

# OPTIMIZED FUZZY C-MEANS (FCM) CLUSTERING FOR HIGH-PRECISION BRAIN IMAGE SEGMENTATION AND DIAGNOSIS USING DENSENET FEATURES

PRIYA KANTAMANENI<sup>1</sup>, D.VETRITHANGAM<sup>2</sup>, M MAITHILI SAISREE<sup>3</sup>, S.SHARGUNAM<sup>4</sup>,  
S.SRINIVAS KUMAR<sup>5</sup>, ASHOK BEKKANTI<sup>6</sup>

<sup>1</sup>Assistant Professor, P.B Siddhartha college of Arts and Science, Vijayawada, Andhra Pradesh,  
Department of Computer Science, India.

<sup>2</sup> Professor, Chandigarh University, Mohali, 140413, Department of Computer Science and Engineering,  
India.

<sup>3</sup>Assistant Professor, R.V.R & J.C College of Engineering, Chowdavaram, Guntur, Andhra Pradesh-  
522019,  
Department of Computer Science and Engineering, India.

<sup>4</sup>Assistant Professor, Kalasalingam Academy of Research and Education, Virudhunagar, Srivilliputhur,  
Tamilnadu, Department of Computer Science and Engineering, India.

<sup>5</sup>Assistant Professor, Madanapalle Institute of Technology & Science, Madanapalle-517325, Andhra  
Pradesh,  
Department of Computer Science and Engineering, India.

<sup>6</sup>Assistant Professor, Koneru lakshmaiah Education Foundation, Vaddeswaram, Guntur, Andhra Pradesh,  
Department of Computer Science and Engineering, India.

E-mail: <sup>1</sup>ppriyamca@gmail.com, <sup>2</sup>vetrigold@gmail.com, <sup>3</sup>mvsaisree@gmail.com,  
<sup>4</sup>s.shargunam@klu.ac.in

<sup>5</sup>srinivaskumar4u@gmail.com, <sup>6</sup>ashok.bakkanti@gmail.com

## ABSTRACT

Brain imaging techniques play a crucial role in identifying the causes of brain cell injury. Consequently, early diagnosis of such conditions can yield significant benefits, improving treatment prospects and minimizing potential patient complications. Among the most formidable challenges in medical image analysis is brain tumor segmentation. Challenges include limited spatial context, increased occurrences of false positives and negatives, the inability to distinguish tumor components, and a lack of preprocessing. To address these issues, we propose an approach that combines Optimized Fuzzy C-Means (FCM) Clustering with DenseNet Features and employs efficient preprocessing techniques. Our improved DenseNet architecture meticulously extracts relevant features from preprocessed images. FCM assigns each feature vector to one or more clusters based on their degrees of membership and its output encompasses cluster centers and membership values, indicating the degree of association for each data point with each cluster. Hence, FCM improves interpretability by distinctly delineating tissue regions through the utilization of these features. Markov Random Field (MRF) Optimization is probabilistic graphical model that capture spatial dependencies among neighboring pixels or regions in an image. As each MRI modality possesses the unique ability to emphasize distinct tissue characteristics. All the MRI Modalities (Flair, T1, T1c, T2) can be combined to get valuable and complementary wealth of information regarding the tissues and structures undergoing examination. Our optimized FCM model is experimented on the Original FLAIR -MR images of patients and Combined MRI Modalities (Flair, T1, T1c, T2).The Optimized Fuzzy C-Means (FCM) Clustering achieved train Dice Coefficient score of 99.18% and test Dice Coefficient score 98.64%, and the Optimized Fuzzy C-Means (FCM) Clustering with Combined MRI modality feature achieved train Dice Coefficient score 100% and test Dice Coefficient score of 99.413%.The results shows that the proposed model out performs the existing models.

**Keywords:** Brain Image, Segmentation, DenseNet, Fuzzy C-Means, Optimization, Diagnosis

## 1. INTRODUCTION

Medical imaging analysis has been commonly involved in basic medical research and clinical treatment, e.g. computer-aided diagnosis [1]. Among various tasks in medical image analysis, brain tumor segmentation has attracted much attention in the research community [2]. Medical imaging techniques, such as positron emission tomography (PET) [3], magnetic resonance imaging (MRI) [4], computed tomography (ct) [5], x-ray [6], and ultrasound have been widely employed for disease detection, diagnosis, and treatment during the last few decades [7]. The development of anomalous cell clusters within or near the brain triggers the onset of a brain tumor [8], these irregular cells disrupt brain function and impact the patient's health [9]. Brain tumors can be broadly categorized into two types: malignant tumors, which are cancerous, and benign tumors, which are noncancerous [10].

Numerous image-processing techniques and methods have been employed in the diagnosis and treatment of brain tumors. Among these, segmentation serves as a foundational step in image processing, allowing for the extraction of the affected brain tissue region from MRI scans [11]. Tumor region segmentation is a crucial undertaking in the realm of cancer diagnosis, treatment, and treatment outcome assessment. a wide array of both semi-automatic and automatic segmentation methods and techniques are employed for the purpose of tumor segmentation [12]. MRIs offer a range of features that are utilized in studies focused on the segmentation of brain tumors, including image textures [13], local histograms [14] and other features [15].

Machine learning techniques are frequently employed for pattern classification in research related to the segmentation of tumors [16][17]. MRI includes various sequences, including t1-weighted (t1) and t1-weighted contrast-enhanced (t1c), as well as t2-weighted and t2-weighted fluid attenuated inversion recovery (flair) techniques. These sequences are utilized in the segmentation of brain tumors [18][19][20]. Deep learning methods have demonstrated cutting-edge performance in automatically segmenting brain tumors using Multi-modal MRI data [21][22][23]. A model based on optimal feature selection has been developed for the efficient prediction of breast cancer, utilizing a modified logistic regression approach [39]. An artificial neural network model in conjunction with a Meta-heuristic algorithm worked

well on the types of datasets for coronary artery disease prediction [40].

Multi-disease prediction was done by the use of deep reinforcement Boltzmann machines [41]. The modified resnet152v2 model demonstrated effective performance in predicting pneumonia from chest x-rays [42]. the accuracy of brain tumor prediction is improved by enhancing the convolutional neural network layers, transfer learning fully connected layers, and weights of the layers in the vgg-19 model [43][44][45]. the objectives of this research work are to improve brain tumor segmentation accuracy and dice coefficient score by fulfilling the gaps such as limited spatial context, inability to distinguish tumor components, increased false positives and negatives, and the risk of misinterpretation.

The research paper effectively bridges critical technical gaps identified within existing models for brain image segmentation. the paper employs a well-rounded approach that systematically addresses these gaps through the utilization of various techniques: firstly, image preprocessing techniques, enhanced with augmentation, are deployed to tackle issues such as "limited spatial context" and "inability to distinguish tumor components." this preprocessing step enhances image quality and fosters improved spatial context by readying the data for subsequent analysis, including noise reduction and intensity normalization, which aids in distinguishing between different tumor components.

Secondly, the paper leverages densenet feature extraction to combat concerns related to "increased false positives and negatives" and "less accuracy." by employing modified densenet architecture, relevant features are meticulously extracted from the preprocessed images. This strategic feature extraction approach significantly diminishes the occurrence of false positives and negatives, concurrently elevating the overall precision of segmentation. Thirdly, fuzzy c-means (FCM) clustering takes center stage, primarily addressing the "risk of misinterpretation." FCM clustering partitions the feature space into distinctive clusters representing different regions of brain tissue. Consequently, this process alleviates the risk of misinterpretation by providing a lucid delineation of tissue regions grounded in the extracted features.

Lastly, the integration of Markov random fields (MRFs) for optimization firmly addresses concerns related to "limited spatial context" and "increased false positives and negatives." by incorporating MRFs as an optimization step, the

methodology substantially bolsters spatial context. MRFs adeptly model spatial relationships between voxels, fostering spatial coherence within the segmentation process. Consequently, this meticulous approach diminishes the likelihood of false positives and negatives, ultimately culminating in more precise and dependable segmentation outcomes. In summation, the research paper presents a holistic methodology systematically tailored to bridge identified technical gaps in current models for brain image segmentation. This multifaceted approach combines image preprocessing techniques with augmentation, densenet feature extraction, FCM clustering, and MRF-based optimization. The result is a robust and potent approach that not only amplifies segmentation accuracy but also diminishes misinterpretation, thereby significantly enhancing the overall performance of brain image segmentation.

## 2. LITERATURE REVIEW

In 2018, Sharif et al.[24] proposed a new method for the segmentation and classification of brain tumors based on improved saliency segmentation and the best feature selection approach. The proposed method achieved an average classification accuracy of above 90%, but this approach suffers from an over segmentation problem, because of which the classification accuracy is affected by irrelevant features. In 2021, Hu et al.[25] introduced a fuzzy system for predicting brain diseases. They employed the HPU-Net (Hybrid Pyramid U-Net Model) to enhance the model's safety and performance. The HPU-Net achieved impressive results with a DSC (Dice Similarity Coefficient) of 93.6% and an accuracy coefficient of 84.5%. One notable advantage of this model is its lower energy consumption and greater stability compared to other models operating under similar conditions.

However, it's worth mentioning that this model did not incorporate texture and shape features into its experimental setup. In 2020, Kwon et al. [26] introduced an uncertainty-quantification-based Bayesian neural network approach for classification and segmentation applications. This method effectively leverages both aleatoric and epistemic uncertainty. The proposed approach offers several advantages compared to existing methods. Notably, it expresses inherent variability through the underlying distribution of outcomes, ensuring numerical stability. However, it's important to note

that this method has not been explored from various angles in terms of experimentation.

In 2021, Díaz-Pernas et al. [27] proposed an automated model for brain tumor segmentation and classification, leveraging a Deep Convolutional Neural Network (CNN). To enhance the training dataset and mitigate overfitting, data augmentation was implemented through elastic transformation. This approach yielded impressive results, achieving a tumor classification accuracy of 97.3%, an average Dice index of 82.8%, an average sensitivity of 94.0%, and an average positive predictive total agreement score (PTAS) of 96.7%. However, it's worth noting that this method did not involve the removal of skull and vertebral column parts, and it encountered challenges related to the variability of the three tumor types, which led to occasional false positives in some images.

In 2020, Ali et al. [28] introduced an ensemble technique that incorporates both 3D CNN and U-Net architectures. Through this approach, they achieved dice scores of 75% for the enhancing tumor, 90.6% for the whole tumor, and 84.6% for the tumor core. One limitation of this approach is that it did not undergo extensive preprocessing of neither the dataset nor employ comprehensive post-processing of the results.

In 2021, Gunasekara et al.[29] introduced a systematic approach for MRI brain tumor localization and segmentation, leveraging deep learning-based active contouring techniques. This method yielded a Dice Score of 92% and demonstrated a high level of accuracy in regions of interest (RI) with a score of 99.36%. One limitation of this approach is the absence of a discussion regarding the number of training epochs and the complexity of the model, which could impact the method's reproducibility and understanding.

In 2020, Inbarani and Azar [30] introduced an innovative approach called the Hybrid Histogram-Based Soft Covering Rough K-Means Clustering (HSCRKM) algorithm for segmenting leukemia nucleus images. This method heavily relied on features derived from gray level co-occurrence matrix (GLCM), color, and shape information. The HSCRKM clustering algorithm achieved a prediction accuracy of 80%, while logistic regression and neural network models consistently delivered accuracy rates exceeding 90%. However, it's worth noting that this approach did not incorporate optimization principles into its methodology.

In 2022, Habib et al. [31] presented a hybrid approach for brain tumor segmentation, classification, and feature extraction. This approach

employed threshold segmentation and the watershed algorithm. The experimental results demonstrate that this novel method improves the detection of brain tumor images, achieving an accuracy rate exceeding 90%. However, it's worth noting that the accuracy falls somewhat short when compared to certain recent methods. In 2022, Dang et al.[32] introduced a novel deep learning framework that incorporated preprocessing techniques in conjunction with the Unet architecture, as well as utilizing VGG and GoogleNet implementations to classify various types of gliomas. Their model achieved a notable Dice coefficient score of 82% and exhibited high accuracy, reaching approximately 93%.

However, a notable limitation of this framework is its struggle to accurately segment regions of the glioma images that fall outside the established ground truth annotations. This limitation introduces a significant bias into the classification results, particularly when dealing with the exclusion of poorly performing data records. In 2022, Li et al. [33] introduced a region-based framework for EDL (Edge Detection and Labeling) segmentation that generated dependable uncertainty maps. This framework achieved a Dice score of 76.9%, highlighting its effectiveness in segmentation tasks. However, one notable drawback of this approach is its substantial computational cost. In 2023,

Balamurugan and Gnanamanoharan [34] introduced an innovative hybrid deep Convolutional neural network (DCNN). This DCNN leveraged the LuNet classifier to effectively detect and classify brain tumors. Impressively, this network achieved an accuracy rate of 99.7%. However, it's worth noting that this model exhibits a certain level of complexity within its network architecture. In 2023, Asiri et al. [35] introduced an innovative tumor detection and classification approach. Their method harnessed the power of a Fine-Tuned CNN, incorporating both ResNet50 and U-Net models. Remarkably, this methodology achieved impressive performance metrics, with a Dice Similarity Coefficient (DSC) of 95%, an F1 score of 93%, and an accuracy rate of 94%. However, it is important to note that this method did not provide specific information regarding the types of tumors it was designed to detect and classify.

Table-1 explains the gaps in existing brain tumor segmentation models are outlined here. These include the absence of optimization techniques for refining reproduced models, the potential introduction of errors due to cross-entropy loss usage, and the model's relatively high computational complexity. There are also issues related to

sensitivity to irrelevant features, the omission of critical texture and shape features, variability problems, misinterpretation issues and the absence of comprehensive preprocessing steps. Furthermore, the model's high complexity, combined with the lack of optimization principles, gives rise to concerns regarding computational costs and model interpretability. Additionally, the challenging task of detecting and segmenting small or subtle lesions in brain images, especially in early-stage diseases, remains a formidable obstacle.

### 3. PROPOSED METHODOLOGY

#### 3.1 Dataset

The "RSNA-MICCAI Brain Tumor Radiogenomic" dataset is a collection of medical images and associated data used for brain tumor segmentation and radiogenomic analysis. This dataset was created as part of the RSNA-MICCAI Brain Tumor Radiogenomic Classification Challenge, an initiative that aims to advance the field of brain tumor research and classification using machine learning techniques. The dataset includes a variety of brain MRI images of 2040 patients available at the source <https://www.kaggle.com/competitions/rsna-miccai-brain-tumor-radiogenomic-classification/data>.

The dataset also provides metadata and clinical information for each patient, including genomic data. The primary data type in this dataset is medical images in the form of DICOM (Digital Imaging and Communications in Medicine) files. DICOM is a standard format for storing and transmitting medical images. These images capture various types of MRI sequences (T1-weighted, T1-weighted contrast-enhanced (T1c), T2-weighted, FLAIR, etc.) that offer different perspectives on brain structures and pathology. The dataset provides annotations that segment brain tumors in the images. These annotations are often in the form of pixel-level masks or region-of-interest labels, indicating the boundary and location of tumor regions within the images.

#### 3.2 Preprocessing

The techniques include smoothing, filtering, normalization, and histogram equalization. The resulting images and the differences between them are visualized, and annotations are added to explain the effects of each preprocessing step. Here, DICOM files are loaded from the specified path using the pydicom library. DICOM files are commonly used in medical imaging to store data such as MRI or CT scans. The pixel data from the DICOM image is extracted into a NumPy array

called `pixel_array`. The pixel values are then rescaled to the range [0, 255] to ensure consistent visualization across different images.

A Gaussian filter with a specified sigma value is applied to the `pixel_array`. Gaussian smoothing helps reduce noise in the image by blurring it slightly. A median filter with a specified kernel size is applied to the `pixel_array`. Median filtering helps remove noise while preserving edges in the image. The pixel values of the `pixel_array` is Z-score normalized using the mean and standard deviation of the image.

This process brings the pixel values to a standard distribution with a mean of 0 and a standard deviation of 1. Histogram equalization is applied to the `pixel_array` to enhance the contrast of the image. This process redistributes the intensity values to cover a wider range and improve visual clarity. Difference images are calculated by subtracting the preprocessed images (smoothed, filtered, normalized, and equalized) from the original `pixel_array`. These images highlight the changes introduced by each preprocessing step.

### 3.3 System Model

Figure-1 illustrates the Proposed architecture of optimized FCM clustering with DenseNet-169. The architecture begins with an initial convolutional layer featuring numerous filters (e.g., 64 filters) using a small kernel size (e.g., 7x7) and is followed by a max-pooling layer (3x3 pool size, stride of 2) to reduce spatial dimensions. DenseNet introduces dense blocks, comprised of multiple dense layers stacked together. Each dense layer consists of convolutional layers, batch normalization, and ReLU activation. Crucially, each layer receives input from all prior layers in the same dense block. This "dense connectivity" fosters feature reuse and gradient flow. Transition layers separate dense blocks, incorporating batch normalization, 1x1 convolutions for dimensionality reduction, and average pooling to reduce spatial dimensions, controlling model parameters and computation.

Global Average Pooling (GAP) follows multiple dense blocks, resulting in 1x1 spatial dimensions and averaged feature maps. A fully connected layer processes GAP output, with neurons equating class count for classification tasks. Softmax activation yields class probabilities. To work with features from DenseNet-169, select a layer to extract features depending on desired abstraction levels (e.g., lower layers capture textures, while higher layers capture abstract patterns). Features are flattened into 1D vector for each image and normalized for consistent scale. For

Fuzzy C-Means (FCM) clustering, apply a custom membership function to calculate data point (feature vector) membership degrees to clusters.

Normalized feature vectors serve as input to FCM, specifying the desired number of clusters (K). In Markov Random Field (MRF) optimization, nodes (voxels) represent random variables for tissue labels (e.g., gray matter). An energy function combines data likelihood (label fit to MRI data) and smoothness (neighbor similarity) terms. The final output is a segmentation map assigning each voxel to a tissue class, aiding brain structure identification.

Figure 2 illustrates the overall flow diagram of Optimized Fuzzy C-Means (FCM) Clustering with DenseNet-169. DenseNet-169 is designed specifically for handling grayscale images, usually with dimensions of 224x224 pixels and a sole grayscale channel. In grayscale imagery, pixel intensity serves as a measure of brightness, where elevated values correspond to brighter regions, while diminished values correspond to darker areas. Feature Extraction from DenseNet-169: Features are gleaned from images using the pre-trained DenseNet-169 model. Typically, these features are extracted from one of the intermediate layers, depending on the desired level of abstraction. Feature Preprocessing: Normalization of extracted features is imperative to ensure consistent scales.

This normalization is crucial for subsequent clustering and optimization algorithms. Fuzzy C-Means (FCM) Clustering: The Fuzzy C-Means (FCM) clustering algorithm is applied to the preprocessed feature vectors. FCM is a soft clustering method that assigns each feature vector to one or more clusters based on their degrees of membership. The FCM output encompasses cluster centers and membership values, indicating the degree of association for each data point with each cluster. The segmentation process is guided by cluster assignments or membership values derived from Fuzzy C-Means (FCM). This can involve assigning each pixel to the cluster with the highest membership value.

Alternatively, membership values can be utilized as weights in a segmentation algorithm to generate a segmented image. Markov Random Field (MRF) Optimization is probabilistic graphical model that capture spatial dependencies among neighboring pixels or regions in an image. They are instrumental for modeling smoothness constraints in image processing tasks. Construction of an MRF model is undertaken, where nodes represent pixels or image regions, and edges denote pairwise interactions. An energy function is defined as consisting of two components: a data term, which

reflects how well the segmentation fits the data, and a smoothness term, which encodes continuity constraints between neighboring entities.

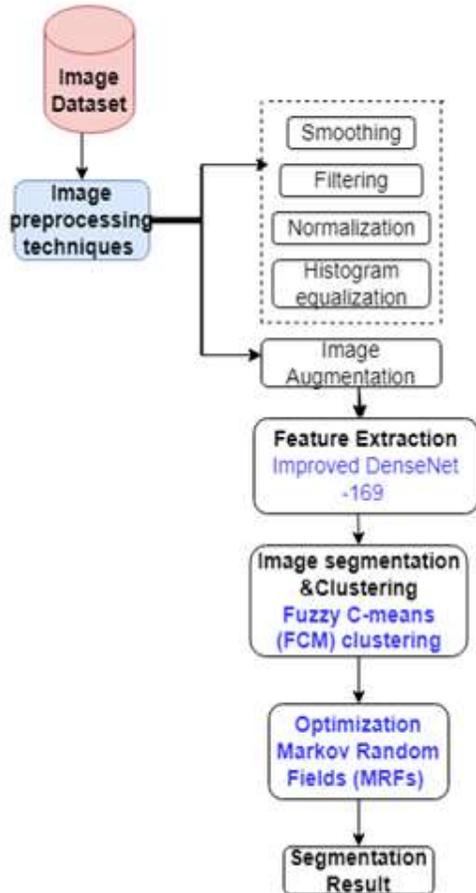


Figure 2: Flow Diagram of Optimized Fuzzy C-Means (FCM) Clustering with DenseNet 169

The energy function is carefully formulated to incentivize consistency between the FCM-derived segmentation and spatial relationships among pixels. The outcome of MRF optimization yields the ultimate segmented image, where pixels or regions are allocated to specific classes or clusters based on both data and spatial considerations. By combining FCM clustering, which groups features effectively, with MRF optimization, which enhances spatial coherence, we create a powerful image segmentation approach. This method effectively utilizes both feature similarity and smoothness constraints, making it especially valuable in tasks where achieving precise results depends on balancing local and global information, such as image segmentation.

## 4. RESULTS AND ANALYSIS

This section explains the results derived from the proposed model of the Optimized Fuzzy C-Means (FCM) Clustering method for High-Precision Brain Image Segmentation and Diagnosis utilizing DenseNet features.

### 4.1 Performance Metrics

Normally, the results of brain tumor segmentation consist of four types of measures: Dice Similarity Coefficient (DSC) and Accuracy. The ground truth mask and expected segmentation mask are compared using the Dice coefficient to determine how similar or overlapped they are. The masks must perfectly match for the Dice coefficient to be 1, which ranges from 0 to 1. The formula for calculating the Dice coefficient is shown in equation (1).

$$\text{Dice coefficient} = \frac{(2 * |A \cap B|)}{(|A| + |B|)} \quad (1)$$

Where A denote the predicted segmentation mask (as a set of pixels), B represents the ground truth segmentation mask (a collection of pixels),  $|A \cap B|$  demonstrates the cardinality (number of elements) of the intersection between A and B (similar pixels between the expected and ground truth masks),  $|A|$  represents the cardinality of A (total number of pixels in the predicted mask), and  $|B|$  represents the cardinality of B (The ground truth mask's overall pixel count). The numerator  $(2 * |A \cap B|)$  represents the predicted and ground truth masks both share twice as many pixels. The total of the number of pixels in the predicted and ground truth masks is represented by the denominator  $(|A| + |B|)$ .

The anticipated and ground truth masks must match exactly for the Dice coefficient to be 1; otherwise, there is no overlap or similarity. The Dice coefficient is frequently employed in the segmentation of medical images since it gives an indication of how well and closely the segmented regions match the ground truth annotations. It is frequently employed in additional picture segmentation tasks to assess the accuracy of the results. Accuracy measures the overall correctness of the segmentation predictions. It measures how many pixels in the image were correctly identified (including true positives and true negatives) as shown in equation (2).

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (2)$$

## 4.2 Results of the preprocessing Stage

As illustrated in the figure 3, the techniques encompass smoothing, filtering, normalization, and histogram equalization. The resulting images and the disparities between them are presented visually, accompanied by annotations to elucidate the impacts of each preprocessing step.

## 4.3 Segmentation Results and Analysis

The input for the proposed Optimized Fuzzy C-Means (FCM) Clustering for High-Precision Brain Image Segmentation and Diagnosis Using DenseNet Features consists of original FLAIR-MR images from patients. These images undergo a series of preprocessing steps to enhance their suitability for analysis. Following preprocessing, the improved DenseNet-169 model is employed to extract features from the images. These extracted features then undergo further preprocessing to refine and prepare them for subsequent analysis. The next step involves the application of Fuzzy C-Means (FCM) Clustering to segment the preprocessed features, effectively grouping similar elements within the images.

Subsequently, the segmented features are optimized using Markov Random Field techniques, enhancing the accuracy and coherence of the segmentation results. Finally, the outcomes of this comprehensive process are presented in the form of three key images: Figure 4a) is the original image with the tumor, which provides an unaltered view of the input image. Figure 4b) is an image with the tumor clearly highlighted, showcasing the segmented regions of interest. Figure 4c) is an image displaying the predicted segmentation, offering a visual representation of the identified areas of interest within the brain images. This workflow aims to provide precise brain image segmentation and diagnosis, leveraging advanced techniques and optimized feature extraction for improved accuracy and clinical relevance.

Figure 5a displays the Combined MRI Modalities (FLAIR, T1, T1c, T2), while 5b illustrates the Predicted Segmentation. The fusion of various MRI (Magnetic Resonance Imaging) modalities within MRI scans offers a valuable and complementary wealth of information regarding the tissues and structures undergoing examination. Each MRI modality possesses the unique ability to emphasize distinct tissue characteristics. For example, T1-weighted images excel at revealing anatomical intricacies, T2-weighted images are adept at detecting fluid content and edema, and diffusion-weighted imaging unravels insights into tissue microstructure. Incorporating T1c in conjunction with complementary modalities such as

FLAIR, T1, and T2 expands the scope of visualization, resulting in a more comprehensive and intricate portrayal of tumor boundaries. This enhancement significantly boosts the ability to detect and characterize tumor lesions and their specific attributes. By uniting these modalities, both radiologists and clinicians gain a comprehensive and all-encompassing perspective of the tissues under scrutiny. The amalgamation of MRI modalities in imaging stands as an adaptable approach that fosters a deeper and more informative understanding of imaged tissues and structures. This holistic approach is particularly invaluable in realms such as clinical diagnosis, treatment planning, and advanced research, enabling a profound exploration of the intricacies within brain imaging.

We examine the following key metrics: "Training Accuracy," "Validation Accuracy," and the "Dice Coefficient." Training Accuracy assesses the model's proficiency in correctly assigning segmentation labels to the training dataset. It provides insight into how well the model performs on the data it was trained on. Validation Accuracy, on the other hand, offers an indication of the model's generalization capability. It measures the model's accuracy in predicting segmentation labels for previously unseen data. Higher validation accuracy implies that the model excels at precisely segmenting objects or identifying regions of interest in new and unprocessed data. As shown in figure 6, the Optimized Fuzzy C-Means (FCM) Clustering achieved train accuracy of 99.78% and test accuracy of 98.25%, and the Optimized Fuzzy C-Means (FCM) Clustering with Combined MRI modality feature achieved train accuracy of 100% and test accuracy of 99.813% for the Epochs 35.

The Dice Coefficient, typically used as an evaluation metric rather than a training metric, quantifies the degree of overlap between the predicted segmentation and the ground-truth segmentation. It provides a valuable measure of the segmentation model's performance in terms of accuracy and consistency with the ground-truth data. As shown in figure 7, the Optimized Fuzzy C-Means (FCM) Clustering achieved train Dice Coefficient score of 99.18% and test Dice Coefficient score 98.64%, and the Optimized Fuzzy C-Means (FCM) Clustering with Combined MRI modality feature achieved train Dice Coefficient score 100% and test Dice Coefficient score of 99.413% for the Epochs 35.

The given figure-8 illustrates a comparative analysis between the Optimized FCM model, integrated with combined MRI modalities, and an existing segmentation model. This analysis

is based on accuracy, a common metric for evaluating segmentation accuracy. Notably, the Optimized FCM model exhibits significantly higher Dice coefficient values compared to the existing models. Specifically, the Dice coefficients for the Optimized FCM model are 9.04, 1.74 and 1.6, surpassing the corresponding values achieved by the following existing models: Improved saliency segmentation method[24], Deep CNN[27], and DL framework [32].

The given figure-9 illustrates a comparative analysis between the Optimized FCM model, integrated with combined MRI modalities, and an existing segmentation model. This analysis is based on the Dice coefficient. Notably, the Optimized FCM model exhibits significantly higher Dice coefficient values compared to the existing models. Specifically, the Dice coefficients for the Optimized FCM model are 5.8, 16.61, 8.81, 7.41, 39.4, 22.51, 10.913, and 20.213, surpassing the corresponding values achieved by the following existing models: HPU-Net [25], Deep CNN [27], Ensemble technique [28], contouring techniques [29], K-Means Clustering [30], Edge Detection and Labeling [33], Multimodal AD-Net [36], Hybrid Transformer [37], and Semi-supervised multiple evidence fusion [38]. Our Optimized Fuzzy C-Means technique significantly differs from existing brain tumor segmentation methods, particularly in the realm of preprocessing. While most methods focus solely on image augmentation techniques, our proposed technique incorporates both image augmentation and preprocessing methods. This dual approach has proven effective in refining the brain tumor image dataset, contributing to the enhanced accuracy and dice scores observed in our results. The inclusion of combined MRI modality features further distinguishes our model, leading to notable improvements in segmentation outcomes compared to traditional methods.

## 5. CONCLUSION AND FUTURE SCOPE

Our research work introduces an innovative approach that combines Optimized Fuzzy C-Means (FCM) Clustering with DenseNet Features, coupled with efficient preprocessing techniques. This enhanced DenseNet architecture adeptly extracts pertinent features from preprocessed images, leading to enhanced interpretability. Furthermore, the integration of Markov Random Fields (MRFs) ensures seamless spatial coherence during the segmentation process. The results of our study are highly promising. The Optimized FCM Clustering achieves a training Dice Coefficient score of 99.18% and a testing Dice

Coefficient score of 98.64%. Notably, the Optimized FCM Clustering with Combined MRI modality features attains even more impressive results, with a training Dice Coefficient score of 100% and a testing Dice Coefficient score of 99.413%. In terms of accuracy, the Optimized FCM Clustering demonstrates a training accuracy of 99.78% and a testing accuracy of 98.25%, while the Optimized FCM Clustering with Combined MRI modality features achieves a training accuracy of 100% and a testing accuracy of 99.813%. These outcomes underscore the significant advancements our proposed model has achieved, showcasing a remarkable test accuracy of 99.813% and a test Dice Coefficient score of 99.413%. These results notably outperform existing models, emphasizing the substantial potential impact of our approach in the realm of medical image analysis and brain tumor segmentation. Most of the existing brain tumor segmentation methods used only image augmentation techniques for preprocessing, but our proposed Optimized Fuzzy C-Means techniques used both image augmentation techniques and image preprocessing techniques, which has given good results in refining the Brain tumor image dataset. Because of the combined MRI modality features, the overall accuracy and dice score of the segmentation have improved.

In future endeavors, we plan to augment our proposed approach by incorporating alternative feature extraction methods and integrating it with diverse optimization techniques. We aim to assess its performance on various medical image datasets, thereby ensuring its versatility and robustness across different clinical scenarios. Additionally, we intend to extend the model's capabilities to handle 3D medical images, a prevalent format in brain imaging. This 3D analysis will enable a more comprehensive exploration of the spatial characteristics of tumors, further enhancing our understanding of their complexity and distribution.

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Table 1: Literature on Brain Tumor Segmentation and Diagnosis

S. No	Methods	Performance metrics (Dice score)	Advantages	Gap identified
1	Improved saliency segmentation method[24]	90% (Accuracy)	Produced Good accuracy	classification accuracy is affected by irrelevant features
2	HPU-Net[25]	93.6%	lower energy consumption	this model did not incorporate texture and shape features
3	Deep convolutional Neural Network[27]	82.8% to 97.3% (accuracy)	Produced Good accuracy	This model has variability problem
4	Ensemble technique[28]	75% to 90.6%	Produced Good Result	This model did not undergo extensive preprocessing
5	Contouring techniques[29]	92%	Produced Good Result	The model complexity is high.
6	Soft Covering Rough K-Means Clustering[30]	90%	Produced Good Result	did not incorporate optimization principles
7	Edge Detection and Labeling[33]	76.9%	Model produced generated dependable uncertainty maps effectively	computational cost
8	multimodal AD-Net [36]	90%	The model constrained the convolutional weights for downsampling, thereby hastening the convergence of the overall model weights.	The model did not employ an optimization method to refine the reproduced models. Instead, it utilized cross-entropy loss, which could potentially introduce errors.
9	Hybrid Transformer [37]	88.50 %	The integration of multiple modalities enhanced the quality of the segmentation results.	The computational complexity is little bit higher.
10	Semi-supervised multiple evidence fusion [38]	79.2%	The decrease in performance with only 50% of labeled data has been mitigated	Average dice score

