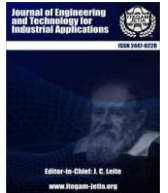




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RESEARCH ARTICLE

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AN EFFICIENT AND AUTOMATED BRAIN TUMOR SEGMENTATION IN MRI IMAGES USING NON-SUPERVISED MODEL

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ABSTRACT

Brain neoplasm is life-threatening abnormalities that require accurate segmentation for effective diagnosis along with treatment planning. Existing segmentation methods often depend on manual annotations or supervised learning, which are time-consuming, subjective, and not scalable. To overcome these challenges, this study proposes a fully unsupervised brain tumor segmentation framework using multimodal MRI data. The 3D MRI volumes are first sliced into 2D axial views and preprocessed to enhance quality. K-means clustering is then applied to generate pseudo-labels that distinguish tumor from healthy regions. These labels guide M-Net CNN training process, which produces coarse tumor localization. A U-Net model further refines the segmentation by fusing the original sliced MRI inputs with M-Net CNN outputs to enhance boundary precision and anatomical alignment. The proposed pipeline achieved a high Dice coefficient of 84.2%, demonstrating its accuracy and robustness. This multi-stage, annotation-free approach enables precise tumor delineation and is suitable for large-scale clinical integration.



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I. INTRODUCTION

Neoplasma of the brain is an extensive category of brain pathologies of high morbidity and mortality. High-accuracy volumetric segmentation and early detection are valuable to clinical applications like longitudinal monitoring, radiotherapy, and surgical planning. The main imaging modality in neuro-oncology is Magnetic Resonance Imaging (MRI) because it is a non-invasive procedure. Varying MRI sequences offer complementary diagnosis information: T1, T2, T1ce, and FLAIR. A combination of these modalities allows a complete tumor characterization and subregion definition. Radiologists usually annotate the tumors manually, and it represents the clinical reference used in a diagnosis and the basis used to train segmentation models. Nonetheless, the manual segmentation is labor-intensive, time-consuming and it is highly variable, making it difficult to scale up in other large datasets. This has been highlighted by supervised deep learning methods, particularly the U-Net and its variants [1], [2], to make an effective use of the spatial and contextual information in multimodal MRI samples to identify tumor subregions. However, they need large annotated datasets that are expensive to generate due to privacy limitations and require experts to be available. To eliminate these difficulties, unsupervised techniques of segmentation are studied. Unsupervised techniques identify tumor based on voxel intensities yet tend to produce inaccurate borders and poor generalizability [3]. The proposed work overcomes these limitations by using a combination of methods by exploiting the statistical intensity-based grouping and Deep learning (DL) in the context of learning the features in brain tumor segmentation based on convolutional neural networks (CNN) that is unsupervised. In the suggested framework, an MRI preprocessing step is followed by pseudo-label construction via intensity grouping and the structural accuracy refinement using CNN. The main research findings of the proposed work are as follows:

- To access the 2D images, the input 3D MRI volumes are sliced in the axial level where it is then preprocessed to increase contrast and image quality.
- To distinguish between healthy and tumor area an initial pseudo-labels are created by using K-means clustering on the unlabeled 2D slices.

- The pseudo-labels are used to train an M-Net CNN to learn spatial tumor features and generate improved and detailed segmentation maps.
- The U-Net has the raw slices of MRI data combined with the M-Net CNN outputs to complete segmentation with a greater precision of boundaries and consistency of anatomies.

II. LITERATURE REVIEW

The MRI image represents the standard in diagnosis of brain tumors by non-invasive technique, although manual segmentation is time-consuming and susceptible to error due to inter-observer variability. To automate this process, ML methods were initially applied. The [4] proposed a two-stage system that entailed refined binomial thresholding in localizing the tumor and feature-based classification using SVM, and Random Forest. [5] were able to improve upon the boundary refinement using a hybrid SVM-fuzzy classifier, albeit based on handcrafted features, in which little generalization was done across imaging modalities. Deep learning (DL) approaches advanced the field by learning hierarchical representations directly from data. [6] proposed a symmetrical encoder-decoder framework with a Threefold Attention Mechanism to enhance tumor boundary prediction across multimodal MR images. In [7] a deep neural network pipeline was constituted that detects tumor at early stage, and [8] improved the U-Net architecture by altering depth and skip interconnections to provide more structural detail forecasting. Model TACA-RNet proposed by [9] utilized the idea of tri-planar context and enhanced multimodal tumor segmentation. This binary tumor prediction utilised a traditional CNN in [10], though Z-Net demonstrated in [11] improvement at predicting the tumor boundaries using pyramid pooling to generate finer predictions in 2D slices. [12] decided to use a multi-scale attention mechanism with an EfficientNetB4 backbone since it proved useful in capturing tumor variations. Other more recent approaches leveraged a Transformer-GAN was done in [13] to provide more robust boundary prediction, as well as a hybrid ViT-CNN model was presented in [14], to enable explanatory glioma segmentation across MRIs. To address the dependency on annotated labels, unsupervised approaches have emerged. [15] proposed a two-stage GAN-based pipeline that synthesizes tumor-free and tumor-bearing images to generate pseudo-masks for segmentation prediction. [16] introduced a prompt-based unsupervised framework (PL-BTS) that predicts tumor-like regions through intensity prompts and pseudo-label refinement (PL-BTS+). [17] adopted a spatially variant finite mixture model with RJMCMC sampling to predict tumor regions based on probabilistic tissue distributions, offering label-free yet interpretable segmentation. These models shift the field toward scalable annotation-independent solutions, though trade-offs in computational demand and data quality remain. Current techniques used in segmenting the brain tumor have a number of limitations. Conventional methods of ML depend on handcrafted features that are weak on complex tumor structures and also noise-sensitive [4], [6]. Transformer-based and hybrid deep learning models have higher segmentation accuracy, but they are usually associated with high cost of computation and decreased interpretability under the clinical setting [13], [14]. In addition, DL models usually need a huge amount of labeled MRI data to be qualified which are costly and time-consuming to acquire [9], [10]. To address these challenges, the proposed method employs K-means clustering to generate pseudo-labels from unlabeled MRI slices, which guide an M-Net CNN for segmentation. A subsequent U-Net model refines this output by enhancing feature fusion and spatial consistency, enabling accurate tumor delineation in an unsupervised setting.

III. METHODOLOGY

As shown in Figure 1, the proposed approach performs brain neoplasm segmentation utilizing an unsupervised models framework for unlabeled MRI images. The 3D MRI volumes will be originally sliced in the axial plane in order to give 2D slices. Then preprocessing modalities used to improve image quality and contrast. The K-means clustering is then used to produce pseudo-labels that indicate tumor and non-tumor areas. These pseudo-labeled masks guide an M-Net convolutional neural network (CNN) towards segmenting a tumor. M-Net CNN's outputs, together with the corresponding raw sliced MRI images, are then given as input to a U-Net model. The U-Net performs feature fusion and spatial refinement, producing a precise and anatomically consistent tumor segmented part.

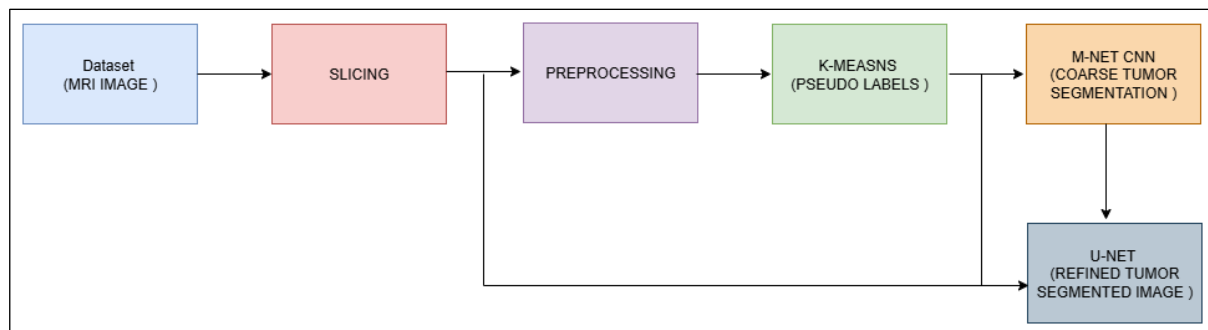


Figure 1: Overall architecture unsupervised learning pipeline.
Source: Authors, (2026).

III.1 DATASET

The proposed unsupervised brain tumor segmentation framework uses the BraTS 2019 dataset [18], which comprises 335 co-registered, skull-stripped, and multimodal MRI volumes of the T1, T1ce T2, and FLAIR sequences. These volumes are acquired with a uniform voxel resolution and follow standardized clinical acquisition protocols. In this study, the dataset is incorporated into an unsupervised learning pipeline, whereby ground-truth segmentation masks supplied in the training set are excluded from the learning procedure.

III.2 SLICING

In the BraTS 2019 set of data, each subject is represented by a 3D volumetric MRI scan acquired using 4 modalities: T1, T1ce, T2, and FLAIR. To enable efficient training of 2D DL models and reduce computational overhead, a slicing process is applied to convert 3D MRI volumes into 2D axial slices. Slicing is carried out in the axial plane, giving a sequence of 2D slices that retain spatial fidelity and tumor-related anatomical structures. These slices are extracted in a modality-wise manner, ensuring that for each 2D position, corresponding slices across all modalities are available and aligned. The stacked multi-modal 2D slice at axial index k is represented as:

$$S^{(k)} = [S_{T1}^{(k)}, S_{T1ce}^{(k)}, S_{T2}^{(k)}, S_{FLAIR}^{(k)}] \in R^{H \times W \times 4} \quad (1)$$

Where $S^{(k)}$ denotes the composite input formed by concatenating slices from all four modalities at position k , with H and W representing the spatial dimensions.

III.3 DATA PREPROCESSING

Following the slicing of 3D MRI volumes into 2D axial slices, a sequence of preprocessing operations is applied, all aimed at improving image quality and normalizing intensity characteristics across samples. First, average filtering is used to remove random noise and smoothen the image while conserving important structural and anatomical boundaries. This helps suppress high-frequency distortions and assists in achieving homogeneity of non-tumor regions. Then, histogram equalization is invoked as a means of contrast enhancement, meaning to redistribute pixel intensities uniformly across the dynamic range. This operation maximizes the visibility of subtle tumor boundaries and paves the way for effective segmentation of the slices. For model evaluation along with generalization analysis, a set of data was randomly split into train and test subsets using 80:20 ratio.

III.4 K-MEANS CLUSTERING PROCESS

Following the completion of the slicing and preprocessing stages, the enhanced multimodal two-dimensional MRI slices are utilized for pseudo-label generation using the K-means clustering algorithm. This unsupervised method segments each slice into two distinct clusters that correspond to tumor and healthy regions, based on pixel-wise intensity similarity patterns across modalities. For each axial position, the corresponding slices from a T1, T1ce, T2, and FLAIR modalities are stacked to form a tensor of size $H \times W \times 4$. In this representation, each pixel is described by a four-dimensional feature vector comprising the intensity values from four MRI sequences. Entire image is reshaped into a two-dimensional feature matrix of size $(H \times W) \times 4$, which is provided as input to the K-means clustering algorithm. The objective of K-means is to minimize intra-cluster variance, mathematically defined by

$$J = \sum_{j=1}^k \sum_{i=1}^n \|x_i^{(j)} - c_j\|^2 \quad (2)$$

Here, k denotes the number of clusters, n is a total number of pixels, $x_i^{(j)}$ represents pixel i^{th} assigned for cluster j , and c_j denotes corresponding centroid. The entire process of clustering commences with initialization of two centroids randomly in the feature space. Next, given data points are assigned to the most nearest centroid using Euclidean distance. Centroids are also updated by computing mean of all the vectors which are in a single cluster. This assignment along with update process continues repeated until convergence, which is reached when centroid positions remain stable across iterations. After convergence, the cluster assignments are reshaped to match the spatial dimensions $H \times W$, resulting in a binary pseudo-label mask that delineates tumor from healthy one.

III.5 M-NET CNN

Following the generation of pseudo labels through K-means clustering, the tumor segmentation stage employs an end-to-end trainable CNN based on the M-Net architecture to identify brain tumor regions in an unsupervised manner. The input to this M-Net CNN consists of co-registered and preprocessed two-dimensional axial MRI slices from 4 modalities: FLAIR, T1, T1ce, and T2. These modalities are stacked along the channel dimension to form a single composite tensor of shape $H \times W \times 4$, allowing the network to exploit anatomical, structural, and contrast-related cues for accurate segmentation. M-Net CNN is symmetrically structured along the lines of encoder decoder, as illustrated in Figure 2. The architecture of M-Net is symmetrical where it has four different paths, one is the main encoder path, one is decoder path, and the other two are side paths which are conventionally named as the left leg and the right leg which can provide deep supervision and multi-scale features. Every encoder unit has two conv layers 3x3 kernel size, then batch normalization and ReLU. These cascade convolutional layers allow a gradual refinement of each layer. Each unit is concluded with 2x2 max pooling operation which decreases spatial dimensions with a maximum feature abstraction. The output of encoder layer feature map is as:

$$E(l) = \text{MaxPool}(\sigma(W^{(l)} * E^{(l-1)} + b^{(l)})) \quad (3)$$

Where, $E^{(0)}$ represents stacked multimodal MRI input, $W^{(l)}$ and $b^{(l)}$ denote the learnable weights and biases, $*$ represents convolution, and $\sigma(\cdot)$ is the ReLU activation function. The left leg of M-Net CNN applies four successive 2x2 max pooling operations to the input, providing multi-scale contextual features to the encoder blocks.

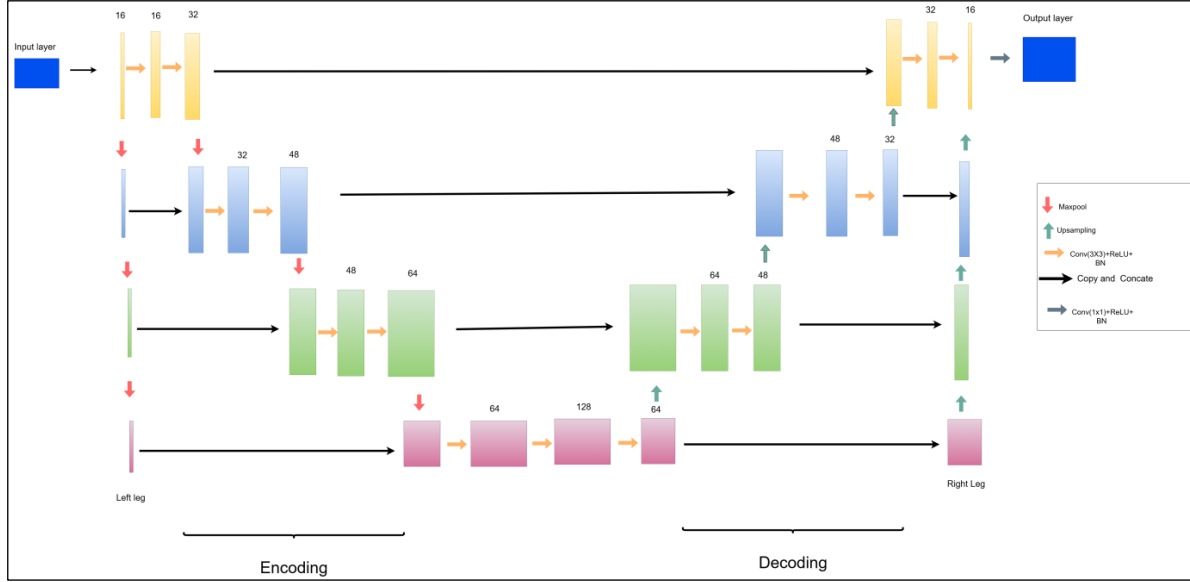


Figure 2: M-Net CNN architecture.
Source: Authors, (2026).

The bottleneck block adopts convolutional layers of deeper filter depth to acquire semantic feature in high level. The decoder is the reverse of the encoder where the first layer of each block involves a transposed convolution to upsample the block, and then the skip connections with the previous layers of the encoder are used to maintain fine-grained spatial information. The decoder path restores original spatial dimensions using transposed convolution operations and includes skip connections from encoder. The decoder feature map at level is obtained by:

$$D(l) = \sigma(W_{up}(l) * U_p(D^{(l+1)}) + W_{skip}^l * E^{(l)} + b^{(l)}) \quad (4)$$

Where $U_p(\cdot)$ denotes upsampling through transposed convolution, W_{up} and W_{skip} are the weights for upsampling and skip connections, respectively. Simultaneously, the right leg upsamples the outputs of each decoder block to the original resolution of input, enabling deep supervision. These auxiliary paths enhance the network's multi-scale learning and segmentation accuracy. The last stage of decoder performs a 1×1 convolution layer followed by a sigmoid, the output is a binary mask segmented of size $H \times W \times 1$ with pixel-wise tumor probabilities. The network is trained using pseudo labels generated by K-means clustering, eliminating the requirement for manually annotated ground truth. Dice loss function is used to optimize the segmentation learning by calculating overlap of predicted segmentation with pseudo label Y . The loss is defined as:

$$L_{Dice} = 1 - \frac{2 \sum_{i=1}^N \hat{Y}_i Y_i + \epsilon}{\sum_{i=1}^N \hat{Y}_i + \sum_{i=1}^N Y_i + \epsilon} \quad (5)$$

Where $\hat{Y}_i$ is a predicted value at pixel, Y_i gives pseudo label, N represents number of pixels, and ϵ denotes small constant to prevent division by zero. The output of M-Net is a binary segmentation mask aligned with spatial dimensions of input multimodal slice, effectively delineating tumor regions from healthy tissue. This is achieved using pseudo supervision derived from K-means clustering, thereby eliminating the requirement for manually annotated ground truth.

III.6 U-NET

Following the coarse tumor localization obtained from the M-Net CNN, a U-Net is employed to refine the tumor segmentation in an unsupervised manner. The input to the U-Net consists of preprocessed axial MRI slices from four modalities, along with the binary tumor mask from M-Net. These five inputs are stacked to form a composite tensor of shape $H \times W \times 5$. Such setup allows the U-Net to couple the anatomical differences between modalities with the crude localization of the tumor, to increase the ability of network for detecting refined tumor margins. U-Net design follows the symmetric encoder-decoder design which makes hierarchical feature learning easy. The encoder path has two convolutional blocks in each block are two convolutional layers of 3×3 kernels, batch normalization, ReLU activation, and a 2×2 max pooling layer as a spatial resizing block to detect high level and abstract features. Bottleneck layer is relating encoder and decoder, and it makes an aggregation of the contextual semantic representations. Spatial resolution is upscaled step by step through transposed convolutions in the decoder route. In order to maintain the spatial accuracy, the connection between related encoder and decoder layers is done using skip connections. These interactions make feature fusion possible by adding the encoder features of the high resolutions to decoder features which are increased through addition, which is mathematically expressed as:

$$D(l) = \sigma(w(l) * U_p[(D^{(l+1)}) || E^{(l)}] + b^{(l)}) \quad (6)$$

where $U_p(D^{(l+1)})$ is the upsampled decoder feature, $E^{(l)}$ is the encoder feature map, $||$ denotes channel-wise concatenation, and $\sigma(\cdot)$ gives ReLU activation. At the final stage of decoding, a 1×1 convolutional layer followed by a sigmoid activation function generates a binary segmentation mask of dimensions $H \times W \times 1$, indicating the pixel-wise probability of tumor presence.

The K-means predictions are used as pseudo labels to train the network, so no manually annotated ground truth is required. Dice loss function is used to optimize the overall segmentation level which measures the overlap between the mask generated in the segmentation and the pseudo label. Such features as feature fusion achieved with skip connections and multimodal plus auxiliary input channels allow the U-Net to demonstrate the refined and anatomic-consistent form of segmentation, which elevated the accuracy of tumor delineation.

IV. RESULT AND ANALYSIS

The suggested unsupervised brain tumor segmentation method was examined on 2D axial slices on four modalities in data records of the BraTS2019 database. The M-Net CNN model has been learned in regard to tumor-specific features using pseudo-labels generated through K-means clustering. Raw sliced MRI data is then merged with the M-Net CNN output to form a U-Net model to allow a more accurate segmentation. The framework is considered by computing the Dice coefficient, Intersection over Union (IoU), precision, recall, and accuracy. The qualitative results of segmentation application on test images are shown in Figure 3, and these have proven how the method used is accurate in locating and outlining the tumor area by segmentation process in the test images.

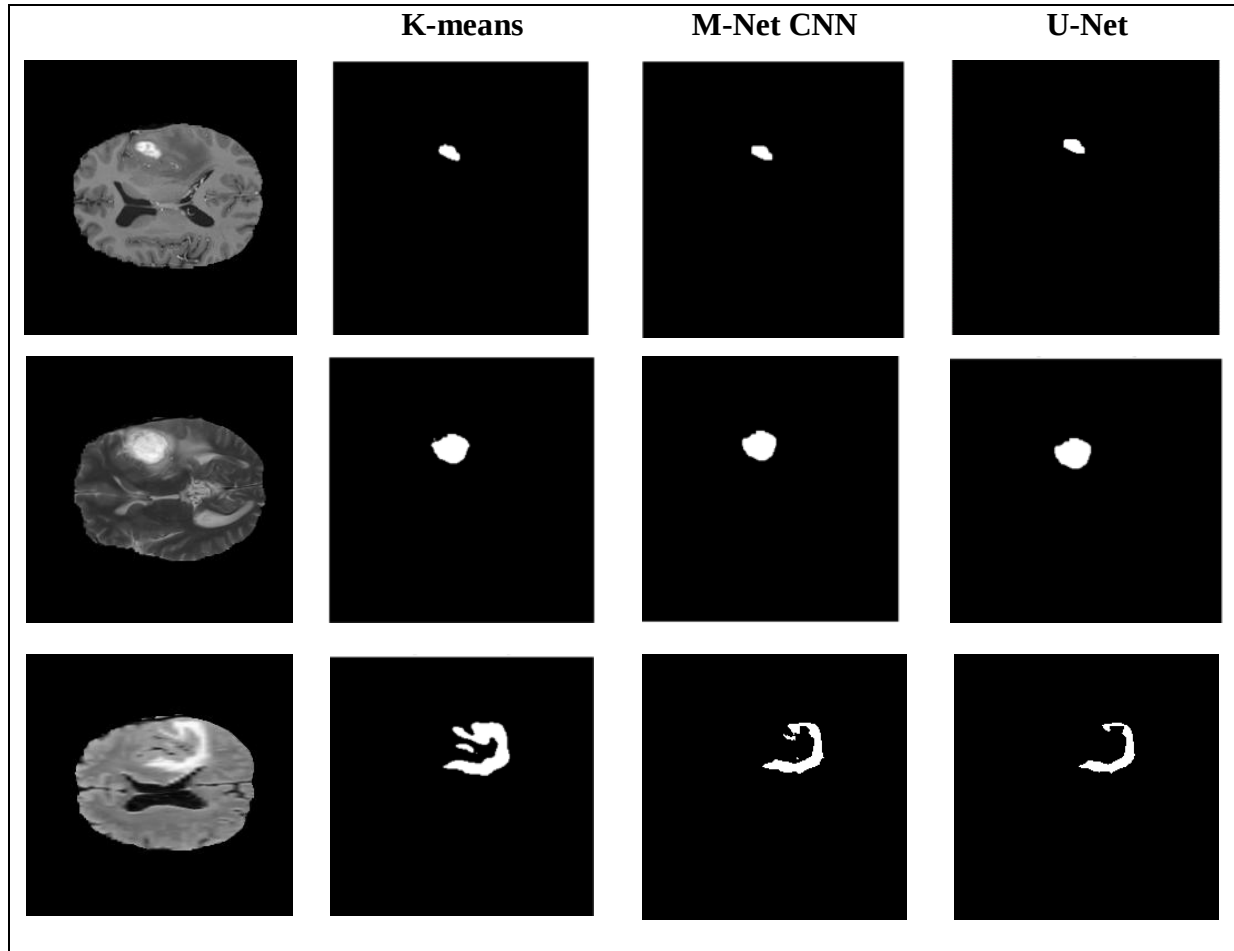


Figure 3: Samples of brain tumour segmentation results on test images of BraTS2019.

Source: Authors, (2026).

The evaluation metrics for K-means clustering models on unlabeled MRI slices will be represented in the Figure 4 for generation of pseudo-labels. Through intensity-based clustering where K-means does not require any manual annotations, it would distinguish tumor and non-tumor regions. It attained a Dice coefficient of 78.0%, IoU at 65.0%, thus showing itself adept at spatially delineating tumor regions with moderate accuracy. It records also 85.3% in accuracy, 76.5% precision and 79.2% recall which authenticate its reliability in pseudo-label generation, paving the way for further training of CNN-based segmentation models. Figure 5 presents a segmentation performance of the M-Net CNN model trained using pseudo-labels generated from K-means clustering. The model achieved a Dice coefficient of 83.0%, 72.4% IoU, 82.7% precision, 84.2% recall, and overall accuracy of 88.5%. These results demonstrate M-Net's ability to leverage pseudo supervision for accurate and consistent tumor segmentation in unlabeled MRI slices. Figure 6 illustrates a comparative evaluation between the proposed M-Net CNN model and two existing unsupervised segmentation methods: SynthTumour [15] and PL-BTS [16]. M-Net achieved a Dice coefficient of 83.0 %, outperforming SynthTumour at 78.03 % and PL-BTS at 79.5 %. It also recorded the highest recall of 84.2%, compared to 78.54 % for SynthTumour and 82.90 % for PL-BTS, highlighting its improved ability to detect tumor regions. In terms of precision, M-Net CNN reached 82.7%, closely matching SynthTumour at 82.50 % and exceeding PL-BTS at 80.36%. These comparisons confirm that the proposed M-Net CNN, guided by pseudo-labels and a structured CNN architecture, surpasses existing methods in segmentation accuracy, consistency, and sensitivity.

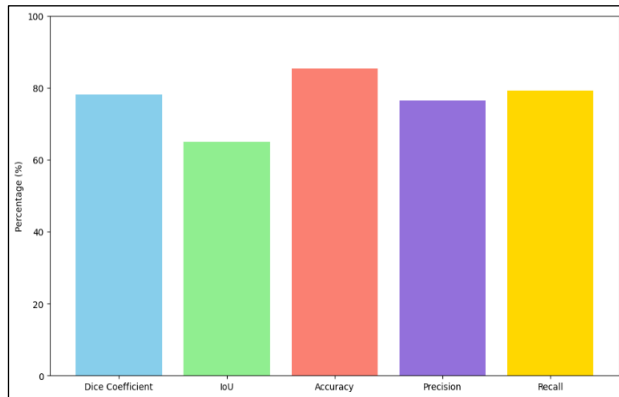


Figure 4: K-means Model performances.
Source: Authors, (2026).

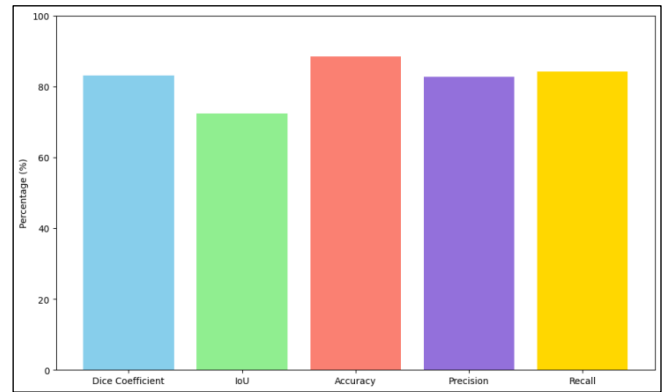


Figure 5: Evaluation of M-Net CNN.
Source: Authors, (2026).

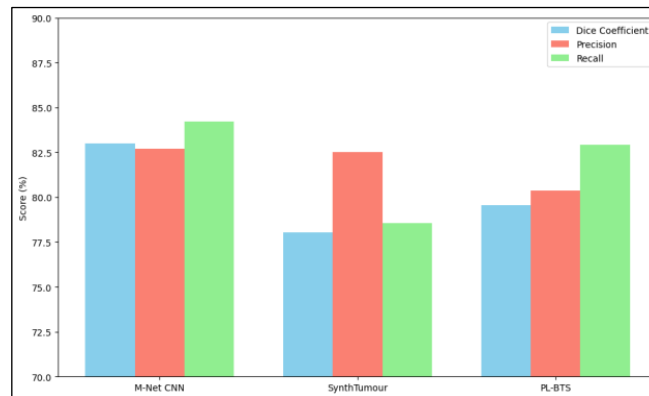


Figure 6: Comparative Performance of M-Net CNN against Existing Unsupervised Segmentation Methods.
Source: Authors, (2026).

The final refined segmentation was performed using a U-Net model, which used both the raw MRI slices and feature maps extracted from the preceding M-Net CNN. As illustrated in Figure 7, the U-Net demonstrated superior performance by achieving a Dice coefficient of 84.2 %, IoU at 73.9 %, It also attained a precision of 83.7 %, 85.0% recall and accuracy of 89.6 %. These improvements confirm the effectiveness of integrating multimodal inputs and intermediate deep features, enabling more accurate and anatomically aligned tumor segmentation. As shown in Figure 8, the various performance comparisons of the U-Net, ResNet [7], and BrainSegNet [19] models proposed were carried out using pseudo-labeled MRI data. U-Net achieved the highest score, with a Dice coefficient of 84.20%, followed by ResNet with 80.50% and BrainSegNet with 79.80%. In terms of precision, U-Net scored 83.70%, while ResNet and BrainSegNet scored 81.00% and 80.30%, respectively. U-Net again scored highest in recall at 85.00%, while ResNet and BrainSegNet scored 82.00% and 81.70%, respectively. These results clearly indicate that U-Net performed the best in terms of segmentation using pseudo-labeled data. The Dice Coefficient is provided for three stages of the modeled unsupervised segmentation pipeline in Table 1. The process begins with pseudo-label generation by K-means clustering, yielding a Dice coefficient of 78.0%. The pseudo-labels are then used to train the M-Net CNN, which improves segmentation performance to 83.0%. The refined U-Net model is finally applied, achieving the highest Dice score of 84.2%, demonstrating the effectiveness of the multi-stage enhancement and feature learning in the unsupervised framework. The performance gains across stages indicate the robustness of the refinement strategy as well as the U-Net's ability to adapt to pseudo-supervised inputs.

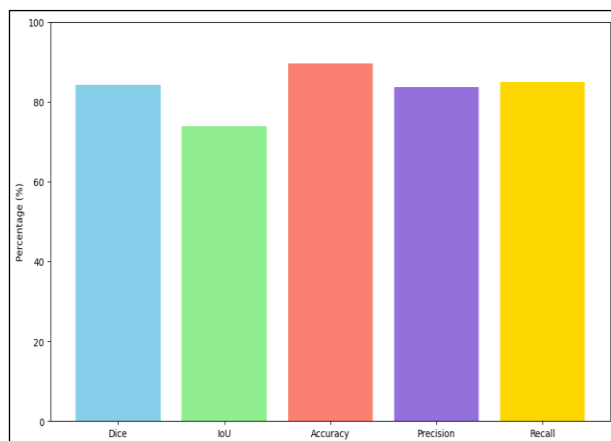


Figure 7: Evaluation of U-Net.
Source: Authors, (2026).

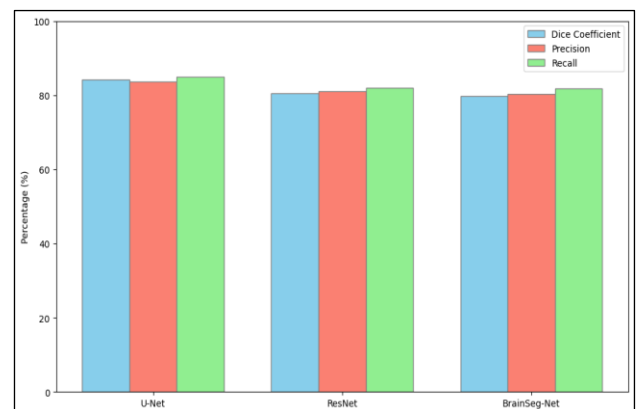


Figure 8: Comparative Performance of U-Net, ResNet-50, and BrainSegNet on Pseudo-Labeled image.
Source: Authors, (2026).

Table 1: Evaluation of Proposed models.

Models	Dice Coefficient
K-means	78.0%
M-Net CNN	83.0%
U-Net	84.2%

Source: Authors, (2026).

V. CONCLUSION

This work proposed a pseudo-supervised segmentation pipeline using the BraTS 2019 multimodal MRI dataset. K means generated pseudo labels trained an M-Net CNN, whose output was refined by a U Net model for enhanced accuracy. The final segmentation achieved a Dice coefficient of 84.2 %, showing effective tumor localization. The integration of multiple MRI modalities enhanced tissue characterization and model robustness. This framework reduces dependence on manual annotations, making it suitable for large-scale neuroimaging studies. As future work, the method can be extended to other diagnostic modalities, including CT scans for broader applicability across clinical environments. Additionally, incorporating self-supervised learning, attention-based mechanisms, and cross-modal consistency may further improve segmentation quality and generalization across heterogeneous datasets.

VI. AUTHOR'S CONTRIBUTION

Conceptualization: J. N. Adlin and Arockia Selva Saroja.

Methodology: J. N. Adlin and Arockia Selva Saroja.

Investigation: J. N. Adlin and Arockia Selva Saroja.

Discussion of results: J. N. Adlin and Arockia Selva Saroja.

Writing – Original Draft: J. N. Adlin.

Writing – Review and Editing: J. N. Adlin and Arockia Selva Saroja.

Resources: Arockia Selva Saroja.

Supervision: J. N. Adlin and Arockia Selva Saroja.

Approval of the final text: J. N. Adlin and Arockia Selva Saroja.

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Data Availability: The dataset used in this study is publicly available and was obtained from the Kaggle repository. Specifically, the Brain Tumor Segmentation (BraTS 2019) dataset can be accessed at: <https://www.kaggle.com/datasets/aryashah2k/brain-tumor-segmentation-brats-2019>. No additional permissions were required for its use in this research.

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