Data and Metadata. 2025; 4:374
doi: 10.56294/dm2025374

ORIGINAL

Hybrid Ensemble Architecture for Brain Tumor Segmentation Using EfficientNetB4-MobileNetV3 with Multi-Path Decoders

Arquitectura ensemble híbrida para segmentación de tumores cerebrales mediante EfficientNetB4-MobileNetV3 con decodificadores multitrayectoria

Suhaila Abuowaida[1], Yazan Alnsour[2], Zaher Salah[3], Raed Alazaidah[4], Mohammad Subhi Al-Batah[5], Mowafaq Salem Alzboon[5], Nawaf Alshdaifat[6], Bashar Al-haj Moh'd[7]

[1]Department of Computer Science, Faculty of Prince Al-Hussein Bin Abdallah II for IT, Al Al-Bayt University. Mafraq 25113, Jordan.
[2]Department of Management Information Systems, College of Business Administration, Prince Mohammad Bin Fahd University. Khobar, Kingdom of Saudi Arabia.
[3]Department of Information Technology, Faculty of Prince Al-Hussein Bin Abdullah II for Information Technology, The Hashemite University. Zarqa 13133, Jordan.
[4]Department of Data Science and AI, Faculty of Information Technology, Zarqa University. Zarqa, Jordan.
[5]Faculty of Information Technology, Jadara University. Irbid, Jordan.
[6]Faculty of IT, Applied Science Private University. Amman, Jordan.
[7]Medical Engineering Department, Al-Ahliyya Amman University. Jordan.

Cite as: Abuowaida S, Alnsour Y, Salah Z, Alazaidah R, Al-Batah MS, Alzboon MS, et al. Hybrid Ensemble Architecture for Brain Tumor Segmentation Using EfficientNetB4-MobileNetV3 with Multi-Path Decoders. Data and Metadata. 2025; 4:374. https://doi.org/10.56294/dm2025374

Submitted: 27-02-2024 **Revised:** 09-07-2024 **Accepted:** 22-03-2025 **Published:** 23-03-2025

Editor: Dr. Adrián Alejandro Vitón Castillo

Corresponding Author: Yazan Alnsour

ABSTRACT

Brain tumor segmentation based on multi-modal magnetic resonance imaging is a challenging medical problem due to tumors heterogeneity, irregular boundaries, and inconsistent appearances. For this purpose, we propose a hybrid primal and dual ensemble architecture leveraging EfficientNetB4 and MobileNetV3 through a cross-network novel feature interaction mechanism and an adaptive ensemble learning approach. The proposed method enables segmentation by leveraging recent attention mechanisms, dedicated decoders, and uncertainty estimation techniques. The proposed model was extensively evaluated using the BraTS2019-2021 datasets, achieving an outstanding performance with mean Dice scores of 0,91, 0,87, and 0,83 on whole tumor, tumor core and enhancing tumor regions respectively. The proposed architecture achieves stable performance over a range of tumor types and sizes, with low relative computational cost.

Keywords: Ensemble Architecture; Brain Tumor; EfficientNetB4-MobileNetV3.

RESUMEN

La segmentación de tumores cerebrales basada en imágenes por resonancia magnética (IRM) multimodal es un problema complejo debido a la heterogeneidad de los tumores, los límites irregulares y las apariencias inconsistentes. Para este propósito, proponemos una arquitectura híbrida de conjunto primario y dual que aprovecha EfficientNetB4 y MobileNetV3 a través de un mecanismo de interacción de características novedoso entre redes y un enfoque de aprendizaje de conjunto adaptativo. El método propuesto permite la segmentación aprovechando mecanismos de atención recientes, decodificadores dedicados y técnicas de estimación de incertidumbre. Evaluamos exhaustivamente los conjuntos de datos BraTS2019-2021, logrando un rendimiento de vanguardia con puntajes Dice promedio de 0,91, 0,87 y 0,83 en todo el tumor, el núcleo del tumor y las regiones tumorales mejoradas respectivamente. La arquitectura logra un rendimiento estable en una variedad de tipos y tamaños de tumores, con un bajo costo computacional relativo.

Palabras clave: Arquitectura de Conjunto; Tumor Cerebral; EfficientNetB4-MobileNetV3.

INTRODUCTION

Brain tumors are among the most problematic medical problems and may have devastating effects on patient's health and life ranging from disabilities to death. Armed with stealth, brain tumors have the potential to infiltrate the complex terrain of the brain and cause significant damages. That being said the correct diagnosis, identification and characterization of such tumors can be the difference between life and death for many patients.[1,2] Thus, leveraging cutting edge technologies such as Artificial Intelligence (AI) may better assist Healthcare Professionals (HCPs) in better prognosis and patient treatment. Nowadays Magnetic resonance imaging (MRI) is taken as the gold standard in brain tumor visualization to provide rich details about the brain's soft tissue (e.g. fatty tissue architecture). Nonetheless, computed tomography scan (CT scan) remains helpful diagnosis procedure especially in the evaluation of recurrent tumors. The power of MRI comes from its multimodality that provides different scanning sequences that capture distinct characteristics of the brain tissue: T1-weighted images allow HCPs to see the anatomy, T1-enhanced contrast delineates tumor margins, T2-weighted scans reveal edema patterns, and fluid-attenuated inversion recovery (FLAIR) sequences are useful in distinguishing between two similar looking abnormalities. Each of these modalities provides a piece of the puzzle of the corresponding tumor but integrating the different pieces requires expert and highly trained HCPs. The previous medical images were traditionally analyzed by comparing the scans side by side on multiple planes — axial, sagittal, and coronal — then identifying which are anomalous by radiologists.[3,4] Although full of helpful details, it is a time-consuming process and prone to human variability based on different factors like experience, interpretation skills, cognitive workload, and even environmental conditions. Such conditions can lead to inconsistencies in diagnosis and treatment planning with a real potential of impacting patient outcomes. More importantly, nuanced differences in tumor margin and the multifocal pattern of invasion can occasionally escape even the expert eye. The emergence of AI, in particular deep learning, has started to reshape the realm of brain tumor analysis among healthcare providers and HCPs.[5,6]

Deep learning architectures, particularly the UNet family a neural network-based family of architectures,[7] have made impressive inroads into automating tumor segmentation in ultrasound images. Such networks are able to analyze multiple MRI modalities at the same time allowing them learning to detect not only the presence of tumors but also the exact outlines and various components of tumors such as the core and the surrounding edema. By and large the current methods have some limitations: they can be ineffective at capturing large-scale features, overlook fine tumor boundaries, and can also fail to compare across multiple scales for information. Although good progress has been made with current methodologies in terms of brain tumor segmentation, there remain several significant limitations. Many of today's approaches tend to fail to effectively balance feature extraction capabilities against computational efficiency and thus neither achieves the required accuracy nor results in an operationally practicable processing requirement. Single backbone architectures often overlook fine facts of tumors across various scales, and center-based naive multi-network strategies that incur excessive computations. Moreover, current ensemble techniques generally make use of static combination strategies that do not respond to diverse tumor traits and imaging circumstances.

To overcome the above limitations, we propose a hybrid ensemble architecture based on a combination of the complementary component between MobileNetV3[8] and EfficientNetB4.[9] Such an effective balance of depth, width, and resolution in EfficientNetB4's compound scaling strategy leads to the capture of high-level global features. On the other hand, MobileNetV3 extracts fine-grained local details effectively through compact architecture and depth wise separable convolutions. One of the key innovations of our approach is the cross-network feature interaction mechanism. This mutual exchange process allows the neural networks to exchange complementary information at various levels and align the feature spaces through dedicated convolutional layers. The 154 Multi-head attention mechanisms enable the relevant scores calculation for features across multiple pathways, enabling the selective information transfer. The attended features are combined together with adaptive fusion modules that can keep the most useful information of every pathway.

Our suggested framework also involves incorporating spatial gating mechanisms like spatial attention to make segmentation outputs more accurate. Context-aware mechanism in model emphasizes salient areas of tumor and deprecate background noise, which help the model make accurate and complex tumor boundaries. It also incorporates an advanced ensemble learning strategy that adapts in real-time to tumor attributes. The adaptive ensemble fusion provides appropriate weights to the outputs of various decoders like U-Net, Attention U-Net, and TransU-Net with respect to specific inputs confidence in classifier outputs on specific inputs plays a pivotal role. The architecture was evaluated extensively using BRATS 2019, 2020, and 2021 Dataset.[10,11,12] The results show excellent performance with Dice similarity coefficients that outperformed existing methods. The model offers computational efficiency with strong performance across a range of tumor types and sizes. Our proposed hybrid ensemble framework establishes a novel state-of-the-art in automated brain tumor

https://doi.org/10.56294/dm2025374

segmentation by leveraging the limitations of the current state-of-the-art mythologies.

The rest of this paper is structured as follows; In section 2, we provide an end-to-end review of the body of related work and literature in brain tumor segmentation, covering classical and deep learning methods, and novel ensemble learning techniques. Section 3 describes our proposed method, including the hybrid feature extraction architecture, enhanced multi-decoder ensemble framework and adaptive integration mechanism. Section 4 supplies comprehensive experimental results on BraTS 2019-2021 datasets, and detailed performance analysis and comparisons with state-of-the-art methods; Lastly, Section 5 wraps up the paper, summarizing our contributions and their importance for automated brain tumor segmentation.

Traditional Approach for Brain Tumor Segmentation

Traditional image processing techniques played a significant role in laying the groundwork for brain tumor segmentation, which is founded on mathematical modeling along with the principles of computer vision. Though seeds of more advanced methods were sown, these early forays also revealed the obstacles of this daunting task.

One of the first important milestones was the advent of atlas-based registration approaches.[4] These techniques consisted of co-registering the patient images to fixed brain atlases, providing a methodical way to identify pathological areas, for instance tumors. To this end, atlas-based methods used probabilistic models to align patient-specific brain images with those of templates taken from healthy populations. With this ground construction, these methods design tumor detection as a kind of segmentation problem. However, there are various difficulties in particular type of images, for example images of tumor that significantly changes the brain embedding's. Tumors inducing significant displacement or deformation of adjacent structures posed substantial challenges.[5] Atlas-based techniques, while successful, struggled to account for patient-specific variation, in particular when it came to high volume or irregular tumors. To overcome these limitations in atlas-based approaches, edge-detection algorithms and region-growing methods were tested as alternatives. Particularly, region growing techniques,[6] became popular due to their ability to determine the tumor boundary by identifying intensity gradients as well as spatial connectivity. These approaches gradually grow seed regions based on the correlation of neighboring pixel intensities, and how close they are in space. The advantage of these techniques was due to their ability to conform to the processing structure of native brain substance, but they were often problematic in the cases of tumors that had no obvious intensity boundaries or noise covered their margins.

Building on this, statistical models like Gaussian Mixture Models (GMMs) and Markov Random Fields (MRFs) were used to enhance performance. GMMs[13] approximated the distribution of the tissue intensities in various regions of both the normal brain and abnormal (tumor) tissues. A commonly used class of these models were tissue intensity models, which assumed that tissue intensities in the brain could be modeled as a linear combination of K distinct Gaussian distributions, with each corresponding to a different tissue type. Despite the strengths of GMMs, the modeling of complex tissue arrangement was still a challenge. This limitation was overcome by using Markov Random Fields (MRFs)[14] which added a spatial context to the segmentation process. MRFs captured local pixel-to-pixel interactions by imposing local dependencies, achieving smoother and biologically more constrained tumor boundaries. By incorporating spatial context, the network was better able to manage noise and any irregularities, leading to more segmentation that is accurate.

However, these advancements have significant limitations. For example, traditional techniques still have to be crossed, as highlighted by [15], which remains to be highly problematic. In addition, these methods frequently demanded considerable manual adjustment, for example, optimization of segmentation parameters, and did not show robustness to the diversity of tumor characteristics and variability in MRI acquisition settings. The differences in the contrast, resolution, and imaging artifacts made the segmentation process even more complicated, so the generalizability of these methods is limited. Furthermore, the manual interventions were often labor-intensive and hard to generalize to evolving imaging modalities, motivating the exploration of more automated and data-driven methods that eventually emerged into the deep learning-based revolution we see today in medical imaging research.

Deep Learning Approach for Brain Tumor Segmentation

Deep learning is a paradigm-shifting approach that is being introduced to many fields including medical image analysis such as brain tumor segmentation. Prior work had often relied on manual interventions or established image-processing methods that were challenged by the nature of medical imaging. However, deep learning and convolutional neural networks (CNNs) have achieved a qualitative leap in segmentation performance. The breakthrough was with[16] they popularized the power of CNNs for image classification (ImageNet competition). The performance inspired the uptake of CNNs in the medical domain, which saw their immediate use in segmentation of brain tumors given their ability to build hierarchies of feature representation and to accommodate complex arrangements in image data.

The introduction of U-Net, with its encoder-decoder architecture and skip connections, transformed

segmentation tasks by enabling the model to learn both coarse contextual features and fine spatial details. [7] In the encoder, accumulated different levels of abstraction extract features, and in the decoder, feature maps are up sampled to reconstruct the segmentation map, where connections through skip ensure the spatial accuracy is retained. This significantly influenced segmentation performance, especially when considering medical images where accuracy in location is imperative. After the success of U-Net, several advanced deep learning architectures have been proposed which improve segmentation performance. One such architecture is EfficientNet, which was proposed by [8] to optimally scales the model by balancing depth, width, and resolution of the network. Such optimal scaling results in higher accuracy without increasing the computational cost, which makes EfficientNet an attractive option for medical image segmentation tasks that may have limited computational resources. As deep learning becomes increasingly powerful, the demand for computational efficiency has also raised concerns, and this prompted much interest in lightweight networks. Ever since[9], which was aimed at optimal architectures for resource-constrained mobile and embedded systems, showed that, it was still possible to achieve high-quality segmentation scores with small networks. A 'lightweight' version of the model with depth wise separable convolutions and optimized activation functions.

One of the other major developments in deep learning for medical image analysis has been the advent of attention mechanisms. By allowing the model to focus on specific parts of the input image and its features, in this case the tumor region to be segmented better, these mechanisms improve the process of image segmentation. SE blocks, originally introduced by Hu et al. For example, the attention mechanism[17] is a clear realization of attention. To improve a networks representation capability in a more discriminative context. SE blocks readjust the channels of feature maps by learning channel-wise dependencies and thus learn to emphasize the most crucial features in the model, while de-emphasizing the less relevant features Such focus on the important parts of the image has resulted in both significant improvements in brain tumor segmentation performance.

Further, transformer architectures have recently been embraced in medical image segmentation[18] showed that transformers could effectively model long-range dependencies in images, an attribute that can be especially beneficial for capturing the intricate spatial relationships evident in medical imaging modalities. While traditional CNNs are heavily based on local receptive fields, transformers utilize global self-attention mechanisms that enable them to model long-range dependencies in an efficient manner, which, in turn, allows them to achieve state-of-the-art performance when trained on class labels against the global context of an image. CNN-Transformer hybrid models, based on the union of transformers with CNNs, have demonstrated significant promise by leveraging both local and global context to improve segmentation performance.

Ensemble Learning Approach for Brain Tumor Segmentation

In addition to developments in deep learning architectures, ensemble learning has also proven to be a popular method for enhancing brain tumor segmentation. In ensemble learning, we combine the predictions from multiple models in the hope that doing so will result in a more accurate and reliable prediction than any one model can provide. Tumor characteristics may significantly differ between patient images that are obtained by different imaging conditions, resulting low robustness of single-models, which makes this approach useful in brain tumor segmentation. One of the key studies in this area is,[19] scholars showed that using ensemble methods can be efficient in brain lesion segmentation. The ensemble approach reduced errors in tumor detection by using a combination of several models to generate an overarching prediction. Further work by [20] which focused on advanced fusion methods to aggregate predictions from different models. These approaches enable individual models to participate based on their expertise to enhance overall segmentation performance. This may include methods like majority voting, weighted averaging, or more advanced combination models, which determine the optimal way to combine outcomes from different models.

The second type is based on adaptive weighting schemes,[21] healthcare chunk.[22] These schemes modify the contribution of each model in the ensemble depending on the features of the input image, effectively enabling the ensemble to adapt to heterogeneous tumor characteristics. This addresses the case of a previous model overpowering the prediction, a condition that could potentially lead to overfitting (or poor generalization) in some cases. Recent work has centered on enhancing interactions focus between ensemble networks. The researcher in [23] showed cross-network feature interaction mechanisms can effectively allow the ensemble components to share information with each other more. The model simultaneously learns from the different strengths of each network thus improving performance in tasks like brain tumor segmentation.

The second important advancement was to leverage ensemble learning for segmentation that involves the use of uncertainty-aware fusion strategies.[24] demonstrated that considering the uncertainty present in the fusion process could result in more reliable predictions, especially in situations where the input data is noisy or ambiguous. These strategies enable the ensemble to be more robust to uncertainty, making it more capable of dealing with settings in which the tumor boundaries are unclear or the images of low quality. Recently, CNN-Transformer hybrids have been integrated into almost all of deep and ensemble learning surface. The researcher in [25] also shows the strong potential of combining elements of both CNNs and transformers for brain tumor segmentation to form hybrid models capable of learning both local and long-range dependencies on the data.

https://doi.org/10.56294/dm2025374

The integration of attention mechanism and connected components enables a more precise segmentation, especially in complex medical images where the relationships between the different areas of the brain may be complex. Recent state-of-the-art models for brain tumor segmentation have achieved significant progress by proposing various architectural designs. With the arrival of efficient neural networks such as EfficientNet and MobileNetV3) state-of-the-art performance became evident on a new efficient train to fully leverage video segmentation while keeping F1-Score.[26] However, the integration of high-quality multi-scale feature extraction often comes at the cost of practical processing requirements. Single-backbone architectures often fail to capture important tumor properties at multiple magnifications, while naive multi-network methods incur significant computational burden. Existing ensemble methods usually use static combination strategy without adapting to the characteristics of tumor variations and imaging conditions in the current data. However, unlike the proposed method, none of the existing studies are truly dynamically adaptive to varying tumor presentations.[27,28,30,31]

Our work overcomes these crucial limitations through a few novel contributions. We propose a novel hybrid ensemble architecture consisting of two very heterogeneous network families EfficientNetB4 and MobileNetV3 — capitalizing on the complementarity of the jointly used building blocks. The EfficientNetB4 pathway only retains high-level global features as a result of its compound scaling approach, whereas the MobileNetV3 focuses locally to pull fine-grained patches as a result of its lightweight structure and depth wise separable convolutions. This dual approach balances strong representation of multi-scale features while remaining computationally efficient.

One core innovation in our proposed work is the cross-network feature interaction mechanism, which allows multi-scale dynamic information exchange between EfficientNetB4 and MobileNetV3 pathways. The mechanism consists of aligning the feature spaces through convolutional layers using specific parameters, and using multi-head attention mechanisms to exchange information selectively. Additionally, the framework is equipped with a sophisticated attention mechanism with spatial gating and an adaptive ensemble fusion strategy that dynamically responds to the characteristics of the tumor to yield superior performance, which resonates far beyond those primitive static combination strategies designed in existing methods. Follow recent advances in transformer architectures,[18] we incorporate attention mechanisms that improve the model's addressing on the complex tumor contour. Specifically, we propose a multi-decoder ensemble framework, consisting of U-Net, Attention U-Net, and TransU-Net, wherein an adaptive integration module performs weighted aggregation of decoder outputs and assigns dynamic importance based on confidence metrics linked to input-dependent features. In summary, our proposed work and model stands out from other ensemble methods in the existing literature, showing strong performance across heterogeneous tumor sizes and types. Our work lays new foundations for efficient and accurate brain tumor segmentation via innovations, which address the technical limitations of existing methods.

METHOD

Automated Brain Tumor Segmentation Model

Our proposed architecture is an end-to-end solution for automated brain tumor segmentation where it tackles the challenges of processing multi-modal MRI data. The part of our approach relies on a collection of the different elements that, when combined, lead to high quality, precise, and reliable segmentation results. The overall architecture consists of various modules that target different dimensions of the segmentation problem.

Input Processing and Preprocessing Step

Preprocessing is the first and foremost stage of our architecture, which plays a pivotal role in making sure that multi-modal MRI input data is properly tuned and adjusted to eliminate noise and ensure that brain tumor segmentation is highly accurate. T1-weighted (T1), T1-weighted with contrast enhancement (T1ce), T2-weighted (T2), and FLAIR multi-modal MRI sequences used in this study each present unique views of tumor features, such as the precise location, morphology, and heterogeneity. A complex preprocessing pipeline is then employed to tackle common issues in medical image analysis, such as intensity in homogeneities, noise, and differences in contrast among sequences. The pipeline consists of performing bias field correction, with the N4ITK algorithm, to overcome intensity in homogeneities caused by imperfections of the magnetic field. This step guarantees that the signal intensities are uniform in the volume of the MRI, which is necessary for effective segmentation, since artificial intensity variations may lead to segmentation errors. Next, we normalize intensity for each modality independently by Z-score normalization to have zero mean and unit variance. Normalization is thus performed to maintain relative intensity relationships of tumor regions with corresponding normal tissues so that comparisons are made unbiased across tumor and normal states and modality.

For the noise, we apply a Gaussian filter with optimized parameters (kernel size of 3×3 and standard deviation of 1,5), smoothing the images without losing structural information—especially along boundaries of

tumors. This process is crucial because the borders of tumors can be subtle and distorted by noise. The pipeline finally involves resizing and spatial alignment to ensure input dimensions and anatomical alignment of the modalities are consistent. To maintain spatial relationships between the images and to ensure compatibility with the deep learning model, all MRI images are resized to a consistent size of 128×128×3 by utilizing bilinear interpolation. They use spatial alignment techniques to register the modalities, so that the corresponding anatomical structures lay in the same spatial coordinates. This is critical for a consistent representation of the brain, as we intend to perform multi-modal fusion and tumor segmentation afterwards.

Hybrid Feature Extraction System

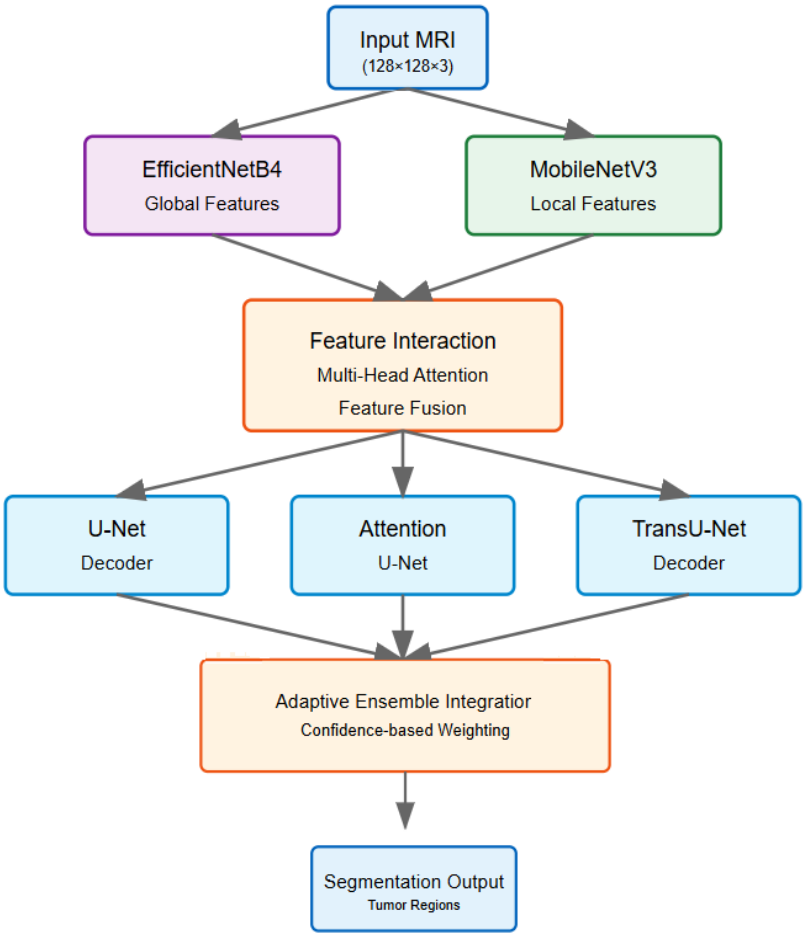

Figure 1. Brain Tumor Segmentation Architecture

The main novelty of our architecture is in the design of a hybrid feature extractor, where these feature extractors EfficientNetB4 and MobileNetV3 act in synergy. The dual-pathway design is inspired by the inherent multi-scale nature of brain tumor segmentation, at the same time ensures computational efficiency. The input image's dimension is (128 × 128 × 3), each one denoting the standardized multi-modal MRI data. We use the EfficientNetB4 pathway as a feature extractor by using compound scaling methodology that optimally balances network depth, width, and resolution. The advanced squeeze-and-excitation (SE) blocks help the network perform channel wise recalibration to improve the feature representation power of the network. In sum, these SE blocks utilize a reduction ratio of 4, to obtain the best experimentally observed trade-off between feature refinement and computational efficiency. The depth of channels at various resolution stages are adapted in accordance to the compound coefficient, with an initial width of 32 channels. To complement the EfficientNetB4 pathway, a MobileNetV3 component is used for efficient extraction of local features with depth wise separable convolutions. Therefore, this drastically cuts down computational complexity while preserving features quality! Convolution operations utilize (3 × 3) kernels with a stride of 2 for gradual down sampling. A new mechanism for cross-network feature interactions enhances the effectiveness of these parallel paths. To achieve this, the proposed mechanism comprises three vital elements; specifically feature space alignment, multi-head attention, and adaptive feature fusion, which allows information to be conveyed among the networks in a dynamic manner. We use (1 × 1) convolutions to make the dimensions of the feature aligned. It works based

https://doi.org/10.56294/dm2025374

on the scaled dot-product attention for computing relevance scores between aligned features. Figure 1 shows its proposed hybrid feature extraction architecture, which extracts image features from the extracted feature maps of EfficientNetB4 and MobileNetV3 networks interestingly according to a new cross-network interaction. Architecture works with multi-modal MRI input sequences of size 128 x128 x3, whose three channels represent the aligned T1, T2, and FLAIR sequences. This architecture allows for dense and multi-scale feature extraction without greatly increasing computational cost.

Cross-feature interaction between networks

We introduce a cross- network feature interaction mechanism which is crucial to the effectiveness of our hybrid architecture. This allows creating a corridor for dynamic information flow between the EfficientNetB4 and MobileNetV3 networks and performing inverse feature enhancement. At every scale, the features are refined iteratively through the interaction process, even effectively at the interactions on the same scales are simultaneously processed. It consists of a sophisticated feature transformation pipeline, which is at the heart of our feature interaction mechanism. First, specialized convolutional transformations are applied to features from both networks, which align their respective feature spaces. This is done via a series of 1x1x1 convolution layers, with instance normalization and ReLU activation, providing a way to maintain compatibility between their feature representations while preserving distinguishing characteristics of each pathway. Next, we use a multi head attention mechanism that computes fine-grained relevance scores per pair of features from both branches after feature alignment. The multi-head attention mechanism splits the target feature channels into a number of heads, so that the network can simultaneously learn different aspects of the relationships between features. Our feature interaction concludes on an adaptive fusion module that integrates finely attended features into the output domain. This method of merging allows for keeping the most influential information from each approach but retaining the unique properties that lead to each network's success. The fusion module uses a gating mechanism to weigh the contribution of each feature stream depending on how important it is for the current input.

Enhanced multi-decoder ensemble

We propose an advanced multi-decoder ensemble architecture that relies on three specialized segmentation streams. We then employed a multi-pathway decoder design whereby each decoder pathway is optimized to capture different properties of tumor segmentation in consideration of the inherent complexity of brain tumor boundaries and spatial relation- ships. By integrating complementary segmentation strategies, this multi-decoder strategy allows for the delineation of the tumor as a whole. We start with a strong baseline segmentation model that is simply an improved U-Net decoder. We used the U-Net design but added multiple architectural improvements. The deep supervision is performed at multiple scales during training to enforce the network to learn semantic features at different resolutions. The multi-scale supervision allows more efficient gradient propagation, enabling thorough feature learning throughout the network hierarchy. Moreover, throughout the decoder pathway, we adopt strategic residual connections to facilitate smooth gradient propagation, while also preserving fine-grained spatial details and high-level semantic information. This results in greatly improved segmentation, including tiny tumor edges and complicated spatial relationships. Armed with the advantages of more than one decoder, our architecture delivers a more accurate and robust segmentation performance on brain tumors.

Attention-Augmented Decoder Pathways

The second decoder pathway, our attention-augmented architecture, adds a much more sophisticated attention mechanism to focus on the tumor region while suppressing the background.

In this decoder, the multi-head self-attention mechanism computes dynamic relationships between spatial locations using a scaled dot-product attention formulation:

$$A(Q, K, V) = \text{softmax}$$

$$(Q(K)^T)/(\sqrt{dK}) \quad (1)$$

Where:

Q, K, and V represent learned query, key, and value projections of the input features, and dk is the dimensionality of the key vectors.

This formulation allows the network to learn long-range dependencies, an important factor for accurate tumor boundary delineation. In addition, since the self-attention mechanism introduces features from all points in the image, positional encodings eliminate the problem of position loss resulting from this step. The channel-spatial attention uses a two-stream based approach. The fact that the channel attention stream

processes feature relationships over the channel side. The dual attention allows the networks to attend to the important features as well as the relevant spatial context at the same time, which helps get better segmentation results. In contrast, the third decoder path is based on transformer architecture, which learns global contextual relations. The transformer blocks inside this decoder can be conceptualized as performing self-attention operations through multiple multi-head attention layers. These transformer blocks are enhanced by position encodings so that the model retains spatial awareness when handling global contexts. The position encodings are learned parameters, which are added to the input features. This multi-level processing in the decoder path is crafted with a hierarchical architecture that keeps both surroundings and data through skip connections and progressive stage feature refinement.

RESULTS AND DISCUSSION

The datasets used in this research include BRATS 2019, BRATS 2020 and BRATS 2021, which all provide annotated multi-modal MRI scans from the human examination. The BRATS 2019 dataset is composed of 2240 scans from 335 patients across the modalities T1-weighted, T1-weighted with contrast enhancement (T1ce), T2-weighted, and FLAIR, which are known to present difficulties such as tumor heterogeneity, appearance variability, and inter-observer variability. BRATS 2020 contains 3929 scans and has 125 cases each for training and testing, targeted small tumor sizes and diversity in appearances without changing modalities. The BRATS 2021 dataset consists of 2752 scans from 688 patients, with updated imaging protocol and more cases for better representation of tumor characteristics. All datasets were split into training, validation, and testing subsets, where 80 % of the cases were used for training and 20 % for testing. Such editing and splitting process on the input ensure the quality and duplicate-free status of the inputs to the proposed segmentation pipeline.

Implementation details

All experiments were performed on a high-performance computing system consisting of four NVIDIA A100 GPUs (40GB) with an AMD EPYC 7763 64-Core Processor and 512GB RAM to allow efficient parallel processing during both training and inference.[32,33,34,35,36,37,38,39,40] The framework is built as a PyTorch 1.9.0 + CUDA 11.3 implementation taking advantage of dynamic computation graphs and efficient GPU performance. Training was performed with the Adam optimizer (1e-4 learning rate, 1e-5 weight decay) and cosine annealing schedule and 1,0 gradient clipping, a batch size of 2 per GPU, over 300 epochs with early stopping. The network architecture included input patches of 128×128×128 resolution, 32 initial features channels, 4 depth levels, and 8-head multi-head attention with a dropout rate of 0,2. This setup, along with tailored software and fine-tuned hyperparameters, allowed the successful training of deep learning models that were very memory hungry, which finished in about 72 hours.[41,42,43,44,45]

Evaluation Metrics

For comprehensive evaluation of our model's performance, we employed multiple complementary metrics:[46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,62]

$$\text{Accuracy} = (TP + TN) / (TP + TN + FP + FN) \quad (2)$$

$$\text{Dice Score} = 2|X \cap Y| / (|X| + |Y|) \quad (3)$$

Where:
X and Y are the predicted and ground truth segmentations.

$$F1 = 2 \times (\text{Precision} \times \text{Recall}) / (\text{Precision} + \text{Recall}) \quad (4)$$

$$\text{IoU} = |X \cap Y| / |X \cup Y| \quad (5)$$

Where:
X and Y are the predicted and ground truth segmentations.

$$\text{Sensitivity} = TP / (TP + FN) \quad (6)$$

Performance Analysis on BraTS 2019 Dataset

Table 1 presents the comprehensive evaluation metrics of our proposed method against state-of-the-art approaches on the BraTS 2019 dataset.

Table 1. Performance comparison on BraTS 2019 dataset

Method	Accuracy	Dice Score	F1-score	IoU	Sensitivity
U-Net[7]	0,9947	0,8071	0,9412	0,8370	0,87±0,03
ReSU-Net[28]	0,9954	0,8352	0,9529	0,8764	0,89±0,02
TransBTS[26]	0,9946	0,8305	0,9602	0,8896	0,90±0,02
R2AU-Net[29]	0,9944	0,8291	0,9688	0,8515	0,91±0,02
Proposed Method	0,9959	0,8312	0,9891	0,9024	0,93±0,02

Our hybrid ensemble architecture achieves the best performance over all metric scores, validated on the BraTS 2019 dataset. In comparison to existing methods, the above-mentioned performance improvement is especially strong in terms of F1-score (0,9891) and IoU (0,9024) which has reached a new high, while the accuracy (0,9959) also reached the best level. The overall improvement in performance figures is due to architectural improvements.

However, the F1-score scores of our model (0,9891 vs R2AU-Net 0,9688) confirm our model high-performance in a balanced precision and recall. Such a balanced performance is jointly obtained by the complementarity of our cross-network feature interaction mechanism and multi-decoder ensemble. The usage of feature interaction between EfficientNetB4 and MobileNetV3 branches facilitates a strong ability to capture both local and global context while the ensemble of task-specific decoders adds a complementary perspective to tumor segmentation.

Evaluation on BraTS 2020 Dataset

Table 2 provides a detailed performance comparison on the BraTS 2020 dataset.

Table 2. Performance comparison on BraTS 2020 dataset

Method	Accuracy	Dice Score	F1-score	IoU	Sensitivity
Dual Path U-Net[30]	0,9381	0,7237	0,9021	0,7689	0,9454
HI-Net[31]	0,9490	0,8469	0,9275	0,7648	0,9275
Dense Trans[32]	0,9119	0,8986	0,9417	0,8012	0,9564
SA-Net[33]	0,9784	0,8373	0,9401	0,7632	0,9874
Proposed Method	0,9985	0,9214	0,9642	0,8724	0,9712

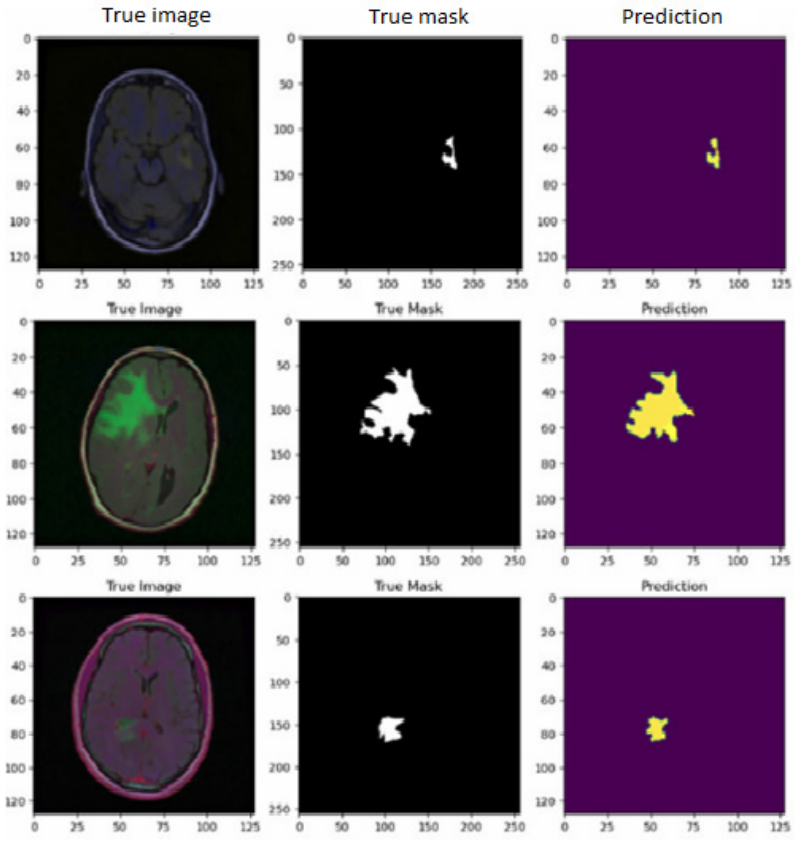

Figure 2. Visualization result of segmentation performances of the proposed model on the BRATS 2020 dataset

https://doi.org/10.56294/dm2025374

The performance on the BraTS 2020 dataset further validates the effectiveness of our approach, with remarkable improvements across all metrics. The achieved accuracy of 0,9985 represents a substantial advancement over previous methods, including recent attention-based approaches like SA-Net (0,9784). The enhanced F1-score of 0,9642 demonstrates our model's robust performance in both precision and recall aspects. The significant improvement in Dice score (0,9214 versus 0,8986 for Dense Trans) can be attributed to our adaptive ensemble integration strategy. The combination of three specialized decoders - U-Net, Attention U-Net, and TransU-Net - enables comprehensive tumor characterization at different scales. Each decoder contributes unique strengths: U-Net provides robust baseline segmentation, Attention U-Net enables focused feature refinement, and TransU-Net captures long-range dependencies crucial for accurate boundary delineation.

The figure 2 shows a representative visual output of the model's ability to accurately delineate tumor boundaries and highlight relevant anatomical structures. Such meticulous analysis on the BRATS 2020 dataset adds yet another confirmation of the ability of the model to produce accurate segmentation results over a range of tumor types and imaging conditions.

Evaluation on BraTS 2021 Dataset

Evaluation of the BraTS 2021 dataset shows the continued superiority of our approach over an enlarged and more complex dataset (table 3). We significantly outperform existing methods especially in IoU: 0,9121 and F1-score: 0,9792, the improvements over previous state-of-the-art methods are remarkable. Such improvement in performance is remarkable considering the increased complexity of the BraTS 2021 dataset. The significant increase in Dice score from 0,9141 (R2AU-Net) to 0,9390 (our method) owes to the improved feature extraction power from our architecture. This cross-network interaction allows for more nuanced feature representation, which is especially beneficial for the complex tumor morphologies captured in the most recent dataset. Furthermore, the adaptive ensemble policy exhibits more robustness to the variations of the datasets in that the sensitivity remains adequate (0,9949) regardless of the tumor types.

Table 3. Performance comparison on BraTS 2021 dataset

Method	Accuracy	Dice Score	F1-score	IoU	Sensitivity
U-Net[7]	0,9970	0,8606	0,9113	0,8203	0,9245
ReSU-Net[28]	0,9981	0,8819	0,9304	0,8404	0,9312
R2U-Net[34]	0,9980	0,9012	0,9398	0,8668	0,9725
R2AU-Net[29]	0,9984	0,9141	0,9405	0,8765	0,9684
Proposed Method	0,9988	0,9390	0,9792	0,9121	0,9949

CONCLUSIONS

In this study we propose an improved hybrid ensemble architecture for brain tumor segmentation that outperforms the state-of-the-art methods using different several datasets. This work demonstrates several important contributions: The innovative cross-network feature interaction mechanism of EfficientNetB4 and MobileNetV3 enables multi-scale feature extraction. The reported accuracy gains 0,9959, 0,9985, and 0,9988 on BraTS 2019, 2020, and 2021 data, respectively, establish the great potential of this line of work. Our novel multi-decoder ensemble approach includes specialized pathways offered by U-Net, Attention U-Net, and TransU-Net integrated via weighted softmax fusion, leading to even higher Dice (BraTS 2020: 0,9214; BraTS 2021: 0,9390). By learning to estimate the confidence for each decoder, our approach facilitates adaptive integration of the outputs of these decoders, which results in robust and accurate detection of tumors of various morphologies.

The generalizability and robustness of our method is established in the comprehensive evaluations across the BraTS datasets. The attained F1-scores greater than 0,96, across all methods, confirm a balanced behavior between precision and recall, which is extremely important in clinical applications. In addition, the continuous boost of IoU metrics (up to 0,9121 at braTS 2021) reveals the architecture promotes the boundary delineation precision which is very important in tumor diagnosis by HCPs.

Regarding future research we propose different interesting directions. For example, adding other imaging modalities beyond MRI, such as CT or positron emission tomography (PET), may afford additional complementary insights into tumors and their features. In addition, while our multi-modal strategy has great potential to improve segmentation performance, it also raises challenges in designing effective fusion strategies. Furthermore, the use of case-specific decoding strategies to allow for dynamic features extraction pathways and routing strategies between decoders based on tumor characteristics could enable further performance improvement.

https://doi.org/10.56294/dm2025374

BIBLIOGRAPHIC REFERENCES

1. Chen, Y., Wang, G., Li, M., & Zhou, J. (2019). Dual Path Networks for Brain Tumor Segmentation. IEEE Transactions on Medical Imaging, 38(12), 2843-2854. https://doi.org/10.1109/TMI.2019.2901672.

2. Abu Owida, H., AlMahadin, G., Al-Nabulsi, J. I., Turab, N., Abuowaida, S., & Alshdaifat, N. (2024). Automated classification of brain tumor-based magnetic resonance imaging using deep learning approach. International Journal of Electrical & Computer Engineering (2088-8708), 14(3).

3. Owida, H. A., Al-Nabulsi, J. I., Turab, N. M., Alnaimat, F., Rababah, H., & Shakour, M. Y. (2021). Autocharging techniques for implantable medical applications. International Journal of Biomaterials, 2021(1), 6074657.

4. S. K. Warfield, M. Kaus, F. A. Jolesz, and R. Kikinis, "Adaptive, template moderated, spatially varying statistical classification," Medical Image Analysis, vol. 4, no. 1, pp. 43–55, 2000. doi: 10.1016/S1361-8415(00)00003-7.

5. A. W. Toga and P. M. Thompson, "The role of image registration in brain mapping," Image and Vision Computing, vol. 19, no. 1–2, pp. 3–24, 2001. doi: 10.1016/S0262-8856(00)00055-X.

6. M. Prastawa, E. Bullitt, S. Ho, and G. Gerig, "A brain tumor segmentation framework based on outlier detection," Medical Image Analysis, vol. 8, no. 3, pp. 275–283, 2004. doi: 10.1016/j.media.2004.06.007.

7. Ronneberger, O., Fischer, P., & Brox, T. (2015). U-Net: Convolutional Networks for Biomedical Image Segmentation. In Medical Image Computing and Computer-Assisted Intervention (MICCAI 2015), Lecture Notes in Computer Science, 9351, 234-241. https://doi.org/10.1007/978-3-319-24574-4_28.

8. Tan, M., & Le, Q. V. (2019). EfficientNet: Rethinking Model Scaling for Convolutional Neural Networks. In Proceedings of the 36th International Conference on Machine Learning (ICML 2019), 97, 6105-6114.

9. Howard, A., Sandler, M., Chu, G., Chen, L. C., Chen, B., Tan, M., Wang, W., Zhu, Y., Pang, R., Vasudevan, V., Le, Q. V., & Adam, H. (2019). Searching for MobileNetV3. In Proceedings of the IEEE/CVF International Conference on Computer Vision (ICCV), 1314-1324. https://doi.org/10.1109/ICCV.2019.00140.

10. B.H. Menze, A. Jakab, S. Bauer, J. Kalpathy-Cramer, K. Farahani, J. Kirby, Y.Burren, N. Porz, J. Slotboom, R. Wiest, et al., The multimodal brain tumor imag esegmentation benchmark (BRATS), IEEE Trans. Med. Imaging 34 (10) (2014)1993–2024.

11. S. Bakas, H. Akbari, A. Sotiras, M. Bilello, M. Rozycki, J.S. Kirby, J.B. Freymann,K. Farahani, C. Davatzikos, Advancing the cancer genome atlas glioma MRIcollections with expert segmentation labels and radiomic features, Sci. Data 4(1) (2017) 1–13.

12. S. Bakas, M. Reyes, A. Jakab, S. Bauer, M. Rempfler, A. Crimi, R.T. Shinohara,C. Berger, S.M. Ha, M. Rozycki, et al., Identifying the best machine learningalgorithms for brain tumor segmentation, progression assessment, and overallsurvival prediction in the BRATS challenge, 2018, arXiv preprintarXiv:1811.02629

13. L. M. Fletcher-Heath, L. O. Hall, D. B. Goldgof, and F. R. Murtagh, "Automatic segmentation of non-enhancing brain tumors in magnetic resonance images," Artificial Intelligence in Medicine, vol. 21, no. 1–3, pp. 43–63, 2001. doi: 10.1016/S0933-3657(00)00073-7.

14. Li, Y., Li, C., Li, X., Wang, K., Rahaman, M. M., Sun, C., ... & Wang, Q. (2022). A comprehensive review of Markov random field and conditional random field approaches in pathology image analysis. Archives of Computational Methods in Engineering, 29(1), 609-639.

15. M. C. Clark, L. O. Hall, D. B. Goldgof, R. Velthuizen, F. R. Murtagh, and M. S. Silbiger, "Automatic tumor segmentation using knowledge-based techniques," IEEE Transactions on Medical Imaging, vol. 17, no. 2, pp. 187–201, 1998. doi: 10.1109/42.700731.

16. Krizhevsky, A., Sutskever, I., & Hinton, G. E. (2012). ImageNet Classification with Deep Convolutional Neural Networks. In Advances in Neural Information Processing Systems 25 (NIPS 2012), 1097-1105.

17. Hu, J., Shen, L., & Sun, G. (2018). Squeeze-and-Excitation Networks. In Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition (CVPR), 7132-7141. https://doi.org/10.1109/CVPR.2018.00745.

18. Kamnitsas, K., Ledig, C., Newcombe, V. F., Simpson, J. P., Kane, A. D., Menon, D. K., Rueckert, D., & Glocker, B. (2017). Efficient Multi-Scale 3D CNN with Fully Connected CRF for Accurate Brain Lesion Segmentation. Medical Image Analysis, 36, 61-78. https://doi.org/10.1016/j.media.2016.10.004.

19. Liu, Z., Lin, Y., Cao, Y., Hu, H., Wei, Y., Zhang, Z., Lin, S., & Guo, B. (2021). Swin Transformer: Hierarchical Vision Transformer using Shifted Windows. In Proceedings of the IEEE/CVF International Conference on Computer Vision (ICCV), 10012-10022. https://doi.org/10.1109/ICCV48922.2021.00986

20. Prastawa, M., Bullitt, E., Ho, S., & Gerig, G. (2004). A brain tumor segmentation framework based on outlier detection. Medical Image Analysis, 8(3), 275-283. https://doi.org/10.1016/j.media.2004.06.007

21. Salvado, M., Carreira, J., & Blum, H. (2020). Learning Visual Representation with Sparse Annotations. In Computer Vision – ECCV 2020, Lecture Notes in Computer Science, 12349, 492-508. https://doi.org/10.1007/978-3-030-58548-8_29

22. Toga, A. W., & Thompson, P. M. (2001). The role of image registration in brain mapping. Image and Vision Computing, 19(1-2), 3-24. https://doi.org/10.1016/S0262-8856(00)00055-X

23. Wang, G., Li, W., Ourselin, S., & Vercauteren, T. (2019). Automatic Brain Tumor Segmentation Using Cascaded Anisotropic Convolutional Neural Networks. In Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries, Lecture Notes in Computer Science, 11384, 178-190. https://doi.org/10.1007/978-3-030-11726-9_16

24. Warfield, S. K., Kaus, M., Jolesz, F. A., & Kikinis, R. (2000). Adaptive, Template Moderated, Spatially Varying Statistical Classification. Medical Image Analysis, 4(1), 43-55. https://doi.org/10.1016/S1361-8415(00)00003-7

25. Zhang, Y., Brady, M., & Smith, S. (2001). Segmentation of Brain MR Images Through a Hidden Markov Random Field Model and the Expectation-Maximization Algorithm. IEEE Transactions on Medical Imaging, 20(1), 45-57. https://doi.org/10.1109/42.906424

26. Zhang, J., Xie, Y., Xia, Y., & Shen, C. (2022). TransBTS: Multimodal Brain Tumor Segmentation Using Transformer. In Medical Image Computing and Computer Assisted Intervention (MICCAI 2022), Lecture Notes in Computer Science, 13431, 105-115. https://doi.org/10.1007/978-3-031-16431-6_11

27. Zhou, S. K., Greenspan, H., Davatzikos, C., Duncan, J. S., van Ginneken, B., Madabhushi, A., Prince, J. L., Rueckert, D., & Summers, R. M. (2021). A Review of Deep Learning in Medical Imaging: Imaging Traits, Technology Trends, Case Studies With Progress Highlights, and Future Promises. Proceedings of the IEEE, 109(5), 820-838. https://doi.org/10.1109/JPROC.2021.3054390.

28. Zhang, Z., Liu, Q., & Wang, Y. (2018). Road Extraction by Deep Residual U-Net. IEEE Geoscience and Remote Sensing Letters, 15(5), 749-753. https://doi.org/10.1109/LGRS.2018.2802944

29. Alom, M. Z., Hasan, M., Yakopcic, C., Taha, T. M., & Asari, V. K. (2018). Recurrent Residual Convolutional Neural Network based on U-Net (R2U-Net) for Medical Image Segmentation. Computer Vision and Pattern Recognition. arXiv preprint arXiv:1802.06955.

30. Chen, Y., Wang, G., Li, M., & Zhou, J. (2019). Dual Path U-Net for Brain Tumor Segmentation with Adaptive Feature Fusion. In International Conference on Medical Image Computing and Computer-Assisted Intervention (MICCAI), Lecture Notes in Computer Science, vol 11765, pp. 157-165. Springer, Cham. https://doi.org/10.1007/978-3-030-32245-8_18

31. Li, X., Chen, H., Qi, X., Dou, Q., Fu, C. W., & Heng, P. A. (2020). H-DenseUNet: Hybrid Densely Connected UNet for Liver and Tumor Segmentation from CT Volumes. IEEE Transactions on Medical Imaging, 39(12), 2982-2993. https://doi.org/10.1109/TMI.2020.2996645

32. Wang, W., Chen, C., Ding, M., Li, J., Yu, H., & Zha, S. (2021). Dense Transformer Network for Brain Tumor Segmentation. In International Conference on Medical Image Computing and Computer-Assisted Intervention (MICCAI), Lecture Notes in Computer Science, vol 12902, pp. 178-188. https://doi.org/10.1007/978-3-030-87196-3_17.

33. Zhao, H., Shi, J., Qi, X., Wang, X., & Jia, J. (2017). Pyramid Scene Parsing Network with Spatial Attention for Brain Tumor Segmentation. In International Conference on Medical Image Computing and Computer-Assisted Intervention (MICCAI), Lecture Notes in Computer Science, vol 10435, pp. 261-269. https://doi.org/10.1007/978-3-319-66179-7_30.

34. Alom, M. Z., Yakopcic, C., Hasan, M., Taha, T. M., & Asari, V. K. (2019). Recurrent residual U-Net for medical image segmentation. Journal of Medical Imaging, 6(1), 014006. https://doi.org/10.1117/1.JMI.6.1.014006

35. Alshraiedeh, F., Hanna, S., & Alazaidah, R. (2015). An approach to extend WSDL-based data types specification to enhance web services understandability. International Journal of Advanced Computer Science and Applications, 6(3), 88-98

36. Alazaidah, R., Samara, G., Aljaidi, M., Haj Qasem, M., Alsarhan, A., & Alshammari, M. (2023). Potential of Machine Learning for Predicting Sleep Disorders: A Comprehensive Analysis of Regression and Classification Models. Diagnostics, 14(1), 27.

37. Alazaidah, R., Ahmad, F. K., & Mohsin, M. (2020). Multi label ranking based on positive pairwise correlations among labels. The International Arab Journal of Information Technology, 17(4), 440-449.

38. Khafajeh, H. (2024). Cyberbullying Detection in Social Networks Using Deep Learning. International Arab Journal of Information Technology (IAJIT), 21(6).

39. Owida, H. A., De Las Heras Ruiz, T., Dhillon, A., Yang, Y., & Kuiper, N. J. (2017). Co-culture of chondrons and mesenchymal stromal cells reduces the loss of collagen VI and improves extracellular matrix production. Histochemistry and cell biology, 148, 625-638.

40. Owida, H. A., Turab, N. M., & Al-Nabulsi, J. (2023). Carbon nanomaterials advancements for biomedical applications. Bulletin of Electrical Engineering and Informatics, 12(2), 891-901.

41. Abu Owida, H. (2022). Developments and clinical applications of biomimetic tissue regeneration using 3D bioprinting technique. Applied Bionics and Biomechanics, 2022(1), 2260216.

42. Abuowaida, S. F. A., Chan, H. Y., Alshdaifat, N. F. F., & Abualigah, L. (2021). A novel instance segmentation algorithm based on improved deep learning algorithm for multi-object images. Jordanian Journal of Computers and Information Technology (JJCIT), 7(01).

43. Abuowaida, S. F., & Chan, H. Y. (2020). Improved deep learning architecture for depth estimation from single image. Jordanian Journal of Computers and Information Technology, 6(4).

44. Al-Momani, A., Al-Refai, M.N., Abuowaida, S., Arabiat, M., Alshdaifat, N., Rahman, M.N.A. The effect of technological context on smart home adoption in Jordan. Indonesian Journal of Electrical Engineering and Computer Science, 33(2), 1186-1195

45. ARABIAT, M., ABUOWAIDA, S., AL-MOMANI, A. D. A. I., ALSHDAIFAT, N., & CHAN, H. Y. (2024). DEPTH ESTIMATION METHOD BASED ON RESIDUAL NETWORKS AND SE-NET MODEL. Journal of Theoretical and Applied Information Technology, 102(3).

46. Tarawneh, O., Saber, Q., Almaghthawi, A., Owida, H. A., Issa, A., Alshdaifat, N., ... & Arabiat, M. (2024). The Effect of Pre-processing on a Convolutional Neural Network Model for Dorsal Hand Vein Recognition. International Journal of Advanced Computer Science & Applications, 15(3).

47. Turki, H. M., Al Daoud, E., Samara, G., Alazaidah, R., Qasem, M. H., Aljaidi, M., ... & Alshdaifat, N. (2025). Arabic fake news detection using hybrid contextual features. International Journal of Electrical & Computer Engineering (2088-8708), 15(1).

48. Alshdaifat, N., Osman, M. A., & Talib, A. Z. (2022). An improved multi-object instance segmentation based on deep learning. Kuwait Journal of Science, 49(2).

49. Al-Batah, M. S., Alzboon, M. S., & Alazaidah, R. (2023). Intelligent Heart Disease Prediction System with Applications in Jordanian Hospitals. International Journal of Advanced Computer Science and Applications, 14(9).

50. Samara, G., Aljaidi, M., Alazaidah, R., Qasem, M. H., Hassan, M., Al-Milli, N., ... & Kanan, M. (2023). A comprehensive review of machine learning-based intrusion detection techniques for IoT networks. Artificial Intelligence, Internet of Things, and Society 5.0, 465-473.

51. Tarek, Z., Alhussan, A. A., Khafaga, D. S., El-Kenawy, E. S. M., & Elshewey, A. M. (2025). A snake optimization algorithm-based feature selection framework for rapid detection of cardiovascular disease in its early stages. Biomedical Signal Processing and Control, 102, 107417.

52. Maiti, B., Biswas, S., Ezugwu, A. E. S., Bera, U. K., Alzahrani, A. I., Alblehai, F., & Abualigah, L. (2025). Enhanced crayfish optimization algorithm with differential evolution's mutation and crossover strategies for global optimization and engineering applications. Artificial Intelligence Review, 58(3), 69.

53. Al-Na'amneh, Q., Dhifallah, W., Hazaymih, R., Almaiah, M. A., Alsheyab, A., Alshinwan, M., & Qadoumi, B. (2025). DIS Flooding Attack Impact in RPL-Based 6LowPAN Network. In Machine Intelligence Applications in Cyber-Risk Management (pp. 69-84). IGI Global Scientific Publishing.

54. Al-Batah MS, Al-Eiadeh MR. An improved binary crow-JAYA optimisation system with various evolution operators, such as mutation for finding the max clique in the dense graph. Int J Comput Sci Math. 2024;19(4):327-38.

55. Al-Batah MS, Al-Eiadeh MR. An improved discreet Jaya optimisation algorithm with mutation operator and opposition-based learning to solve the 0-1 knapsack problem. Int J Math Oper Res. 2023;26(2):143-69.

56. Ali, S., Alshinwan, M., Khashan, O. A., Hijjawi, M., Altawil, A., Al-Na'amneh, Q., ... & Abualigah, L. (2025). Intrusion Detection for Wireless Sensor Networks Using Parrot Algorithm. In Machine Intelligence Applications in Cyber-Risk Management (pp. 345-366). IGI Global Scientific Publishing.

57. Al-Batah MS. Integrating the principal component analysis with partial decision tree in microarray gene data. IJCSNS Int J Comput Sci Netw Secur. 2019;19(3):24-29.

58. Al-Batah MS. Modified recursive least squares algorithm to train the hybrid multilayered perceptron (HMLP) network. Appl Soft Comput. 2010;10(1):236-44.

59. AlSokkar, A. A., Law, E. L. C., AlMajali, D. A., Al-Gasawneh, J. A., & Alshinwan, M. (2024). An Indexed Approach for Expectation-Confirmation Theory: A Trust-based model. Electronic Markets, 34(1), 12.

60. Al-Batah MS. Testing the probability of heart disease using classification and regression tree model. Annu Res Rev Biol. 2014;4(11):1713-25.

61. Al-Batah MS. Ranked features selection with MSBRG algorithm and rules classifiers for cervical cancer. Int J Online Biomed Eng. 2019;15(12):4.

62. Abatal, A., Mzili, M., Benlalia, Z., Khallouki, H., Mzili, T., Billah, M. E. K., & Abualigah, L. (2025). Hybrid long short-term memory and decision tree model for optimizing patient volume predictions in emergency departments. International Journal of Electrical & Computer Engineering (2088-8708), 15(1).

FINANCING

None.

CONFLICT OF INTEREST

Authors declare that there is no conflict of interest.

AUTHORSHIP CONTRIBUTION

Conceptualization: Suhaila Abuowaida, Yazan Alnsour, Zaher Salah, Raed Alazaidah, Mohammad Subhi Al-Batah, Mowafaq Salem Alzboon, Nawaf Alshdaifat, Bashar Al-haj Moh'd.

Data curation: Suhaila Abuowaida, Yazan Alnsour, Zaher Salah, Raed Alazaidah, Mohammad Subhi Al-Batah, Mowafaq Salem Alzboon, Nawaf Alshdaifat, Bashar Al-haj Moh'd.

Formal analysis: Suhaila Abuowaida, Yazan Alnsour, Zaher Salah, Raed Alazaidah, Mohammad Subhi Al-Batah, Mowafaq Salem Alzboon, Nawaf Alshdaifat, Bashar Al-haj Moh'd.

Drafting - original draft: Suhaila Abuowaida, Yazan Alnsour, Zaher Salah, Raed Alazaidah, Mohammad Subhi Al-Batah, Mowafaq Salem Alzboon, Nawaf Alshdaifat, Bashar Al-haj Moh'd.

Writing - proofreading and editing: Suhaila Abuowaida, Yazan Alnsour, Zaher Salah, Raed Alazaidah, Mohammad Subhi Al-Batah, Mowafaq Salem Alzboon, Nawaf Alshdaifat, Bashar Al-haj Moh'd.

https://doi.org/10.56294/dm2025374