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A Hybrid FCM Based Ensemble Framework for Brain Tumor Segmentation

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Abstract

Precise brain tumor segmentation in Magnetic Resonance Imaging (MRI) is challenging for healthcare providers and many researchers because of variability in size and boundaries. Conventional clustering and ensemble feature selection methods for complex tumor regions are characterized by uncertainty and can result in overfitting. To address these shortcomings, the proposed Hybrid FCM Ensemble framework integrates Fuzzy C-Means (FCM) clustering and wrapper filter feature selection with an ensemble classifier to address the segmentation challenges in MRI tumors. The multimodel magnetic resonance images are preprocessed using z-score normalization, Gaussian smoothing filtering and morphological techniques. The FCM wrapper filter method is used to reduce MRI heterogeneity, clustering and select unique tumor features. The three primary filtering criteria, such as solidity, area and major axis length are analyzed and set to standardized limits to ensure accurate segmentation results across multiple sizes of MRI images. These selected features are then processed by a weighted ensemble classifier and morphological refinement to enhance the segmentation process. The proposed framework is evaluated on the Multimodal Brain Tumor Segmentation Challenge (BraTS) 2018 dataset and the performance is evaluated with accuracy, dice, sensitivity and specificity metrics. The performance of 97.87 percent accuracy, 91.73 percent dice score with 92.38 percent sensitivity and 98.49 percent specificity indicates that the proposed method can effectively diagnose brain tumors compared with traditional methods.

Keywords: Brain Tumor, Clustering, Ensemble Techniques, Fuzzy Clustering, Segmentation, Wrapper-filter.

Introduction

Magnetic Resonance Imaging (MRI) based brain tumor detection and segmentation play a crucial role in diagnosis and prediction estimation (1). However, brain tumor segmentation remains challenging due to variations in MRI intensity, heterogeneity, irregular tumor boundaries and inter-patient variability. Various tumor types and their grades were explored using MRI features and statistical and machine learning techniques (2-4). Early studies for automated segmentation and classification of medical image analysis were based on neural and knowledge-based systems (5-7). Several machine learning algorithms such as Support Vector Machine (SVM), Bayesian classifiers and kernel-based learning techniques were introduced to improve diagnostic accuracy in tumor prediction. While these methods achieved promising classification performance, they were designed for tumor classification rather than accurate pixel-level segmentation and ignored spatial relationships (8–10). To address these research challenges, the proposed study primarily focuses on tumor segmentation, which aims to delineate tumor boundaries at the pixel level. To improve tumor diagnostic accuracy, MRI and Magnetic Resonance Spectroscopic Imaging (MRSI) feature selection framework using Least Square SVM was implemented. In their framework, feature selection methods were utilized to reduce data dimensionality while preserving the most informative biomarkers. This method integrates automatic relevance determination and probabilistic outputs to improve tumor type classification and 98.26% prediction accuracy was achieved. MRI images are sensitive to noise and may vary with respect to acquisition protocols. Hence, this method was highly dependent on MRI and MRSI data quality and was sensitive to noise and acquisition variations (11). Another hybrid method combined a genetic algorithm, wavelet transform and SVM to improve tumor detection accuracy. Initially, wavelet-based texture features

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are extracted to capture important structural information from MR images. Then appropriate features are selected using a genetic algorithm. The selected feature subset is provided to an SVM classifier to classify brain tissues into normal, benign and malignant classes. These models achieved prediction accuracies of 96.29% and 99.35%, respectively. While these classification techniques provide significant diagnostic accuracy, they do not address pixel-level segmentation challenges. These models focus only on classification accuracy but do not ensure spatial consistency in segmentation (12, 13). Semi-supervised learning approaches were studied to handle partially labelled datasets, but caused limitations in boundary detection accuracy (14). A pre-trained VGG16 encoder was utilized to enhance brain tumor segmentation accuracy. MaxPooling layers with a 2 × 2 kernel in the VGG16 encoder were utilized to preserve critical data and derive hierarchical features from input images. Class imbalance in the VGG16 encoder was addressed with a gradient descent-based loss function. The framework achieved an average Dice score of 89% for complete tumor segmentation (15).

A hybrid approach integrated K-means clustering, Moth Flame Optimization (MFO), and Convolutional Neural Networks (CNN) for brain tumor segmentation. A custom fitness function was used to extract tumor regions. Experimental results showed that traditional clustering did not achieve high accuracy. This research demonstrated that traditional clustering was sensitive to noise and exhibited poor spatial coherence, resulting in fragmented regions. It was shown that integrating clustering with optimization techniques significantly improved tumor detection efficiency (16).

Several studies combine Bayesian discriminant methods, neural networks, logistic regression and decision trees within ensemble frameworks. Ensemble methods have shown improved robustness in tumor diagnostic systems (17, 18). Many researchers have analyzed the performance of a brain tumor segmentation framework using different filtering and automated hybrid feature selection techniques. Their results show that selected spectral features significantly enhance diagnostic performance, but feature selection is critical in reducing redundancy. Wrapper based neural network feature selection strategies were also proposed for efficient subset optimization. These techniques mainly focused on dimensionality reduction, classification accuracy but spatial and structural information was often ignored (19-22).

A transformer-based multimodal brain tumor segmentation framework with masking and noise-masking strategies was studied (23). This model was able to handle missing modalities and achieved a Dice similarity coefficient of approximately 0.93% more than conventional CNN-based models. However, the model is not robust to heterogeneous clinical noise and lacks explicit spatial consistency constraints. These limitations may lead to fragmented or anatomically inconsistent segmentations.

A two-stage multimodal brain tumor segmentation approach was proposed using transfer learning for tumor detection. This method reduces segmentation complexity by converting a multiclass problem into a binary classification of healthy and non-healthy tissue to improve robustness. The model achieved a Dice Similarity Coefficient of 92.08% for segmentation. It also detected 95.42% of blood vessel samples in structural segmentation. However, this approach depends heavily on pseudo-label quality and errors may be introduced due to the automatic generation of pseudo-labels. It also struggles with distinguishing tumors from highly vascularized regions, which leads to misclassification. Further, sparse annotations and lack of spatial consistency constraints may affect segmentation reliability in complex clinical scenarios (24).

Although considerable advancements have been shown for brain tumor segmentation using MRI data, current methods have some limitations. Traditional clustering methods, such as Fuzzy C-Means are susceptible to noise or intensity change. Noise caused by these issues leads to inaccurate boundary definition. Deep learning and machine learning techniques are also powerful but may not work well with heterogeneous clinical data. Finally, single model approaches do not do a good job of representing the spatial and texture variations of tumor areas. Therefore, there is a need for a hybrid framework utilizing the benefits of FCM in combination with an optimized ensemble strategy to improve the accuracy and reliability. This necessity leads to the proposed hybrid FCM-based wrapper optimized ensemble framework for automated brain tumor segmentation.

Methodology

The Hybrid FCM Ensemble framework is proposed for accurate brain tumor segmentation from multimodal MRI images. As shown in Figure 1, the framework integrates five major stages: preprocessing, Fuzzy C-Means clustering, hybrid wrapper-filter feature selection and segmentation, weighted ensemble classification and morphological post-processing refinement to improve segmentation performance.

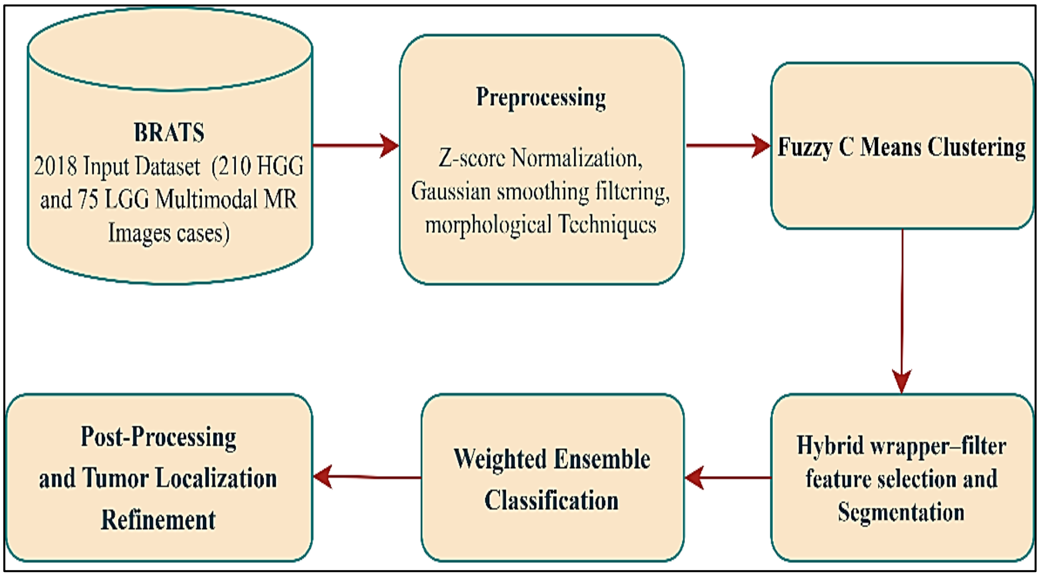

Figure 1: Proposed Hybrid FCM Ensemble Framework

Preprocessing

Noise in medical imaging often hinders the classification of lesions and the identification of patient conditions. On the BraTS 2018 input dataset (25), intensity normalization is performed first using Z-score normalization to standardize pixel intensities among different patient images. Then Gaussian smoothing filtering is employed to remove noise from MRI brain images. This filtering efficiently eliminates Gaussian noise while preserving the original image texture. In addition, Magnetic Resonance (MR) brain scans often include images of non-brain structures, including the skull and the outer membrane. To minimize computational complexity and enhance segmentation, skull stripping and non-brain tissues are removed using morphological techniques such as erosion, dilation and opening. Morphological techniques are also used to identify the borders and skeletons of image objects.

Dilation and erosion are the most prevalent morphological processes. Dilation enlarges the image edges, filling the target's outer or inner depressions. Erosion reduces the sawtooth artifacts along the target's edge. The opening operation is a combination of erosion and dilation processes, in which erosion is performed first, followed by dilation using the same structuring element. To acquire a full brain parenchymal area, the morphological opening technique is utilized to eliminate nonbrain anatomy from the MR image database and the hole-filling approach is employed for restoration. The goal of this phase is to lower the algorithm's complexity and the suggested clustering algorithm's precision is also increased to some degree.

Fuzzy C-Means Clustering

A variety of fuzzy logic systems have been implemented over a decade and results in reduction in ambiguity associated with improved modelling of uncertainty. In a fuzzy logic system, fuzzy rules, an inference engine, a fuzzifier and a defuzzifier are the major components of fuzzy sets. These sets are used to handle intensity overlap between tumor and healthy tissues. Unlike hard clustering, Fuzzy C-Means (FCM) clustering is employed to assign soft membership values to each pixel and enables better modelling of uncertain tumor boundaries.

The optimal objective function is estimated using Equation [1]. The clustering algorithm is executed multiple times until an optimal solution is attained.

The number of clusters depends on the images that do not include any areas of tumor or extensive edema. The ideal number of clusters has been selected to avoid manual interference.

The objective function minimized by FCM is given as,

$$Jm = \sum_{i=1}^{N} \sum_{j=1}^{C} u_{ij}^{m} \|x_i - c_j\|^2 \quad [1]$$

Where, N is the number of pixels and C is the number of clusters. u_{ij} is membership of pixel i in cluster j , m is the fuzzifier parameter, typically $m = 2$ and c_j is cluster centroid.

The number of clusters C is determined through an adaptive data-driven approach. First, the method evaluates a range of candidate cluster values that depends on the intensity distribution and structural properties of the MRI. Finally, the optimal cluster value is selected based on the best clustering stability and segmentation consistency over many iterations. This process ensures that the selected C value effectively captures the heterogeneity between tumor, edema and healthy tissues without manual intervention.

Hybrid Wrapper–filter Feature Selection and Segmentation

This hybrid strategy balances computational efficiency and predictive accuracy. A tumor is identified by first locating its three constituent pieces in separate modalities and then piecing them together. Hence, initially, a single tumor feature component is identified across all imaging modalities using the feature relevance score. Then a hybrid feature selection strategy detects the best features and reduces redundant features to enhance segmentation robustness.

$$S_f = MI(X_i, Y) \quad [2]$$

In filter stage, Mutual information MI is used to measure the relevance score S_f of each feature X_i with respect to the Y target tumor class labels as in Equation [2].

This stage eliminates irrelevant features efficiently. During the filtering phase of selection, Mutual Information scores are computed for each feature with respect to the target class labels. The feature set is ranked by MI values and a threshold is set to include only the most informative features within the feature set. The threshold is determined through empirical analysis of the distribution of MI scores, which excludes low-relevance and redundant features.

In the Wrapper Stage, selected subset features X_{subset} are further evaluated using the classifier performance accuracy to evaluate the wrapper score S_w as defined in Equation [3].

$$S_w = Accuracy(Classifier(X_{subset})) \quad [3]$$

During the wrapper phase of selection, the selected feature sets are evaluated again based on the performance of a classifier. The accuracy of each subset is determined by performing iterative evaluations of different subset combinations on a validation set. The subset combination that produces the highest level of validation accuracy is classified as optimal. The result is a balance of feature reduction and predictive performance that avoids overfitting. The selected features improve the discriminative capability between tumor and non-tumor regions, thereby directly enhancing segmentation accuracy and boundary delineation.

With the BraTS 2018 dataset, the filtering criteria are set as

a) object solidity larger than 0.7,

b) object area larger than 500 pixels and

c) object length of main axis larger than 35 pixels.

These value for each filtering criterion was chosen based on a broad range of empirical evaluation to accommodate MRI images of varying sizes. Figure 2 illustrates the segmentation performance of the proposed framework with uncertainty estimation for both training and testing MRI samples. Figures 2A–2D correspond to the training phase, where Figure 2A indicates the input MRI slice, Figure 2B presents the corresponding ground-truth annotation, Figure 2C depicts the segmentation predicted by the proposed framework and Figure 2D represents the uncertainty map highlighting regions with lower prediction confidence around complex tumor boundaries. Figures 2E–2H demonstrate the testing phase, including the unseen MRI input image, the corresponding ground-truth mask, the predicted tumor segmentation and the final prediction output, respectively. The predicted segmentation and the ground-truth annotations indicate that the proposed framework effectively preserves discriminative tumor characteristics extracted after Fuzzy C-Means clustering. The uncertainty map confirms that the majority of prediction uncertainty is confined to boundary regions with overlapping tissue intensities.

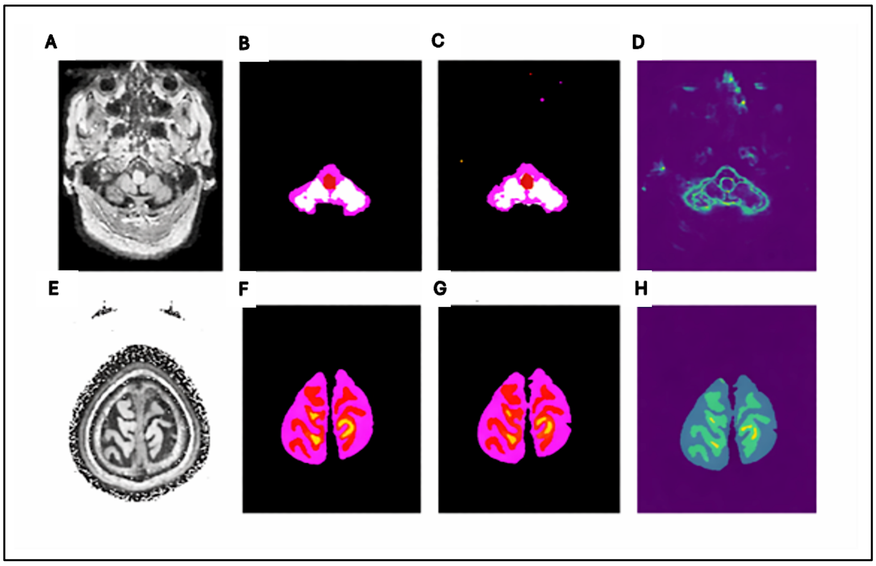

Figure 2: (A) Training Sample Input Image, (B) Ground Truth Mask, (C) Predicted Segmentation, (D) Uncertainty Map, (E) Testing Sample Source Image, (F) Ground Truth, (G) Predicted Segmentation, (H) Prediction Output

Weighted Ensemble Classification

The optimized feature subset obtained from the hybrid wrapper–filter selection is used as the input to an ensemble classification framework. Multiple heterogeneous base classifiers, including Naive Bayes (NB), Support Vector Machine (SVM) and Deep Convolutional Neural Network, are trained independently using the selected feature subset. These classifiers are selected for their complementary strengths, where NB provides probabilistic modeling, SVM ensures robust decision boundaries and Deep CNN captures complex spatial features. In addition, K-means clustering is utilized to enhance feature representation rather than as a classifier. $h_k(x)$ denote the prediction of the k^{th} classifier from M number of base classifiers where classifier weight is represented as w_k. Their outputs are combined using a weighted voting strategy based on individual classifier performance to improve robustness and generalization.

The ensemble classification output is determined by weighted voting as defined in Equation [4].

$$\text{classification output} = \sum_{k=1}^{M} w_k\, h_k(x) \qquad [4]$$

The weights are assigned based on the individual classifier performance. The ensemble strategy reduces prediction variance and minimizes overfitting. This ensemble framework improves robustness resulting in more consistent segmentation outputs across heterogeneous MRI data.

Post Processing and Tumor Localization

The classification output is fed into the postprocessing stage. Then morphological operations are applied to refine the predicted tumor regions. Initially, binary segmentation masks are generated to identify individual tumor candidates. A binary image is considered a valid tumor region if it overlaps the corresponding segmented region with a predefined threshold such as 20 pixels. The images that do not satisfy this threshold are ignored and considered false positives.

To analyze the spatial consistency across consecutive MRI images, tumor structure is verified. Tumor regions typically exhibit measurable changes in size across their neighbors. Therefore, objects detected in adjacent regions are verified to identify whether they belong to the same tumor structure. If an object appears in the same spatial location even with minor size variations, it is confirmed as a valid tumor region. Once the tumor location is identified, the same spatial region is also examined to detect the tumor mass. Then morphological dilation and closing operations are applied to refine the tumor boundary. These operations discover missing tumor pixels, if any and generate a consistent binary tumor mask.

Hybrid FCM-based Ensemble Framework Workflow

The overall workflow of the proposed Hybrid FCM-based Ensemble Framework for brain tumor segmentation is summarized as follows:

Initially, the input MRI brain image is preprocessed by the following steps:

a) Normalize the image intensity values
b) Apply Gaussian filtering for noise removal and morphological operations to remove non-brain tissues

Subsequently, the FCM clustering adopts the following steps iteratively to partition the image into fuzzy clusters:

a) Initialize cluster centers and membership values
b) Until convergence criteria is satisfied – Compute membership values for each pixel and update cluster centers
c) Generate clustered image

The resulting clustered image is given as input for feature extraction where intensity, texture and statistical characteristics are computed from the segmented regions. Next, a hybrid wrapper–filter feature selection strategy is employed to compute the optimal feature subset as follows:

a) Initialize feature subsets
b) Evaluate each subset using classifier performance
c) Select optimal feature subset

The optimized feature subset is subsequently provided to the weighted ensemble classifier, where the following steps are carried out:

a) Train Naive Bayes classifier
b) Train Support Vector Machine classifier
c) Train Deep CNN model
d) Obtain predictions from all classifiers and combine predictions using weighted voting

Finally, the following morphological post-processing operations are carried out to remove small artifacts, refine boundaries and generate the final refined tumor segmentation region.

Results and Discussion

Dataset Description

The proposed framework is analyzed using the BraTS 2018 dataset. This dataset contains 285 multimodal MRI patient cases. It consists of 210 patients with High-Grade Glioma (HGG) and 75 patients with Low-Grade Glioma (LGG). HGG is a fast-growing, aggressive and highly malignant tumor with a poor survival rate when compared to LGG. Each patient dataset consists of multimodal MRI scans of T1, T1c, T2 and FLAIR modalities under varying magnetic field strengths and acquisition protocols. Each MRI volume has a spatial resolution of 240 × 240 × 155 pixels. Figure 3 illustrates the qualitative comparison between the training and testing dataset input FLAIR MRI 75th slice, ground truth and predicted segmentation result. It highlights the model's ability to delineate tumor boundaries. Figures 3A–3C correspond to the training phase, where Figure 3A presents the input FLAIR MRI 75th slice, Figure 3B shows the corresponding ground-truth annotation and Figure 3C depicts the tumor segmentation predicted by the proposed framework. Similarly, Figures 3D–3F represent the testing phase, including the input FLAIR MRI 75th slice, the corresponding ground-truth annotation and the predicted segmentation result, respectively. The close visual agreement between the predicted segmentation masks and the expert-annotated ground truth demonstrates the capability of the proposed framework to accurately identify tumor regions while preserving their structural characteristics. The qualitative results further indicate that the proposed method maintains consistent segmentation performance on both training and unseen testing samples, highlighting its robustness and generalization capability.

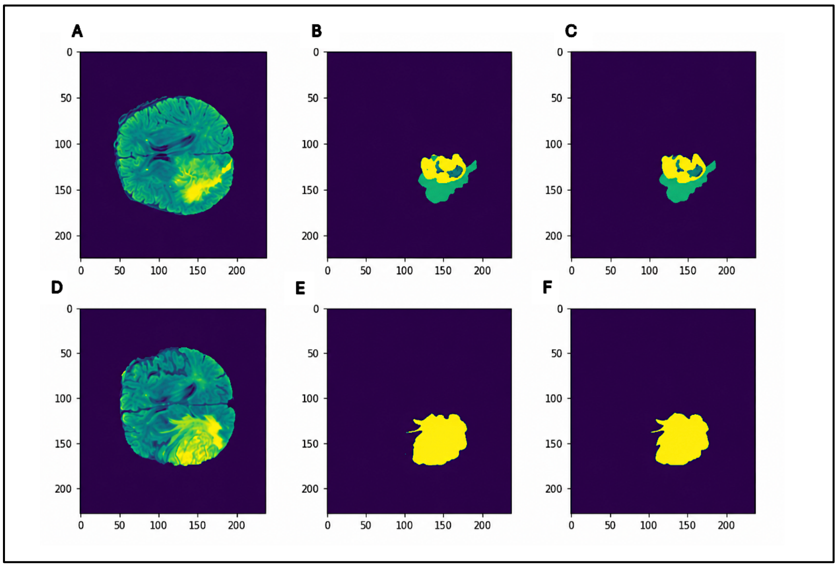

Figure 3: (A) Training Dataset Input FLAIR MRI 75th Slice, (B) Corresponding Ground Truth Annotation, (C) Predicted Segmentation, (D) Testing Dataset Input FLAIR MRI -75th Slice, (E) Ground Truth Annotation, (F) Predicted Segmentation

To evaluate the proposed method, the dataset is split into an 80% training set, a 10% validation set and a 10% testing set to provide an unbiased performance evaluation and prevent overfitting. Neuroradiologists manually annotated the tumor regions in the MRI volumes using predefined label values. Label 0 represents healthy brain tissue. Label 1 corresponds to the necrotic and non-enhancing tumor core, while label 2 represents peritumoral edema surrounding the tumor. Label 4 represents the enhancing tumor region visible after contrast enhancement. Label 3 is not used in the BraTS annotation scheme.

To ensure the robustness and reliability of the results, the proposed model was executed over multiple runs with different random initializations. The final reported performance metrics represent the average values obtained across these runs. The validation set was used for hyperparameter tuning, while the test set was strictly used for unbiased performance evaluation.

Accuracy, Dice, Sensitivity and Specificity are the four evaluation indicators that were used to determine the performance of the proposed system and segmentation quality. The Dice value measures the overlap between predicted and ground-truth segmentation. Accuracy is the overall correctness. Sensitivity indicates the number of true prediction rates. Specificity is a metric that measures the true negative rate.

The performance evaluation indicators are determined using Equations [5-8].

$$\text{Accuracy} = \frac{\text{TP+TN}}{\text{TP+TN+FP+FN}} \quad [5]$$

$$\text{Dice} = \frac{2\,\text{TP}}{\text{2TP+FP+FN}} \quad [6]$$

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP+FN}} \quad [7]$$

$$\text{Specificity} = \frac{\text{TN}}{\text{TN+FP}} \quad [8]$$

where TP, TN, FP, FN are defined as follows:

a) TP denotes the presence of a tumor that has been accurately recognized.

b) TN stands for tumor not existing and it cannot be found.

c) FP refers to a tumor that does not exist yet is discovered.

d) FN indicates that a tumor is present but has not been discovered.

Table 1 evaluation results show notable consistency in segmentation performance across three random patients. The accuracy values consistently vary in the range from 0.926 to 0.942. The dice coefficient indicates significant overlap between predicted and ground truth regions around 0.97. The proposed framework achieves significant sensitivity in the range between 0.924 and 0.960, indicating reliable detection of target regions. The specificity is achieved in the range of 0.982 and 0.998, which shows minimal false positives of the framework.

Table 1: Comparison of Accuracy, Dice, Sensitivity and Specificity Metrics for Qualitative and Representative Comparison of Three Random Patients

Evaluation Metrics	Patient 1	Patient 2	Patient 3
Accuracy	0.926	0.942	0.932
Dice	0.960	0.979	0.973
Sensitivity	0.924	0.958	0.960
Specificity	0.995	0.998	0.982

After evaluating representative patient cases, the overall generalization performance is evaluated using the complete test dataset. As shown in Table 2, the results demonstrate the stability and generalization capability of the proposed model. It shows that the suggested Hybrid FCM Ensemble model works successfully with the BraTS 2018 training, validation and test datasets. The model achieves 97.65% accuracy and a 91.12% Dice score for the test dataset. 91.8% sensitivity and 98.32% specificity results show that the proposed system is consistent in sensitivity and 98.32% of specificity results show that the proposed system is robust and consistent in tumor detection.

Table 2: Proposed Hybrid FCM Ensemble Framework Aggregate Evaluation Across the Entire Test Set

Dataset Split	Accuracy (%)	Dice Score (%)	Sensitivity (%)	Specificity (%)
Training Set (228 cases)	98.12	92.45	93.2	98.75
Validation Set (28 cases)	97.84	91.63	92.15	98.4
Test Set (29 cases)	97.65	91.12	91.8	98.32

While some deep learning approaches often result in a higher Dice score, they require more annotated data and relatively more computational resources. However, the proposed hybrid framework provides a 91% Dice score, indicating a balanced trade-off between segmentation accuracy, robustness and the overall generalization ability.

Table 3 illustrates the comparative analysis of the proposed Hybrid FCM Ensemble method with the conventional framework. It highlights the significantly improved performance of the proposed Hybrid FCM Ensemble framework over other conventional methods in terms of accuracy, Dice score, sensitivity and specificity. SVM (8) and Naive Bayes (9) algorithms exhibit average performance levels when compared with the k-means (10) accuracy and Dice coefficient.

Table 3: Performance Analysis of Proposed and conventional Framework

Method	Accuracy (%)	Dice Score (%)	Sensitivity (%)	Specificity (%)
Naive Bayes (9)	96.84	88.92	90.75	97.63
SVM (8)	97.02	89.63	91.42	97.98
K-means (10)	95.73	87.41	89.96	95.84
Deep CNN (23)	97.45	90.61	91.87	98.12
Proposed Hybrid FCM Ensemble	97.87	91.73	92.38	98.49

The deep convolutional neural network shows itself to be better than other traditional machine learning algorithms. Because Deep CNN has the ability to learn complex feature representations in MRI data. The proposed framework provides better performance than all baseline models with result of 97.87% accuracy and 91.73% Dice score with 92.38% sensitivity and 98.49% specificity. These results demonstrate improved robustness and segmentation accuracy of the proposed system. Although the improvement over Deep CNN (23) is modest, the proposed approach addresses both intensity ambiguity and uncertainty using Fuzzy C-Means clustering. This shows enhanced capability in handling overlapping intensity distributions between tumor and normal tissues, which is often challenging for CNNs.

Conclusion

This study presented a hybrid FCM-based ensemble framework for automated brain tumor segmentation from MRI images using the BraTS 2018 dataset. The primary contribution of this work is the development of a hybrid segmentation framework that integrates fuzzy clustering, wrapper-based feature optimization and ensemble classification within a single methodology. The proposed model achieved an accuracy of 97.87%, a Dice score of 91.73%, a sensitivity of 92.38% and a specificity of 98.49%, compared with conventional methods such as Naive Bayes, SVM, K-means and Deep CNN. The experimental results demonstrate that the proposed framework effectively segments tumor regions despite the complexity and heterogeneity of MRI images. By accommodating structural variations, irregular tumor boundaries and overlapping intensity distributions, the framework provides more reliable segmentation performance. These findings indicate that the integration of fuzzy clustering, wrapper-based feature selection and ensemble learning enhances segmentation accuracy while providing a robust foundation for automated brain tumor analysis. Consequently, the proposed framework will provide a reliable and effective brain tumor segmentation mechanism that provides guidance in clinical decision-making in neuro oncological environments.

The use of fuzzy clustering enables the framework to better represent the gradual transition between tumor and normal tissues by assigning membership values rather than hard boundaries during segmentation. The wrapper-based feature optimization strategy reduces redundant features and selects the most informative attributes, thereby improving classification efficiency and reducing computational complexity. Finally, the ensemble classification stage combines the strengths of multiple classifiers to improve segmentation accuracy and robustness across MRI images with varying tumor characteristics. These methodological components collectively contribute to the improved performance achieved by the proposed framework.

Although the proposed framework produced encouraging results, certain limitations remain. The performance evaluation was conducted only on the BraTS 2018 dataset and therefore its generalization to different clinical datasets, MRI acquisition protocols and patient populations requires further investigation. In addition, the present work processes MRI slices individually and does not utilize the complete three-dimensional spatial information available in volumetric MRI data. Future work will focus on extending the proposed framework to three-dimensional brain tumor segmentation and validating its performance using larger and more diverse clinical datasets. Further improvements can also be achieved by investigating advanced feature optimization methods and enhanced ensemble learning strategies to improve robustness and computational efficiency.

Abbreviations

BraTS: Multimodal Brain Tumor Segmentation Challenge, FCM: Fuzzy C Means, MR: Magnetic Resonance, MRI: Magnetic Resonance Imaging, MRSI: Magnetic Resonance Spectroscopic Imaging, SVM: Support Vector Machines.

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Author Contributions

Ramesh T: Adapted a Fuzzy C-Means wrapper–filter feature selection approach and experimentally validated the results using the BraTS dataset, Faritha Banu J: Formulated the research problem, developed the hybrid FCM ensemble framework and integrated and evaluated the performance of the model, Lakshmi Haritha Medida: Implemented the ensemble classification model, Padmapriya S: Carried out MRI data preprocessing and selective comparison with baseline methods. The final version of the manuscript was discussed, examined and approved by all authors.

Conflict of Interest

The authors declare that they have no conflicts of interest regarding the present study.

Data Availability

The dataset is publicly available. However, the compiled data supporting the findings of this study can be made available from the corresponding author on a reasonable request.

Declaration of Artificial Intelligence (AI) Assistance

The authors written this manuscript without the use of generative AI or any AI-assisted technology. The content of this manuscript was written exclusively by the authors.

Ethics Approval

Not applicable.

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