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Redefining brain tumor segmentation: a cutting-edge convolutional neural networks-transfer learning approach

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ABSTRACT

Medical image analysis has witnessed significant advancements with deep learning techniques. In the domain of brain tumor segmentation, the ability to precisely delineate tumor boundaries from magnetic resonance imaging (MRI) scans holds profound implications for diagnosis. This study presents an ensemble convolutional neural network (CNN) with transfer learning, integrating the state-of-the-art Deeplabv3+ architecture with the ResNet18 backbone. The model is rigorously trained and evaluated, exhibiting remarkable performance metrics, including an impressive global accuracy of 99.286%, a high-class accuracy of 82.191%, a mean intersection over union (IoU) of 79.900%, a weighted IoU of 98.620%, and a Boundary F1 (BF) score of 83.303%. Notably, a detailed comparative analysis with existing methods showcases the superiority of our proposed model. These findings underscore the model's competence in precise brain tumor localization, underscoring its potential to revolutionize medical image analysis and enhance healthcare outcomes. This research paves the way for future exploration and optimization of advanced CNN models in medical imaging, emphasizing addressing false positives and resource efficiency.

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1. INTRODUCTION

Brain tumors present a complex medical challenge that demands accuracy and efficiency in diagnosis [1]. This challenge is further compounded by the diverse morphology of brain tumors, spanning variations in shape, size, and intensity. With advancements in medical imaging technologies, particularly magnetic resonance imaging (MRI), there is an increasing opportunity to improve the precision of brain tumor detection. The accurate segmentation of brain tumors from MRI scans plays a pivotal role in early diagnosis [2]. However, manual segmentation methods are often time-consuming and prone to error [3], making the development of automated and precise segmentation techniques essential [4], [5].

Traditional methods relied on handcrafted features and classical machine learning algorithms [6], paving the way for early endeavors in deep learning for MRI detection. These techniques utilized texture and shape features like gabor filters, gray level co-occurrence matrices (GLCM), zernike moments, region, circularity, and wavelet transformations [7], [8]. Classifiers such as markov random field (MRF), artificial neural network (ANN), and support vector machine (SVM) achieved accuracy rates ranging from 75% to 98%, playing a vital role in tissue categorization [9]. Advanced features and techniques like combining Zernike moments with ANN-Gabor wavelets with SVM classifiers were explored, alongside experiments evaluating texture and shape features with naïve Bayes (NB) classifiers [10].

The advent of deep learning, particularly convolutional neural networks (CNNs), transformed MRI classification in brain tumor detection. However, early attempts with CNNs faced challenges due to limited sample sizes and overfitting risks. The nuances of MRI detection, including the diverse nature of brain tumors and dataset imbalances, added complexity to the quest for automated detection [11]. Proposing transfer learning from pre-trained CNNs addressed these issues, showcasing an initial architecture achieving an 84.19% accuracy in classification [12]. MRI detection encountered challenges in brain tumor variability and dataset imbalances. Researchers aimed to automate detection without manual segmentation, incorporating additional metrics (precision, sensitivity, and specificity) for accurate detection assessment.

Recent advances in deep learning, marked by innovative methods like capsule networks (CapsNets), deep residual networks (ResNets), and inception models, have reshaped brain tumor detection. Integration of multiple architectures, novel approaches, and ensemble techniques addressed spatial boundary complexities in segmentation [13]. However, the journey towards optimal brain tumor segmentation persists, with the application of asymmetric and symmetric network architectures, novel loss functions, and knowledge exchange strategies [14], [15]. These developments highlight the continuous evolution of medical image analysis, steering towards enhanced accuracy and efficiency.

In response to these challenges, our study introduces ensemble CNNs with transfer learning, integrating the Deeplabv3+ architecture with the ResNet18 backbone to redefine the landscape of brain tumor segmentation. Deep learning has shown remarkable potential in automatically learning intricate patterns in complex data, and the concept of transfer learning, which adapts pre-trained CNN models [16], has emerged as a critical factor in enhancing their performance. Our research focuses on developing and implementing a CNN-transfer learning framework tailored explicitly to brain tumor segmentation. By harnessing the knowledge embedded in pre-trained models and fine-tuning them for tumor detection, we aim to significantly improve the accuracy and efficiency of brain tumor segmentation in medical practice.

This article unfolds as follows: section 2 presents our CNN-transfer learning framework's methodology, section 3 unveils experimental results, and section 4 provides a thoughtful conclusion with insights into future research directions. Our article aims to underscore the transformative potential of the CNN-transfer learning framework, promising a revolution in brain tumor detection and, by extension, the broader landscape of medical image analysis

2. METHOD

Our brain tumor prediction model relies on a robust deep learning architecture to harness the predictive power of CNNs and the knowledge transfer capabilities of transfer learning. We have tailored this architecture to excel in medical image segmentation, specifically for brain tumor localization. The core elements of this architecture include:

2.1. Data collection and preprocessing

Data quality and preprocessing are critical pillars in our brain tumor prediction and segmentation methodology. For this task, we sourced a dataset from Kaggle, curated by Nikhil Tomar [17]. This dataset consists of 3,064 MRI images, each paired with its corresponding ground truth image as shown in Figure 1. A subset of MRI images as shown in Figure 1(a) was randomly selected for visual inspection to ensure our data's uniformity and high quality. These images were overlaid with their corresponding ground truth masks as shown in Figure 1(b), a crucial step to verify proper alignment between the MRI and ground truth masks – a prerequisite for practically training our prediction

2.2. Base CNN model: ResNet18

Our ensemble CNN-transfer learning architecture [18] relies on the DeepLabV3+ with ResNet18 model, forming the backbone of our brain tumor prediction system. ResNet18, renowned for its deep architecture as shown in Figure 2 and residual connections, facilitates the direct transfer of information between layers, mitigating the vanishing gradient problem during training. With 18 layers, ResNet18 strikes an optimal balance between depth and capacity, enabling it to discern intricate patterns within medical images. Leveraging pre-trained knowledge from the ImageNet dataset, the model efficiently identifies pertinent features in medical images. Fine-tuning tailors the model to brain tumor segmentation, refining its capacity to make precise predictions. ResNet18's deep structure, residual connections, and pre-trained foundation make it a powerful choice for accurately identifying and segmenting brain tumors in medical images.

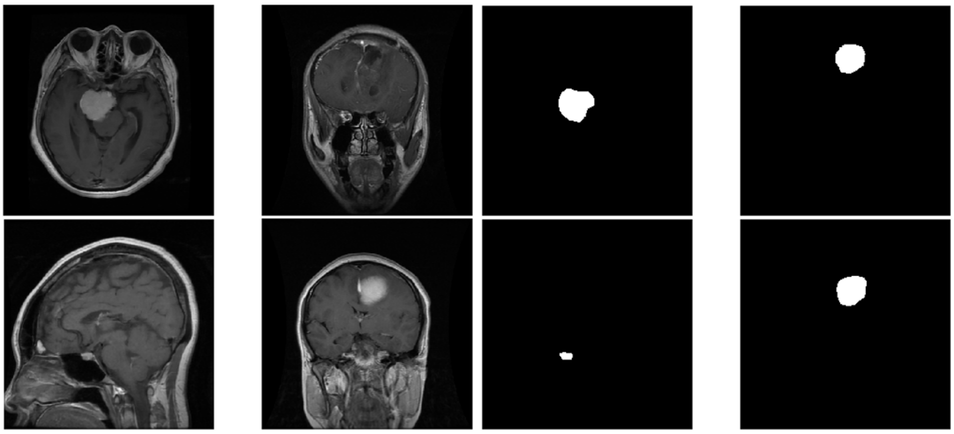

(a) (b)

Figure 1. Dataset of (a) MRI brain images and (b) the ground truth

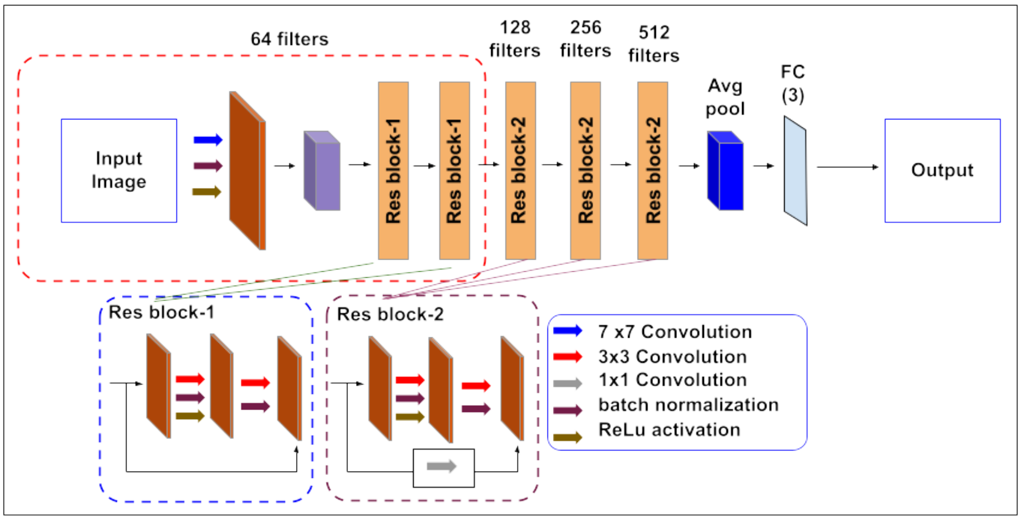


Figure 2. ResNet18 architecture for brain tumor segmentation

2.3. DeepLabv3+ layers and ensemble approach

The efficiency of our ensemble CNN-transfer learning system relies on the innovative architecture of DeepLabv3+, as shown in Figure 3. This model excels in semantic segmentation, emphasizing precise object boundary delineation crucial for medical image analysis [19]. Atrous or dilated convolution expands the receptive field without increasing parameters, ensuring accurate segmentation by capturing features from fine-grained to high-level details. Atrous spatial pyramid pooling (ASPP) and feature refinement modules enhance the model's proficiency in recognizing large and small tumor regions.

Our ensemble leverages multiple CNN outputs to enhance accuracy, particularly in complex tasks like medical image segmentation [20]. Blending ResNet18's feature extraction with DeepLabv3+'s architecture allows the ensemble to capture diverse features at different scales and resolutions. This strategic fusion ensures robust performance, mitigating overfitting risks and promoting generalization to new data. The ensemble achieves high accuracy, showcasing the adaptability of deep learning in medical image analysis.

2.4. Training, validation, and parameter configuration of segmentation

The training and validation phase is crucial for developing our brain tumor segmentation model, involving the meticulous partitioning of the dataset into training, validation, and testing subsets. The training dataset, which contains annotated brain MRI scans, is the foundation for instructing the model to identify tumor regions. Simultaneously, the validation dataset, which is kept separate during training, plays a pivotal role in performance monitoring, overfitting detection, and hyperparameter refinement.

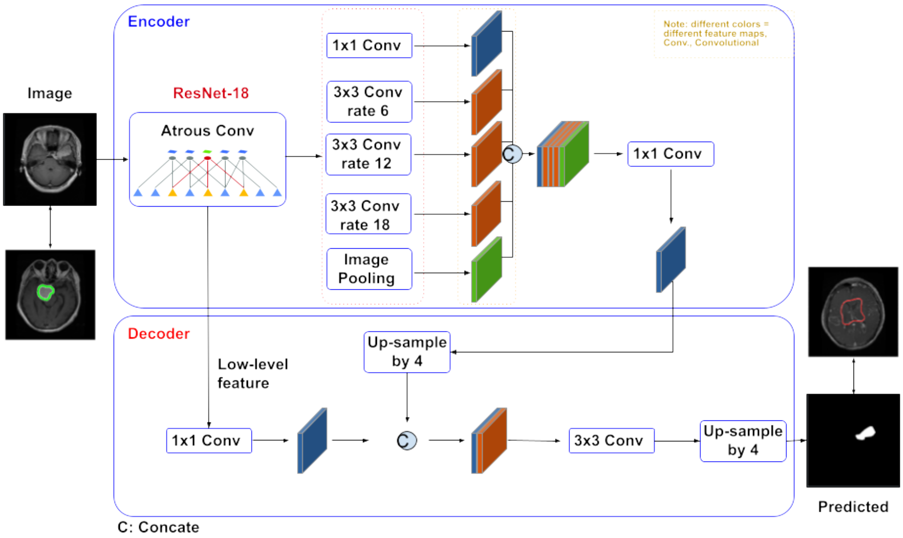


Figure 3. Ensemble CNN-Resnet18 architecture using DeepLabV3+ for brain tumor segmentation

The configuration of training parameters is vital for achieving optimal model performance, preventing overfitting, and ensuring efficient convergence [6]. Leveraging stochastic gradient descent with momentum (SGD) as the optimizer, we dynamically adjust model weights to minimize the loss function. Key parameters, including the learning rate and L2 regularization, are carefully tuned to prevent overfitting. Batch processing enhances training efficiency, and periodic evaluations on the validation dataset facilitate progress tracking. Early stopping ensures prompt conclusion if performance stagnates.

These meticulously adjusted parameters collectively contribute to a model achieving accuracy and robust generalization [6]. Post-training, the inference and segmentation phase marks the practical application of our trained model to previously unseen brain MRI scans. Pixel-wise segmentation maps are generated, aiding accurate diagnosis and treatment planning. This transformative capability showcases the substantial impact of deep learning in advancing medical imaging and healthcare.

2.5. Performance evaluation metrics

Our semantic segmentation model is assessed using key metrics [21]. Accuracy gauges overall classification performance by calculating the ratio of correctly classified samples to the total number ($Accuracy = \frac{(TP+TN)}{(TP+FP+TN+FN)}$). Precision focuses on correctly classifying positive samples, considering true positives and false positives ($Precision = \frac{TP}{(TP+FP)}$). Recall evaluates the model's effectiveness in identifying relevant instances, using true positives and false negatives ($Recall = \frac{TP}{(TP+FN)}$). The F-measure (F1 score), of dice coefficient, a balance of precision and recall, is computed as $F1 = 2x\frac{Precision x Recall}{(Precision+Recall)}$.

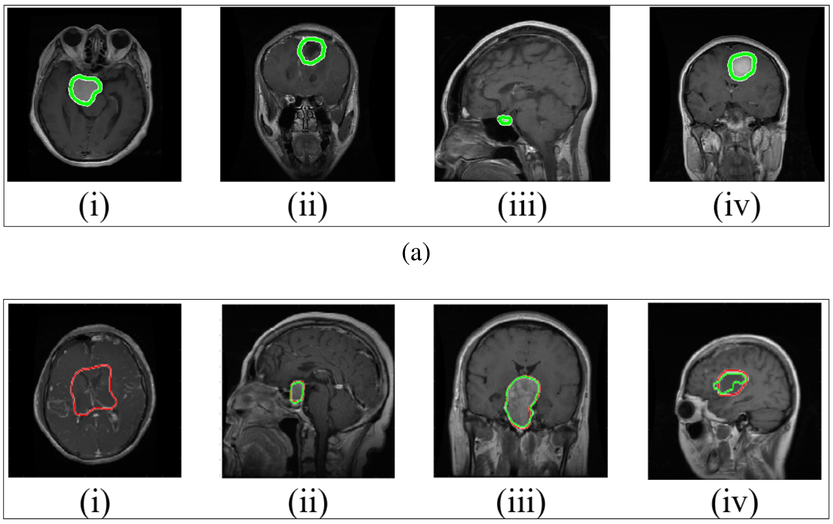
In addition, we utilize global accuracy for overall pixel correctness and mean accuracy for class-specific pixel accuracy, addressing imbalances. Finally, intersection over union (IoU) measures semantic segmentation by assessing the overlap between correctly classified pixels and the ratio of ground truth to predicted pixels. IoU values, ranging from 0 to 1, indicate the similarity between ground truth and model predictions.

3. RESULT AND DISCUSSION

This section outlines the methods employed in the proposed CNN-transfer learning framework for improved brain tumor detection and segmentation. This framework combines the power of convolutional neural networks (CNNs) with transfer learning to enhance the accuracy of MRI-based brain tumor classification and segmentation. The following subsections delve into the critical components of this approach.

3.1. Marker dataset creation and tumor detection (DeepLabv3+ with ResNet18)

This section outlines the creation of marker datasets and brain tumor detection using our ensemble CNN-transfer learning with Deeplabv3+ architecture with ResNet18 backbone. Figure 4 showcases foundational MRI datasets with green-marked tumor boundaries for training and testing. Following the modeling process, experiments with separate datasets as shown in Figure 4(a) reveal accurate tumor detection but precision variations against the ground truth as shown in Figure 4(b). In Figure 4(b), i) closely matches the ground truth, ii) and iii) show close approximations, and iv) exhibit perceptible deviations. Green lines represent the ground truth, and red lines signify model predictions.



(a)

(b)

Figure 4. Samples of (a) dataset with ground truth annotations and (b) segmentation prediction with red (prediction) and green (ground truth) comparisons

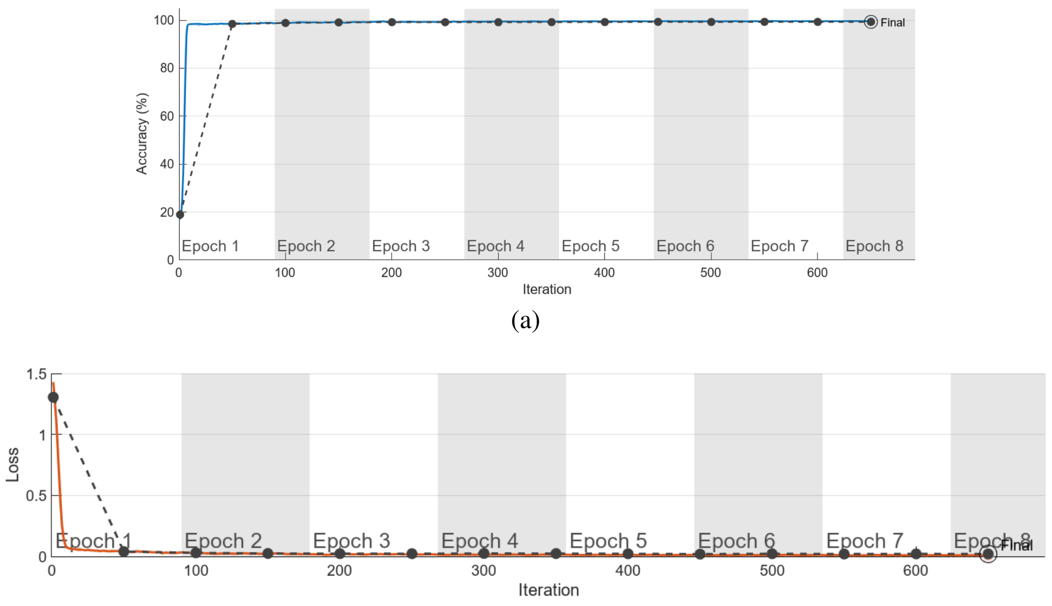
This nuanced analysis illuminates the method's overall effectiveness in brain tumor detection and provides valuable insights into specific areas that could benefit from refinement. The detailed examination of Figure 4(b) reveals the model's successes and underscores the imperative for ongoing fine-tuning to enhance segmentation precision. This emphasis on continuous improvement is particularly crucial when addressing the intricate challenges of certain tumor complexities. By recognizing and addressing these nuances, the model can evolve further, ensuring a more robust and accurate approach to detecting brain tumors in diverse scenarios.

3.2. Performance analysis based on model training and testing

This section comprehensively analyzes our brain tumor prediction model based on CNN-ResNet18. Rigorous training and testing procedures were implemented to ensure the model's accuracy and loss as shown in Figures 5(a) and 5(b). Throughout the training phase, the model exhibited consistent improvement over ten epochs, starting with a modest 15.38% accuracy during the initial epoch and achieving an impressive 99.72% accuracy by the tenth epoch as shown in Figure 6. This significant enhancement in training accuracy underscores the model's effectiveness in learning from the dataset, showcasing its proficiency in accurately detecting brain tumors.

The evolution of accuracy over the training epochs is graphically depicted in Figure 5(a). This visualization showcases the remarkable growth in accuracy, highlighting the model's learning capability as it becomes increasingly adept at identifying and classifying brain tumors. Additionally, Figure 5(b) provides insights into the loss graphs of the model during training. These loss graphs reveal how the model's error decreases as training progresses, emphasizing its ability to refine its predictions over time.

We utilized a normalized confusion matrix to assess the model's classification performance. This matrix provides valuable insights into the model's true positive and false positive rates for brain tumors and background regions. The confusion matrix as shown in Table 1 illustrates the percentages of predicted brain tumors correctly identified (64.5%) and the correctly classified background regions (99.69%). It also indicates that false positives are minimal (0.1134%), signifying the model's precision in classifying non-tumor regions. The confusion matrix suggests several vital observations: high true positive rate, low false negative rate, low false positive rate, and high true negative rate. These observations collectively affirm the model's effectiveness in classifying tumor and non-tumor regions exactly.



(a)

(b)

Figure 5. Training progress (a) accuracy graph and (b) loss graphs

The semantic segmentation results as shown in Table 2 offer crucial insights into the model's accurate prediction of brain tumor regions across two experiments, emphasizing its exceptional proficiency. Metrics, including global accuracy, Mean Accuracy, Mean IoU, Weighted IoU, and Mean BF-Score, showcase the model's consistent and accurate predictions, highlighting its precision in delineating tumor regions and preserving fine-grained details. The remarkable global accuracy of 0.99286 in the first experiment and 0.97480 in the second, along with Mean Accuracy scores of 0.82191 and 0.95860, reflect the model's pixel-wise precision. Mean IoU scores of 0.79900 and 0.93403 demonstrate significant overlap with ground truth regions, while Weighted IoU scores of 0.98620 and 0.95089 highlight the model's versatility in handling class imbalances. Notably, Mean BF-Score values of 0.83303 and 0.91239 underscore the model's exceptional capability in preserving fine-grained tumor details crucial for medical image segmentation, providing valuable evidence of the model's effectiveness.

Table 1. Confusion matrix of segmentation results

Predicted brain tumor	Predicted	Background
True brain tumor	64.5	33.5
True background	0.1134	99.89

Table 2. Performance of semantic segmentation results

Experiment	Global accuracy	Mean accuracy	Mean IoU	Weight IoU	Mean BF-Score
1^{st}	0.99286	0.82191	0.79900	0.98620	0.83303
2^{nd}	0.97480	0.95860	0.93403	0.95089	0.91239

3.3. Comparison with other methods

The performance of our ensemble CNN-transfer learning model in brain tumor segmentation is thoroughly examined in this section. Performance metrics, including dice coefficient (0.91239), mean IoU (0.93403), and accuracy (0.97480), highlight the model's exceptional accuracy and proficiency in tumor segmentation. Our model demonstrates superior performance compared to alternative methods in Table 3, such as cascaded dual-scale LinkNet and segnet-VGG-16. The proposed method has a dice coefficient of 0.91239, indicating precise spatial overlap between predicted and ground truth. Its high Mean IoU of 0.93403 reflects a substantial alignment between predicted and ground truth, highlighting the model's proficiency in delineating tumor boundaries accurately. Moreover, the accuracy score of 0.97480 emphasizes the model's effectiveness in overall classification, showcasing its ability to distinguish between tumor and non-tumor regions with reliability.

Table 3. Comparison of proposed methods with others

No	Methods	Dice coefficient	Mean IoU	Accuracy
1	Proposed method	0.91239	0.93403	0.97480
2	Cascaded Dual-Scale LinkNet [22]	0.8003	0.9074	-
3	Segnet-VGG-16 [23]	0.9314	0.914	0.9340
4	2D-UNet [24]	0.8120	-	92.16
5	CNN with LinkNet [25]	0.73	-	-
6	U-Net with adaptive thresholding [26]	0.6239	-	0.9907
7	O2U-Net [27]	0.8083	-	0.9934
8	CNN U-Net [28]	-	0.8196	0.9854

While competing approaches, including cascaded dual-scale LinkNet and 2D-UNet, demonstrate respectable metrics, the proposed method consistently outperforms both in terms of the Dice coefficient and mean IoU, showcasing its advanced precision in tumor segmentation. Specifically, our method competes closely with Segnet-VGG-16, achieving comparable results in dice coefficient and mean IoU, underscoring its suitability for accurate tumor segmentation. The model's high global accuracy, substantial mean accuracy, and remarkable mean IoU underscore its precision in pixel segmentation and tumor region delineation. Complementary metrics, such as weighted IoU and mean BF-Score, further affirm the model's ability to preserve fine-grained tumor details. These outcomes position the model as a powerful tool in neuroradiology, promising enhanced precision in brain tumor detection, particularly in cases with intricate nuances that challenge human assessment.

4. CONCLUSION

In this study, we have developed and rigorously assessed an ensemble CNN-transfer learning framework, leveraging Deeplabv3+ architecture with ResNet18 backbone, for the intricate task of brain tumor segmentation in medical images. The detailed comparison with various existing methods reinforces the superior performance of our proposed model, demonstrating consistently higher dice coefficient and mean IoU. The research outcomes affirm the model's robustness and accuracy, as evidenced by remarkable global accuracy, class accuracy, intersection over union (IoU), weighted IoU, and Boundary F1 (BF) score—critical metrics in medical imaging. Our model's demonstrated capabilities underscore its potential as a valuable tool for precise brain tumor localization, a crucial aspect of medical diagnosis.

Integrating cutting-edge deep learning techniques into medical image segmentation signifies a significant advancement in the healthcare sector. Beyond reducing subjectivity, these innovations can vastly improve diagnostic precision and enhance the overall quality of patient care. As we look ahead, the research presented here sets the stage for future endeavors to address the pertinent challenges and limitations, such as mitigating false positives and optimizing resource usage. By overcoming these obstacles, we can further refine and elevate the model's performance, solidifying the role of advanced CNN models in various medical imaging applications.

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