Derna Academy Journal for Applied Sciences

E-ISSN: 3006-3159

DAJAS

U-Net Based Approach for Brain Tumor Segmentation

Abdelkader Alrabai

Physics Department, Faculty of Education, Wadi Alshatti University, Alshatti – Libya

E-mail addresses: a.alrabai@wau.edu.ly

Volume: 4 **Issue: 2** **Page Number: 76 - 84**

Keywords:
Brain tumor; CNN; Segmentation; U-net.

Received: 15\08\2025
Accepted: 30\09\2025
Published: 01\10\2025

DOI:https://doi.org/10.71147/25jgwp11

ABSTRACT

Brain tumor segmentation plays a vital role in medical image analysis, offering crucial insights for diagnosis, treatment planning, and surgical guidance. However, manual segmentation by radiologists is often time-intensive, subjective, and susceptible to variability between observers. In this study, an automated segmentation approach is proposed using a U-Net-based convolutional neural network (CNN), which is specifically tailored for biomedical image segmentation tasks. The model is trained and tested on MRI images, with preprocessing and data augmentation techniques applied to improve its generalization performance. To evaluate the effectiveness of the segmentation, commonly used metrics such as dice coefficient, Intersection over Union (IoU), accuracy, and sensitivity are employed. These metrics collectively assess the model's precision in identifying tumor boundaries, ensuring high overlap with tumor regions while minimizing errors like false positives and false negatives. The used model achieved an accuracy of 99.44%, a Dice score of 83.76%, and an IoU of 72.70%. These results demonstrate the U-Net-based framework's robustness and reliability, highlighting its potential to assist radiologists in achieving faster and more consistent brain tumor segmentation.

1. INTRODUCTION

A brain tumor is an atypical growth of cells that can arise in various regions inside the skull, including the brain tissue, cranial nerves, protective membranes (meninges), the bony skull itself, or glands such as the pituitary and pineal. These tumors are generally categorized according to the specific cell type from which they emerge. They may be primary, originating directly within the brain, or secondary (metastatic), having spread to the brain from cancer located in another part of the body *(KK et al., 2013)*. Detecting brain tumors early significantly increases the likelihood of successful treatment. Various brain imaging techniques—like PET, SPECT, CT, and especially MRI—are used to gather vital information about a tumor's location, size, shape, and type. MRI is particularly valuable because it provides detailed images of soft tissues and is widely available. While spotting tumors in MRI scans is relatively simple, outlining the tumor's exact structure is much more complex.

This detailed mapping, known as segmentation, is crucial for understanding the tumor, planning surgery, and choosing the right treatment *(Abd-Ellah et al., 2019)*. Segmenting brain tumors from medical images is essential for improving diagnosis, guiding treatment, and evaluating clinical strategies. This process involves accurately identifying abnormal tissue in brain scans, which sharpens structural understanding and allows for detailed measurement. Segmentation can be done either by experts manually or through automated systems. Manual work, however, is time-consuming, depends heavily on individual skill, and often lacks consistency. Image distortions from scanning limitations, along with the unpredictable shape, location, and unclear edges of many tumors, make this task especially challenging *(Kaifi, 2023)*. Automated segmentation helps speed up medical workflows by reducing the time spent on image analysis and giving doctors more accurate views of anatomical structures or disease. Early in the analysis process, semantic segmentation improves results by filtering out unnecessary details and focusing on key areas like tumors or organ outlines. Segmentation techniques typically fall into two types: semantic segmentation, which labels each pixel based on category, and instance segmentation, which also separates different instances of the same structure. Building reliable models for identifying diseased versus healthy tissue—or mapping specific regions—depends on well-prepared datasets with detailed, expert-labeled examples that reflect the complexity of medical images *(Azad et al, 2024)*. The complexities of diagnosing brain tumors through manual interpretation have driven a growing reliance on advanced computational methods. In particular, researchers are increasingly turning to intelligent algorithms—most notably, machine learning and its deep learning subfield—to streamline and strengthen diagnostic workflows. Among these, Convolutional Neural Networks (CNNs) have had a transformative impact, enabling models to autonomously extract layered, data-driven patterns from raw medical images without the need for handcrafted features. CNNs have proven especially effective in demanding tasks such as tumor localization, segmentation, and classification *(Missaoui et al, 2025)*. Semantic segmentation works by labeling each pixel in an image according to its category. This is often done using models built around an encoder-decoder structure, like FCN, DeepLab, and especially U-Net. These models first simplify the input into compact features, then reconstruct a detailed output. While effective, they do not always make it clear how decisions are made. U-Net stands out in medical imaging for its unique design: it mirrors the encoder and decoder and includes skip connections that link early and late layers. This setup helps the model combine small details with the bigger picture—crucial in medical scans, which often have unclear edges and background noise *(Wang et al., 2022)*. Brain tumor segmentation has seen notable progress, with U-Net models becoming widely used for their strength in handling intricate image features. Researchers have introduced a range of modifications aimed at boosting precision, speed, and reliability. These developments have been tested across different datasets and rely on varied preprocessing methods to refine outcomes and address practical challenges. *Obayya et al.* (2025) introduced a U-Net variant with nested skip connections and custom loss functions, achieving strong results on a low-grade glioma dataset. *Walsh et al.* (2022) developed a lightweight U-Net that performs real-time segmentation with minimal training data, showing solid results on the BITE dataset. *Cherguif et al.* (2019) applied deep convolutional U-Net models to BRATS 2017 data, demonstrating reliable performance on both high- and low-grade gliomas. *Kasar et al.* (2024) compared U-Net and SegNet for tumor segmentation, focusing on fully automated approaches using encoder-decoder structures. *Van Truong and Thao* (2021) incorporated a hybrid loss function combining dice and level set loss to enhance accuracy, especially for finer structures, using a dataset of around 4,000 MRI slices. *Ghosh and Santosh* (2021) compared standard U-Net models with versions using a ResNeXt50 backbone and feature pyramid networks, showing competitive results on the TCGA-LGG dataset. *Hamim and Jony* (2024) proposed a deeper U-Net model with multi-inception modules and normalization techniques, tested on BraTS 2019 data, to reduce manual effort and improve segmentation precision. Segmenting brain tumors from MRI scans is a key step in diagnosing and treating patients; however, manual methods are often slow, inconsistent, and subjective. This study develops an automated segmentation system based on a U-Net. The model is trained on MRI data using preprocessing and augmentation techniques to improve accuracy and reliability, aiming to support radiologists with consistent and precise tumor identification.

2. METHOD

The proposed method focuses on the development of an automated brain tumor segmentation system utilizing the U-Net architecture, specifically tailored for processing MRI images. This approach leverages the strengths of U-Net in capturing both global context and fine-grained localization, which are essential for accurately delineating tumor regions within complex brain structures. The overall process involves several key stages, including data preprocessing, model training, and prediction. The structure of the method and its sequential pipeline is illustrated in Figure 1, outlining the complete workflow from data input to the ultimate segmented output.

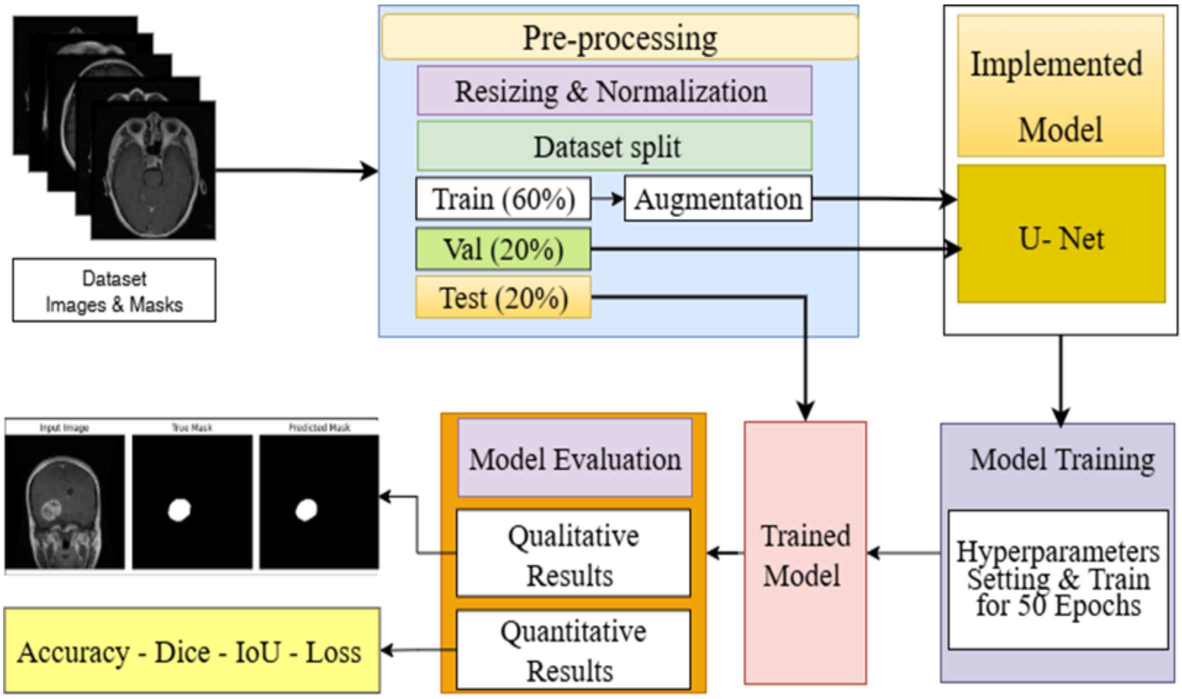

Fig. 1 Methodological Workflow

2.1. DATASET AND PRE-PROCESSING

The dataset used in this study is from Figshare (Cheng, 2017), comprising 3064 MRI images along with their corresponding 3064 segmentation masks. These images are used to train and evaluate the model for medical image analysis. Figure 2 displays few representative samples illustrating both the original MRI images and their corresponding masks taken from dataset used in this study.

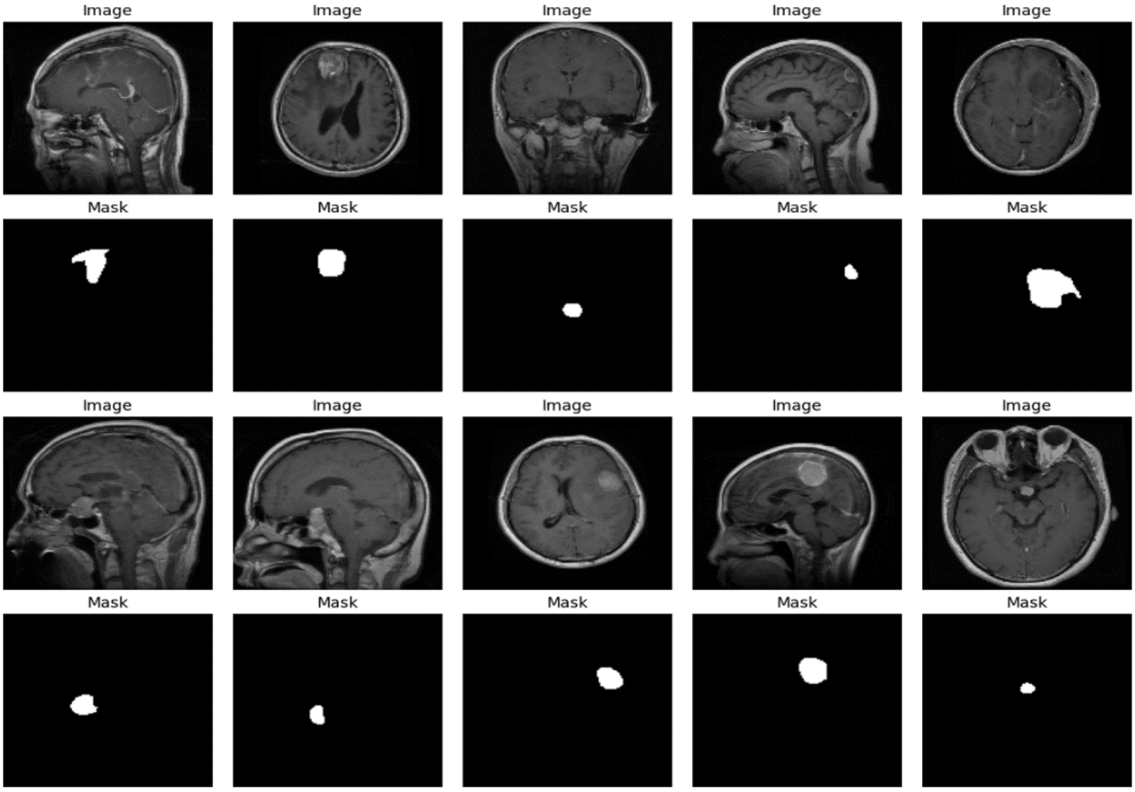

Fig. 2 Dataset Example Samples

Preprocessing is essential for improving the quality and consistency of MRI input data. The dataset is split into 60% for training, 20% for validation, and 20% for testing to ensure a balanced evaluation of the model's performance. The training set is used to fit the model, the validation set helps tune hyperparameters and prevent overfitting, and the test set is reserved for final performance assessment on unseen data. All images and their corresponding masks are resized to 256×256 pixels to ensure compatibility with the U-Net model's input requirements. Intensity normalization is applied to minimize variations across scans. During training, the U-Net model learns to segment tumor regions, producing binary masks that highlight tumor boundaries. In addition, to enhance generalization and reduce overfitting, various data augmentation techniques—such as random horizontal mirroring, positional and dimensional adjustments through shifting, scaling, and rotation, and intensity-based enhancements via brightness and contrast alterations—are used, simulating real-world variability and improving model robustness.

2.2. IMPLEMENTED MODEL

U-Net (Ronneberger et al., 2015) is a pioneering deep learning architecture designed specifically for biomedical image segmentation, where pixel-level accuracy is essential for identifying structures such as cells, tumors, and organs. Unlike traditional classification tasks that assign a single label to an entire image, segmentation requires labeling each pixel, making the task more complex—especially in medical contexts where annotated data is limited. U-Net was developed to address this need, particularly in high-resolution medical imaging applications like microscopy. The architecture is characterized by its distinctive U-shaped structure, composed of a contracting path (encoder) and an expansive path (decoder). The encoder extracts contextual features through repeated convolution and max-pooling layers, reducing spatial dimensions while capturing semantic information. The decoder then reconstructs the spatial resolution using transposed convolutions. A key innovation of U-Net is its skip connections between corresponding layers in the encoder and decoder. These connections ensure that fine-grained spatial information, lost during downsampling, is retained and integrated into the upsampling process—thereby enabling precise localization crucial for segmentation tasks. Figure 3 illustrates the U-Net architecture, highlighting the symmetric design and the role of skip connections in feature preservation.

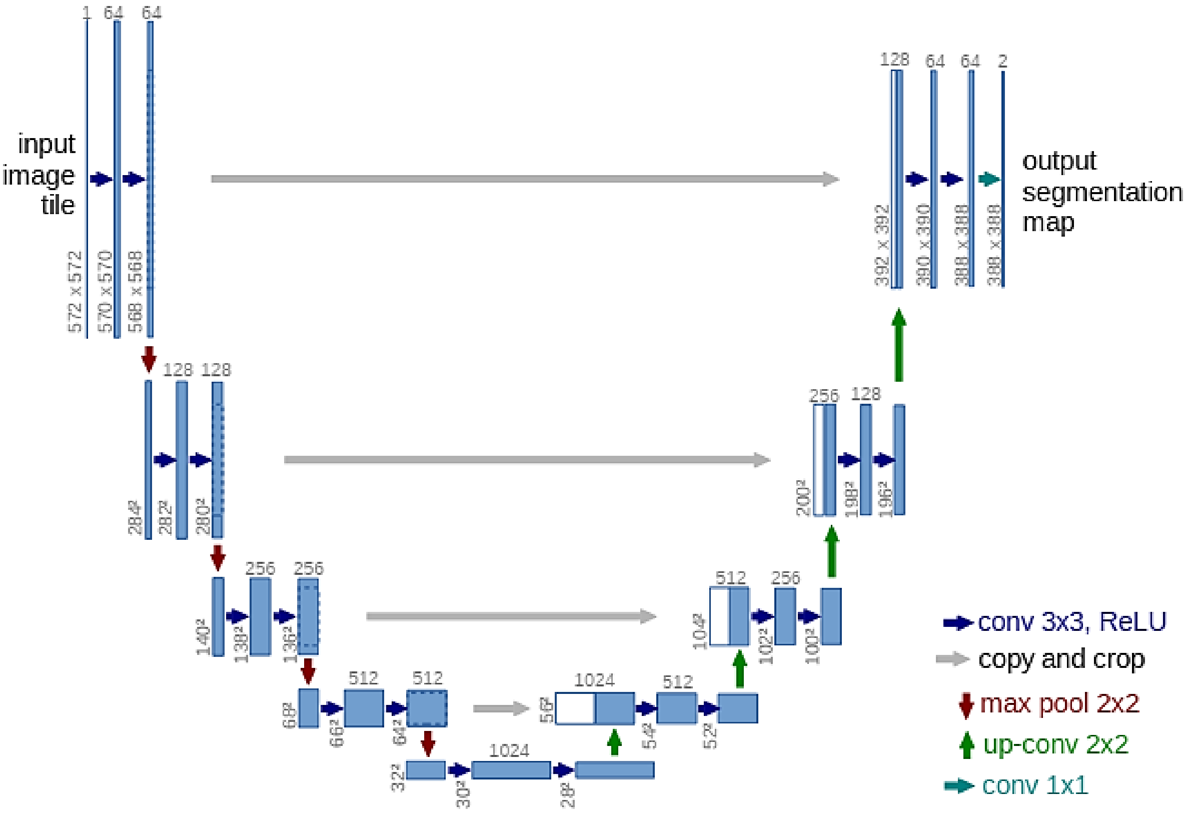

Fig. 3 U-net blueprint [15]

The implemented U-Net follows the same architectural structure illustrated in Figure 3, with minor modifications. These include the addition of extra convolutional layers within each block to enhance feature extraction, and an adjustment to the input image dimensions, which are resized to 256×256 pixels for compatibility with the network.

2.2. TRAINING AND EVALUATION

The model is trained using a set of carefully selected parameters to optimize performance. The key training hyperparameters and their respective values are detailed in Table 1, providing insight into the training configuration used for this study.

Table 1 Training Parameters

Parameters	**Configuration**
Optimizer	Adam
Loss	Combination (Dice and Binary)
Initial learning rate	0.0001
Batch Size	16
Epochs	50

To assess segmentation performance, several evaluation measures are employed, each capturing a different aspect of model behavior. The Dice Score, a key indicator, reflects how closely the predicted regions align with the actual tumor areas—higher values signify better overlap. Similarly, the IoU gauges the accuracy of shape and size by comparing the overlap area to the total combined area of predicted and true segments. Pixel-wise accuracy is also considered, though it may be misleading in datasets with class imbalance, where non-tumor regions dominate. Throughout training, the loss value is monitored to indicate how far the predictions deviate from the ground truth, playing a central role in model optimization. Collectively, these measures offer a layered understanding of the model's ability to deliver precise, consistent, and clinically meaningful segmentation results.

3. ETHIC APPROVAL

This study utilized the publicly available brain tumor MRI dataset published by Jun Cheng on Figshare (Cheng, 2017).

4. RESULTS AND DISCUSSIONS

The performance of the segmentation model is evaluated through both quantitative and qualitative analyses. The quantitative assessment involves key evaluation metrics, which collectively measure the effectiveness of the model's segmentation capabilities. Complementing these numerical results, the qualitative evaluation presents visual comparisons between the predicted segmentation masks and the ground truth, providing deeper insight into the model's ability to accurately capture fine structural features. Figure 4, displays four plots illustrating the training and validation performance of a model over 50 epochs.

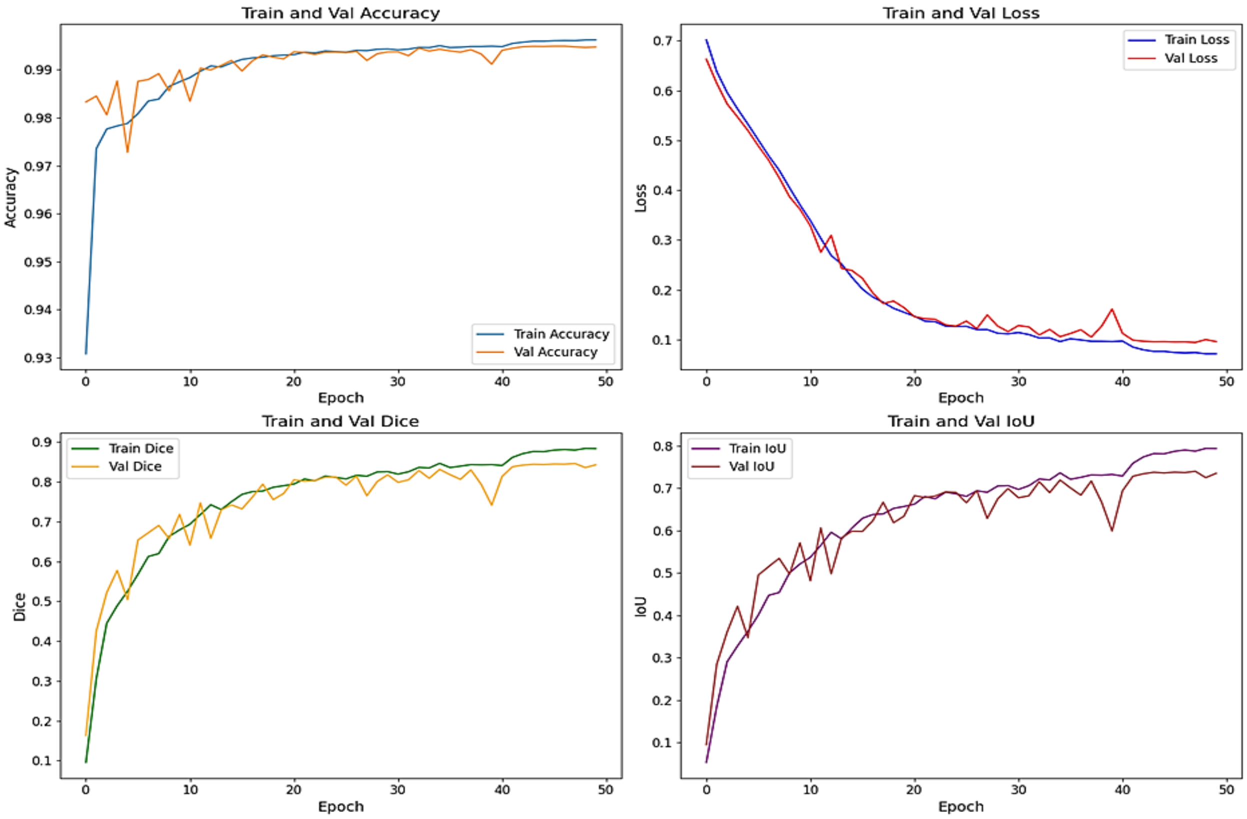

Fig. 4 Train and Validation Performance

Training and validation accuracy reflect how well the model performs on both the training and unseen validation datasets. During the initial epochs, there is a steep rise in accuracy for both sets, quickly exceeding 95%. As training continues, the accuracy steadily improves and ultimately stabilizes above 99%, indicating that the model is effectively learning the task and generalizing well to new data. Training and validation loss track the model's error on the respective datasets. Both loss curves exhibit a sharp decline early in training, highlighting rapid improvements. Over time, the rate of decrease slows, and the loss values settle below 0.1, suggesting that the model is approaching convergence with minimal error. Training and validation Dice scores capture how well the model segments images, with the Dice coefficient being a standard measure in this domain. Both training and validation Dice values rise swiftly in the first few epochs. As training progresses, the scores level off above 0.8, with the validation set typically showing slightly lower values than the training set—an expected outcome in most learning scenarios. Training and validation IoU measure the overlap between predicted and actual segmentation masks. Similar to the Dice trend, both IoU curves rise significantly in the early stages, then gradually plateau. Final IoU values range between 0.7 and 0.8, suggesting a strong match between predictions and ground truth. Ultimately, as illustrated in Figure 4, the upward trends in accuracy, Dice, and IoU—alongside the downward trend in loss—demonstrate that the model is learning effectively and has largely converged by the 50th epoch. These metrics together indicate solid performance across training and validation phases. The experimental results of performance of the U-Net model are summarized in Table 2.

Table 2 Performance Results

Metrics	**Accuracy**	**Dice**	**IoU**	**Loss**
U-net	0.9944	0.8376	0.7270	0.0998

The model achieved an accuracy of 99.44%, indicating that the vast majority of pixel classifications were correct. However, while accuracy is high, it can sometimes be misleading in segmentation tasks with class imbalance. Therefore, more informative metrics such as Dice and IoU were also considered. The U-Net model reached a dice score of 0.8376, reflecting a good balance between precision and recall in the predicted segmentation masks. This suggests that the model effectively captures the overlap between predicted and ground truth regions.

Additionally, the IoU score of 0.7270 further confirms the model's ability to produce accurate segmentation boundaries, although slightly lower than the Dice score, as expected due to its stricter calculation. Moreover, the loss value of 0.0998 indicates effective convergence during training, with relatively low prediction error. Overall, the results in Table 2 highlight U-Net's robustness and effectiveness in medical image segmentation tasks. These results support the effectiveness of the proposed approach in providing a reliable and automated solution for brain tumor segmentation in clinical settings.

Figure 5 presents qualitative results from a random test sample, illustrating the model's segmentation performance. It includes the original input images, the corresponding ground truth masks highlighting the target regions, and the predicted masks generated by the model. Visual comparison between the true and predicted masks allows for an intuitive assessment of how accurately the model identifies and segments the regions of interest.

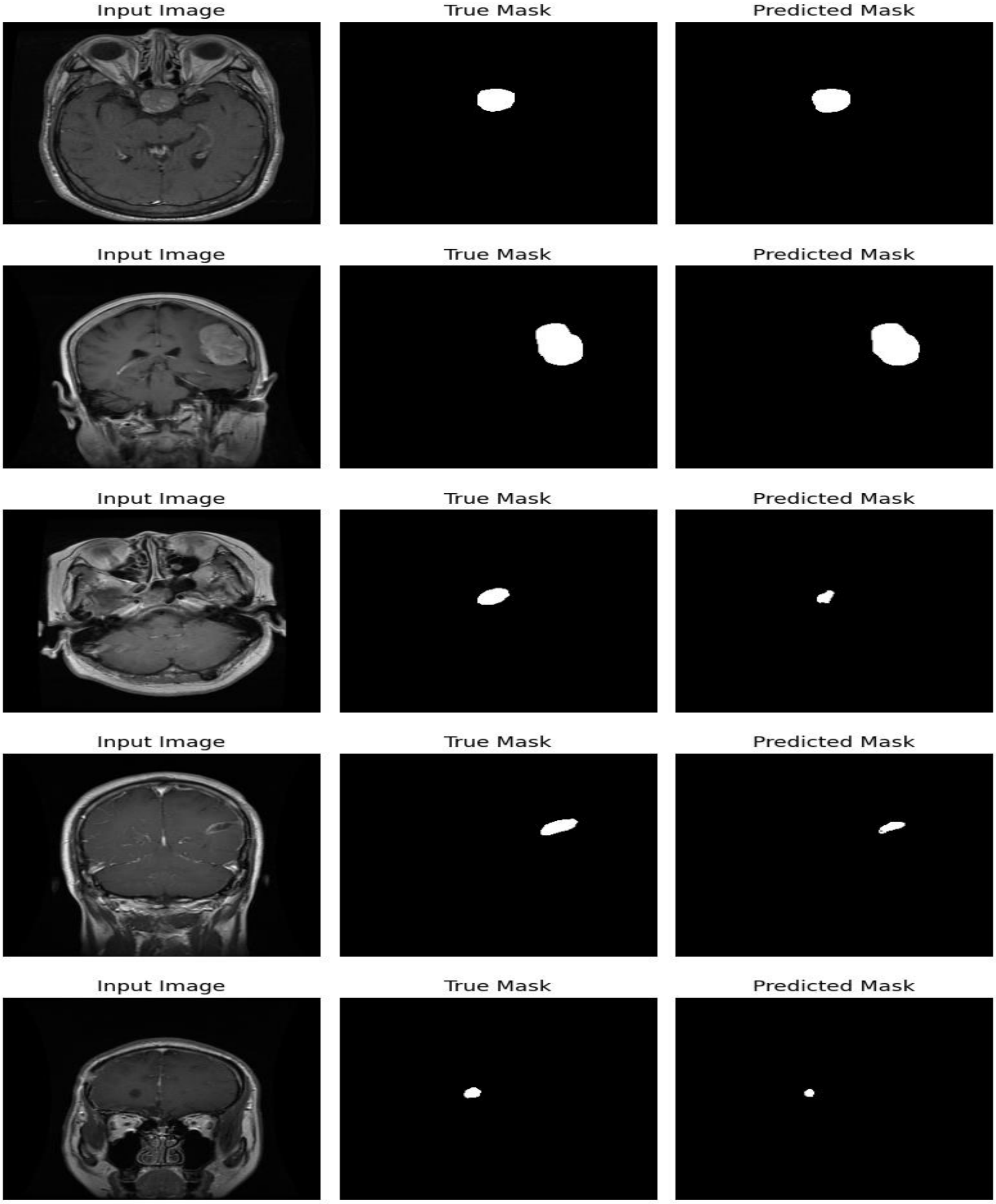

Fig. 5 Visual Results

In most instances in Figure 5, the predicted masks appear to closely resemble the true masks in terms of shape, size, and location, suggesting that the model is performing well in identifying the target structures. There might be slight variations in boundary precision or small discrepancies, but overall, the visual comparison indicates effective segmentation by the model.

Ultimately, Figure 5 provides a visual validation of the segmentation model's performance by showcasing its ability to accurately predict masks that closely align with the true, manually annotated masks across various input medical images.

5. CONCLUSION

This study presented an automated framework for brain tumor segmentation using a U-Net-based CNN, specifically designed for biomedical image analysis. By leveraging MRI images, along with comprehensive preprocessing and data augmentation techniques, the model effectively learns to identify and delineate tumor regions. The use of standard evaluation metrics, including Dice, IoU, accuracy, and loss, demonstrates the model's strong performance. The proposed approach addresses the limitations of manual segmentation by offering a faster, more consistent, and objective alternative, which can assist radiologists in clinical decision-making and treatment planning. Overall, the results validate the potential of deep learning–based methods to enhance the accuracy and efficiency of brain tumor analysis. Future work may explore integrating multi-modal data, refining model architecture, and applying the framework to larger and more diverse datasets to further improve performance and generalizability.

6. REFERENCES

Abd-Ellah, M. K., Awad, A. I., Khalaf, A. A., & Hamed, H. F. (2019). A review on brain tumor diagnosis from MRI images: Practical implications, key achievements, and lessons learned. Magnetic resonance imaging, 61, 300-318.

Cheng, Jun (2017). brain tumor dataset. figshare. Dataset. https://doi.org/10.6084/m9.figshare.1512427.v8

Cherguif, H., Riffi, J., Mahraz, M. A., Yahyaouy, A., & Tairi, H. (2019, December). Brain tumor segmentation based on deep learning. In 2019 International Conference on Intelligent Systems and Advanced Computing Sciences (ISACS) (pp. 1-8). IEEE.

Ghosh, S., & Santosh, K. C. (2021, June). Tumor segmentation in brain MRI: U-Nets versus feature pyramid network. In 2021 IEEE 34th International Symposium on Computer-Based Medical Systems (CBMS) (pp. 31-36). IEEE.

Hamim, S. A., & Jony, A. I. (2024). Enhancing brain tumor MRI segmentation accuracy and efficiency with optimized U-Net architecture. Malaysian Journal of Science and Advanced Technology, 197-202.

Kaifi, R. (2023). A review of recent advances in brain tumor diagnosis based on AI-based classification. Diagnostics, 13(18), 3007.

Kasar, P., Jadhav, S., & Kansal, V. (2024, October). Brain Tumor Segmentation using U-Net and SegNet. In International Conference on Signal Processing and Computer Vision (SIPCOV-2023) (pp. 194-206). Atlantis Press.

KK, K., Rajan, M. S., Hegde, K., Koshy, S., & Shenoy, A. (2013). A COMPREHENSIVE REVIEW ON BRAIN TUMOR. International Journal of Pharmaceutical, Chemical & Biological Sciences, 3(4).

Missaoui, R., Hechkel, W., Saadaoui, W., Helali, A., & Leo, M. (2025). Advanced Deep Learning and Machine Learning Techniques for MRI Brain Tumor Analysis: A Review. Sensors, 25(9), 2746.

Obayya, M., Alshuhail, A., Mahmood, K., Alanazi, M. H., Alqahtani, M., Aljehane, N. O., ... & Al-Hagery, M. A. (2025). A novel U-net model for brain tumor segmentation from MRI images. Alexandria Engineering Journal, 126, 220-230.

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: 18th international conference, Munich, Germany, October 5-9, 2015, proceedings, part III 18 (pp. 234-241). Springer international publishing.

Van Truong, P., & Thao, T. T. (2021). Brain tumor segmentation based on U-Net with image driven level set loss. Vietnam Journal of Science and Technology, 59(5), 634-642.

Walsh, J., Othmani, A., Jain, M., & Dev, S. (2022). Using U-Net network for efficient brain tumor segmentation in MRI images. Healthcare Analytics, 2, 100098.

Wang, R., Lei, T., Cui, R., Zhang, B., Meng, H., & Nandi, A. K. (2022). Medical image segmentation using deep learning: A survey. IET image processing, 16(5), 1243-1267.