



Deep learning-based robust brain tumor detection via fuzzy C-means and LSTM networks

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Abstract

AI-based segmentation enables longitudinal tracking of tumor growth and changes over time. This helps clinicians monitor disease progression, assess treatment efficacy, and make informed decisions regarding patient management. The combination of fuzzy C-means (FCM) clustering and short-term memory (LSTM) networks enhances the robustness of brain tumor segmentation in MR images by leveraging the complementary strengths of both techniques. FCM clustering provides initial segmentation based on intensity distributions, while LSTM networks refine the segmentation by incorporating contextual information from neighboring regions, making the segmentation more robust to noise and artifacts in the images. To evaluate our segmentation system, we conducted experiments on the BraTS benchmark using different distance metrics. The True positive rate and True negative rate are highest on Mahalanobis, moreover, false positive rate and false negative rate are highest on Euclidean distance, and these results show that the Mahalanobis distance is more suitable for the proposed hybrid approach compared to the Euclidean distance. The experimental findings demonstrate that our own approach can yield comparable results to the ground truth segmentation of brain tumors, the proposed computer-aided diagnosis (CAD) system achieved promising results in the detection and segmentation of brain tumors on MR images, and demonstrated a Dice similarity coefficient of 91.8% and 91.5%. The integration of FCM-clustering and LSTM-networks often leads to improved segmentation accuracy compared to traditional methods. This improvement is due to the ability of FCM to handle intensity variations and spatial characteristics of the tumor while LSTM networks refine the segmentation by incorporating contextual information.

Keywords Brain tumor · Automatic segmentation · MRI · Computer-aided diagnosis system · Deep learning · Image processing

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1 Introduction

Brain tumors represent one of the most critical and complex medical challenges, affecting millions of people globally. Timely and accurate segmentation of brain tumors in medical imaging, particularly Magnetic Resonance Imaging (MRI) scans, is essential for diagnosis, treatment planning, and monitoring of tumor progression. Segmentation refers to the process of partitioning an image into meaningful regions, and for brain tumor cases, this means isolating tumor regions from healthy brain tissue to facilitate targeted therapies (Krishnakumar and Manivannan 2021). Despite advances in medical imaging, achieving robust and reliable segmentation remains challenging due to the inherent variability in tumor shapes, sizes, locations, and textures, as well as the similarity in intensity between tumors and normal tissues in MRI scans. Traditional image processing techniques have been used extensively for brain tumor segmentation; however, they often struggle with the complex structures and heterogeneous nature of tumor tissues (Veerabatheran et al. 2024). Recently, deep learning methods have emerged as powerful tools for medical image analysis, achieving significant success in various segmentation tasks (Souza et al. 2023). Convolutional neural networks (CNNs) and other deep learning architectures can automatically learn hierarchical features that capture spatial dependencies and complex patterns in medical images. However, while CNNs are well-suited for spatial feature extraction, they sometimes lack the

temporal sensitivity required to model pixel- or voxel-level transitions effectively, particularly in cases where image slices are analyzed in sequence. Furthermore, deep learning models often require large amounts of labeled data for effective training, which can be challenging to acquire in the medical field (Ghosh et al. 2024). To address these challenges, we propose a hybrid model that integrates Fuzzy C-Means (FCM) (Höppner et al. 1999) clustering with Long Short-Term Memory (LSTM) networks within a deep learning framework for robust brain tumor segmentation. FCM is a soft clustering technique that allows each data point to belong to multiple clusters with varying degrees of membership, making it well-suited to handle the uncertainty and ambiguity often present at the tumor boundaries in medical images. FCM can effectively preprocess MRI images, providing an initial segmentation by grouping pixels based on intensity similarity (Vishnuvartanan et al. 2017). This clustering information, which captures spatial features and regional continuity, can then be used to guide the LSTM network, which excels at learning temporal dependencies, to refine the segmentation. The LSTM's ability to retain information over time steps is adapted in our model to capture complex patterns within image slices, producing a more cohesive and robust segmentation output.

The Fig. 1 presents the architecture of the proposed FCM-LSTM method for brain tumor segmentation. It begins by applying the Fuzzy C-Means (FCM) clustering algorithm to an input slide, producing a segmented image that distinguishes different regions based on intensity variations,

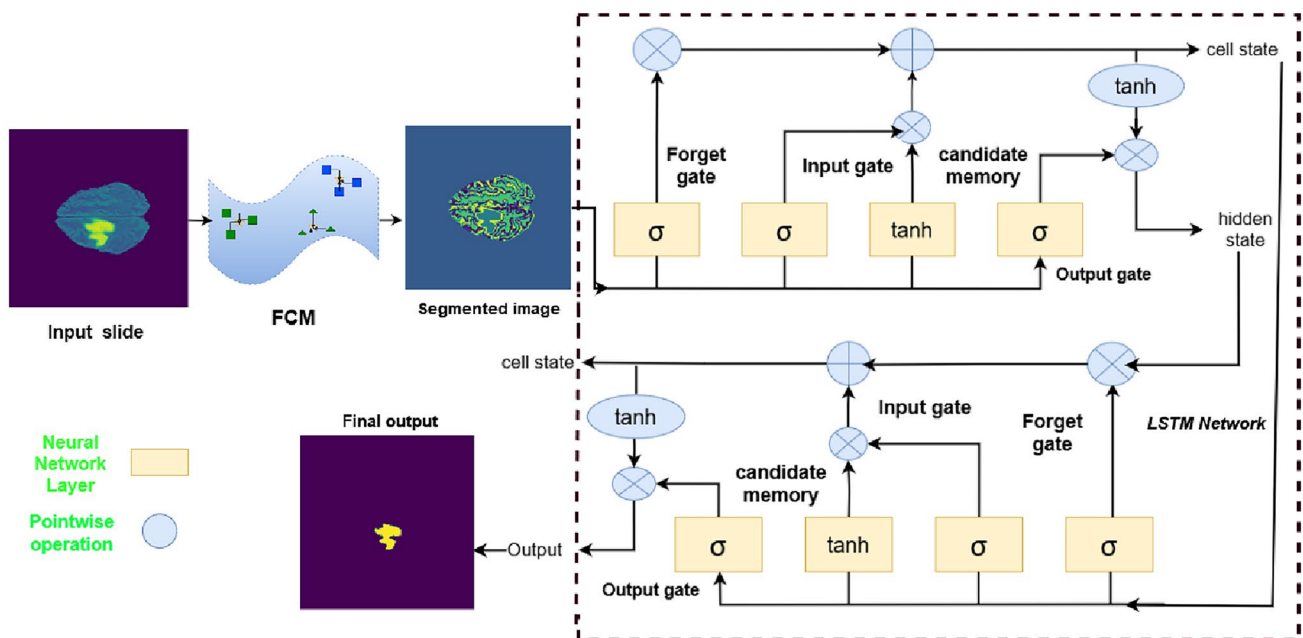


Fig. 1 The overall architecture of the proposed FCM-LSTM method

enhancing tumor region identification. This segmented image is processed by an LSTM network, which leverages its cell states and gates (forget, input, candidate memory, and output) to retain and refine spatial features. The integration of FCM's clustering capabilities with LSTM's feature learning strengths enhances segmentation accuracy and ensures robust tumor boundary delineation. FCM clustering effectively identifies boundaries, while the LSTM network provides contextual understanding critical for handling diverse tumor characteristics. Furthermore, incorporating LSTM within a deep learning pipeline introduces temporal continuity, addressing the variability in tumor presentation across patients. Our proposed FCM-LSTM model is designed to outperform traditional methods, particularly in cases with challenging tumor morphologies. The primary contributions of this research can be summarized as follows:

- We developed a fully functional brain tumor segmentation and detection system based on unsupervised and supervised techniques, this system relies on machine learning at all stages, making it suitable for real-time applications.
- We trained our proposed approach model on NVIDIA GPU (T4x2), proposed segmentation and detection model achieves high Dice similarity coefficient rates, with running times of about 0.08 s.
- Reduced Dependence on Extensive Labeling: The FCM preprocessing step reduces the requirement for extensive manual labeling, making the proposed framework more feasible for clinical applications where annotated data is limited.
- To address the problems of cluster brain tumor detection, we proposed a lightweight and operational long short-term memory (LSTM) network; this proposed architecture can be deployed on CPUs or low-resource devices.
- We performed experimental analysis on the benchmark BraTS datasets provided by the Medical Segmentation Decathlon12 and collected from the BraTS 2016–2017 versions and on the BraTS 2023. Our results confirmed that the proposed brain tumor detection system based on FCM and LSTM network could outperform the state-of-the-art works regarding the Dice similarity coefficient rate.

This paper is structured as follows. Section 2 reviews related work on brain tumor segmentation and the application of FCM and LSTM in medical imaging. Section 3 details our proposed FCM-LSTM model, including the preprocessing and segmentation stages. Section 4 presents the experimental setup and results, demonstrating the effectiveness of our model in comparison with existing methods. Finally, Sect. 5 discusses the conclusion and suggests directions for future research. The proposed model aims to achieve robust

and accurate brain tumor segmentation by combining the interpretative strengths of FCM with the contextual learning capabilities of LSTM, providing a comprehensive tool for aiding diagnosis and treatment planning in brain tumor cases.

2 Related works

Accurate brain tumor segmentation in MRI images has been an active area of research in medical image processing. The variability in tumor appearance due to different types, sizes, and locations has posed significant challenges, necessitating robust approaches that can adapt to complex and diverse tumor characteristics (Zhang et al. 2021). Traditional segmentation methods relied on techniques such as thresholding, region growing, and edge detection, which are limited in handling noise and often fail when faced with the high variability in brain tumor morphology (Mohan and Subashini 2019).

2.1 Brain tumor segmentation using traditional and deep learning methods

Over the past decade, deep learning has revolutionized medical image segmentation by introducing architectures that can automatically learn hierarchical features from imaging data. Convolutional Neural Networks (CNNs) have been widely used for brain tumor segmentation. For instance, Pereira et al. (2016) proposed a CNN architecture that segments brain tumors by capturing both high- and low-level features through multiple layers and achieved considerable success on the BraTS (Brain Tumor Segmentation) dataset. Similarly, Kamnitsas et al. (2017) developed a deep learning model that combines 3D CNNs with a fully connected Conditional Random Field (CRF) to capture both spatial and contextual information in brain tumor segmentation, demonstrating the advantage of combining CNNs with probabilistic methods and cements in deep learning have introduced the use of U-Net, a fully convolutional network for biomedical image segmentation. Ronneberger et al. (2015) proposed U-Net, which has since become one of the most popular architectures for segmentation tasks, building upon the success of U-Net, researchers have further extended this model to 3D volumetric data, resulting in the development of the 3D U-Net model (Çiçek et al. 2016). U-Net-based models perform well in brain tumor segmentation due to their ability to capture fine details through symmetric skip connections, which merge information from the encoding and decoding paths. These models, however, often require large annotated datasets for training and may suffer from generalization issues in cases of high tumor variability. Also, Attention

mechanisms have been incorporated into deep learning models for brain tumor segmentation (Ranjbarzadeh et al. 2021) to highlight informative regions within input data, these mechanisms, including spatial and channel-wise attention mechanisms, aim to enhance the precision of tumor segmentation by emphasizing specific spatial locations and informative channels, respectively. Conditional generative adversarial networks (cGANs) (Rezaei et al. 2018) have been used for brain tumor segmentation to generate accurate tumor masks; these networks utilize both a generator and a discriminator to improve segmentation performance by considering the spread of tumor regions in the training set. In Das et al. (2022), the authors used ensemble approaches to further enhance the accuracy and robustness of tumor segmentation, the principal behind these approaches is to train different models with different architectures, then, data augmentation strategies was used during the training to introduce diversity into the training samples, thereby aiding ensemble models in achieving better generalization capacity and robustness, finally, the output of each model is then combined to generate a final segmentation outcome.

2.2 Fuzzy C-means in medical imaging

FCM clustering is a soft clustering technique that has shown success in handling segmentation tasks where boundary ambiguity is present. Unlike traditional hard clustering methods, where each data point is assigned to only one cluster, FCM allows for partial membership across multiple clusters (Bezdek 2013). This flexibility makes FCM particularly suited for medical imaging, where tumor boundaries are often unclear. Ahmed et al. (2002) introduced a modified FCM for MRI segmentation that accounted for noise and intensity inhomogeneity, showing improved robustness in noisy images. This adaptation of FCM has become influential in brain tumor segmentation, where noise and irregular tumor boundaries are prominent challenges. More recently, research explored combining FCM with other deep learning models to enhance segmentation performance. For example, Özyurt et al. (2020) utilized FCM in conjunction with deep neural networks to preprocess MRI images, segmenting brain tumors by identifying regions of interest for further refinement by a neural network, this hybrid approach demonstrated that FCM could effectively enhance initial segmentation, providing a baseline that improves the accuracy of subsequent processing stages. Integrating FCM as a preprocessing step also has the benefit of reducing the dependency on extensive manual annotation, as the FCM clustering can provide an initial partition of the image into tumor and non-tumor regions.

2.3 LSTM in medical image segmentation

Recurrent Neural Networks (RNNs), particularly LSTM networks, have been applied to various medical imaging tasks, with promising results in segmentation. LSTM networks are designed to capture long-range dependencies within sequential data [19], which can be beneficial in medical imaging when considering a sequence of slices in 3D MRI scans. Unlike CNNs, which primarily capture spatial features, LSTMs can model dependencies across slices, enabling them to capture both spatial and contextual relationships within the sequence. In the domain of brain tumor segmentation, LSTMs have shown potential, especially when combined with CNNs. For instance, Dhaniya and Umamaheswari (2023) proposed a hybrid CNN-LSTM model that combined CNN layers for spatial feature extraction with LSTM layers for temporal modeling across MRI slices. Their results indicated that incorporating LSTM improved the consistency and accuracy of tumor boundary detection, particularly in cases of high inter-slice variability. Another notable work by Faryna et al. (2020) introduced an attention mechanism within an LSTM framework for liver segmentation, highlighting the effectiveness of attention-guided LSTM networks in improving segmentation accuracy and robustness against image noise and artifacts. Hybrid models that integrate clustering methods with deep learning architectures have emerged as an effective solution for addressing the challenges in brain tumor segmentation. By combining FCM with deep learning models, researchers can leverage the interpretability of FCM clustering with the predictive power of neural networks. The integration of FCM and LSTM is particularly promising as it enables the initial segmentation through FCM, which can capture the spatial regions of interest, followed by LSTM layers that model the spatial continuity across slices. In this work, we build upon these approaches by proposing a hybrid FCM-LSTM model for robust brain tumor segmentation in MRI images. This model aims to exploit the fuzzy clustering capability of FCM to create a soft partitioning of the image, which serves as input to an LSTM network for sequence-based refinement. By doing so, the model captures both spatial consistency and temporal dependencies, addressing the limitations of purely CNN-based approaches. To our knowledge, this study is one of the first to apply an FCM-LSTM combination to brain tumor segmentation, providing a novel approach that enhances segmentation accuracy and robustness.

3 Materials and methods

In this study, we propose a hybrid segmentation model that combines Fuzzy C-Means (FCM) clustering and Long Short-Term Memory (LSTM) networks within a deep learning

framework for brain tumor segmentation. This section outlines the dataset used, the preprocessing steps, and the architecture of the proposed FCM-LSTM model, followed by a description of the training and evaluation protocols.

3.1 Experimental data

The BraTS database (Center for Biomedical Image Computing and Analytics (CBICA) 2024) is a widely used benchmark dataset in medical image processing; it is specifically designed for brain tumor segmentation and can be used for tumor-grade prediction and survival prognosis tasks, the BraTS database provides multimodal MRI data for studies and the development of brain tumor analysis algorithms. Indeed, MRI images are commonly used in medical practice for diagnosing and evaluating various anomalies, such as cancer, inflammation, or injury, owing to their ability to provide detailed information about the anatomy and pathology of various body structures (Nishikawa et al. 2023). However, accurately distinguishing between different brain components such as gray matter, brainstem, white matter, cerebral cortex, and cerebellum, can be challenging in MR-intensity images. The database consists of MRI slices of brain tumor patients and the related ground truth segmentations, indicating the tumor locations. The MRI scans include four different modalities: T1-weighted (T1), T1-weighted with contrast enhancement (T1Gd), T2-weighted (T2), and T2 fluid-attenuated inversion recovery (FLAIR). These modalities offer supplementary knowledge about brain tissue and tumor characteristics. Medical experts annotate the ground truth segmentations in the BraTS dataset. This dataset is publicly available and can be accessed from the official BraTS challenge website or other repositories hosting medical imaging datasets. As a preprocessing phase, we selected five representative volumes from the BraTS2023 dataset and three representative volumes from the BraTS16-17 dataset for the training phase, each containing 152 slices. This selection allowed us to work with a diverse subset of slices while keeping the computational load manageable. Each slice in these volumes provides unique intensity patterns, contributing to effective learning of tumor characteristics and reducing the likelihood of overfitting. Subsequently, each volume was reshaped from its original $240 \times 240 \times 152 \times 1$ plane to a $15257,600 \times 152$ plane. This transformation was necessary to process the data in a format compatible with both clustering and sequence-based models, with each row representing a flattened slice that retains spatial information for subsequent segmentation. Moreover, to capture local spatial features, we applied a sliding window of size 3×3 to each slice. This window extracts feature vectors by scanning through the image in small patches. By moving one pixel at a time, the model gains a comprehensive view of the pixel neighborhoods, which aids in identifying subtle texture variations critical for tumor boundary delineation. This feature extraction strategy

is particularly useful in the presence of noise and intensity variations across slices

3.2 Proposed FCM-LSTM hybrid model

FCM is a soft popular clustering algorithm that permits a feature point to be a part of several groups with different membership levels. Unlike traditional K-means clustering, FCM assigns a probability or degree of membership to each data point for each cluster rather than a hard assignment to a single cluster. This is achieved through a membership function that computes each point's membership level in each cluster based on a distance metric between each feature value and the cluster centroids. Moreover, our proposed model combines FCM clustering and LSTM networks to leverage both spatial and sequential information in brain tumor segmentation. This section describes the model's architecture and its components in detail. FCM method operates by first initializing the cluster centroids and membership degrees; it then iteratively modifies the membership degrees and the cluster centroids up to the convergence. The objective function of FCM aims to minimize the average of the squared distances between the cluster centroids and every feature value, weighted by their membership degrees. Compared to traditional clustering techniques, FCM has several advantages. It can handle noisy and overlapping data and give more details about the structure of the features. However, it also is computationally expensive and requires tuning several parameters, such as the value of clusters and the fuzziness parameter. Therefore, Fuzzy C-Means clustering was used as an initial step to segment the MRI images into tumor and non-tumor regions, FCM is an unsupervised clustering technique that enables each data point to belong to multiple clusters, each with a different degree of membership. This property is particularly useful in brain tumor segmentation, where tumor boundaries are often unclear and may overlap with healthy tissue. In fact, the FCM algorithm groups pixels based on intensity values and assigns them to one of three primary clusters: Background (non-brain tissue), Healthy Brain Tissue and Tumor Region. Algorithmically speaking, FCM considers a given matrix of feature points, denoted as x_i , to be clustered.

$$x_j = [x_{j1} \ x_{j2} \ \dots \ x_{jm}]^T, \quad 1 \leq j \leq N \quad (1)$$

where N represents the matrix rows and the number of columns for each feature point equals the feature's dimensionality. Initially, FCM computes the cluster centers and stores in the array c_i , as indicated in equation (2). Each cluster center is represented by a row in this array, and the number of columns in this array corresponds to the number of columns in the feature point's matrix x_i .

$$c_i = [c_{i1} \ c_{i2} \ \dots \ c_{in}]^T, \quad 1 \leq i \leq c \quad (2)$$

Next, FCM determines the dissimilarity between each data point and the cluster centers. This step allows FCM to assign each data point a degree f membership for each cluster considering relative distances to the cluster centers. Therefore, the selection of the adapted distance metric is crucial. Euclidean distance and Mahalanobis distance are the two most often used distance measures. The Euclidean distance between two points, A and B, in a d -dimensional space is calculated as:

$$\text{distance}(A, B) = \sqrt{(x_1 - y_1)^2 + (x_2 - y_2)^2 + \dots + (x_d - y_d)^2} \quad (3)$$

where $(x_1, x_2, \dots, x_d)$ and $(y_1, y_2, \dots, y_d)$ are the coordinates of points A and B, respectively. A modified version of the traditional fuzzy C-means clustering algorithm, namely Gustafson-Kessel FCM, has been proposed to improve the segmentation results further. This modified algorithm considers the covariance matrix of the features and uses the Mahalanobis distance as a metric. The Mahalanobis distance is a measure that computes the distance between the feature vector and cluster center, considering the correlation between features. Gustafson-Kessel FCM can handle data with different covariance structures and non-spherical clusters. This approach is beneficial when dealing with high-dimensional datasets where the assumption of isotropic clusters (equal variances in all dimensions) is invalid. The Mahalanobis distance is described using equation (4):

$$\text{distance}(A, M, C) = \sqrt{(A - M)^t \cdot C^{-1} \cdot (A - M)} \quad (4)$$

where $(A - M)$ is the difference vector between point A and the mean M, C^{-1} is a covariance matrix's inverse, and $(\cdot)^t$ denotes the transpose of a vector or matrix. For the FCM technique, the objective function is designed to optimize the clustering algorithm. The objective function for FCM is often called the fuzzy objective function or the fuzzy partition coefficient. The FCM objective function aims to reduce the fuzziness or uncertainty of the cluster assignments. It calculates the distance between every cluster center and each feature point, assigning a membership value that represents the level of belongingness of the feature point to every cluster. The objective function seeks to minimize the combination of these membership rates for each data point. The FCM objective function is typically determined as follows:

$$J = \sum \left(\sum u_{ij}^m \cdot d_{ij}^2 \right) \quad (5)$$

where: J is the objective function value. u_{ij} is the membership value of feature point i to cluster j . The fuzziness exponent m in the clustering determines the level of fuzziness. d_{ij} is the distance between feature point i and cluster center

j . In our adaptive approach, the FCM algorithm was initialized with 15 clusters. This choice was based on preliminary experiments and was optimized to balance detail in segmentation without overwhelming computational resources. Each cluster aims to represent specific intensity ranges associated with various tissues (e.g., gray matter, white matter, and tumor tissue). Furthermore, we set the maximum number of FCM iterations to 20. This ensures that clustering converges within a reasonable time frame while effectively partitioning the data into meaningful regions, the iteration limit also helps manage computational cost without compromising segmentation quality. Additionally, FCM assigns a membership value to each pixel based on its similarity to cluster centroids, allowing for soft clustering where pixels can partially belong to multiple clusters, this approach is ideal for MRI segmentation, where tumor boundaries are often unclear and intensities vary, as it enables nuanced segmentation that better captures these transitions. In addition, during each iteration, cluster centroids are updated based on pixel membership values, and the process repeats until convergence is achieved, this iterative refinement helps to enhance the accuracy of initial tumor boundary delineation.

3.3 LSTM network for sequential refinement

To refine the initial segmentation generated by FCM, we proposed LSTM network architecture to classify tumor and non-tumor textures to select the best tumor cluster index. The LSTM network is a recurrent neural network (RNN) architecture specifically designed to address the limitations of traditional RNNs in capturing long-term dependencies within sequential data, the proposed architecture network processes the soft segmentation maps from FCM in a slice-by-slice manner, allowing it to model the spatial continuity and dependencies across the slices in the MRI volume. The key idea behind LSTM networks is the introduction of memory cells that can store information over long periods, these memory cells are connected through gates that control the flow of information into, out of, and within the cells. The gates, implemented using sigmoid and element-wise multiplication operations, enable the LSTM to learn which information to keep, forget, and update in the memory cells. Therefore, we used three hidden layers of sizes: 300, 400, and 300, respectively, the entire architecture of our LSTM model is described in Fig. 2. The sequence folding layer turns a batch of slide sequences into an array of images. The first convolution layer, conv_1 , filters the 240-by-240 input images with 16 kernels of size 3×3 , the second convolution layer, conv_2 , filters images with 16 kernels of size 5×5 , where we have followed up each convolution layer with a batch-normalization layer for improved training stability and speed up convergence, it normalizes the inputs of the layer by subtracting the batch mean and dividing by the batch

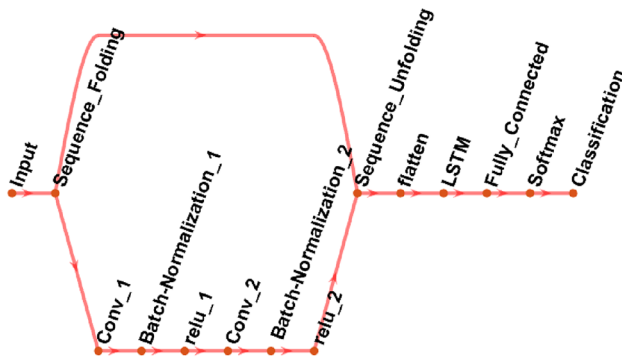


Fig. 2 The model architecture diagram of the LSTM network implemented in the case study

standard deviation, the total number of trainable parameters is 13,089,301. The ReLU (Rectified Linear Unit) layer is a popular activation function in neural networks. It introduces non-linearity to the network by replacing negative values with zero and leaving positive values unchanged. The ReLU function is defined as follows:

$$\text{ReLU}(x) = \max(0, x) \quad (6)$$

where x is the input to the layer, if the input is negative, the ReLU function returns zero; otherwise, it returns the value itself. After completing these processes, we changed this array of images back to image sequences by utilizing a sequence unfolding layer to regain the sequence structure, we used the flattening layer to convert images to feature vectors, and then we applied the vector sequences to the LSTM layers, we trained the proposed model with a mini-batch size of 16 for a learning rate 0.001. In the training phase, we used 28 volumes from the BraTS dataset, which mean 4256 slides for each sub-dataset (positive and negative).

4 Results

4.1 Quantitative results

The combination of FCM clustering and LSTM networks enables automatic segmentation of brain tumors in MR images, reducing the need for manual intervention and subjective interpretation by radiologists. This automation streamlines the segmentation process, making it more efficient and less labor-intensive, especially in clinical settings where timely diagnosis and treatment planning are critical. Therefore, our proposed FCM-LSTM model was evaluated on the BraTS16-17 and BraTS2023 datasets using several performance metrics to measure its effectiveness in accurately segmenting brain tumors. These metrics include True Positive Rate (TPR), True Negative Rate (TNR),

Table 1 The results of the proposed detection method on the BraTS datasets

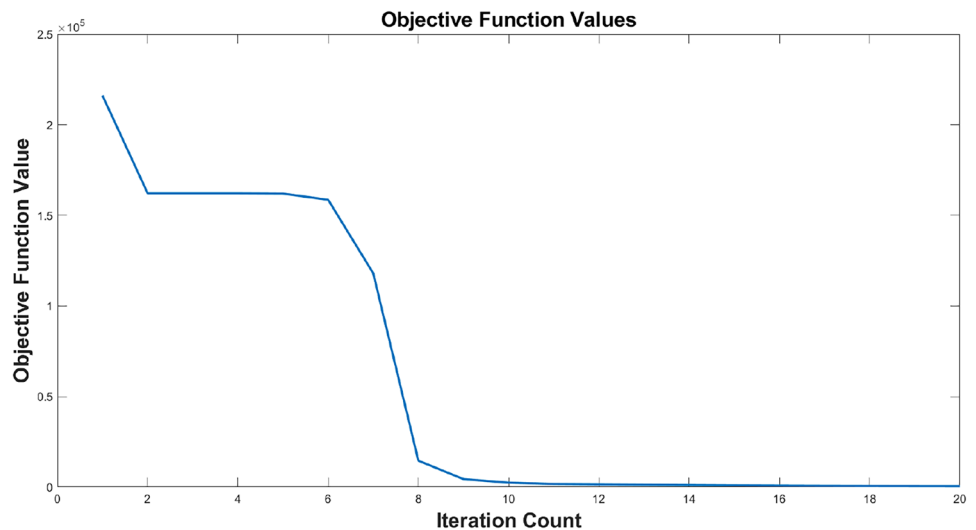
Dataset	Distance	TPR (%)	TNR (%)	FPR (%)	FNR (%)
BraTS16-17	Euclidean	62.88	88.41	11.59	37.12
	Mahalanobis	84.91	91.33	8.97	15.09
BraTS2023	Euclidean	60.45	88.05	11.95	39.55
	Mahalanobis	81.93	90.13	9.87	18.09

False Positive Rate (FPR), False Negative Rate (FNR), and the Dice Similarity Coefficient (DSC) of the whole tumor region, we also investigated the effectiveness of two distance metrics: Euclidean and Mahalanobis.

Table 1 presents the results of the proposed detection method on the BraTS datasets; the training stage used a total of 5320 slides for the BraTS2023 dataset and 4104 slides for BraTS16-17 dataset. These rates are essential performance metrics in evaluating machine learning models, especially brain tumor segmentation task, as they provide insights into the model's ability to correctly classify positive and negative cases. It can be observed that for both datasets, the Mahalanobis distance metric significantly outperforms the Euclidean distance in TPR, achieving 84.91% on BraTS16-17 and 81.93 % on BraTS2023 compared to 62.88% and 60.45%, respectively, for the Euclidean metric. This improvement indicates that Mahalanobis is more effective in accurately identifying tumor regions. The TNR is also higher with Mahalanobis, reaching 91.33% on BraTS16-17 and 90.13% on BraTS2023, as opposed to 88.41% and 88.05% with Euclidean. This suggests a reduced number of false positives with Mahalanobis, aligning with the lower FPR observed. Furthermore, Mahalanobis reduces the FNR on both datasets (15.09% on BraTS16-17 and 18.09% on BraTS2023) compared to Euclidean (37.12% and 39.55%). The results indicate that Mahalanobis provides a more reliable performance in detecting true tumor pixels and minimizing both false positives and false negatives across datasets, making it a preferable choice for accurate tumor segmentation.

Figure 3 shows the progress of the clustering objective function, the clustering objective function is a standard metric used to measure the effectiveness of FCM models, while both the Euclidean and Mahalanobis distance metrics are used for pixel-level anomaly detection, the Mahalanobis distance generally results in fewer false positives, this is due to its ability to consider the correlations between pixel values and scale the distance accordingly, providing a more accurate representation of anomalies in complex image data. Therefore, for applications requiring precise anomaly detection with minimal false positives, the Mahalanobis distance is often the preferred choice. From the obtained curve, we

Fig. 3 The progress of the clustering objective function

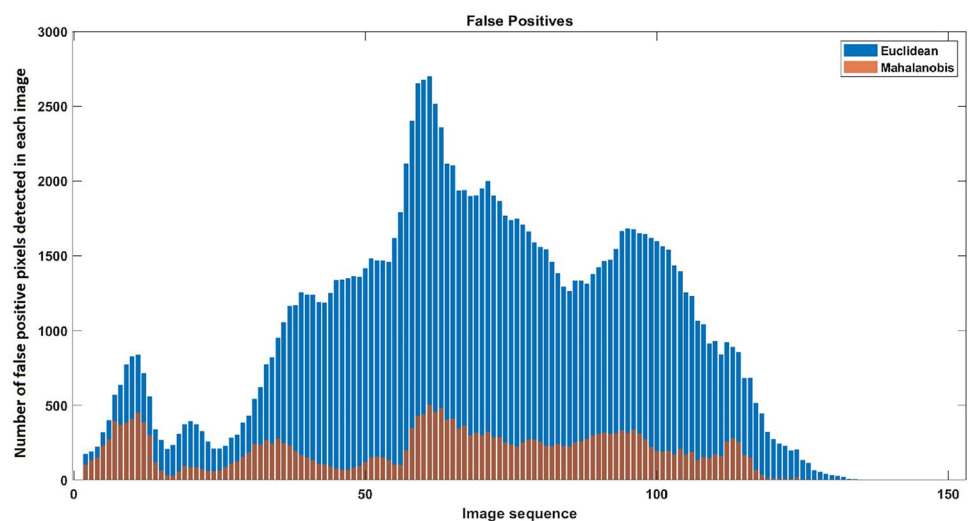


can observe that the objective function fluctuates considerably and converges to a value of 0 after iteration 17, the FCM algorithm has a stable curve in the segmentation task, so the model can learn better to classify tumor and non-tumor textures. The model learns to classify tumor and non-tumor textures better, indicating that the model is adjusting to the complexity of the data, which means that the objective function is minimized, these models create clusters as compact and separated from each other as possible, with each data point having a high membership value in its corresponding cluster and low membership values in other clusters.

Figure 4 shows the number of false positive pixels at each image slice for brain tumor segmentation on volume BraTS-449 from the BraTS dataset, comparing the performance of Euclidean and Mahalanobis distance metrics. The x-axis represents the sequence of MRI slices through the volume, while the y-axis indicates the number of false positive pixels identified in each slice, the Euclidean distance metric

generally produces a higher number of false positives across the slices. Peaks can be seen in certain regions, indicating that the Euclidean metric struggles to distinguish between tumor and non-tumor areas, especially in complex regions or where the intensity variations within the brain are subtle. The Mahalanobis distance consistently yields fewer false positives across the volume, this improvement is due to the Mahalanobis metric's ability to account for correlations among features, allowing for better discrimination between tumor and non-tumor tissues. Moreover, the Mahalanobis distance metric shows relatively stable performance across slices, with fewer fluctuations in the number of false positives, this stability indicates that it is more resilient to intensity variations and noise across different slices. It is important to note that the Euclidean distance used is typically used when data features are independent or weakly correlated. In contrast, the Mahalanobis distance is preferred in cases where the data features have strong correlations or when the

Fig. 4 Number of false positives pixel-level results using the Mahalanobis and Euclidean distance metrics applied to volume BraTS-449 from the BraTS2017 dataset



data does not conform well to a spherical distribution. The Dice similarity coefficient, also known as the Dice coefficient or Sorensen-Dice coefficient, is a measure of the similarity or overlap between two sets of binary variables. It is commonly used in brain tumor segmentation. The formula for calculating the Dice similarity coefficient of two sets, A and B, is:

$$\text{Dice}(A, B) = \frac{2 \times |A \cap B|}{|A| + |B|} \quad (7)$$

The metrics true positives (TP), false positives (FP), and false negatives (FN) can also be used to describe the Dice coefficient:

$$\text{Dice}(A, B) = \frac{2 \times \text{TP}}{2 \times \text{TP} + \text{FP} + \text{FN}} \quad (8)$$

The results in Table 2 present a comparative analysis of various methods for brain tumor segmentation on different versions of the BraTS dataset, evaluated using the Dice similarity coefficient for the whole tumor region. This table highlights the performance of several state-of-the-art approaches developed between 2017 and 2023. Notably, traditional convolutional neural network (CNN)-based architectures, such as those used by Tseng et al. (2017) (Encoder-Decoder CNN) and Iqbal et al. (2018)

(Sequential Multiple CNN), show modest accuracy with Dice scores ranging from 85% to 87% on the BraTS 2015 dataset. More advanced architectures, like U-Net used by Li et al. (2019) improve upon these results, achieving a Dice score of 89% on the 2015 dataset and 87.6% on the 2017 version. Moreover, recent approaches employing capsule networks (CapsNet) by Elmezain et al. (2022) and particle swarm optimization by Atia et al. (2022) in 2022 report even higher accuracies, with Dice scores reaching up to 92% on BraTS 2021. Similarly, multi-task methods by Zhou et al. (2020) and dynamic feature learning (FDL) by Wang and Chung (2022) in 2022 achieve Dice scores above 90%, emphasizing the continuous advancements in segmentation accuracy across newer datasets. Our proposed method, which integrates LSTM-based fuzzy C-means (FCM) clustering, demonstrates competitive results, yielding a Dice score of 91.8% on the BraTS 2016–2017 dataset versions and 91.5% on the 2023 dataset version. This performance indicates that the proposed hybrid approach is on par with recent state-of-the-art methods, successfully leveraging LSTM's temporal capabilities and FCM clustering for effective tumor segmentation. Overall, these findings highlight the robustness of the proposed approach in achieving high segmentation accuracy, comparable with or even surpassing other recent models on similar datasets.

Fig. 5 Tumor texture used for the training of LSTM model from the BraTS dataset

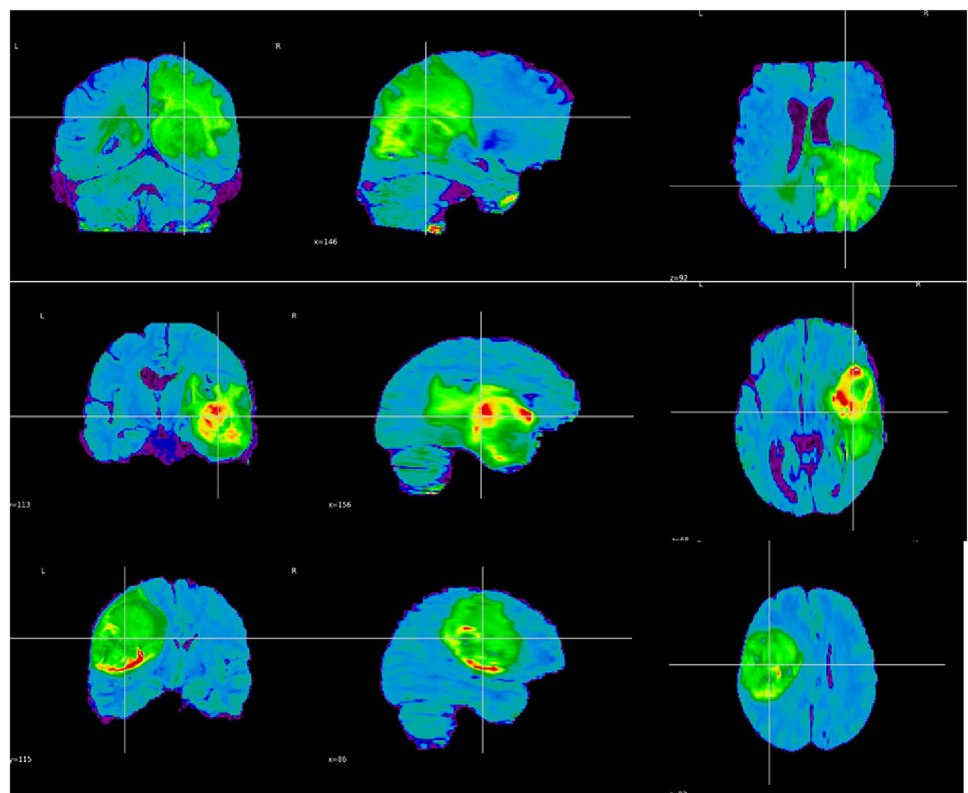


Table 2 The comparison results of our method to the state-of-the-art on BraTS dataset using the Dice similarity coefficient applied to the whole brain tumor region

Reference	Year	BraTS version	Methods	Dice (%)
Tseng et al. (2017)	2017	2015	Encoder-Decoder CNN	85
Iqbal et al. (2018)	2018	2015	Sequential Multiple CNN	87
Li et al. (2019)	2019	2015	U-Net network	89
		2017		87.6
Elmezain et al. (2022)	2022	2015	CapsNet	91
		2021		92
Atia et al. (2022)	2022	2015	Particle swarm optimization	91
Zhou et al. (2020)	2020	2015	One-Pass Multi-Task	87
		2017		90.71
		2018		91.8
Zhang et al. (2020)	2020	2017	Task Structure	88.3
		2018		89.6
Wang and Chung (2022)	2022	2019	Dynamic FDL	91.6
Proposed method	2023	2016–2017	LSTM based-FCM	91.8
		2023		91.5

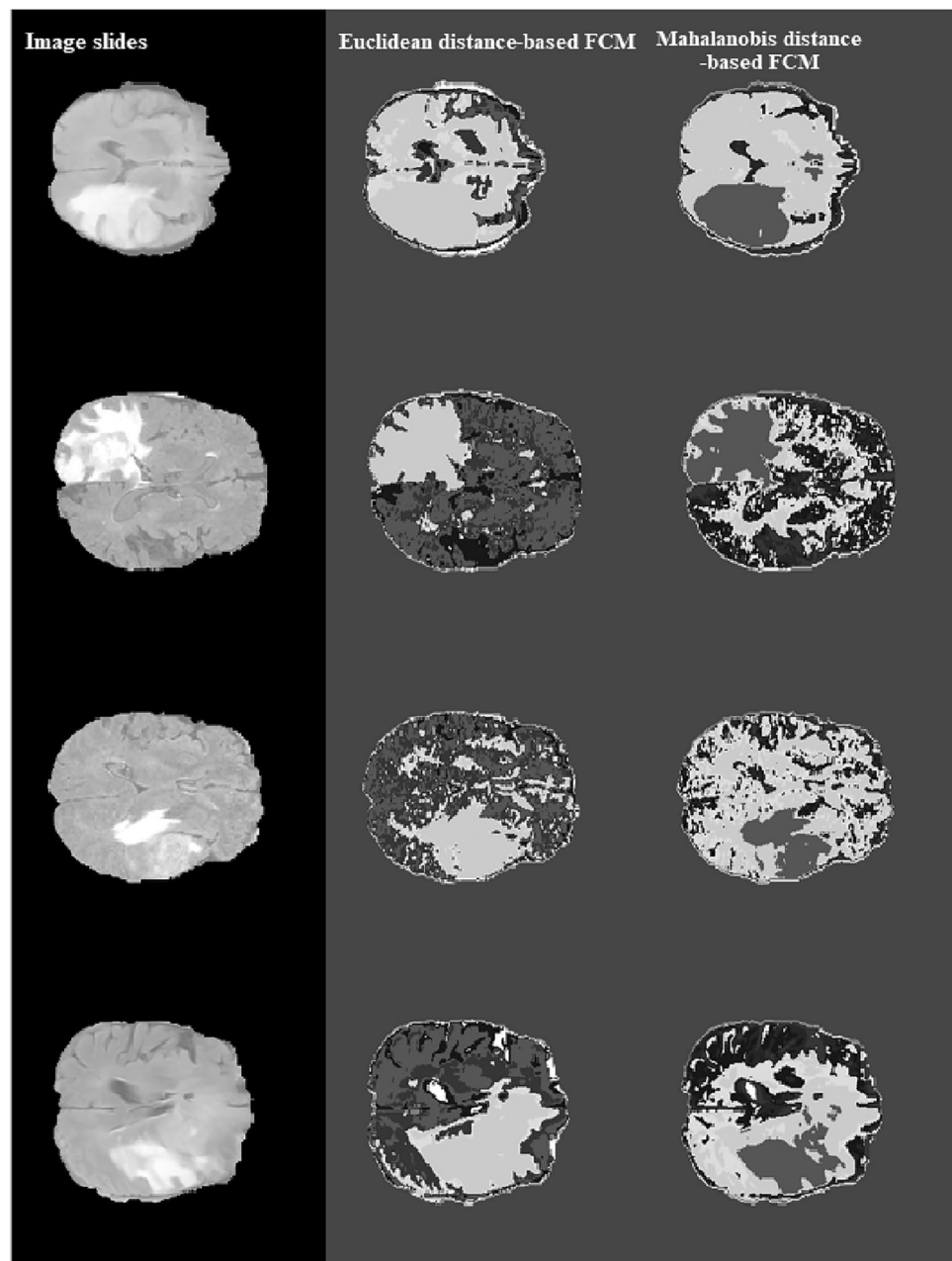
4.2 Visual results

Figure 5 displays various MRI brain scans from the BraTS dataset, highlighting the tumor texture features used to train the LSTM model, each image shows different cross-sectional views of brain scans, with color variations representing various intensities and textures within the tumor regions. These texture patterns provide critical information for the LSTM model, enabling it to learn intricate details about tumor morphology and intensity variations, the distinct layers and color gradations across the tumor regions contribute to the LSTM's ability to capture spatial dependencies and identify tumor boundaries more accurately, by leveraging these texture features during training, the model can improve its segmentation performance, effectively distinguishing tumor tissue from normal brain tissue. Figure 6 compares brain tumor segmentation results using the Fuzzy C-Means clustering algorithm with two different distance metrics: Euclidean and Mahalanobis. The left column displays the original MRI brain slices for reference. The middle column shows segmentation results using the Euclidean distance metric, which groups pixels based on spatial proximity and may capture larger areas, including some non-tumor regions. The right column presents segmentation results with the Mahalanobis distance metric, which considers both spatial and intensity differences, leading to more focused segmentation on actual tumor regions and reducing false positives. By comparing each row across columns, we can observe how each metric influences the accuracy of tumor segmentation with the Fuzzy C-Means clustering algorithm, it is clear that the Mahalanobis distance-based FCM algorithm efficiently segments various brain tissues, especially tumors, in comparison with the Euclidean distance, whose results were far from the ground truth. We used the LSTM network to detect

and isolate the brain tumor cluster from the rest brain clusters; therefore, we collected two datasets from the BraTS database. This database includes images of positive (tumor texture) and negative (non-tumor texture).

Figure 7 illustrates brain tumor detection results using the LSTM network-based FCM method applied to the BraTS16–17 dataset. Each row represents a different brain image slide. The columns display the following: the original image slides, labeled images (ground truth), Euclidean distance-based segmentation, and Mahalanobis distance-based segmentation. Additionally, the LSTM network, combined with FCM clustering, segments the tumor regions, producing Euclidean and Mahalanobis distance maps that capture the tumor's structure by distinguishing it from the surrounding healthy tissues. The Euclidean and Mahalanobis distance representations highlight differences in segmentation accuracy, where the Mahalanobis distance often provides a more refined result, potentially due to its sensitivity to data distribution, enhancing tumor region distinction compared to Euclidean distance. This comparative visualization allows for evaluating the method's effectiveness in accurately segmenting and identifying tumor boundaries. The segmented images typically show a clear delineation of the tumor region. The LSTM-FCM approach can highlight the tumor boundaries more sharply. Figure 8 demonstrates brain tumor segmentation results using Euclidean and Mahalanobis distance metrics, highlighting their performance differences on the BraTS 2023 dataset. While the Euclidean distance provides an initial segmentation, it struggles with boundary accuracy, resulting in fragmented predictions. In contrast, the Mahalanobis distance metric achieves smoother, more cohesive tumor boundaries by accounting for feature correlations, showing improved alignment with the ground truth. However, both methods face challenges in detecting

Fig. 6 Brain tumor segmentation results using the Euclidean and Mahalanobis distances-based FCM

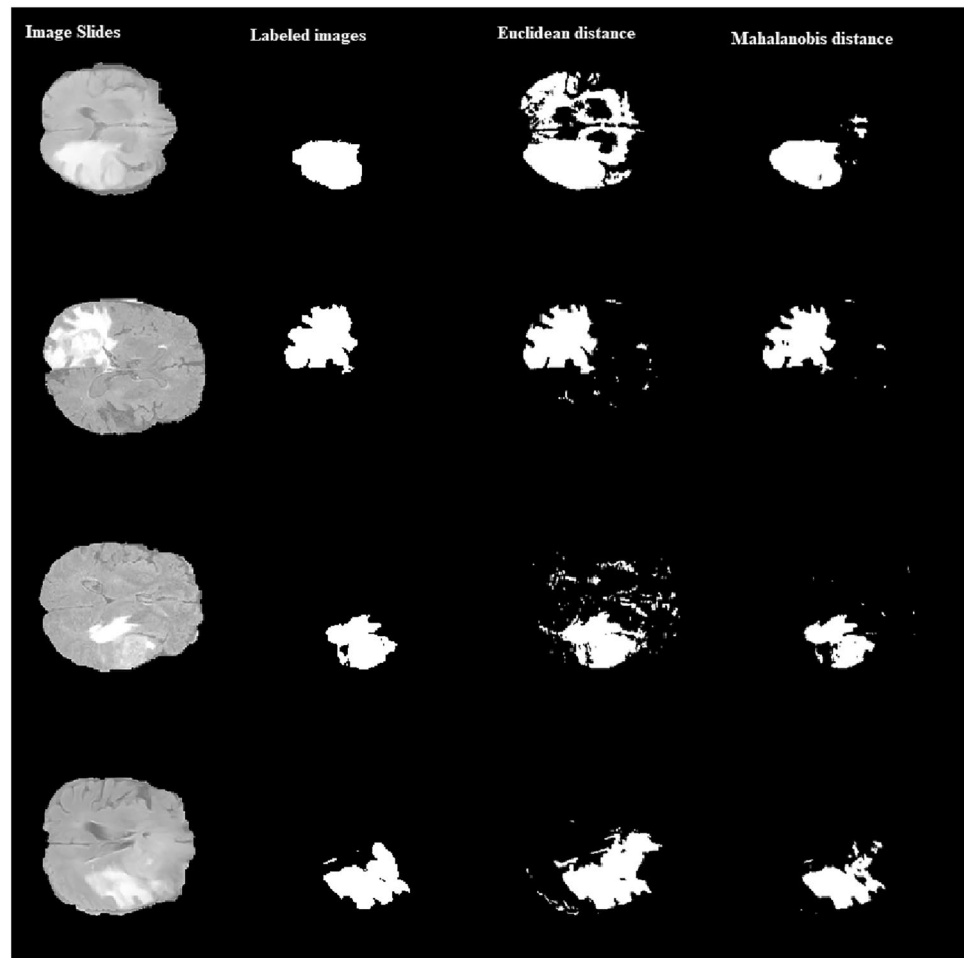


small or low-contrast tumors. This comparison underscores the potential benefit of integrating LSTM-based sequential refinement to enhance segmentation accuracy and consistency across MRI slices. Figure 9 shows an example of incorrect detection results from the BraTS dataset using the proposed LSTM network-based FCM with Euclidean distance.

In our study, we utilized the NVIDIA GPU (T4x2) for model training and testing, the FCM-LSTM hybrid model's computational requirements are moderate, making it feasible on standard GPU resources without excessive runtime. Compared to conventional CNN-based approaches for brain tumor segmentation, our hybrid model requires slightly more computation due to the sequential processing of slices by the

LSTM network. However, this added computational cost is justified by the improvement in segmentation performance. Specifically, FCM's initial clustering reduces the complexity of the LSTM's input by pre-segmenting regions of interest, enabling the LSTM to focus on refining these regions rather than segmenting from scratch. This division of tasks allows for efficient processing without a significant increase in computational load. In terms of performance gains, the improvement in Dice Similarity Coefficient metric demonstrates that the hybrid model's additional computational cost is offset by its robust handling of complex tumor structures and intensity variations. This increase in accuracy supports the use of the FCM-LSTM approach, especially for applications

Fig. 7 Brain tumor detection results using the LSTM network-based FCM applied to BraTS16-17 dataset



where segmentation accuracy is critical, such as treatment planning and longitudinal tumor monitoring. Segmenting a single BraTS volume of size 240x240x155 typically takes around 15 s for FCM clustering on the NVIDIA T4x2.

5 Conclusion

In this study, we presented a novel hybrid model that combines FCM clustering and LSTM networks within a deep learning framework to address the challenges in brain tumor segmentation from MRI images. The FCM clustering step effectively handles spatial ambiguities by producing an initial segmentation based on pixel intensities, while the LSTM network refines this segmentation by capturing sequential dependencies across MRI slices. By leveraging both spatial and temporal information, the proposed FCM-LSTM model enhances segmentation accuracy and boundary precision, particularly in cases of tumors with complex structures and

variable intensities. Furthermore, our approach demonstrates several key advantages. First, the FCM clustering stage provides a robust initial segmentation that reduces reliance on extensive labeled data, a common limitation in medical imaging tasks. Second, by incorporating the LSTM network, our model captures inter-slice continuity, which enhances segmentation consistency across slices and helps mitigate the variability in tumor morphology. Experimental results on the BraTS datasets show that the FCM-LSTM model achieves competitive performance compared to traditional methods, with improved Dice Similarity Coefficient (DSC) indicating its robustness in diverse tumor cases, the findings highlight the potential of combining fuzzy clustering with deep learning architectures for complex medical segmentation tasks. Future work could explore integrating attention mechanisms within the LSTM network to further refine segmentation accuracy, as well as extending this model to other tumor types and imaging modalities.

Fig. 8 Brain tumor detection results using the LSTM network-based FCM applied to BraTS2023 dataset

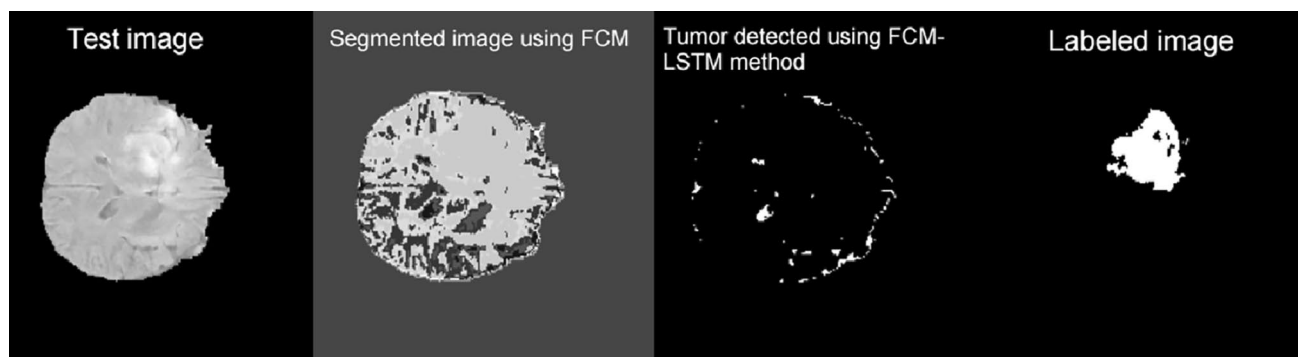
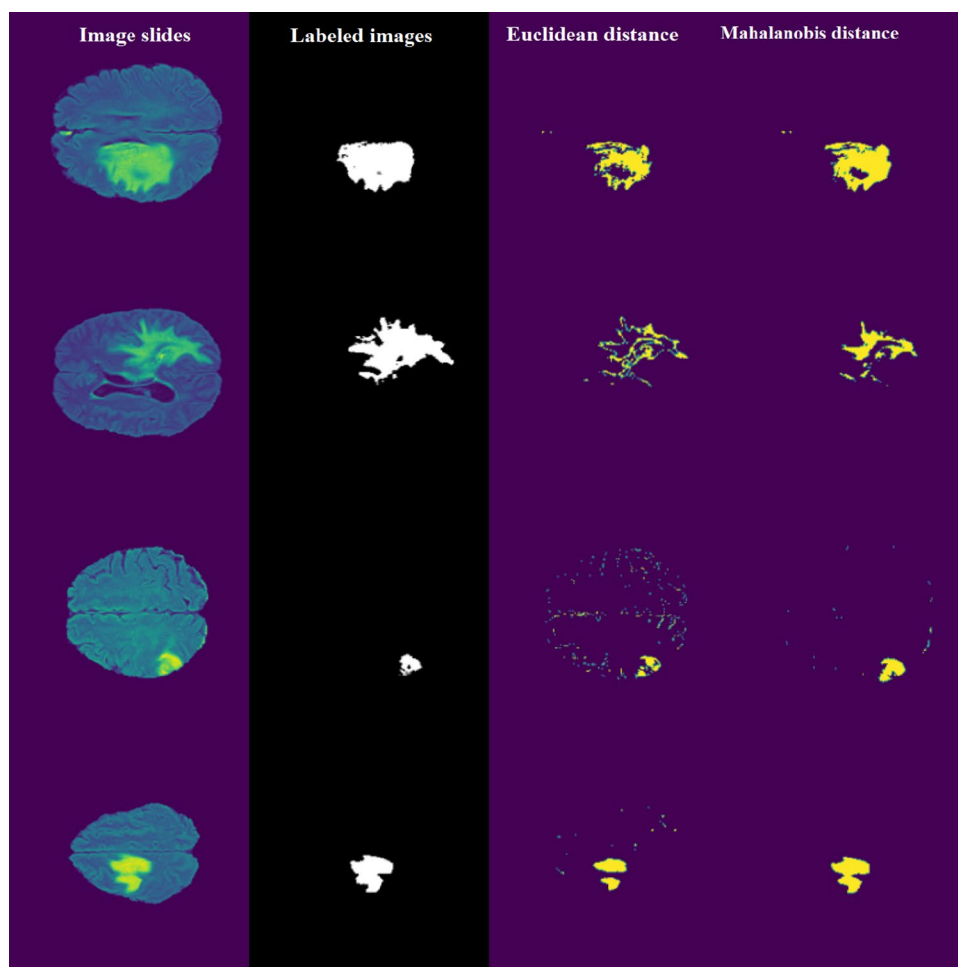


Fig. 9 Example of incorrect detection results using the proposed LSTM network

Data Availability The data used in this study are publicly available from the Brain Tumor Segmentation (BraTS) challenge. The BraTS datasets can be accessed through the Medical Image Computing and Computer-Assisted Intervention (MICCAI) website at <https://www.med.upenn.edu/cbica/brats2021/>. Researchers must comply with the terms and conditions of use specified by the dataset providers.

Declarations

Conflict of interest The authors declare that they have no Conflict of interest.

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