



Brain Tumor Detection Using Improved Fuzzy Logic Classifier Model Based on K-folds Validation

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Abstract.

Purpose: This study aims to improve brain tumor detection by integrating Fuzzy Logic with K-folds validation to enhance classification accuracy and robustness. The research addresses the challenge of distinguishing between normal and abnormal brain MRI images.

Methods: This study utilized a public dataset from Kaggle comprising 2,660 MRI images, initially categorized into four classes: Glioma, Meningioma, Pituitary, and No Tumor. For the study, Glioma, Meningioma, and Pituitary were combined into one abnormal label, resulting in two classes: Normal and Abnormal. The methodology involved pre-processing the images, applying Fuzzy Logic with K-folds validation (K=3), and evaluating the model's performance using single prediction tests.

Result: The proposed approach achieved an exceptional accuracy of 99.88% during the K-folds validation process. The model demonstrated strong performance across all test samples, accurately classifying both normal and abnormal cases, with true positive results in single prediction tests.

Novelty: This study introduces a novel combination of Fuzzy Logic with K-folds validation, demonstrating a significant improvement in classification accuracy compared to existing methods. The integration of these techniques offers a robust framework for brain tumor detection, enhancing diagnostic precision and addressing the challenge of distinguishing between various tumor types in MRI images.

Keywords: Brain tumor, Computer vision, Fuzzy logic, GLCM extraction, K-folds validation.

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INTRODUCTION

Brain tumor is one of the deadliest cancers in the world, with significant morbidity and mortality [1], [2]. Worldwide, the incidence of brain tumors is increasing along with advances in medical technology that allow earlier detection [2]. However, despite advances in diagnostic and treatment techniques, the survival rate of patients with brain tumors is still relatively low, mainly due to the complexity and biological variation of these tumors [3]. The main difficulties in treating brain tumors lie in their sensitive location, which often limits treatment options such as surgery, and the ability of the tumor to spread aggressively within the brain tissue [4], [5]. In addition, current detection methods still have limitations in terms of accuracy and speed, which can affect clinical decisions and patient outcomes [6], [7]. Therefore, the development of more efficient and accurate detection methods is essential to improve patient prognosis and provide more timely and effective treatment.

To address the challenges in brain tumor detection, this study proposes a solution through the application of an improved fuzzy logic model, combined with K-fold validation to improve the accuracy and precision of detection. This improved fuzzy logic model is designed to better handle the sharpness and biological variability in brain tumor images, allowing for more precise and adaptive classification of conditions that are difficult to identify by conventional methods. K-fold validation is used to ensure that the model is not only effective on a specific dataset, but also has good generalization to various variations in the data, thus providing consistent and robust results. With this approach, the study is expected to offer a more efficient and accurate detection method, which can ultimately improve patient prognosis and accelerate clinical decision making.

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Research [8] combines Support Vector Machine (SVM) with Fuzzy Logic Classifier to detect brain tumors. This integration produces the highest accuracy of 99.24%, indicating that the combination of SVM with fuzzy logic can significantly enhance classification capabilities, particularly in managing the variability often present in medical images. The model's ability to classify with such high accuracy demonstrates its effectiveness in distinguishing between tumor and non-tumor regions. However, despite these impressive results, the approach still faces limitations, particularly in its generalizability to larger and more diverse datasets. The reliance on specific training data may lead to overfitting, where the model performs exceptionally well on the data it was trained on but struggles to maintain the same level of accuracy when applied to new, unseen data. Moreover, the integration of SVM and fuzzy logic, while powerful, can be computationally intensive, which may hinder its scalability and practical application in real-time clinical settings. Research [9] utilized a Bayesian Fuzzy Logic Classifier for brain tumor classification, achieving a remarkable classification accuracy of 98.5%. The Bayesian approach in this method effectively integrates probabilistic information with fuzzy logic, offering a significant advantage in managing the inherent uncertainty and ambiguity often found in medical data. This integration allows the model to make more nuanced decisions, particularly in cases where the boundaries between healthy and abnormal tissues are not clearly defined. However, despite the high accuracy, the study has some limitations. The primary focus on probabilistic reasoning means that the model excels in estimating the likelihood of tumor presence but may not perform as effectively when it comes to tasks like segmentation or the detailed analysis of specific features within the medical images. This can be a significant drawback in clinical applications where precise localization and characterization of the tumor are crucial for effective treatment planning. Research [10] combined Convolutional Neural Network (CNN) with Fuzzy Logic Clustering for brain tumor detection and classification, achieving an impressive accuracy of 98.64%, with sensitivity reaching 100% and specificity at 99%. This hybrid approach capitalizes on the strengths of CNN for feature extraction and fuzzy clustering for precise segmentation, resulting in superior performance in accurately identifying tumor regions within brain images. Despite these notable results, there are significant limitations associated with this method. The combined use of CNN and fuzzy clustering is computationally intensive, requiring substantial processing power and time, which may be impractical for real-time applications or scenarios where rapid analysis is critical. Additionally, the approach depends heavily on the availability of large, high-quality datasets for effective training, which can be a major constraint in settings where data is limited or difficult to obtain.

This study proposes the use of Improved Fuzzy Classifier validated using K-Folds with a value of $K = 3$ to detect brain tumors. Although the three previous studies have utilized deep learning techniques, this study offers an alternative approach by improving the fuzzy logic algorithm. With the K-Folds validation technique, this model is expected to not only achieve higher accuracy but also have better generalization capabilities on various data variations. This approach is believed to produce superior performance compared to studies that have used deep learning, with the hope of significantly increasing the accuracy and reliability of brain tumor detection.

The structure of this paper is organized as follows: first, the Introduction, presenting background, motivation, and a summary of the problem; the second section describes the Research Methodology, stating the techniques applied, the datasets, the tools used for conducting research work, and any special algorithm or model applied. The third section contains the Results, in which important findings are selected and their meaning contextualized to outline the achievements and main lessons learned from the study. Finally, the Conclusion summarizes the contributions of the research, discusses implications, and identifies potential lines of future work.

METHODS

The research methodology begins with data collection from a public dataset, followed by splitting the data into 80% for training and 20% for validation [11]–[13]. Next, the initialization of the K-value for K-fold cross-validation is performed, along with the hyperparameters for the fuzzy classifier model during training. The fuzzy classifier is then trained on the training set to predict whether a brain tumor is present. If the prediction yields "ABNORMAL," the process continues with segmentation to locate the tumor, followed by GLCM extraction to analyze the texture of the tumor region. If the prediction results in "NORMAL," the process ends without further processing. Flow of research methodology can be seen in Figure 1.

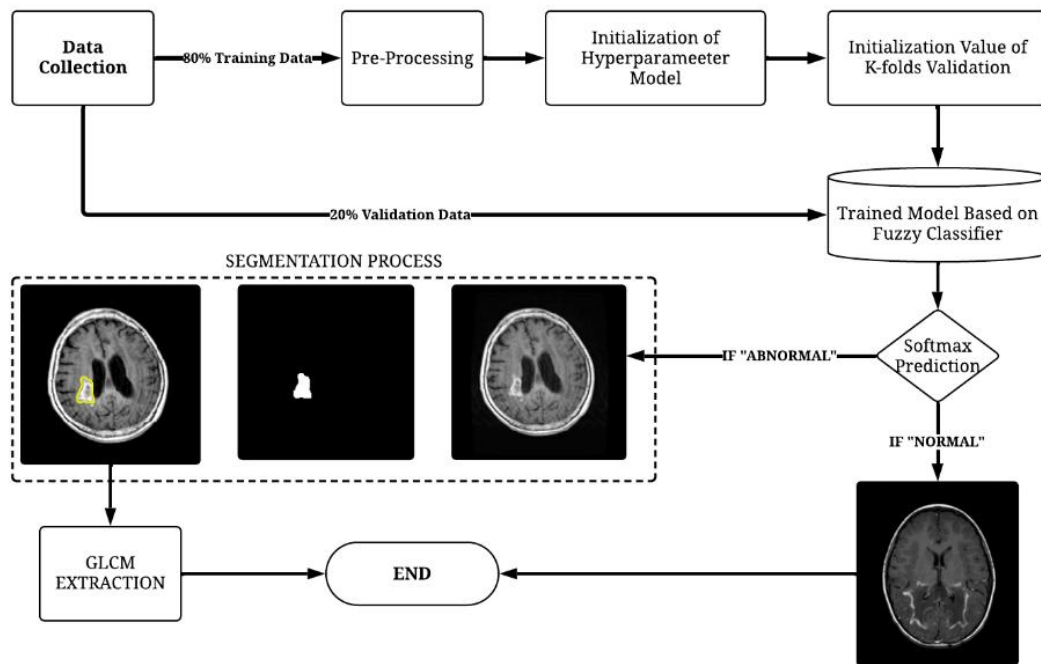


Figure 1. Research methodology

Data collection and tools

The dataset used in this research was sourced from a public dataset available on Kaggle [14], which contains a total of 2,660 MRI images with random dimensions. This dataset contains MRI images with random dimensions and is categorized into four classes: Glioma, Meningioma, Pituitary, and No Tumor. To simplify the classification process and increase the complexity of the data, the three tumor types (Glioma, Meningioma, Pituitary) were combined into a single label, resulting in two classes for this study: Normal (No Tumor) and Abnormal (Glioma, Meningioma, Pituitary). This combination introduces greater variability within the Abnormal class, which presents a more challenging scenario for the model during the training phase, thereby testing its robustness and ability to generalize across different tumor types. Sample data collection can be seen in Figure 2.

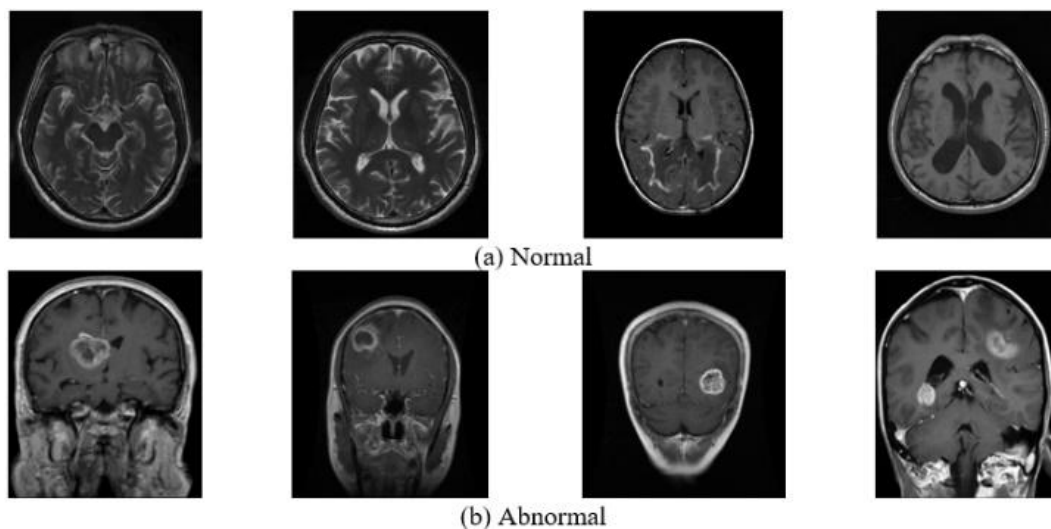


Figure 2. Proposed model

The study employed both MATLAB 2020a and Python (Google Colab) to carry out the suggested approach. MATLAB was utilized for image segmentation, enhancement, resizing, and other pre-processing tasks due to its rich libraries and strong features in the field of image processing. During the training and classification stages, the Improved Fuzzy Logic Model was implemented and hyperparameter tuning was performed

using Python on Google Colab. The researchers utilized Python's deep learning frameworks and Google Colab's computational resources for efficient training. This included implementing K-Folds validation to ensure the model performed effectively. The combined use of MATLAB and Python improved the workflow by letting MATLAB handle early data preparation stages while Python managed model training, resulting in accurate predictions of brain tumor presence.

Pre-processing

In the pre-processing stage, image enhancement techniques were applied to improve the overall quality of the MRI images, making them more suitable for subsequent analysis [15], [16]. The enhancement process involves adjusting the contrast and brightness of the images to ensure that the critical features, such as tumor regions, are more distinguishable [17]. Following enhancement, denoising was performed to remove any noise that could interfere with accurate segmentation and feature extraction [18]. This step is crucial for reducing artifacts and preserving important image details. Finally, the images were resized to a consistent dimension of 227 x 227 pixels with three color channels (227 x 227 x 3) to standardize the input data. The enhancement, denoising, and resizing equation can be seen in eq (1) - (3). Where α is contrast adjustment, β is brightness adjustment, σ is the standard deviation of the Gaussian filter, u and v are the coordinates in the resized image.

$$enhanced(x, y, z) = \alpha \cdot original_{image}(x, y, z) + \beta \quad (1)$$

$$denoised(x, y, z) = \frac{1}{2\pi\sigma^2} \exp\left(-\frac{x^2 + y^2}{2\sigma^2}\right) \cdot enhanced(x, y, z) \quad (2)$$

$$resized(x, y, z) = denoised\left(\frac{x \cdot M}{X}, \frac{y \cdot N}{Y}, \frac{z \cdot O}{Z}\right) \quad (3)$$

Training hyperparameter

Specific parameters and hyperparameters were carefully selected to optimize the performance of the Improved Fuzzy Logic Model in categorizing brain tumors. The learning rate was deliberately chosen to regulate the size of each step-in optimization, ensuring successful convergence without surpassing the best solution [19]. The batch size was chosen to enable the model to handle a reasonable number of images simultaneously, striking a balance between computational efficiency and model precision [20]. The training took place over a set number of epochs to ensure enough learning opportunities, and the Adam optimizer was used for its ability to adjust the learning rate, leading to faster convergence and increased stability [21]. During training, a validation split was included to evaluate how well the model performs on new data, thus reducing the risk of overfitting. Triangular membership functions were utilized for the fuzzy logic component to represent input features. The final classification output was generated through the use of Mamdani inference and the centroid defuzzification method. The strength of the model was confirmed using K-Folds Cross-Validation, which guarantees consistent performance on various portions of the dataset [22]. The parameters and hyperparameters used in this study can be seen in Table 1.

Table 1. Measurement instrument

Models	Number of Learning Rate	Number of Max Epoch	Batch Size	K-Folds Validation	Defuzzification	Optimizer
Base Parameter	0.001	28	-	-	Centroid	Adam
Modified Parameter	0.0001	28	32	3	Centroid	Adam

Image segmentation

Specific methods, such as dilation and analysis of region properties, were utilized in the segmentation process to accurately identify the location of brain tumors in abnormal cases. The segmented binary images underwent dilation to improve and link separate areas, making it easier to identify and highlight tumor regions [23]. This process aids in enlarging the tumor's boundaries, making it easier to differentiate from the nearby brain tissue. After expanding, region properties (regionprops) were used to examine the geometric characteristics of the interconnected areas in the image, including size, center point, and enclosing rectangle [24]. This examination allowed for the accurate pinpointing and mapping of the tumor by gathering key details regarding its location, dimensions, and form. The equation based on proposed segmentation method can be seen in eq (4) – (6). Where eq (4) represents the dilation operation, eq (5) and eq (6) correspond to the region properties calculation, including area and centroid determination. In these equations, I is the binary input image, and S is the structuring element used for dilation, which modifies the

shape and size of objects in the image. The variable z denotes a point in the output image, while $[(S)]_z$ refers to the structuring element S shifted by z . signifies the dilation operation, which expands the boundaries of objects in the image. In the context of region properties, R represents the set of pixels within a region of interest, and (x,y) are the coordinates of these pixels within the region R .

$$I \oplus S = \{z \mid (S)_z \cap I \neq \emptyset\} \quad (4)$$

$$Area = \sum_{(x,y) \in R} 1 \quad (5)$$

$$Centroid = \left(\frac{1}{Area} \sum_{(x,y) \in R} x, \frac{1}{Area} \sum_{(x,y) \in R} y, \right) \quad (6)$$

GLCM extraction

The Gray Level Co-occurrence Matrix (GLCM) extraction is a helpful method in texture analysis that captures the spatial connection between pixel intensities within an image [25], [26]. The GLCM creates a matrix that represents the texture of an image by calculating the occurrence of certain pixel intensity pairs at a specified spatial relationship, such as distance and direction [2]. Every value in the GLCM corresponds to the frequency of a specific intensity pair, which can be used to calculate different texture characteristics like contrast, correlation, energy, and homogeneity [27]. These characteristics play a vital role in identifying various textures present in an image, highlighting the significance of GLCM extraction in medical image interpretation. It is especially valuable in detecting subtle changes in texture that may signal the existence of abnormalities like tumors. The equation based on GLCM Extraction can be seen in eq (7) – (10). Where $P(i,j)$ is the probability of occurrence of a pixel with intensity i being adjacent to a pixel with intensity j . μ_x and μ_y are the means of the rows and columns of the GLCM, and σ_x and σ_y are their standard deviations. Correlation measures the degree of correlation between pixel pairs. N is the number of gray levels.

$$Contrast = \sum_i \sum_j (i - j)^2 p_{(i,j)} \quad (7)$$

$$Correlation = \sum_i \sum_j \frac{(i - \mu_i)(j - \mu_j)p_{(i,j)}}{1 + |i - j|} \quad (8)$$

$$Homogeneity = \sum_i \sum_j \frac{p_{(i,j)}}{1 + |i - j|} \quad (9)$$

$$Energy = \sum_i \sum_j p_{(i,j)}^2 \quad (10)$$

Fuzzy classifier

Fuzzy classifier is a machine learning model that uses fuzzy logic principles to categorize data into distinct groups [28], [29]. Fuzzy classifiers differ from traditional classifiers by allowing for varying degrees of membership, which means that an input can be assigned to multiple classes to different degrees. This approach is especially beneficial for handling uncertainties and ambiguities in data, offering a more nuanced and adaptable way of categorizing information. In a fuzzy classifier, input features are initially translated into fuzzy sets through the use of membership functions, which assign a level of membership ranging from 0 to 1 [30]. Fuzzy classifier layer can be seen in Figure 3.

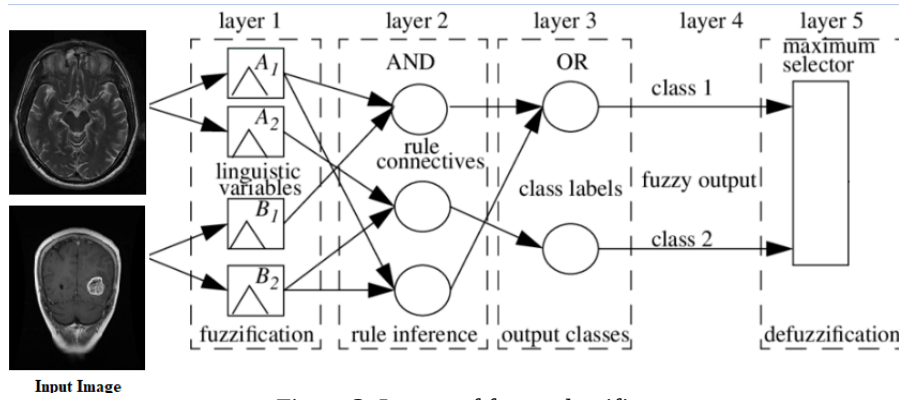


Figure 3. Layers of fuzzy classifier

These fuzzy sets are analyzed using fuzzy rules that imitate human logic by considering multiple conditions and producing an output that falls within fuzzy sets as well. Defuzzification is the last stage where the fuzzy result is transformed into a clear class label or a probability score. The fuzzy classifier operates through a sequence of layers, involving fuzzification, rule evaluation, and defuzzification. The equation each layer can be seen in eq (11) – (13). Where $\mu_{A_i}(x_i)$ is the membership function value for the input x_i in the fuzzy set A_i . $\mu_{Rule\ Inference}$ is the firing strength of the j^{th} rule. y_j is the output associated with the j^{th} . And m is the number of rules.

$$Fuzzification = \mu_{A_i}(x_i) \in [0,1] \quad (11)$$

$$Rule\ Inference = IF\ x_1\ is\ A_1\ AND\ x_2\ is\ A_2\ AND\ ...AND\ x_n\ is\ A_n\ THEN\ y\ is\ B \quad (12)$$

$$Defuzzification = \frac{\sum_{j=1}^m \mu_{Rule\ Inference} \cdot y_j}{\sum_{j=1}^m \mu_{Rule\ Inference}} \quad (13)$$

RESULTS AND DISCUSSIONS

The Results and Discussion section begins by outlining the training process based on the proposed method. The model was trained using 80% of the total dataset, with the remaining 20% reserved for validation. Training was conducted utilizing the modified hyperparameters, as presented in Table 1, which highlights key differences between the base and modified parameters. The modified parameters, including a reduced learning rate, defined batch size, and the incorporation of K-folds validation, were specifically adjusted to improve the model's performance. The model was optimized using the Adam optimizer, and the defuzzification process employed the centroid method. The training procedure included using K-folds validation with a value of $K = 3$ to train and validate the model on various parts of the data, enhancing its ability to generalize and preventing overfitting. This approach involved the model going through three rounds, with one-fold serving as a validation set in each round and the other two folds being used for training. The results of the K-folds validation process produced three separate charts, illustrating various performance metrics for each fold, as depicted in Figure 4.

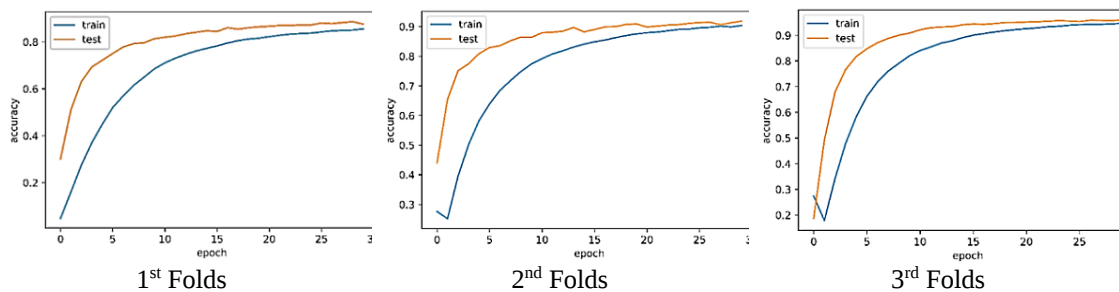


Figure 4. Training accuracy each folds

According to the graph shown in Figure 4, the model reached its highest accuracy of 99.88% on the 3rd fold, demonstrating outstanding performance on that particular portion of the dataset. On the other hand, the accuracy dropped to 92.16% in the first fold, indicating that the model encountered more difficult data

during this round. The second fold achieved a precision rate of 96.48%, indicating a better performance than the first fold but falling slightly short of the third fold. The differences in accuracy between the folds emphasize the need for K-fold validation to assess the model's consistency and effectiveness in generalizing across varied data subsets. After obtaining the highest accuracy result of 99.88% from the 3rd fold, which demonstrated the model's optimal performance, single prediction was performed on several test samples to further evaluate its effectiveness. The predictions for these samples are detailed in Table 2, showcasing the model's capability to accurately classify individual instances of brain tumors. This step was crucial for validating the model's precision in practical scenarios, ensuring that the high accuracy achieved during training translates effectively to real-world testing conditions.

Table 2. Testing using single prediction

Class	Testing Sample	True Label	Predicted	Conclusion
Normal	Normal (2).png	Normal	Normal	True Positive
	Normal (31).png	Normal	Normal	True Positive
	Normal (22).png	Normal	Normal	True Positive
Abnormal	Abnormal (7).png	Abnormal	Abnormal	True Positive
	Abnormal (16).png	Abnormal	Abnormal	True Positive
	Abnormal (28).png	Abnormal	Abnormal	True Positive

Based on Table 2, the single prediction performance of the model demonstrates a high level of accuracy in classifying test samples. All samples, including both normal and abnormal cases, were correctly identified by the model, resulting in true positive outcomes for each prediction. Specifically, the model accurately classified normal samples such as Normal (2).png, Normal (31).png, and Normal (22).png as "Normal," and abnormal samples like Abnormal (7).png, Abnormal (16).png, and Abnormal (28).png as "Abnormal." These results confirm the model's robustness and reliability in distinguishing between normal and abnormal brain scans, effectively validating its high accuracy achieved during training. Following the performance testing, the next step involved conducting segmentation and GLCM extraction to analyze the tumor regions in detail. As depicted in Figure 5, the segmentation process effectively isolated the tumor areas from the rest of the brain images, providing clear delineation of the regions of interest. The results of the GLCM extraction for each single prediction are presented in Table 3, which includes detailed texture metrics for the segmented tumor regions.

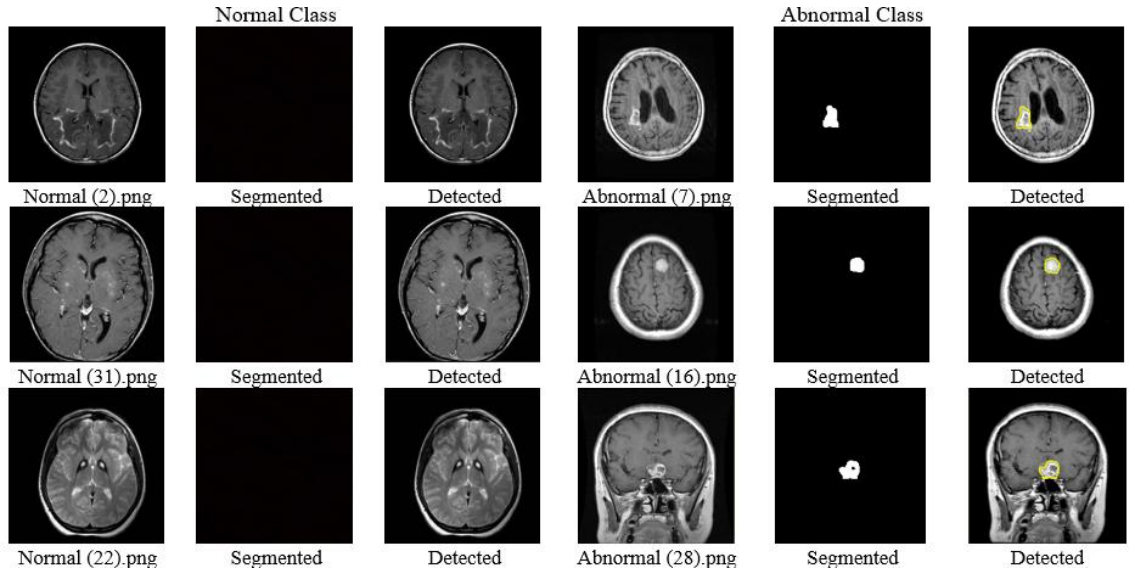


Figure 5. Results of detected tumor each single prediction

Based on Table 3, the GLCM extraction results for the detected tumor regions reveal significant texture characteristics that provide further insights into the nature of the abnormalities. The contrast values range from 0.16 to 0.27, indicating varying degrees of intensity contrast within the tumor areas, while the correlation values are between 0.132 and 0.155, suggesting moderate relationships between pixel intensities. Homogeneity values are consistently high, ranging from 0.92 to 0.93, reflecting a uniform texture within the tumor regions. Additionally, the energy values, which range from 0.71 to 0.76, highlight the amount of information contained in the textures. Based on Table 4, the performance of the proposed

methodology, which integrates Fuzzy Logic with K-folds validation, shows a notable improvement compared to related methods. Our approach achieved an impressive accuracy of 99.88%, surpassing the results reported by previous studies. Specifically, the SVM combined with Fuzzy Logic reported an accuracy of 99.24% [6], the Bayesian Fuzzy Logic method achieved 98.5% [7], and the Neural Network coupled with Fuzzy Logic obtained 98.64% [8]. This superior performance indicates that the integration of K-folds validation with the Fuzzy Logic model enhances the classification accuracy, demonstrating the efficacy of our proposed approach in accurately detecting brain tumors.

Table 3. Results of GLCM extraction

Sample Image	Contrast	Correlation	Homogeneity	Energy
Abnormal (7).png Detected Tumor	0.22	0.155	0.93	0.76
Abnormal (16).png Detected Tumor	0.27	0.132	0.92	0.71
Abnormal (28).png Detected Tumor	0.16	0.144	0.93	0.73

Table 4. Comparison with related method

Researcher	Method/Novelty	Datasets Protocol	Accuracy
[8]	SVM + Fuzzy Logic	MRI Brain Tumor	99.24%
[9]	Bayesian Fuzzy Logic	MRI Brain Tumor	98.5%
[10]	NN + Fuzzy Logic	MRI Brain Tumor	98.64%
Our	Fuzzy Logic + K-folds	MRI Brain Tumor	99.88%

CONCLUSION

In this study, we proposed an innovative methodology combining Fuzzy Logic with K-folds validation to enhance brain tumor detection. Using a dataset of 2,660 MRI images, the approach achieved a remarkable accuracy of 99.88% with a K-folds validation value of 3. This high level of accuracy was further supported by single prediction tests, which consistently identified tumors correctly, yielding true positive results across all samples. The use of K-folds validation allowed for rigorous evaluation and demonstrated the model's robustness and precision. The successful integration of Fuzzy Logic with K-folds validation showcases the potential for improved diagnostic performance in brain tumor detection. Future research could explore several enhancements to build upon this study's findings. Investigating advanced deep learning techniques, such as hybrid models combining Convolutional Neural Networks (CNNs) with Fuzzy Logic, may offer further improvements in accuracy and efficiency.

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