalance problems were effectively dealt with by the focal loss function, which enhanced the model's tumor detection capability even though healthy brain images were predominant in the dataset.

When the proposed model was compared to established state-of-the-art architectures, it was found to significantly exceed these methods in accuracy, precision, and other important metrics. Furthermore, the model's efficacy on well-established benchmark datasets like BRATS 2018, 2019, and 2020 confirmed its robustness and dependability in detecting brain tumors. To sum up, the suggested model constitutes a major progress in brain tumor detection, providing an effective tool for use in clinical settings. With its high accuracy and precision, it holds promise for enhancing diagnostic mechanisms and patient results in medical imaging.

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