

# **Brain Tumor Segmentation using a Hybrid Multi-Resolution U-Net with Residual Dual Attention and Deep Supervision on MR Images**

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## **Abstract**

Tumors are the uncontrolled multiplication of cells in the human body. Benign tumors are non-cancerous and do not spread to other body parts. Even though benign tumors are less aggressive, they can increase in mass and become malignant. If a tumor spreads to other organs, it is called metastasis. Malignant tumors are cancerous, may penetrate nearby tissues, and migrate to other organs. These cells aggressively multiply at an unpredictable rate and can be life-threatening. Diagnosing a tumor, and treatment planning are important for improving the prognosis of a patient.

In the diagnosis phase, clinicians and radiologists use medical radiology images of the brain to locate and analyze the characteristics of any likely tumor. The general literature focuses on using MR imaging as it provides a non-invasive, non-ionizing, and information-rich Spatio-temporal image. They show good contrast over the softer body tissues that help the clinician get a better understanding of the tumor and its surrounding tissues. From the MR images, identification of tumor volumes, shape, and size is important for treatment planning. However, manual identification of brain tumors from MR images is laborious, time-consuming, and human error-prone. Automatic segmentation of brain tumors from MR images aims to bridge the gap.

Computationally segmenting the tumor region from MR images is a difficult task due to image artifacts like image noise, low contrast, and intensity inhomogeneity. U-Net, a deep learning model, has delivered promising results in generating brain tumor segments. However, the model tends to over-segment the tumor volume than required. It will have a significant impact on deploying the model for practical use. The work focuses on the baseline U-Net model with the addition of residual, multi-resolution, dual attention, and deep supervision blocks. The goal of residual blocks is to efficiently extract features to reduce the semantic gap between low-level features from the decoder and high-level features from skip connections. The multiple resolution blocks have been added to extract features and analyze tumors of varying scales. The dual attention mechanism has been incorporated to highlight tumor representations and reduce over-segmentation. Finally, deep supervision blocks have been added to utilize features from various decoder layers to obtain the target segmentation. The proposed model has been trained and evaluated on the BraTS2020 training and validation datasets. On the validation data, the proposed model has achieved a dice score of 0.60, 0.75, 0.62 for enhancing tumor (ET), whole tumor (WT), and tumor core (TC), respectively, and a Hausdorff95 score of 46.84, 11.05, and 22.5, respectively. Compared to the baseline U-Net, the proposed model has outperformed WT and TC volumes in the Hausdorff95 distance metric except for the ET volume.