

Improved Brain Tumor Detection and Classification in Brain MRI using Deep Learning Techniques

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Abstract—Since early detection may strongly support appropriate treatment decisions, brain tumor analysis utilizing magnetic resonance imaging (MRI) is a crucial duty in medical diagnosis. The demand for automated solutions arises due to the time-consuming nature of manual MRI scan evaluation and its heavy reliance on expert interpretation. This study proposes a computer-aided system for brain tumor analysis that integrates a deep learning-based classification method with fuzzy thresholding-based picture segmentation. MRI brain pictures are processed initially to improve clarity and minimize undesired noise. Fuzzy thresholding, which aids in controlling intensity changes found in medical images, is then used to segregate tumor areas. Following segmentation, the pictures are classified into appropriate tumor classifications using a deep learning model. When compared to conventional methods, the experimental results show that the suggested structure offers dependable and consistent performance. Overall, the established method provides an effective and automated way to help medical practitioners identify and categorize brain tumors.

Index Terms—Brain tumor detection, MRI analysis, fuzzy thresholding, tumor classification.

I. INTRODUCTION

Over 14 million people globally have been impacted by brain tumor malignancies in the last thirty years [1]. Because of their aggressive character and detrimental effects on neurological function, these cancers remain

leading cause of death. According to epidemiological forecasts, the number of brain tumors worldwide may increase to around twenty-one million cases by 2030, despite improvements in treatment. This pattern emphasizes how urgently better diagnostic tools that facilitate early detection and promote sustainable healthcare development objectives are needed. It is expected that 30 Medical specialists' visual evaluation of MRI data is the mainstay of conventional brain tumor diagnosis. But this is a very difficult and time-consuming method. Radiologists may differ in their diagnostic precision, and even the same doctor may give contradictory conclusions based on the circumstances. The recognition of tumor areas is further complicated by differences in MRI contrast, lighting, and scan quality. These drawbacks highlight the significance of automated brain tumor detection technologies, which can boost patient outcomes, save diagnostic time, and improve consistency. The processing of brain MRI images for therapeutic purposes has changed as a result of recent improvements in intelligent computing techniques. MRI has become a preferred imaging modality for Because it presents a thorough picture of soft tissues with distinct contrast changes, it can be used to detect problems in the brain. However, brain tumors are difficult to identify and classify because they can have complicated forms, uneven borders, and changing intensities. It takes a lot of skill and time to rely just on visual evaluation of MRI images, which raises the risk of diagnostic variability. These difficulties emphasize the necessity of dependable and automated

computational techniques for exact brain tumor identification and analysis. To get over these drawbacks, convolutional neural networks (CNNs) have been extensively utilized in automated brain tumor determining tasks. Unlike classic methods that rely on manually constructed features, CNN-based algorithms develop selective representations directly from MRI data, avoiding the need for manually generated feature extraction. This automation lessens reliance on manual preprocessing methods while increasing categorization accuracy. Clinicians are further supported with computer-aided diagnostic (CAD) systems, which expedite diagnosis, minimize recurrent tests, and decrease human error. Many current machine learning and DL-based algorithms have drawbacks such as excessive computational complexity, lack of resilience, and inadequate attention to tumor segmentation quality, despite significant advancements. Furthermore, the majority of research only focuses on classification accuracy, ignoring clinically crucial factors like tumor size estimation. Eliminating these constraints is still a significant scientific challenge. This research presents a hybrid system integrating tumor segmentation utilizing fuzzy logic and a classification technique driven by deep learning. The main objectives of the proposed method are reliable MRI classification into four categories (no tumor, glioma, meningioma, and pituitary tumor), accurate tumor region extraction, and percentage-based tumor size determination. The designed system is totally automated, and standard assessment measures are used to evaluate its performance. When compared to traditional brain tumor detection methods, the experimental findings show that the suggested strategy achieves higher accuracy and efficiency.

II. LITERATURE REVIEW

Over time, MRI data has been utilized to assess brain tumors using a range of computer algorithms. Early research concentrated on rule-based and pattern-driven systems that needed to extract visual descriptors by hand in order to make decisions. These techniques were not very flexible between datasets because they heavily relied on expert knowledge and predetermined picture features. Discriminative data may now be automatically extracted from MRI images thanks to recent developments in data-driven learning systems. These techniques have decreased reliance on manually generated feature design and greatly increased classification reliability. Convolution-based architectures are now widely used for brain MRI analysis due to recent developments in data-driven learning techniques, which allow them to automatically identify significant patterns without the need for human feature generation. To enhance the accuracy of tumor identification, a number of research studies have examined

various pre-processing, segmentation, and feature extraction methods. To improve segmentation and classification performance, several researchers used wavelet modifications, fuzzy logic, principal component analysis (PCA), and histogram-based methods. In order to improve brain tumor classification accuracy, recent research has investigated hybrid frameworks that integrate deep neural architectures with complementary methods for learning. Although the excellent classification accuracy reported by these approaches, issues including restricted interpretability, high computational costs, and enormous dataset needs still exist. In addition, only a small number of studies have combined tumor size estimation with categorization, which is crucial for making choices regarding treatment. An accurate and unified framework that includes segmentation accuracy, tumor size computation, and trustworthy classification is obviously needed, according to the literature currently under publication. By fusing fuzzy-based segmentation with a CNN-based classification model, the technique developed in this work seeks to close these gaps. Numerous studies have examined neural network-oriented methods to enhance the detection and categorization of brain tumors from MRI scans. High classification accuracy has been demonstrated by sophisticated methods for extracting features, including attention-driven strategies and pretrained feature learning frameworks. To increase the efficacy of tumor detection, hybrid deep learning models and multi-label classification techniques have been further investigated. Many of these methods depended on small datasets, which limits their capability to successfully generalize across a variety of MRI samples, even when they attained promising accuracy levels.

Fuzzy logic has been used with deep learning models in recent research to enhance the accuracy of segmentation and classification. Prior to classification utilizing CNN-based architectures, tumor areas have been separated using fuzzy rule-based techniques. Previous techniques for brain tumor analysis mostly used segmentation architectures like U-Net, but problems with few datasets and tumor size changes remained. Conventional manual feature extraction methods, such as statistical and frequency-based techniques like dimensionality reduction and wavelet transformations, were often used. Usually, these recovered attributes were combined with more conventional classifiers, including support vector-based models, nearby-neighbor techniques, and artificial neural networks. Although these techniques produced respectable classification accuracy, noise, inconsistent intensity, and changes in lighting in MRI images frequently affected their performance, necessitating substantial feature engineering work.

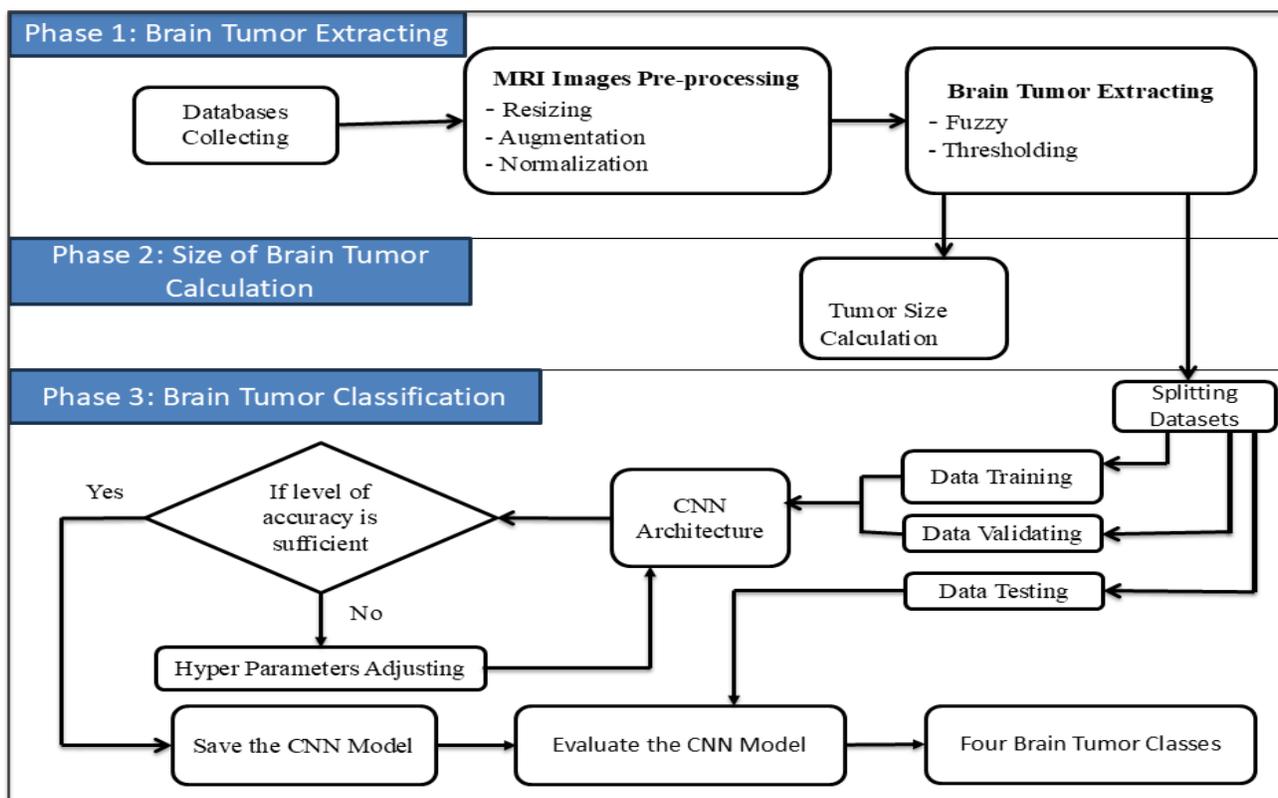


Fig 1: A schematic showing how the suggested MRI image-based brain tumor detection and categorization system work

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unprocessed MRI data. However, a lot of methods using deep learning require big annotated datasets and a lot of processing power, which restricts their application in actual clinical settings. In addition, a number of current research projects lack an integrated assessment framework and approach tumor detection, classification, and size estimation as distinct procedures. Their efficacy for extensive diagnostic analysis is diminished by this division. This paper offers a unified architecture that integrates a convolutional neural network for classification with fuzzy logic-based tumor extraction in order to overcome these drawbacks. Automated tumor site identification, precise tumor size computation, and dependable multi-class classification are all made achievable by the approach suggested in an effective and organized way.

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III. THE PROPOSED MODEL

In this study, a totally automated system for magnetic resonance imaging (MRI)-related brain tumor identification, size estimate, and classification is presented. To accomplish accurate and trustworthy analysis, the suggested method combines deep learning models, fuzzy logic-based segmentation, and picture preparation approaches. Figure 1 depicts the system's overall processing flow, which is divided into many continuous stages to guarantee efficiency and reliability. Brain MRI images are extracted from publicly accessible benchmark datasets in the first stage. To improve visual quality and boost model generalization, these pictures are initially preprocessed using techniques like scaling, intensity leveling, and data augmentation. Preprocessing increases dataset heterogeneity, simplifies picture dimensions, and lowers noise, all of which improve the classification model's increased stability. After preprocessing, fuzzy thresholding is used to effectively remove tumors by separating tumor areas from normal brain tissues. Estimating the tumor size shown in the MRI pictures is the main goal of the second stage.

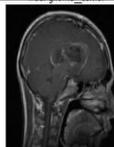
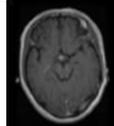
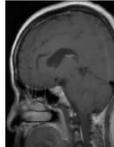
To calculate the relative tumor area in relation to the full brain picture, the segmented tumor region gathered via fuzzy thresholding is applied. By showing the severity of the tumor and allowing subsequent medical investigation, this quantitative assessment offers extra clinical data. The processed dataset is separated into subsets for testing, validation, and training in the last step. A convolutional neural network (CNN) can classify brain tumors into several groups. While validation data serves to adjust hyperparameters and improve classification performance, the training dataset is utilized to train the network. When the desired level of accuracy occurs, the trained model is evaluated using test data that has not yet been seen. The approach categorizes MRI images into four groups: meningioma, pituitary tumor, glioma, and no tumor. Standard performance measurements like accuracy and confusion matrices are used to measure the efficacy of the suggested structure. In accordance with experimental results, the system is appropriate for automated MRI-based brain tumor analysis, as it offers precise tumor identification, trustworthy tumor size calculation, and effective categorization.

A. DATABASE COLLECTION

The provided classification system is trained and assessed using a publically accessible brain MRI dataset. 3,264 MRI pictures in all, divided into four groups glioma tumor, meningioma tumor, pituitary tumor, and no tumor—make up the dataset.

This dataset offers enough variation for performance evaluation and is often used in brain tumor research. To ensure accurate analysis, the dataset is divided into subsets for testing, validation, and training. The model parameters are learned from the 2,870 pictures in the training set. The validation set serves to track progress throughout training and prevent overfitting, while the testing set, which consists of 394 images, is used for final inspection. This structured data organization supports balanced learning and fair performance analysis.

TABLE 1: Class-wise composition of the brain tumor MRI dataset.

Class Name	Total	Training Images	Testing Images	Samples
Glioma Tumors	926	826	100	
Meningiomas Tumors	937	822	115	
No Tumors	500	395	105	
Pituitary Tumors	901	827	74	
Total MRI Images	3264	2870	394	

B. MRI IMAGES PRE-PROCESSING

All MRI images go through a number of preprocessing processes prior to model training in order to enhance consistency and classification accuracy. To guarantee consistent input dimensions, pictures are first scaled to a fixed resolution of 250×250 pixels. Normalizing pixel intensity levels helps to speed up model convergence and stabilize training. Augmentation techniques are used to prevent overfitting and enhance data variety. These include flipping images horizontally and vertically and rotating them at angles of 0° , 90° , 180° , and 270° . By providing equal representation across classes, augmentation enhances the

CNN algorithm, its ability. folders following preprocessing and data augmentation. Figure 2 displays examples of the improved pictures. The produced dataset is then split into three subsets, with the majority being used as training models as well as the remaining portion for testing and validation in order to provide consistent and fair performance evaluation across all tumor classifications.

• For resizing images:

1- If the original image's width and height are equal, then:

$$\text{new_width} = \text{old_width} / r \text{ where } r > 1 \tag{1}$$

$$\text{new_height} = \text{old_height} / r \text{ where } r > 1 \tag{2}$$

If the original width and height are different:

$$\text{new_width} = \sqrt{(\text{original_width} / \text{original_height} \times \text{target_area})} \tag{3}$$

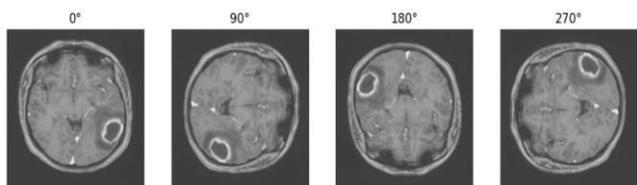


Fig 2: Augmented brain MRI images at different rotation angles.

$$\text{new_height} = \text{target_area} / \text{new_width} \tag{4}$$

In which target area is determined by

$$\text{Target_area} = \text{original_width} * \text{original_height} \tag{5}$$

• To normalize images:

$$\text{Imgout}(i,j) = \text{imgin}(i,j) * (1/255) \tag{6}$$

C. BRAIN TUMOR DETECTION

Tumor region extraction plays a vital role in this study for two primary reasons. First, accurate identification of tumor areas significantly reduces the overall diagnostic time required by medical experts. Second, determining the tumor region helps in estimating the severity and progression level of the disease, which is essential for effective clinical decision-making. The proposed approach identifies tumor regions through a structured two-step procedure. In the first step, an optimal gray-level threshold value is computed using fuzzy thresholding techniques. This method evaluates pixel intensity values and assigns membership degrees to a tumor or non-tumor region. In the second step, MRI images are segmented into distinct tumor and non-tumor areas based on the calculated fuzzy threshold using a fuzzy controller. This fuzzy-based segmentation strategy improves accuracy by effectively handling intensity variations present in MRI images. The

detailed implementation of the fuzzy threshold calculation and segmentation process is described in the following subsections.

1) THRESHOLD VALUE CALCULATION

Classifying pixels into two different groups (black and white) is possible with approaches built around thresholding images. To differentiate image objects from the backgrounds, the following adjustment is applied. A limit called T is used to compare the values of every pixel created in this binary image; any value below the threshold is regarded as an object, while values over the threshold are part of the background. Based on the defined threshold value, pixel intensities are assigned to different classes depending on whether they fall below or above the threshold

$$G = \{0, 1, \dots, L - 1\} \begin{cases} 0 & \text{black} \\ L - 1 & \text{white} \end{cases}$$

An upper threshold value is introduced to ensure stable transformation and accurate segmentation.

$$y_{ij} = \begin{cases} 0 & \text{if } x_i < T \\ L - 1 & \text{if } x_i > T \end{cases} \tag{7}$$

To choose the threshold value T, there are multiple options. The most popular techniques for calculating thresholds depend on histogram analyses. These techniques for calculating the threshold value depend on counting the number of times each level is repeated. Therefore, it requires reading the image 256 times in order to calculate the number of times 256 levels are repeated. This will incur significant costs for hardware implementation. Therefore, the proposal is to rely on fuzzy logic to calculate the best value for the threshold after reading the image only once. The suggested method is predicated on using fuzzy logic to determine the threshold T. According to an analytical perspective, this method just involves computing the mean that is subsequently fitted to the image's distribution. One benefit of using this approach is that the computation methodology speeds up the processing cycle because it simply requires analyzing the image one time. This makes it possible to determine the threshold value directly, which may result in reducing the cost of hardware realization. Each pixel that will be analyzed is fed into the fuzzy technique's inputs, and the consequence represents the outcome of the fuzzy inferences. Following the MRI image reading, the outcome displays its threshold T value. Essentially, the process that creates the fuzzy structure is equivalent to using the formula that follows to calculate the image's histogram's center of weight as follows:

$$T = \frac{\sum_{i=1}^M \sum_{j=1}^R \alpha_{ij} c_{ij}}{\sum_{i=1}^M \sum_{j=1}^R \alpha_{ij}} \quad (8)$$

In which T is the value of the threshold, M indicates the image’s pixel count, R represents the fuzzy mechanism’s total number of rules, c denotes the rules sub- sequently, and provides the rule’s activation degrees If the model recommended has been normalized, the for mula given in issue can be optimized. The iitotal extended to the rule base of the consequent’s activation degrees in this instance bears value 1:

$$\sum_{j=1}^R \alpha_{ij} = 1$$

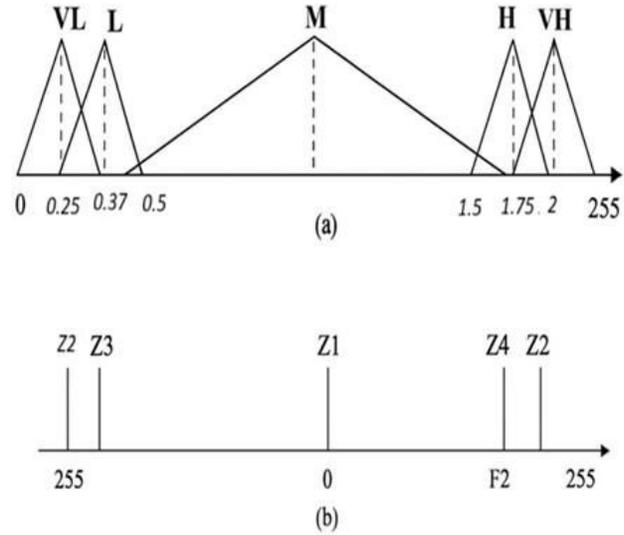
After that, formula becomes:

$$T = \frac{1}{M} \sum_{i=1}^M \sum_{j=1}^R \alpha_{ij} c_{ij} \quad (9)$$

2) MRI HUMAN BRAIN SEGMENTATION

MRI images of the human brain exhibit noticeable differences when abnormal growths are present. In healthy brain scans, intensity values are generally consistent across regions, whereas MRI images containing tumors show distinct in- tensity variations in specific areas. These variations allow abnormal regions to be clearly distinguished from normal brain tissues. In tumor-affected MRI images, the intensity of pixels within the tumor region is often significantly higher or lower compared to surrounding healthy tissue. Based on this observation, the proposed approach utilizes a fuzzy controller to effectively separate tumor regions from normal brain areas. This fuzzy-based segmentation strategy handles uncertainty in pixel intensity values and improves robustness against noise. MRI pixels are categorized into several intensity classes by the fuzzy inference technique, including very low, low, moderate, high, and extremely high.. Every group matches different patterns of brightness seen in MRI data. The fuzzy system calculates appropriate membership degrees for each pixel by examining the overall pixel value distribution. The range of gray-level intensity values determines the fuzzy infer- ence system’s universe of language.Five triangle membership functions—Very Low (VL), Low (L), Medium (M), High (H), and Very High (VH)—are generated to represent various intensity levels. To manage uncertainty in pixel categorization and guarantee seamless transitions between intensity areas, these membership functions partially overlap.

Based on the fuzzy inference rules, pixel classification is performed as follows. If a pixel belongs to the VL or VH intensity range, it is classified as part of the tumor region.



- If U is VL then Z is Z2;
- If U is L then Z is Z3;
- If U is M then Z is Z1;
- If U is H then Z is Z4;
- If U is VH then Z is Z2;

Fig 3: Fuzzy Membership Functions for MRI Intensity Levels

Pixels falling within the L or H ranges are generally associated with normal brain tissue. In cases where a pixel is classified under the medium intensity range, its classification depends on the relative dominance of neighboring intensity regions. If the pixel intensity is closer to the tumor-related range, it is labeled as tumor; otherwise, it is treated as normal tissue. This fuzzy-based segmentation mechanism enables accurate identification of tumor regions by effectively managing intensity overlaps between healthy and abnormal tissues. As illustrated in the corresponding figures, the proposed method successfully distinguishes tumor regions from normal brain areas, even in cases where intensity variations are subtle.

$$F1 = \begin{cases} 255 & \text{if } 0.375T < X < 0.5T \\ 0 & \text{if } X > 0.5T \end{cases} \quad (10)$$

$$F2 = \begin{cases} 0 & \text{if } 1.5T < X < 1.75T \\ 255 & \text{if } X > 1.75T \end{cases} \quad (11)$$

D.PHASE OF BRAIN TUMOR CLASSIFICATION

Brain cancer classification using MRI images is the focus of the framework's last stage. The images are separated by four categories at this phase: glioma, meningioma, pituitary tumor, and non-tumor. Deep learning-generated convolutional neural networks (CNNs) are utilized to implement an automated multi-class classification approach. The CNN uses the tumor areas that were segmented in the earlier phases as input to make its final conclusion. Without the need for manually generated feature extraction, the CNN learns substantial spatial and structural data straight from MRI scans. The network successfully distinguishes between multiple tumor types based on intensity patterns and anatomical features by using convolution, pooling, and non linear activation techniques.

1) ARCHITECTURE OF THE PLANNED CNN MODEL

To accomplish accurate classification, the CNN architecture is developed with many convolutional blocks followed by fully linked layers. Before being fed into the network, the input MRI pictures are reduced to a fixed dimension. Low-level features like edges and texture information are collected by the first convolutional layer utilizing a collection of filters with a small kernel size. A max-pooling layer comes after to lower computational complexity and spatial dimensions. To add non-linearity and improve feature learning, a ReLU activation function is used following each convolutional operation. Higher-level and more discriminative characteristics are obtained from the MRI images by adding additional convolutional layers. To gradually enhance feature representations, max-pooling and ReLU activation come after each convolutional layer. In order to minimize overfitting and increase generalization, dropout layers are added after certain layers to randomly deactivate neurons during training. The convolutional feature extraction step is followed by the flattening and delivery of the generated feature maps to fully linked layers. The final output layer uses the Softmax activation function to provide probability evaluations for each of the four types of brain tumors. From the class that has the highest probability, the predicted output is selected.

2) HYPER-PARAMETERS TUNING OF OUR SUGGESTED CNN MODEL

The CNN model's accuracy is greatly impacted by the choice suitable hyperparameters. Several hyperparameters are changed in this study to guarantee consistent training and good classification accuracy. Important variables include the variety of filters in every convolutional layer, the size of the kernel, the activation function, the batch size, the number of training epochs, the learning rate, and

the dropout ratio. In order to balance accuracy and computing efficiency, these values were selected based on experimental analysis. The convolutional layers use different filter sizes to progressively learn complex features from MRI images, while a consistent kernel size is maintained across layers. The ReLU activation function is employed due to its simplicity and effectiveness in accelerating convergence. The Adam optimizer is selected for weight optimization because of its adaptive learning rate and faster convergence behavior. A suitable batch size and number of epochs are chosen to avoid overfitting while ensuring sufficient training. Dropout is applied to enhance model robustness by preventing dependency on specific neurons. Through proper tuning of these hyper-parameters, the CNN model achieves reliable and consistent classification performance across all tumor categories.

$$MAE = \frac{1}{N} \sum_{i=1}^N |y_i - \bar{y}_i|$$

IV. RESULTS AND DISCUSSION

This section displays the experimental results from the proposed structure for the extraction and categorization of brain tumors. The successful operation of the structure is evaluated using qualitative as well as quantitative techniques. The two main stages of the experimental evaluation are brain tumor extraction and brain tumor classification.

A.RESULTS OF BRAIN TUMOR EXTRACTION

The effectiveness of the proposed brain tumor extraction approach is evaluated both quantitatively and visually. In brain MRI imaging, fuzzy thresholding is used to differentiate atypical tumor patches from the surrounding healthy tissues. Since precise tumor extraction impacts the efficacy of the subsequent classification phase, this stage is essential to the system as a whole. In order to separate tumor areas from healthy brain tissues, the fuzzy-based extraction technique examines the pixel intensity distribution inside MRI images. The suggested technique successfully manages intensity ambiguity and gradual transitions between tumor and non-tumor areas, which are frequently seen in brain MRI images, using fuzzy logic.

1) VISION ASSESSMENT

The qualitative performance of the indicated tumor extraction technique is measured visually. The separation findings show that the fuzzy thresholding approach effectively suppresses background and non-tumor areas while highlighting tumor positions. The extracted tumor

regions appear continuous and well-defined, indicating accurate localization of abnormal tissues. In MRI images containing tumors, abnormal regions are clearly distinguished from healthy brain tissues, even in cases where tumor boundaries are not sharply defined. The method exhibits robustness against noise and intensity variations and does not introduce false tumor regions. These observations confirm that the proposed fuzzy-based extraction technique is capable of reliably identifying tumor regions across MRI images with different tumor sizes, shapes, and locations.

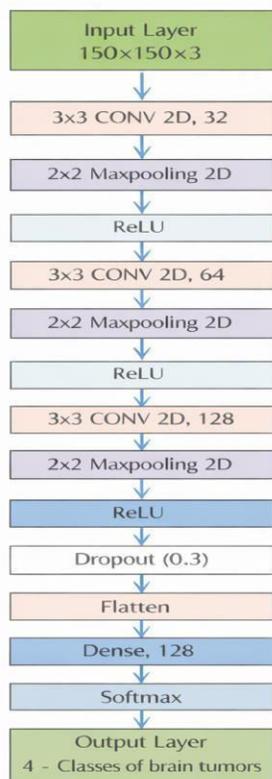


Fig 4: Architecture of the proposed CNN model

2) QUANTITATIVE EVALUATION MEASURE

To complement visual analysis, quantitative evaluation is performed to objectively assess the tumor extraction performance. Numerical measurements are derived from the segmented output images generated using the fuzzy thresholding method. This evaluation focuses on analyzing pixel-level information to distinguish abnormal tumor regions from normal brain tissues. The quantitative analysis provides consistent numerical evidence of tumor presence across different MRI images. Tumor images exhibit significantly higher detected tumor region values compared to non-tumor images, where only minimal or negligible values are observed. The efficacy of the suggested fuzzy-based extraction technique is further supported by this

significant numerical difference. In addition, quantitative evaluation enables comparison of tumor characteristics across multiple MRI samples. Variations in detected region values reflect differences in tumor size, distribution, and intensity patterns within the brain images. The provided framework's dependability increases, and methodical analysis is supported by these numerical insights.

3) COMPUTATION OF DETECTED REGIONS

The detected tumor regions are computed using the binary segmentation masks generated by the fuzzy thresholding algorithm. This process systematically identifies abnormal pixels and separates them from healthy brain tissues. The resulting region information captures both the spatial extent and distribution of tumor regions within the MRI image. The computation of detected regions serves as an important indicator for analyzing tumor characteristics and provides meaningful quantitative information for further processing. Accurate identification of tumor regions establishes a reliable foundation for automated brain tumor classification and decision-support systems.

B.RESULTS OF BRAIN TUMOR CLASSIFICATION

This section evaluates the suggested CNN-based brain tumor detection system's classification performance. The inspection is conducted via the training, validation, and testing stages to fully investigate the model's ability for learning, generalization, and conclusion prediction accuracy. The effectiveness of the classifier is assessed using confusion matrix-based analysis along with standard performance metrics. These results provide a detailed understanding of how accurately the proposed model distinguishes between tumor and non-tumor cases. The confusion matrix outcomes indicate a high rate of true positive and true negative predictions, while maintaining low false positive and false negative values, demonstrating reliable classification behavior. The acquired findings verify that the suggested approach is capable of correctly dividing MRI brain pictures into their appropriate groups. The CNN's capacity to accurately transfer discriminative characteristics from MRI data to the suitable output labels is demonstrated by its excellent classification performance. Furthermore, the consistency of the results across different evaluation phases highlights the robustness of the proposed classification framework. Overall, the experimental outcomes validate that the proposed brain tumor classification approach is effective and dependable, making it suitable for automated medical image analysis and clinical decision-support applications.

TABLE 2: Results of brain tumor identification using K-Means, fuzzy C-Means, and the suggested approach are visually compared

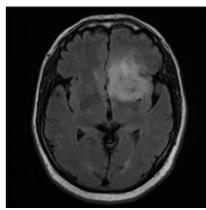
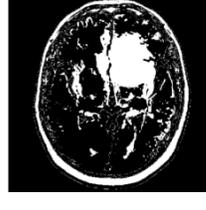
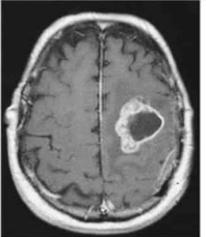
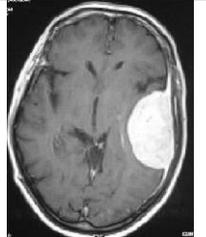
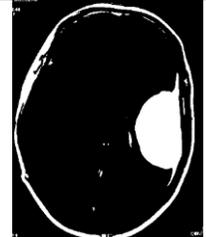
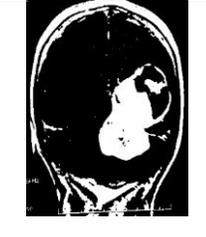
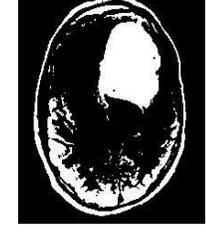
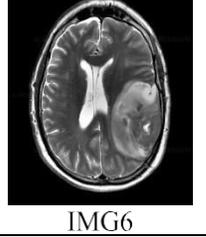
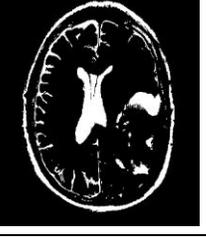
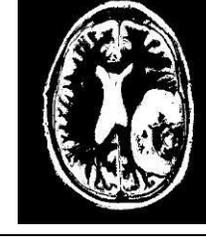
Original image	K-Means Clustering	Fuzzy C-Means	Proposed Method
			
 IMG2			
 IMG3			
 IMG4			
 IMG5			
 IMG6			

TABLE 2: (Continued)Results of brain tumor identification using K-Means, fuzzy C-Means, and the suggested approach are visually compared

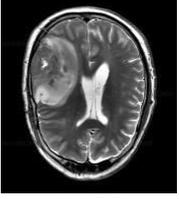
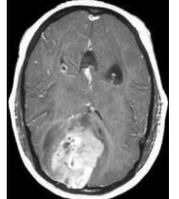
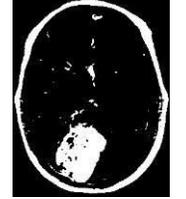
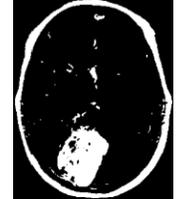
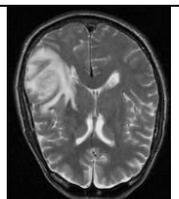
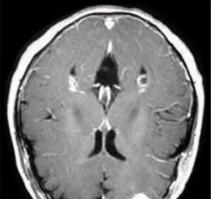
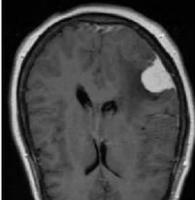
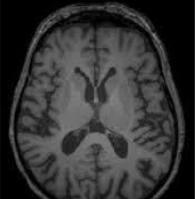
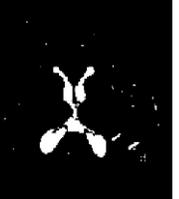
 IMG7			
 IMG8			
 IMG9			
 IMG10			
 IMG11			
 IMG12			

TABLE 3: The suggested algorithm's performance is assessed using a confusion matrix.

Predicted Value		Actual Value		Total Accuracy
		Accuracy of True Positive (TP)	Accuracy of false positive (FP)	100%
Positive		84%-99%	1%-5%	
		Average=96%	Average=3%	
Negative		Accuracy of False Negative (FN)	Accuracy of True Negative (TN)	100%
		1%-16%	95%-99%	
		Average=8%	Average=97%	

TABLE 4: Confusion matrix–based performance evaluation of the Fuzzy C-Means algorithm

Predicted value		Actual Value		Total Accuracy
		Accuracy of True Positive (TP)	Accuracy of false positive (FP)	100%
Positive		61%-92%	8%-39%	
		Average = 76.5%	Average = 23,5%	
Negative		Accuracy of False Negative (FN)	Accuracy of True Negative (TN)	100%
		22%-39%	61%-78%	
		Average = 30.5 %	Average = 69.5%	

TABLE 5: Confusion matrix–based performance evaluation of the K-Means algorithm

Predicted value		Actual Value		Total Accuracy
		Accuracy of True Positive (TP)	Accuracy of false positive (FP)	100%
Positive		60%-91%	9%-40%	
		Average=75.5%	Average=24.5%	
Negative		Accuracy of False Negative (FN)	Accuracy of True Negative (TN)	100%
		21%-45%	55%-79%	
		Average=33%	Average=67%	

TABLE 6: Comparison of brain tumor size (%) across different segmentation methods

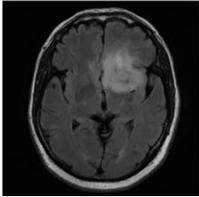
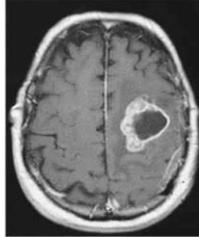
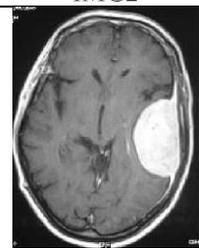
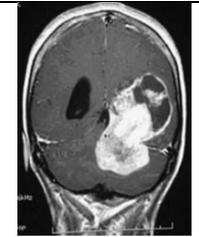
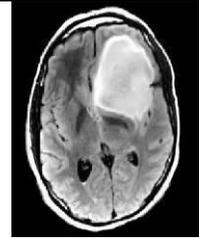
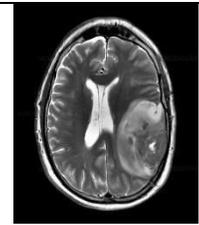
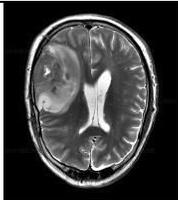
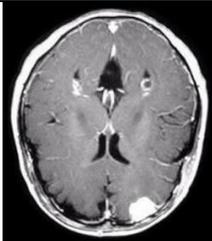
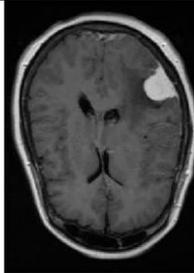
Original image	K-Means Clustering	Fuzzy C-Means	Proposed Method
	12.94%	11.70%	19.06%
 IMG2	8.12%	8.12%	12.56%
 IMG3	15.21%	15.21%	18.67%
 IMG4	21.23	22.42	36.45%
 IMG5	22-92	23.34%	46.12%
 IMG6	17.89%	18.22%	47.32%

TABLE 6: (Continued) Comparison of brain tumor size (%) across different methods

 IMG7	15.55%	16.98%	46.11%
 IMG8	21.11%	21.43%	27.87%
 IMG9	9%	9.11%	18.25%
 IMG10	5%	5%	10.23%

1) TRAINING AND VALIDATING RESULTS OF THE SUGGESTED MODEL

Training and validation tests using a publicly accessible brain tumor MRI dataset were utilized to assess the performance of the suggested CNN model. Glioma tumor, meningioma tumor, pituitary tumor, and no tumor are the four categories into which the dataset's 3,264 MRI pictures fall. To investigate the capacity of the model for both learning and generalization, the data were separated into training and validation sets. The model rapidly picked up discriminative characteristics from the MRI pictures through the training phase. Training accuracy increased steadily across epochs, showing that tumor-related patterns were efficiently learned. Simultaneously, the network showed sustained convergence as the training loss steadily dropped. To make

sure the model works properly when applied to new data, validation performance was studied. The validation loss stayed low during the procedure, and the validation accuracy nearly matched the training accuracy.

The suggested CNN does not experience overfitting and maintains dependable performance on new samples, as seen by the close alignment between training and validation results. At the final epoch, the model achieved high training accuracy along with strong validation accuracy, confirming its capability to accurately differentiate between the four brain tumor classes. All things considered, the training and validation findings show that the proposed CNN model reliably and continually operates well in classification and efficiently extracts important characteristics from MRI images.

2) *CONFUSION MATRIX FOR TESTING THE PROPOSED CLASSIFIER*

It is clear from the confusion matrix study that the provided classifier operates well for every type of tumor. For the glioma tumor class, a total of 100 MRI images were evaluated. Among them, 84 images were accurately classified as glioma, whereas 10 images were incorrectly labeled as meningioma, 5 images were identified as no tumor, and 1 image was misclassified as pituitary tumor. Similarly, for the meningioma tumor category, the test set consisted of 115 images. Out of these, 108 images were correctly recognized, while a small number of samples were misclassified, including 1 image predicted as glioma, 4 images as no tumor, and 2 images as pituitary tumor. In the case of the no tumor class, the classifier successfully detected 97 out of 105 images as normal brain scans. The remaining images were incorrectly classified as tumor cases, indicating a relatively low misclassification rate for healthy MRI images.

TABLE 7: Confusion matrix–based classification results during testing of the proposed model.

Actual class	Predicted class				Class sensitivity
	Glioma	Meningiomas	No Tumors	Pituitary Tumors	
Glioma	84	10	5	1	84%
Meningiomas	1	108	4	2	94%
No Tumors	5	3	97	0	92%
Pituitary Tumors	0	0	1	73	99%
Class Precision	97%	95%	96%	99%	Overall correctness =91%

$$Sensitivity = \frac{TP}{(TP + FN)}$$

$$Precision = \frac{TP}{(TP + FP)}$$

Overall, this detailed class-wise analysis confirms that the proposed model achieves strong discrimination among different brain tumor types while maintaining high accuracy for normal brain image identification.

3) *COMPARISON WITH THE RELATED DEEP LEARNING TECHNIQUES*

The performance of the provided brain tumor classification model is compared with a variety of popular deep learning architectures, such as MobileNetV2, EfficientNet variations, ResNet, VGG, Inception, DenseNet, and Vision Transformer (ViT), in order to determine how successful it is. To guarantee fairness, the comparison is conducted using conventional performance standards measured on the same MRI brain tumor dataset, including accuracy, precision, recall, F1-score, false positive rate (FPR), and inference time. According to the comparing results, the suggested algorithm outperforms a majority of current methods for deep learning in terms of classification accuracy. Even while a number of benchmark models perform effectively, they frequently call for advanced computations or longer inference periods. The suggested method, on the other hand, strikes a better balance between efficiency and accuracy, making it better suited for real-world medical applications. The suggested framework consistently displays good accuracy and recall values across all tumor classifications, signifying accurate tumor position detection with little misclassification of healthy tissues. The robustness of the suggested strategy is further shown by its low false positive rate, which is essential in clinical decision-making to prevent needless alarms. Moreover, when compared to deeper and more complex architectures like Vision Transformers and DenseNet versions, the suggested model’s inference time is considerably shorter. This indicates that the offered architecture enhances computing efficiency in addition to classification performance. Overall, the comparison study indicates the suggested approach performs as well as or better than cutting-edge deep learning methods in terms of efficiency, accuracy, and dependability. These outcomes confirm that the suggested method works for automatically classifying brain tumors from MRI images.

TABLE 8: Validation performance comparison with existing deep learning models

model	Precision	F1-Score	Inference time ms
MobileNetV2	0.88	0.85	11
EfficientNetB0	0.88	0.85	14
EfficientNetB4	0.92	0.90	42
EfficientNetB7	0.93	0.92	114
ResNet50	0.88	0.89	10
ResNet101	0.90	0.91	42
VGG16	0.85	0.84	25
VGG19	0.89	0.87	41
InceptionV3	0.91	0.91	32
DenseNet121	0.92	0.92	41
DenseNet201	0.92	0.93	62
Vision Transformer (ViT)	0.94	0.91	63
Proposed Model	0.9573	0.9573	10

TABLE 9: Validation performance comparison with existing deep learning models

model	FPR	Recall
MobileNetV2	0.150	0.86
EfficientNetB0	0.132	0.87
EfficientNetB4	0.062	0.93
EfficientNetB7	0.063	0.94
ResNet50	0.092	0.90
ResNet101	0.078	0.92
VGG16	0.151	0.85
VGG19	0.142	0.87
InceptionV3	0.052	0.91
DenseNet121	0.078	0.91
DenseNet201	0.049	0.92
Vision Transformer (ViT)	0.059	0.93
Proposed Model	0.093	95.73

V. CONCLUSION AND FUTURE WORKS

This study provided a successful structure for the identification and classification of brain tumors by combining deep learning approaches with segmentation based on fuzzy logic. A publicly accessible MRI brain tumor dataset with four categories—glioma, meningioma, pituitary tumor, and normal cases—was used to assess the suggested technique. The experimental findings show that coupling a CNN-based classifier with fuzzy thresholding for tumor extraction greatly enhances overall performance. By controlling noise and changes in intensity, the segmentation step successfully distinguished tumor areas from MRI images, resulting in precise tumor border identification. In the deep learning step that followed, this dependable extraction method helped enhance classification accuracy. Across all tumor classifications, the CNN model achieved excellent accuracy, precision, recall, and F1-score after effectively learning discriminative features from MRI images. The suggested strategy offers competitive performance while preserving low false positive rates, which is necessary for clinical decision assistance, according to a comparative analysis with current deep learning models. Overall, the results demonstrate that the suggested strategy for automated brain tumor analysis is reliable and efficient. The approach's usefulness for real-world medical imaging applications is shown by its excellent classification accuracy and consistent performance across multiple tumor kinds. Training the suggested framework on greater and more varied MRI datasets can further increase generalization and boost performance in further research. Accurate feature extraction and classification can be further improved by using complex deep learning architectures, such as hybrid or attention-based networks. Furthermore, expanding the framework to handle multi-modal MRI data and real-time clinical deployment could make it more useful in actual healthcare settings. Clinicians may be better able to comprehend model decisions and have more faith in automated diagnostic systems if explainable AI methods are included.

DATA AVAILABILITY

Further The dataset used in this investigation is available to the general public and may be found in free web sources. The suggested research is transparent and repeatable since the brain MRI images utilized for training and evaluation were obtained from publicly accessible sources. These datasets, which are available via the following URLs, provide labeled MRI images suited to tasks involving the categorization of brain tumors:

<https://www.kaggle.com/datasets/sartajbhuvaji/braintumor-classification-mri>
<https://www.kaggle.com/datasets/masoudnickparvar/braintumor-mri-dataset>

These datasets' portability enables further researchers to confirm the findings and develop the suggested strategy.

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