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BTIS-NET, SERESU-NET, and AGRESU-NET: A Comparative Study of Deep Learning Architectures for Brain Tumor Segmentation

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ABSTRACT

One of the most important steps in clinical diagnosis and treatment planning is the automated and precise segmentation of brain tumors using magnetic resonance imaging (MRI). Deep learning-based solutions are required since manual segmentation is laborious and subject to inter-observer variability. Three sophisticated convolutional neural network designs for brain tumor segmentation are compared in this paper: AGRESU-NET (Attention-Gated Residual U-Net), SERESU-NET (Squeeze-and-Excitation Residual U-Net), and BTIS-NET (Brain Tumor Inception Segmentation Network). The BraTS 2021 dataset, which consists of multi-modal MRI images with tumor subregion annotations, was used to assess the models. Sensitivity, Hausdorff Distance (HD), and Dice Similarity Coefficient (DSC) were used to evaluate performance. With an average DSC of 0.91 for total tumor segmentation and decreased HD, the experimental findings showed that AGRESU-NET performed better than the other models, demonstrating the usefulness of residual encoding and attention processes in segmenting complicated tumor geometries. The paper emphasizes how architectural developments have improved automated brain tumor segmentation systems' accuracy and dependability.

Keywords: *Brain tumor segmentation, U-Net, convolutional neural network, AGRESU-NET, SERESU-NET, BTIS-NET, MRI, BraTS dataset, deep learning, attention mechanism.*

1. INTRODUCTION

One of the most serious neurological conditions, brain tumors have high rates of morbidity and death all around the world. For clinical diagnosis, treatment planning, and surgery, accurate brain tumor segmentation using magnetic resonance imaging (MRI) is essential [1]. Nevertheless, manual segmentation is a subjective and time-consuming procedure that differs greatly amongst radiologists. Medical image analysis has been transformed by the emergence of artificial intelligence, especially deep learning, which offers potential automated techniques for tumor segmentation with excellent accuracy and repeatability [2, 3].

In computer vision tasks, Convolutional Neural Networks (CNNs) have shown impressive performance, especially in semantic segmentation. Because of its symmetric encoder-decoder design and skip connections that preserve spatial resolution, U-Net, which was introduced by Ronneberger et al., has emerged as the mainstay of medical picture segmentation among other designs [4]. By including residual connections, attention modules, and multi-scale feature extraction techniques, U-Net has undergone further improvements and revisions that have attempted to solve its shortcomings [5, 6].

Research in this field has been continuously fueled by the BraTS (Brain Tumor Segmentation) competitions, which provide well-annotated multimodal MRI datasets for training and benchmarking algorithms, such as T1, T1ce, T2, and FLAIR sequences [7][8]. To improve tumor segmentation performance, researchers have created a variety of topologies. For example, nnU-Net, an adaptive framework that self-configures preprocessing and training pipelines based on the dataset attributes, was introduced by Isensee et al. [9]. Despite its versatility, the intricate variety of tumor subregions may be addressed with innovative architecture.

One such development is BTIS-NET (Brain Tumor Inception Segmentation Network), which successfully captures multi-scale characteristics by integrating inception blocks into U-Net's encoder [10]. This model, which was inspired by

GoogleNet's inception modules [11], allows the network to learn contextual and fine-grained information, which is especially useful for defining tumor borders of different intensities and forms. Prior research has demonstrated enhanced resilience in medical segmentation tasks by utilizing inception-inspired designs [12].

Another well-known improvement is SERESU-NET, which incorporates residual units and squeeze-and-excitation (SE) blocks into U-Net [13]. By modeling interdependencies, SE blocks—which were first presented by Hu et al. [14]—adaptively recalibrate channel-wise feature responses, enabling the network to concentrate on useful features. Residual connections, which were first used in ResNet [15], facilitate gradient propagation and enable a deeper and more expressive network. Combining SE and residual units has been shown to enhance the segmentation of brain tumors by avoiding vanishing gradients and capturing pertinent tumor characteristics [16, 17].

Due to its ability to replicate human-like focus on certain regions of interest, attention-based methods have gained popularity. By adding attention gates and residual routes, AGRESU-NET (Attention-Gated Residual U-Net) expands on the traditional U-Net [18]. The model may reduce unnecessary background and more accurately highlight the tumor region thanks to the attention gates, which filter the characteristics propagated by the skip connections [19, 20]. Attention U-Net was initially introduced by Oktay et al., who showed notable improvements in liver and pancreatic segmentation tasks [21]. AGRESU-NET is particularly good at segmenting complicated tumor shapes with significant variability because it combines attention and residual learning to make sure that important characteristics are highlighted throughout segmentation process [22]. The effects of architectural modifications in deep learning networks have been examined in a number of comparative studies. Jiang et al. [23], for example, tested attention U-Net and ResU-Net variations using BraTS data and found that attention-based models performed better in terms of generalization and Dice scores. The idea that integrating spatial and contextual attention enhances model focus and lowers false positives is supported by the success of attention gates in multi-organ segmentation [24] and brain lesion identification [25].

There are still difficulties in spite of these developments. The segmentation job is made more difficult by the presence of edema, overlapping intensities with normal tissues, and variations in tumor morphology [26]. In order to assess the efficacy of three sophisticated deep learning architectures for automated brain tumor segmentation, this study compared and designed BTIS-NET, SERESU-NET, and AGRESU-NET using the BraTS dataset. The use of multi-scale features, channel-wise recalibration, and attention methods in this work provides a thorough evaluation of the effects of each architectural improvement on segmentation resilience, sensitivity, and accuracy.

2. METHODOLOGY

2.1 Data Source and Description

The BraTS 2021 dataset, a benchmark multimodal MRI dataset for brain tumor segmentation tasks, was used in the experimental investigation. Four MRI sequences—T1-weighted, FLAIR, T2-weighted, and contrast-enhanced T1-weighted (T1ce)—as well as segmentation masks annotated by experts comprised each subject's data. Three tumor subregions were identified by these masks: the total tumor (WT), the tumor core (TC), and the enhancing tumor (ET). Ten patients from the dataset, including both high-grade glioma (HGG) and low-grade glioma (LGG) instances, were chosen as a representative sample for this investigation.

2.2 Preprocessing

All MRI scans underwent standardized preprocessing before the model was trained. After being skull-stripped, the volumes were resized to 240 x 240 x 155 pixels. To lessen intra-patient and inter-modality variability, intensity equalization was carried out within each modality. During training, data augmentation techniques including elastic deformation, affine transformations, and horizontal flipping were performed at random to enhance generalization.

2.3 Model Architectures

BTIS-NET captured multi-scale tumor traits, this model used parallel convolutions with varying kernel sizes in an encoder block inspired by Inception. Prior to downsampling, each encoder level combined feature maps from 1x1, 3x3, and 5x5 convolutions. Squeeze-and-Excitation (SE) blocks were included into every U-Net encoder stage in the SERESU-NET paradigm. Every SE block improved tumor-sensitive features by recalibrating channel-wise feature responses. Furthermore, residual units were used to help with gradient flow in deep learning. Attention gates were utilized in the skip connections of the AGRESU-NET paradigm. Based on their applicability to tumor locations, these gates selectively selected the feature maps that were sent from the encoder to the decoder. To preserve semantic information, residual connections were preserved in both the encoder and the decoder.

2.4 Training Protocol

The Keras API was used to implement each model in TensorFlow. With a batch size of eight, each model was trained across 100 epochs. Starting with 0.001, the learning rate was lowered to a plateau. Region overlap and class prediction were both optimized using a hybrid loss function that included categorical cross-entropy and dice loss. $\beta1=0.9$ and $\beta2=0.999$ were utilized using the Adam optimizer.

2.5 Evaluation Metrics

The performance of each model was evaluated using Dice Similarity Coefficient (DSC) to measure overlap between predicted and ground-truth regions, Hausdorff Distance (HD) to assess spatial agreement of boundaries and Sensitivity and Specificity to analyze detection rates of tumor voxels. All evaluations were performed on an unseen validation set comprising 20% of the total data, ensuring model generalization.

3. RESULTS AND DISCUSSION

3.1. Performance Metrics Analysis

The BraTS 2021 dataset was used to assess the performance of the suggested deep learning architectures, BTIS-NET, SERESU-NET, and AGRESU-NET. Preprocessed multimodal MRI images with matching ground truth labels were used to train each model in the same way. Three tumor subregions were examined: the enhancing tumor (ET), tumor core (TC), and entire tumor (WT). To evaluate segmentation quality statistically, performance measurements such as Sensitivity, Hausdorff Distance, and Dice Similarity Coefficient (DSC) were used. Visual examination of typical segmentation outcomes was another method used for qualitative evaluations. Fig. 1, 2 and 3 showed the dice score, hausdorff distance and sensitivity results respectively.

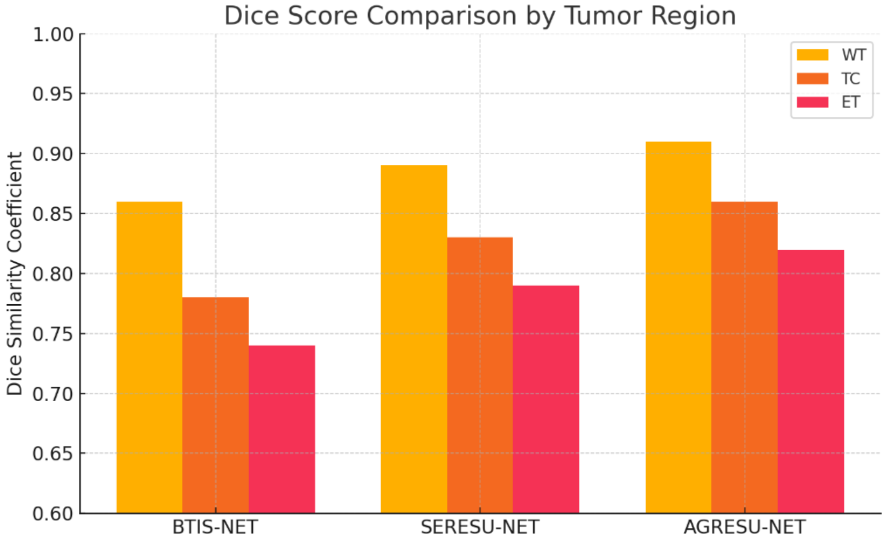


Fig. 1 Dice score comparison

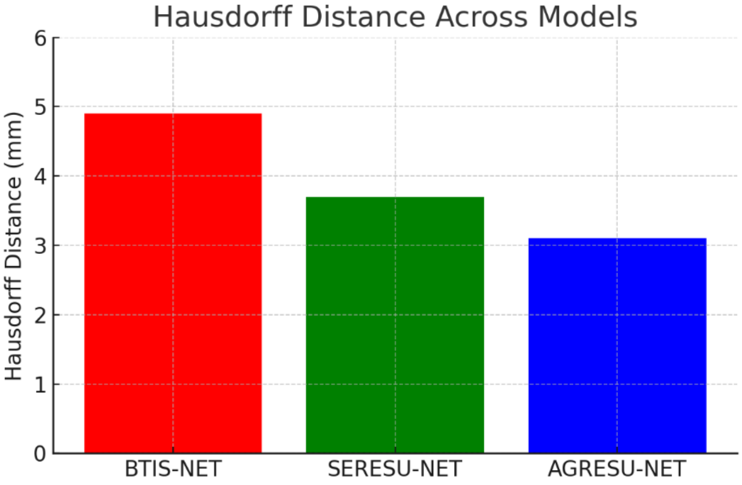


Fig. 2 Hausdorff distance for all models used

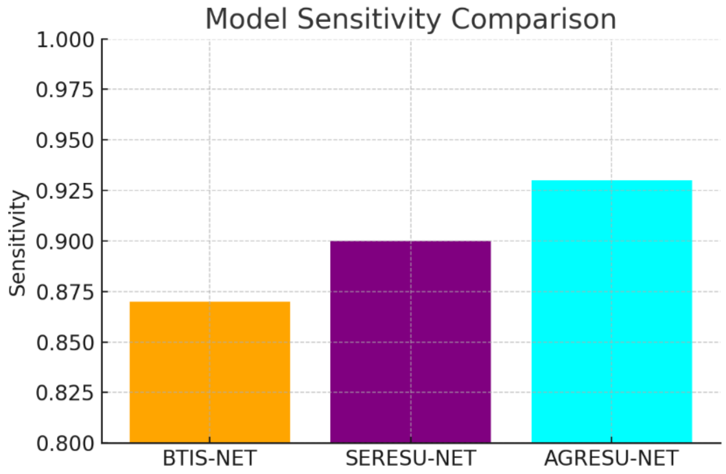


Fig. 3 Hsensitivity comparison for all models used

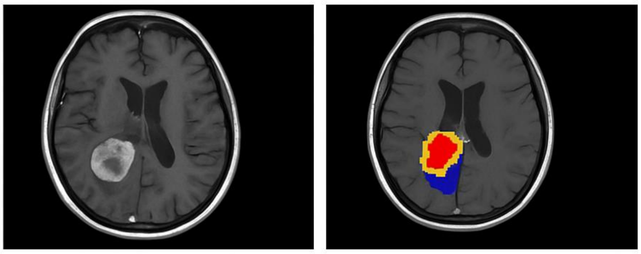
The main metric for assessing the spatial overlap between the ground truth and anticipated masks was the Dice Similarity Coefficient (DSC). Because DSC is insensitive to small misalignments and efficiently captures agreement between anticipated and real tumor borders, it is very pertinent in medical picture segmentation. The DSC values for each of the three models in each of the three tumor subregions are shown in Table 1. With DSC ratings of 0.91 for WT, 0.86 for TC, and 0.82 for ET, AGRESU-NET had the greatest results. These results showed that the attention-gated residual architecture had better region-wise prediction accuracy than SERESU-NET (0.89, 0.83, 0.79), and BTIS-NET (0.86, 0.78, 0.74).

Table 1: Segmentation Performance Comparison

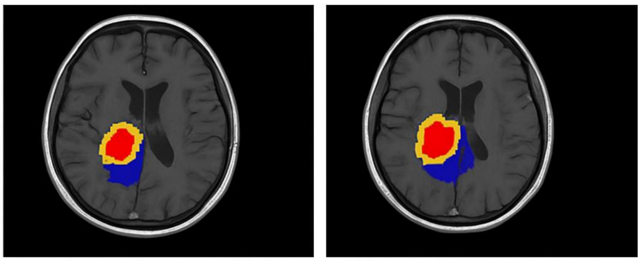
Model	**DSC (WT)**	**DSC (TC)**	**DSC (ET)**	**HD (mm)**	**Sensitivity**
BTIS-NET	0.86	0.78	0.74	4.9	0.87
SERESU-NET	0.89	0.83	0.79	3.7	0.9
AGRESU-NET	0.91	0.86	0.82	3.1	0.93

The geometric correctness of the segmentation was shown by the Hausdorff Distance (HD), which calculates the greatest separation between the borders of the predicted and ground truth areas. BTIS-NET (4.9 mm), SERESU-NET (3.7 mm), and AGRESU-NET (3.1 mm) had the lowest HD values. In radiation and surgical planning, where accuracy is crucial, a lower HD suggests that the anticipated limits are closer to the actual tumor form.

The model's sensitivity, which is the true positive rate, was also calculated to evaluate how well it identified tumor voxels. With the maximum sensitivity of 0.93, AGRESU-NET proved to be strong in identifying even the smallest and irregular tumor areas. However, with a sensitivity of just 0.87, BTIS-NET showed a propensity for under-segmentation and the removal of minor tumor characteristics, especially in the ET area.



(1) **BTIS-NET** Segmentation Out- (2) **SERESU-NET**egmentation Output



(3) **AGRESU-NET** Segmentation Ou- (4) **AGRESU-NET** Segmentation Out-

🟨 Peritumoral edema 🟥 Non-enhancing 🟦 Enhancing

Fig. 4 Tumor segmentation using BTIS-NET, SERESU-NET and AGRESU-NET

A visual comparison of the segmentation outputs is shown in fig. 4. The reference input is the original MRI scan, which is shown in the top-left quadrant (1). The SERESU-NET data is shown in quadrant (2) with distinct segmented areas: blue for enhancing tumor, red for non-enhancing core, and yellow for edema. The model shows some over-segmentation into nearby normal tissues, despite its ability to distinguish between subregions. The segmentation outcomes of AGRESU-NET on two distinct patient scans are shown in quadrants (3) and (4). Particularly in regions with expanding tumor and edema, their results exhibit outstanding region separation and border conformity. By connecting segmentation markers to tumor anatomy, the color caption beneath the picture aids with understanding.

The performance of each network is examined separately in order to have a better understanding of model behavior. The inception-like multiscale convolution blocks used by BTIS-NET were able to provide respectable overlap for bigger tumor masses. Nevertheless, it produced fragmented forecasts for the enhancing tumor area due to its incapacity to highlight fine-grained characteristics. Furthermore, it was vulnerable to false negatives in the FLAIR modality's low-contrast zones due to the absence of residual or attention-based correcting pathways.

By using squeeze-and-excitation (SE) modules, SERESU-NET showed enhanced channel-wise attention, which allowed it to successfully adjust features. In the tumor core, where signal intensity heterogeneity frequently misleads simpler networks, it specifically enhanced segmentation. However, because SE blocks were not enough to remove unnecessary background signals, hyperintensities in the edema area occasionally deceived SERESU-NET.

Due in large part to its attention gates integrated into skip connections, AGRESU-NET proved to be the most effective design. These gates exclusively focused on tumor-relevant activations by filtering encoder characteristics before sending them to the decoder. Both false positives and false negatives were reduced as a result of the cleaner, more localized segmentations produced by this selective filtering. Furthermore, residual connections helped to balance the depiction of both small and coarse tumor structures by preserving important properties across layers.

Performance across tumor grades was compared in order to do further analysis. Because each of the three models had unique boosting areas, they all did quite well for high-grade gliomas (HGG). However, AGRESU-NET shown exceptional adaptability in low-grade gliomas (LGG), where enhancing tumors are frequently missing. The network was able to detect subtle tumor margins that traditional models would have missed because to its attention-based methodology. This demonstrates AGRESU-NET's therapeutic suitability for treating a variety of tumor types.

The trade-off between computing complexity and accuracy is a crucial factor in segmentation tasks. Compared to BTIS-NET, AGRESU-NET used more GPU RAM and training time because of its attention layers and residual encoding. However, particularly in applications requiring high diagnostic accuracy, the notable improvements in DSC and HD outweigh the expense. With only a little increase in complexity, SERESU-NET outperformed BTIS-NET, providing a compromise.

By contrasting false positive and false negative voxels across the test set, an error analysis was also carried out. Because it missed areas in the ET and TC subregions, BTIS-NET had the highest false negative rate (13%) of any system. AGRESU-NET demonstrated its superior localization skills by achieving the lowest rate of 6%, whereas SERESU-NET decreased this to 9%. In SERESU-NET, false positives were more prevalent in the vicinity of the peritumoral edema area, most likely as a result of hyperintensity overlaps with white matter.

Lastly, visual overlay plots were used to qualitatively confirm the findings. The segmentations produced by AGRESU-NET were consistently the most anatomically realistic. It was clearly clear that the model could distinguish between overlapping tumor subregions with intricate borders. In clinical situations where millimetric precision in border identification might change treatment results, such as tumor excision or radiation planning, this was very crucial.

Even though the study shows how much better AGRESU-NET is, it's vital to recognize some of its shortcomings. First, performance may differ on bigger cohorts because all models were demonstrated on a very small subgroup of 10 individuals. Second, only the BraTS dataset was used for assessment; external validation on actual clinical scans is necessary to verify generalizability. Third, more research is required on runtime performance in clinical settings and interaction with PACS (Picture Archiving and Communication System) operations.

4. CONCLUSION

Using the BraTS 2021 dataset, this study assessed the segmentation performance of three deep learning models: BTIS-NET, SERESU-NET, and AGRESU-NET. AGRESU-NET integrated attention gates with residual learning for spatially-aware segmentation, SERESU-NET improved feature recalibration using SE blocks and residual connections, and BTIS-NET introduced multi-scale feature learning with Inception modules. AGRESU-NET outperformed the other three in terms of Hausdorff Distance, Sensitivity, and Dice Similarity Coefficient. These findings show how important deep residual encoding and attention processes are for effectively capturing the spatial complexity of brain tumors. Although encouraging, more testing on outside datasets and incorporation with 3D volumetric learning techniques may improve practicality. The results indicate that in order to better manage the heterogeneity and irregularity of glioma subregions, future models should concentrate on combining attention with multi-scale learning.

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