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HIGH-PERFORMANCE AND EFFICIENT BRAIN TUMOR SEGMENTATION FOR ENHANCED CLINICAL ANALYSIS

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Abstract

Automated brain tumor segmentation from MRI images is critical for accurate diagnosis and treatment planning. This study presents a novel ResUNet50-based approach, integrating ResNet50 as an encoder within the U-Net framework to achieve robust and precise segmentation. The proposed model was evaluated on two datasets: a Kaggle-based T1-CE MRI dataset and BraTS 2018, ensuring comprehensive assessment across different imaging conditions. ResUNet50 outperformed state-of-the-art models, achieving Dice coefficients exceeding 0.95 and Jaccard indices above 0.91 on the Kaggle dataset. Additionally, experiments on BraTS 2018 Whole Tumor segmentation across multiple MRI modalities (FLAIR, T1, T1-CE, and T2) demonstrated high accuracy on both High-Grade Gliomas (HGG) and Low-Grade Gliomas (LGG), confirming model generalization. Statistical significance tests (Paired t-tests and Wilcoxon Signed-Rank Tests, $p < 0.05$) validated the improvements over existing approaches. Furthermore, ResUNet50 reduced parameters by over 60% and accelerated inference time by 4.8× compared to U-Net, enhancing its potential for clinical deployment. Future work will focus on ensemble learning and bio-inspired optimization for improved robustness across multi-center MRI datasets. Explainable AI techniques such as Grad-CAM and saliency maps will be incorporated to enhance interpretability, improving clinical applicability.

1. Introduction

Brain tumor segmentation plays a pivotal role in the diagnosis and treatment planning of neurological disorders. Accurate delineation of tumor regions from medical images, such as magnetic resonance imaging (MRI) scans, is crucial for assessing tumor size, location, and progression. However, radiologists' manual segmentation is time-consuming and prone to subjective interpretation and interobserver variability. As the volume and complexity of medical imaging data continue to increase, there is a growing need for automated segmentation techniques that can efficiently and reliably analyze such data. Deep learning-based approaches have emerged as promising solutions for automated medical image segmentation tasks. Among these approaches, the U-Net architecture has garnered significant attention due to its effectiveness in capturing spatial context and preserving fine details in segmented regions. The U-Net architecture comprises an encoder-decoder structure with skip connections, allowing the integration of high-resolution features from different levels of abstraction. Despite its success in various medical imaging applications, traditional U-Net models may struggle to capture intricate details and subtle variations in complex structures, such as brain tumors. To address this challenge, researchers have explored the integration of advanced convolutional neural network (CNN) architectures as encoders in the U-Net framework. Among these architectures, ResNet50 stands out for its superior performance in feature extraction tasks and the ability to handle deeper networks without suffering from vanishing gradients. By leveraging ResNet50 as an encoder, the resulting hybrid model, referred to as ResUNet50, aims to enhance the segmentation performance of U-Net while maintaining computational efficiency.

1.1 Background

Brain tumors are among the most complex and life-threatening conditions in medicine. They are characterized by abnormal cell growth within the brain, which may occur in various forms including Meningioma, Glioma (ranging from low-grade to highly malignant glioblastoma multiforme), and Pituitary tumors. Each type presents unique challenges for segmentation due to differing morphological characteristics, sizes, and locations relative to critical brain structures. Medical imaging, particularly MRI, has become the gold standard for brain tumor visualization and assessment. MRI offers excellent soft tissue contrast and can capture structural information across multiple modalities, including T1-weighted, T1-contrast enhanced (T1-CE), T2-weighted, and FLAIR sequences, each highlighting different tissue properties. However, the sheer volume of imaging data and the complexity of tumor appearances make manual segmentation by radiologists both labor-intensive and subject to significant variability. The need for automated, reliable, and clinically relevant segmentation tools has driven extensive research in computer-aided diagnosis (CAD) systems. Early approaches relied on handcrafted image features and classical machine learning algorithms such as support vector machines (SVM) and random forests. These methods, while showing promise for specific datasets, lacked the generalization ability needed for clinical deployment across diverse imaging conditions and tumor types. The advent of deep learning, particularly convolutional neural networks (CNNs), brought a paradigm shift in medical image segmentation. The introduction of the U-Net architecture marked a major milestone, offering an elegant encoder-decoder design with

skip connections that enabled precise spatial localization while capturing semantic context. Subsequent research built upon U-Net by incorporating attention mechanisms, dense connections, residual learning, and transfer learning from large natural image datasets.

1.2 Problem Statement

Despite significant advances in deep learning for medical image segmentation, several key challenges persist. Existing U-Net variants face limitations including limited generalization to diverse tumor morphologies, ineffective handling of small or irregular tumor regions, sensitivity to dataset imbalance, and challenges in maintaining segmentation accuracy across datasets with varying contrast and noise levels. These issues necessitate a more efficient and adaptable solution for brain tumor segmentation that can generalize across imaging protocols and tumor types.

The following are the main goals of this research:

1. To develop and evaluate a hybrid ResUNet50 model that integrates ResNet50 as the encoder within the U-Net framework for automated brain tumor segmentation from MRI scans.
2. To apply and evaluate PSO-based optimization for adaptive thresholding, morphological refinement, and test-time augmentation to enhance segmentation robustness.
3. To conduct a comprehensive evaluation of the proposed model's diagnostic performance, encompassing Dice coefficient, Jaccard Index, Accuracy, Precision, Recall, F1 Score, and Mean IoU.
4. To validate the generalization capability of ResUNet50 on the BraTS 2018 multi-modal dataset for Whole Tumor segmentation across HGG and LGG cases.
5. To compare the computational efficiency (parameters, training time, inference speed) of ResUNet50 against baseline U-Net and modified U-Net models.

2. Related Work

With the advent of deep learning, particularly convolutional neural networks (CNNs), a paradigm shift occurred in medical image segmentation. The introduction of the U-Net architecture by Ronneberger et al. marked a significant development due to its ability to efficiently capture spatial context and preserve detailed information through skip connections, making it a popular choice for medical segmentation tasks. Subsequent research brought various improvements to the basic U-Net framework. The integration of attention mechanisms with U-Net-based models allowed focusing computational resources on relevant regions to improve accuracy and robustness. The adoption of dense and residual connections, inspired by DenseNet and ResNet architectures respectively, has facilitated feature reuse and supported the training of deeper networks, enhancing the models' ability to learn complex representations without degrading gradient flow.

Further refinements included the adaptation of pre-trained CNNs for medical imaging through transfer learning. Networks pre-trained on large natural image datasets such as ImageNet have been adapted to the medical domain with minimal fine-tuning. This approach has proven effective in enhancing segmentation performance, particularly in scenarios with limited annotated medical images.

2.1 Advanced Architectural Improvements

Recent research has also focused on integrating more sophisticated architectures. ResUNet combines residual connections with the U-Net

structure to allow deeper feature extraction and mitigate the vanishing gradient problem. Emerging techniques such as graph convolutional networks and attention-based models are being explored to improve feature representation and spatial coherence. The Edge U-Net approach utilizes edge detection to refine segmentation boundaries, while ensemble models leveraging multimodal data have shown improved generalization. Despite these improvements, key limitations persist in existing U-Net variants, including limited generalization to diverse tumor morphologies, ineffective handling of small or irregular tumor regions, and sensitivity to dataset imbalance. To address these issues, we propose ResUNet50, a hybrid model that integrates ResNet50 within the U-Net framework. ResNet50's residual connections improve gradient flow and deep feature learning, mitigating the vanishing gradient problem common in deeper networks. Its optimized skip connections enable better spatial detail retention, allowing for precise tumor boundary delineation. This integration enhances generalization, reduces over-segmentation errors, and ensures more accurate segmentation even for small and irregular tumor structures.

3. Methodology

This section outlines the methodologies adopted in this study, including the Brain MRI dataset preparation, the integration of PSO-based preprocessing, the modified U-Net architecture with a ResNet50 encoder, and the evaluation metrics used to assess segmentation performance. The proposed approach leverages bio-inspired optimization techniques to refine segmentation quality, optimize thresholding and morphological refinements dynamically, and enhance test-time augmentation, ensuring robustness across various MRI scans.

3.1 Brain MRI Dataset and Preprocessing

Our research utilizes a specialized dataset from Kaggle, sourced from the T1-CE MRI collection, which includes 3,064 brain MRI images essential for training our tumor segmentation model. Each image maintains a high-quality standard, featuring a resolution of 512 × 512 pixels and a 24-bit color depth. A key component of our methodology is the inclusion of accurate ground truth tumor masks for each image, fundamental to our supervised learning approach. The images are categorized into three tumor types: Meningioma (708 images), Glioma (1,426 images), and Pituitary (930 images). Meningiomas are typically benign but can be aggressive (Grade II-III), causing vision impairment and neurological deficits. Gliomas range from low-grade to highly malignant glioblastoma multiforme (GBM), with a poor prognosis and a median survival of less than 15 months. Pituitary tumors are often benign adenomas that impact hormone regulation. To further evaluate generalization, experiments were also conducted using the BraTS 2018 dataset, a well-established benchmark for brain tumor segmentation. Unlike the Kaggle dataset, BraTS 2018 includes multi-modal MRI scans (FLAIR, T1, T1-CE, and T2), capturing both High-Grade Gliomas (HGG) and Low-Grade Gliomas (LGG). This dataset provides tumor masks for Whole Tumor (WT) segmentation, encompassing edema, non-enhancing tumor, and enhancing tumor regions.

Table 1: ***Brain MRI Dataset Description (Kaggle)***

Tumor Type	Number of Images
Glioma	1,426

Pituitary	930
Meningioma	708
Total	3,064

Preprocessing steps included image resizing to 256 × 256 pixels to standardize data and reduce computational demands, followed by conversion from 24-bit color to 8-bit grayscale to focus on intensity variations relevant to tumor identification and reduce computational load.

3.2 PSO-Optimized Preprocessing for Thresholding and Morphological Refinement

Thresholding is a crucial step in segmentation, determining how predicted probability maps are converted into binary tumor masks. Traditional methods use a fixed threshold (e.g., 0.5), which fails to account for contrast variations across different MRI scans. Instead, Particle Swarm Optimization (PSO) is applied to determine the optimal binarization threshold dynamically. Each particle in PSO represents a candidate threshold value ranging between 0.1 and 0.9, and the algorithm iteratively adjusts these values to maximize the Dice Coefficient between predicted and ground truth masks.

The Dice loss function is defined as: $L_{Dice} = -(2 \Sigma y_{true} \times y_{pred} + \varepsilon) / (\Sigma y_{true} + \Sigma y_{pred} + \varepsilon)$, where y_{true} represents the ground truth mask, y_{pred} represents the binarized model prediction, and ε is a small smoothing constant to prevent division errors. Even with optimized thresholding, segmentation masks may still contain noise artifacts or incomplete tumor regions. PSO is also applied to select the best morphological transformation and kernel size automatically, including opening (for noise removal), closing (to fill gaps), and dilation (to expand tumor regions). Additionally, PSO optimizes Test-Time Augmentation (TTA) strategies, selecting the best set of augmentations (horizontal flipping, vertical flipping, rotations) during testing.

3.3 Modified U-Net with ResNet50 Encoder (ResUNet50)

The U-Net architecture, initially developed for biomedical image segmentation, is renowned for its efficiency and effectiveness. Building on this foundation, our study introduces a significant modification by integrating the ResNet50 architecture as the encoder within the U-Net framework. This modification harnesses the strengths of ResNet50's deep residual learning framework to enhance feature extraction capabilities.

3.3.1 ResNet50 as Encoder

ResNet50 introduces residual learning to address the degradation problem inherent in training deeper networks. By incorporating shortcut connections that skip one or more layers, ResNet50 allows the training of substantially deeper networks by alleviating the vanishing gradient problem. When utilized as an encoder in the U-Net architecture, ResNet50 enables the propagation of gradients through many layers, enhancing feature extraction without significantly increasing the computational burden. The mathematical representation of the residual block is: Output = F(Input) + (Input), where F(Input) represents the transformation performed by the residual block. This residual connection propagates the gradient directly through the shortcut link to address vanishing gradient problems.

3.3.2 U-Net Architecture Enhancement

In the proposed model, the encoder path has been enhanced by replacing it with a ResNet50 backbone. Each convolution block in the ResNet50 encoder is modified with a 2x configuration, allowing double the depth of feature extraction at every layer. In the decoder path, the model retains the traditional U-Net structure enhanced with up-sampling layers and optimized concatenations of corresponding encoded features. The skip connections have been fine-tuned with a dynamic weighting mechanism to prioritize the most relevant features at each resolution level. This ensures that both low-level spatial information and high-level semantic features are effectively used for accurate localization and segmentation of brain tumors.

3.3.3 Integration and Training

Integrating ResNet50 into U-Net requires careful calibration of network layers to ensure that feature map depths match across encoder and decoder paths. Training involves a fine-tuning process in which pre-trained weights of ResNet50 (trained on ImageNet) are adapted to the specific tasks of medical image segmentation. The ADAM optimizer was used with a learning rate of 0.001, and training was set for 50 epochs with early stopping based on validation loss.

3.4 Evaluation Measures

To comprehensively assess segmentation performance, we incorporate the following evaluation metrics:

Accuracy (ACC) = (TP + TN) / (TP + TN + FP + FN): Quantifies the proportion of correctly classified pixels.

Dice Coefficient = $(2 \times |A \cap B|) / (|A| + |B|)$: Measures spatial overlap between predicted and ground truth masks.

Jaccard Index (JI) = $|A \cap B| / |A \cup B|$: Provides a strict measure of overlap (also known as Intersection over Union, IoU).

Precision = TP / (TP + FP): Proportion of correctly predicted tumor pixels among all predicted tumor pixels.

Recall (Sensitivity) = TP / (TP + FN): Proportion of actual tumor pixels correctly identified by the model.

F1 Score = (2 × Precision × Recall) / (Precision + Recall): Harmonic mean balancing precision and recall.

Mean IoU = $(1/N) \Sigma |A_i \cap B_i| / |A_i \cup B_i|$: Averaged IoU across all classes.

4. Result and Implementation

This section presents the results of our experiments and provides detailed discussion. We begin by outlining the experimental setup and implementation details, then present quantitative and qualitative results, analyze evaluation measures, and compare our method with existing state-of-the-art approaches.

4.1 Experimental Setup and Implementation Details

Experiments were conducted on a high-performance computing setup with 8 NVIDIA A100-SXM4-40GB GPUs, using a Jupyter Notebook environment with TensorFlow and Keras. A modified U-Net architecture integrated with a ResNet50 encoder was developed to enhance depth and feature extraction capabilities.

Table 2: ***Summary of the Experimental Setup***

Parameter	Value
GPUs	8 NVIDIA A100-SXM4-40GB
Environment	Jupyter Notebook with TensorFlow and Keras

Architecture	Modified U-Net with ResNet50 encoder
Optimizer	ADAM
Learning Rate	0.001
Epochs	50
Image Size	256 × 256 pixels, 3 channels
Batch Size	64
Train-Test Split	0.8:0.2 (stratified by tumor type)
Evaluation Metrics	Accuracy, Loss, Dice Coefficient, Jaccard Index

MRI scans were standardized to 256×256 pixels with three channels, normalized to the range [0,1], and skull-stripped to remove non-brain regions. A stratified split was employed to ensure balanced distribution of all tumor types (Meningioma, Glioma, and Pituitary) across training and testing datasets.

4.2 Impact of PSO-Based Preprocessing and Post-Processing

To evaluate the effectiveness of PSO-driven thresholding, morphological post-processing, and TTA, segmentation performance was compared before and after applying PSO optimization.

Table 3: ***Effect of PSO on Threshold and Morphology Optimization***

Metric	Before PSO	After PSO	Improvement (pp)
Dice Score	0.9107	0.9298	+1.91
IoU Score	0.8374	0.8690	+3.16
Precision	0.8690	0.8879	+1.89
Recall	1.0000	0.9883	-1.17

The results indicate that PSO-threshold optimization led to a 1.91 percentage point improvement in the Dice coefficient, and IoU increased by 3.16 pp. Morphological refinement improved precision by 1.89 pp, as noise artifacts were effectively removed. Recall decreased slightly by 1.17 pp, indicating that some minor tumor regions were suppressed during post-processing. These findings confirm that PSO-driven preprocessing and post-processing significantly enhance segmentation performance.

4.3 Evaluation and Segmentation Results

The model demonstrated exceptional Accuracy values, surpassing 99.8% in training and 99.9% in validation. Loss values were consistently low, ranging from 0.0020 to 0.0025, indicating minimal classification errors during training. The Dice coefficient ranged from 0.9091 to 0.9576 across all tumor classes, confirming substantial agreement between predicted and ground truth segmentations.

Table 4: ***Evaluation of Proposed Model Using Selected Metrics***

Metric	Value

Accuracy (ACC)	99.9%
Pixel Accuracy (PA)	98.2%
Mean Pixel Accuracy (MPA)	95.4%
Precision	93.5%
Recall (Sensitivity)	94.5%
F1 Score	94.0%
Mean IoU	92.1%
Dice Coefficient	95.7%
Jaccard Index (IoU)	85.17%

The high recall (94.5%) is particularly significant for clinical relevance, reducing under-segmentation risks where portions of the tumor are missed. The F1 Score of 94.0%, which harmonizes precision and recall, confirms that our method achieves an optimal trade-off, ensuring high tumor detection rates while maintaining specificity. For individual tumor classes, the model achieved Dice coefficients of 0.9716 for Meningioma, 0.9703 for Glioma, and 0.9459 for Pituitary tumors, with corresponding Jaccard indices of 0.9448, 0.9423, and 0.8974 respectively. The slightly lower performance for the Pituitary class reflects the inherent challenges of segmenting these smaller and morphologically variable tumors near critical brain structures.

4.4 Comparison with State-of-the-Art Methods

Our comparative analysis demonstrates compelling performance advantages of the proposed ResUNet50 model across all tumor classes and overall segmentation.

Table 5: ***Comparison of Segmentation Efficacy Using Various Approaches***

Method	Class	Dice	Jaccard
Proposed Method (ResUNet50)	All Images	0.9553	0.9151
CNN-based	All Images	0.828	-
U-Net with AT	All Images	0.6239	-
SegNet	All Images	0.9332	0.8827
DFP-Unet	All Images	0.8169	-
Residual-Unet	All Images	0.9011	-
ResNet101-U-Net	All Images	0.8369	0.85
DeepLab Pre-trained	All Images	0.8091	-
Cascaded dual-scale LinkNet	All Images	0.8003	-

SegNet VGG16	All Images	0.9314	0.7622

The superior performance of ResUNet50 is attributed to several key architectural advancements: residual learning that mitigates the vanishing gradient problem, optimized skip connections that enhance spatial refinement, and multi-scale feature learning for strong generalization across diverse tumor types. Statistical significance tests (paired t-tests and Wilcoxon signed-rank tests, $p < 0.05$) validated the improvements over all existing approaches.

4.5 Computational Efficiency Analysis

To assess computational efficiency, a comparative analysis was conducted against U-Net and M-U-Net based on model complexity, training time, inference speed, and segmentation accuracy.

Table 6: ***Computational Efficiency Comparison***

Method	Parameters	μT(s)	ΣT(s)	DSC	JI
U-Net	34,513,410	39.2	1960	0.8759	0.8391
M-U-Net	31,047,105	35.2	1760	0.9220	0.8569
ResUNet50	13,603,649	8.12	406	0.9553	0.9151

ResUNet50 exhibits a significantly lower parameter count of 13.6 million, compared to 34.5 million for U-Net and 31.0 million for M-U-Net. The training time for ResUNet50 is 406 seconds, approximately 4.8 times faster than U-Net (1,960 seconds). The average processing time per step is 8.12 seconds, significantly outperforming U-Net (39.2 seconds). Despite this lower computational burden, ResUNet50 maintains superior segmentation accuracy with a DSC of 0.9553 and Jaccard Index of 0.9151.

4.6 Evaluation on BraTS 2018 for Generalization

To assess generalization capability, the proposed ResUNet50 model was evaluated on the BraTS 2018 dataset for Whole Tumor (WT) segmentation across all MRI modalities (FLAIR, T1, T1-CE, and T2) for both HGG and LGG cases.

Table 7: ***Performance Evaluation on BraTS 2018 MRI Modalities***

Grade	Modality	Accuracy	Loss	Dice	Jaccard
HGG	FLAIR	0.9981	0.0048	0.9187	0.8506
HGG	T1	0.9988	0.0030	0.9157	0.8463
HGG	T1-CE	0.9977	0.0055	0.9133	0.8414
HGG	T2	0.9989	0.0028	0.9201	0.8538
LGG	FLAIR	0.9980	0.0049	0.9251	0.8621
LGG	T1	0.9987	0.0033	0.9215	0.8562
LGG	T1-CE	0.9979	0.0051	0.9234	0.8587
LGG	T2	0.9987	0.0032	0.9234	0.8593

The proposed ResUNet50 model performs consistently across different MRI modalities, with Dice scores ranging from 0.9133 to 0.9201 for HGG and 0.9215 to 0.9251 for LGG cases. The highest Dice coefficient is achieved with T2-weighted images. On BraTS 2018, the proposed method achieves the highest overall Dice coefficient of 0.9202, surpassing U-Net (0.8440), BrainSeg-Net (0.8940), U-Net-prep (0.9000), and ensemble-based approaches. Statistical analysis confirms these improvements are statistically significant (all $p < 0.05$).

5. Conclusion

This study proposed a ResUNet50-based approach for brain tumor segmentation, integrating U-Net with ResNet50 as the encoder to enhance accuracy and robustness. The proposed method consistently outperformed state-of-the-art models, achieving Dice coefficients above 0.95 and Jaccard indices exceeding 0.91. Evaluations across multiple metrics, including Pixel Accuracy, Precision, Recall, F1 Score, and Mean IoU, further confirmed its superior segmentation capability. To assess generalization, we evaluated ResUNet50 on the BraTS 2018 dataset for Whole Tumor segmentation across multiple MRI modalities (FLAIR, T1, T1-CE, and T2). The model demonstrated high segmentation performance on both High-Grade Glioma (HGG) and Low-Grade Glioma (LGG), reinforcing its effectiveness across diverse imaging conditions. Comparative analysis confirmed superiority, and statistical significance tests (Paired t-tests and Wilcoxon Signed-Rank Tests, $p < 0.05$) validated the improvements over existing models. Additionally, ResUNet50 reduced parameters by over 60% and accelerated inference speed by 4.8× compared to U-Net, enhancing its suitability for clinical deployment. The PSO-based preprocessing pipeline, including adaptive thresholding, morphological refinement, and test-time augmentation, further contributed to segmentation robustness without requiring manual parameter tuning.

Future work will address the remaining challenges in segmentation accuracy and model interpretability. Planned directions include integrating ensemble learning techniques such as model averaging and stacked generalization, exploring bio-inspired metaheuristic optimization for automated hyperparameter tuning, and validating ResUNet50 on multi-center MRI datasets to evaluate robustness across imaging protocols and scanner variations. To enhance interpretability, explainable AI (XAI) techniques such as Grad-CAM and saliency maps will be incorporated, allowing clinicians to understand model decisions and increase trust in automated segmentation systems. These advancements will enhance the model's clinical viability and interpretability. This study provides a highly accurate, efficient, and generalizable framework for brain tumor segmentation, contributing to the advancement of AI-driven medical imaging technologies in neuro-oncology.

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