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Discrete Margin-Infused Laplacian Boost Technique for Detecting Early Alzheimer's Disease

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Abstract

Alzheimer's Disease (AD) is a progressive neurodegenerative disorder that mostly affects older adults. It is distinguished by a slow decline in cognitive functions, including impaired reasoning, reduced problem-solving abilities, depression, and irritability. The disease results from the collection of abnormal protein deposits in the brain, leading to the death of neurons and the lessening of brain tissue over time. Recent ML techniques provide an empirical evidence-based approach for detecting the Alzheimer's disease status of patients. However, current techniques face challenges in accurately early diagnosing the disease with minimal time and error. To address these issues, a Discrete Laplacian Margin-Infused Emphasis Boost classifier (DILMIE-boost) technique is introduced for early diagnosing Alzheimer's disease with higher accuracy in less time. It comprises five processes. Initially, brain MRI images are gathered from a database. Discrete Laplacian Filter Pre-processing is carried out to remove noisy pixels from input MRI images. The Discrete Laplacian operator is a finite-dimensional graph for improving image quality. After that, Fuzzy Piecewise Linear Mumford–Shah functional algorithm-based Segmentation is carried out to partition the enhanced image into a number of sub-divisions based on triangular fuzzy membership functions. For every segmented region, RoI features are extracted for efficient classification to perform disease diagnosis. With the extracted features, the Margin-Infused Emphasis Boost classifier utilizes Margin-infused relaxed classification as a weak learner to classify the MRI images into multiple classes for performing disease diagnosis. The performance outcome of the quantitative study demonstrates that DILMIE-boost offers improved accuracy in disease prediction while also reducing time when compared to existing approaches.

Keywords: Alzheimer’s disease (AD) diagnosis, Discrete Laplacian Filter, Fuzzy Piecewise Linear Mumford–Shah functional algorithm, Margin-Infused Emphasis Boost classifier.

1. Introduction

AD is a chronic and progressive neurodegenerative disorder that mainly affects thoughts and behavior. It is the primary cause of dementia, and its occurrence continues to

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increase globally, specifically among the aging population. As the disease progresses, it leads to severe cognitive and functional decline, ultimately impairing an individual's ability to carry out everyday behaviors. Therefore, early and precise diagnosis is necessary for effective disease management, timely intervention, and enhanced quality of life for patients. Principal Component Analysis (PCA) with ANN (PCA+ANN) was developed [1] to detect AD based on noise removal and correction of image distortions using a non-linear filtering approach and extracting relevant features.However, Region of Interest (ROI)-based segmentation was not applied to focus on specific brain areas associated with Alzheimer's disease to enhance detection accuracy. An ensemble of dissimilar locations showing similar modality with a weighted voting classifier model was developed in [2] with the aim of AD diagnosis based on aspect fusion. However, it did not effectively reduce the time complexity of the diagnosis process. An innovative deep learning (DL) ensemble model was developed in [3] for improving disease diagnostic accuracy by integrating image features such as shapes and textures. However, it failed to explore the model's application with hyper-optimization algorithms to minimize the error rate in Alzheimer's disease diagnosis. An extreme gradient-boosting method as well as a SHAP algorithm was designed in [4]; however, more accurate diagnoses were not achieved. Machine learning algorithms were designed in [5] for diagnosing AD with MRI analysis. However, this approach was not efficient for larger datasets and lacked the use of automated feature selection techniques. Additionally, the designed algorithm did not increase the classification accuracy. A stacking ensemble model was developed in [6] for achieving significant accuracy. However, large medical imaging datasets were not applied for AD diagnosis. Error study was challenging in AD analysis. An ELM classifier was developed in [7] to identify as well as categorize intellect MRIs of Alzheimer's cases and forecast different phases of dementia. However, an AI-driven tool was not employed for improving Alzheimer's disease diagnostics. An explainable ensemble-based diagnostic framework was developed in [8] for AD analysis. However, lightweight ensemble models were not developed to improve AD analysis. Hard and Soft Ensemble Voting Techniques were developed in [9] with the aim of improving Alzheimer’s Diagnosis. However, it did not perform well on larger and more diverse datasets, limiting its ability to make more accurate diagnoses. An XGBoost with SHAP method was developed in [10] to give enhanced prognostic accuracy for analyzing Alzheimer's patients based on feature selection. However, the complexity of latent Alzheimer's diagnosing remained high. A deep ensemble modelling approach was introduced in [11]. However, it failed to enhance model fairness in the detection of AD. Ensemble transfer learning was developed [12] to forecast the evolution of AD by automatic ROI extraction. However, advanced machine learning techniques were not employed for premature analysis in AD. XGBoost and ANN networks were developed in [13] by integrating the features to improve accuracy and efficiency. However, it did not minimize the time consumption for large-scale deployments. Three different pre-trained CNN based architectures were designed in [14] for increasing the accuracy of diagnosis of Alzheimer’s disease. However, fine-tuning was not performed to enhance the performance of disease diagnosis. Support vector machine (SVM) models were developed in [15]to predict AD progression with high performance. However, it was not efficient to investigate the utilization of an ensemble model for improving the strengths and reliability of the method.

The proposed DILMIE-Boost model is novel because it integrates discrete laplacian filtering, fuzzy piecewise linear Mumford–Shah segmentation, RoI-based feature extraction, and a Margin-Infused Emphasis Boost classifier into a unified framework for Alzheimer's disease diagnosis. Unlike existing MRI-based methods, the proposed approach enhances image quality while accurately segmenting disease-relevant brain regions under uncertain intensity

variations. The RoI-based feature extraction reduces redundant information and computational complexity. Furthermore, the Margin-Infused Emphasis Boost classifier improves class discrimination by combining margin-based learning with boosting, resulting in higher diagnostic accuracy and faster classification. These technical advancements collectively provide a more robust and efficient solution than conventional MRI-based Alzheimer's disease detection methods.

1.1 The Key Contributions of The Dilmie-Boost Technique Method

To enhance the accuracy of AD, a DILMIE-boost technique is developed.

- The DILMIE-boost technique is developed to improve the accuracy of Alzheimer's disease diagnosis. It comprises image acquisition, pre-processing, segmentation, feature extraction, and categorization.
- The Discrete Laplacian Filter Pre-processing model is employed to enhance image contrast by removing noise, reducing mean square error, and increasing PSNR.
- Fuzzy Piecewise Linear Mumford–Shah functional algorithm-based Segmentation is carried out to extract the ROI based on a triangular membership function and extract image features to reduce Alzheimer's disease diagnosis time.
- The Margin-Infused Emphasis Boost classifier is applied to categorize the different stages of Alzheimer's disease using the Marczewski-Steinhaus coefficient to improve accuracy.

Finally, an experimental assessment is conducted to estimate the results of the DILMIE-boost technique using different parameters and by comparing it with other classification methods.

The structure of this manuscript is as follows: Section 2 provides an appraisal of pertinent literature. In Section 3, the proposed DILMIE-boost technique is detailed, including a schematic illustration of its framework. Section 4 delineates the database employed and describes the experimental process. Section 5 presents a comparison of results among DILMIE-boost and conventional methods, with an assortment of estimation parameters. Finally, Section 6 summarizes the manuscript.

2. Research Foundation

ViT and GRU were developed in [16] to distinguish AD characteristics from MRI images precisely and dependably based on vital aspects.However, its effectiveness in Alzheimer's disease (AD) detection was not evaluated. An EfficientNet algorithm was designed in [17] to recognize dissimilar kinds of AD for achieving remarkable accuracy. However, it did not focus on exploring more efficient DL architectures for AD recognition. DL and image processing techniques were developed in [18] to enhance Alzheimer's Detection based on feature extraction capabilities. However, timely as well as accurate recognition of AD was not performed to enhance patient outcomes. A new ensemble learning technique was designed in [19] for detecting Alzheimer's disease by effectively capturing spatial as well as semantic data from brain images. However, it failed to apply explainable AI techniques for monitoring diseases. A multi-modal deep learning approach was designed in [20] for clinical decision-

making based on an MRI-based method to identify AD. However, accurate diagnosis of AD remained a challenging issue.

A 3D CNN model was developed in [21] to distinguish disease progression in AD patients using MRI. However, a more robust detection method was not applied to increase accuracy. A deep learning model was designed in [22] for diagnosing AD based on MRI images with high accuracy. However, computational efficiency was not achieved on large-scale databases while sustaining elevated accuracy.

A compositional graph-basis ML approach was developed in [23] for AD recognition. However, the framework was not efficient for AD recognition. IW-BS and OSVM classifiers were introduced in [24] with the aim of classifying MRI images into different Alzheimer's disease levels such as Mild, Very Mild, or Normal. However, feature extraction was not performed to further enhance diagnostic precision.

3. Methods

Early-stage Alzheimer's disease (AD) diagnosis is particularly valuable, as it allows healthcare professionals to implement timely interventions and treatment planning, which may slow disease progression and improve patient outcomes. Therefore, the development of a reliable and efficient prediction model is essential for accurately identifying individuals at risk of developing AD. To address this necessity, a novel model known as ROSIF-RASE is introduced. The ROSIF-RASE model is specifically designed to enhance the accuracy of early-stage Alzheimer's diagnosis, thereby supporting more informed clinical decisions. The proposed DILMIE-boost technique, depicted in Figure 1, comprises five key stages: image acquisition, preprocessing, segmentation, feature extraction, and classification. These interconnected stages work together to significantly distinguish between healthy individuals and those with signs of AD. This section provides a detailed explanation of the proposed DILMIE-boost technique, including its ability to analyse clinical and neurological data and identify patient outcomes as either Alzheimer's or non-Alzheimer's.

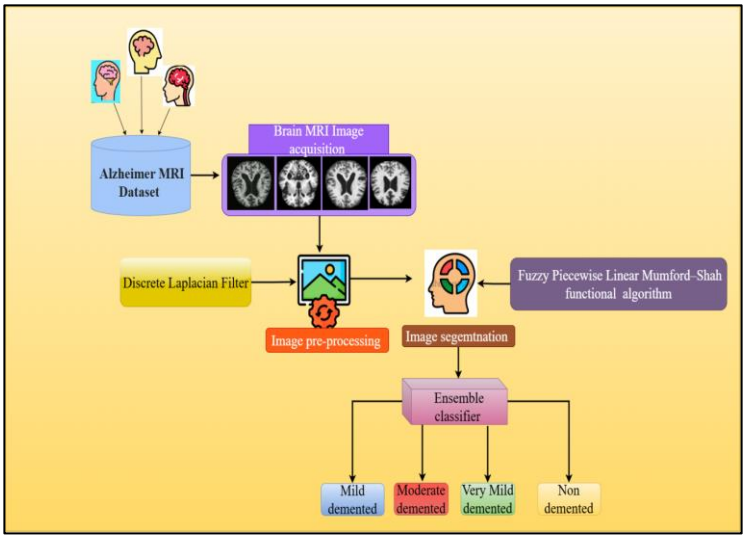


Figure 1. Architecture of DILMIE-boost technique

Figure 1 describes the architecture of the proposed DILMIE-boost technique, developed to enhance the accuracy of Alzheimer's disease (AD) diagnosis. The diagnosis workflow is divided into several key stages: image acquisition, pre-processing, segmentation, and

classification. Each stage in the process plays a critical role in enhancing the accuracy of disease prediction. The first step involves collecting high-quality MRI images of various patients from established datasets. During the pre-processing phase, image clarity is improved by reducing noise and enhancing contrast using a Discrete Laplacian Filter, which helps ensure that the visual data are clean and reliable for further analysis. The subsequent segmentation stage is essential for isolating the region of interest (ROI) and extracting specific features. Finally, an ensemble classifier is employed for classifying the input MRI images into four classes: Mild Demented, Moderate Demented, Non-Demented, and Very Mild Demented. The following subsections offer a comprehensive overview of each stage in the proposed DILMIE-boost technique.

3.1 Image Acquisition

The fundamental step of the proposed DILMIE-boost technique is image acquisition, which involves collecting multiple high-quality MRI brain images to serve as input for the disease prediction process. The Augmented Alzheimer MRI Dataset, extracted from Kaggle [25], is employed for disease diagnosis.

3.2 Image Pre-processing

The second phase of the proposed DILMIE-boost technique is the pre-processing stage, aimed at enhancing image contrast to support accurate recognition of AD. This stage includes a sequence of steps to prepare raw MRI images by removing noise and preserving essential visual features. To attain this, the DILMIE-boost method employs a Discrete Laplacian Filter, a non-linear smoothing method that adaptively minimizes noise and enhances overall image clarity.

The proposed DILMIE-boost technique consists of five processes. Initially, brain MRI images are collected from the database. Subsequently, Discrete Laplacian Filter-based preprocessing is performed to remove noisy pixels and enhance image quality. In this stage, a 3×3 Laplacian kernel is employed to emphasize edge information while suppressing noise. The filter kernel used is

Initially, the raw input dataset, which is represented by D is considered and systematically arranged in the form of a matrix, as represented below.

$$D = \begin{bmatrix} P_1 & P_2 & \dots & P_k \\ R_{11} & R_{12} & \dots & R_{1k} \\ R_{21} & R_{22} & \dots & R_{2k} \\ \vdots & \vdots & \dots & \vdots \\ R_{j1} & R_{j2} & \dots & R_{jk} \end{bmatrix}, j = rows, k = columns \quad (3.1)$$

From the above matrix 3.1, the dataset D consists of k columns representing features or attributes which is represented by $P_1, P_2, \dots, P_k$ and j rows representing the sample instances or student records which is represented by R_{jk}.

Given an input MRI image represented as $G = (V, E)$,V represent vertex or pixel $P = \{P_1, P_2, \dots, P_k\}$and '$E$' indicates an edges or connectivity between adjacent pixels. Therefore, the weighted Laplacian is measured to identify the pixels that differ from their surroundings pixels.

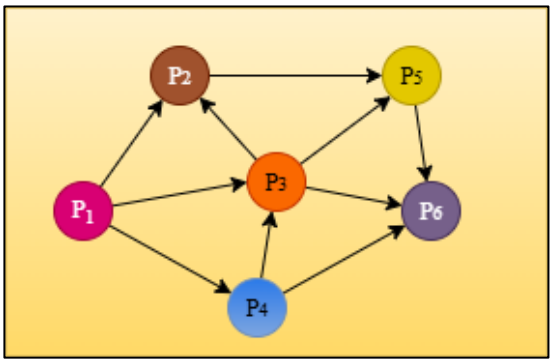


Figure 2. Graphical illustration

Figure 2 illustrates a graph where the image pixels are $P_1, P_2, \dots, P_k$ located into vertexes and edges connecting neighboring pixels. A linear combination of the discrete Laplacian function is expressed as follows,

$$\Delta\phi = \sum W_{jk}\left[\phi(P_j) - \phi(P_k)\right]^2 \quad (1)$$

$$z = \begin{cases} \arg max\, \Delta\phi, & noisy\ pixels \\ otherwise, & normal\ pixels \end{cases} \quad (2)$$

Where, $\Delta\phi$ indicates andiscrete Laplacian function for the filter response, weight of edge attaching pixels P_j and P_k, ϕdenotes a function defined over graph nodes. When the pixel intensity $P_j$is approximately equal to the neighbouring pixels 'P_k', the value of the Laplacian function provides outcomes becomes close to 0, meaning the pixel is preserved in the final output. However, if $P_j$is significantly deviates fromP_k, the Laplacian function output approaches high value. In other words, the pixels with more divergence are identified as noisy. As a result, these noisy pixel values are removed, effectively reducing noise in the image. As a result, enhanced image observed for further processing.

Algorithm 1: Discrete laplacian filter based image denoising

Input: Dataset 'DS', MRI images '$I_1, I_2, \dots, I_n$'
Output: Pre-processed images
Begin
Step 1: **Collect** the number of MRI images '$I_1, I_2, \dots, I_n$
Step 2: **for each input** image 'I'
Step 3: Organize the pixels in graph '$G = (V, E)$'
Step 4: **for each pixel 'P_k' in** graph
Step 5: Measure the Discrete Laplacian function using **(1)**
Step 6: End for
Step 7: if $(\arg max\, \Delta\phi)$ **then**
Step 8: Pixels are determined as noisy
Step 9: **else**
Step 10: Pixels are determined as normal
Step 11: End if
Step 12: **Remove noisy pixels**
Step 13: Return (quality enhanced image)
Step 14: End for
End

Algorithm 1 presents a different process for improving image contrast by identifying and removing noisy pixels. The process begins by acquiring MRI images from the dataset, followed by extracting the pixel intensity values. The pixels are positioned using a graphical structure. Then, a Discrete Laplacian operator is applied to measure the deviation of each pixel from its neighbors. Pixels showing low deviation are treated as consistent or noise-free, while those with high variance are determined to be noisy. Intensity values of noisy pixels are redundant. This targeted filtering improves image clarity, resulting in enhanced contrast. The, processed image shows superior PSNR and minimum MSE, denoting improved quality.

3.3 Fuzzy Piecewise Linear Mumford–Shah Functional Method Basis of Image Segmentation

The DILMIE-boost method carries out image segmentation, which involves dividing an image into pertinent areas. This step shortens image illustration through isolating disease-affected portions to recognize and extract ROIs with superior precision. The DILMIE-boost method employs a Fuzzy Piecewise Linear Mumford–Shah functional developed for segmenting the input pre-processed image to extract the ROI. Compared to conventional segmentation methods, the proposed segmentation algorithm extracts significant edges at images since it clearly comprises a term for border length. This evades over-segmentation and assists in pursuing usual contours.

The segmentation process begins by randomly separating the input pre-processed image into a predetermined number of regions.

$$PI \in \{R_1, R_2, R_3 \dots R_b\} \tag{3}$$

Where, R_b denotes a region of input image 'PI'. Once the regions are initialized, the algorithm proceeds to compute the mean intensity of each region by averaging the pixel values within that region. In the proposed DILMIE-boost method, the mean pixel intensity of each region is computed using the fuzzy concept. Instead of calculating the mean from a hard assignment of pixels, each pixel contributes to a region proportionally to its fuzzy membership value.

$$\mu_p = \frac{1}{m}\sum_{j=1}^{m} P_j \tag{4}$$

Where, μ_p denotes fuzzy mean intensity of each region by averaging the pixel values,$\alpha\ (x, y)$ denotes a triangular fuzzy membership function that helps to allow each pixel to contribute to the mean intensity, $PI\ (x, y)$ denotes the original pixel intensity of image. The triangular fuzzy membership is formulated as follows:

$$\alpha\ (x,y) = \begin{cases} 0 & PI\ (x,y) \le a \text{ or } W \ge c \\ \frac{PI\ (x,y)-a}{b-a} & a < PI\ (x,y) \le b \\ \frac{c-PI\ (x,y)}{c-b} & b < PI\ (x,y) \le c \end{cases} \tag{5}$$

Where a, b, and c denote the lower limit, peak, and upper limit of a triangular membership function for particular region 'R'. The fuzzy membership functions provide an output range [0, 1]. Next, the discrete version of the Mumford–Shah function 'E' compares the pixel's intensity to the mean intensities of all regions.

$$E = \sum_{(x,y\in R)}\left(PI\ (x,y) - \mu_p\right)^2 + \beta.L\ (R) \quad (6)$$

Where, $PI\ (x,y)$ denotes an original pixel intensity of an image, μ_p denotes a mean value, β denotes a regularization parameter to control smoothness,$L\ (R)$ denotes a boundary length of the region, $\left(PI\ (x,y) - \mu_p\right)^2$ indicates a piecewise constant function. This constant term ensures that pixels in a region are closer to the region's mean, supporting homogeneity. The second term handles long or complex region boundaries to smooth the shapes. By minimizing this Mumford–Shah function, the algorithm produces a segmented image in which each region has minimal deviation from the mean.

$$Q = \arg\min E \quad (7)$$

Where, Q denotes an output of segmentation, $\arg\min E$ represents minimizing the Mumford–Shah function. Therefore, Mumford–Shah functional is minimized during the algorithm to produce accurate, smooth, and meaningful segmentation of the ROI. The segmentation algorithm-based crop disease detection is given below.

Algorithm 2: Piecewise linear mumford–shah functional algorithm

Input: pre-processed images 'PI'
Output: Segment the ROI
Begin
Step 1: **For each** pre-processed images 'PI'
Step 2: Divided into number of regions$PI \in \{R_1, R_2, R_3 \ldots R_b\}$
Step 3: **For each** region
Step 4: **Compute** mean value using (4)
Step 5: **Compute** Mumford–Shah function 'E' using (5)
Step 6: **if** $(arg\min E\ )$**then**
Step 7: Segment the ROI
Step 8: **End if**
Step 9: End for
Step 10: End for
Step 11: Obtain the segmented regions
End

Algorithm 2 sketches a procedure employed to enhance segmentation for accurate disease recognition. The procedure begins with pre-processed images that serve as inputs to the segmentation phase. The image is separated into a number of regions. For every region, the mean value of pixel intensity is calculated based on a triangular fuzzy membership function. Instead of assigning pixels entirely to a single region, each pixel contributes proportionally to the region based on its membership value. This fuzzy value ensures that pixels closer to the peak of the membership function have a superior influence on the region's mean, while pixels farther away contribute less leading to smoother and more accurate segmentation. After that, the Mumford–Shah function is calculated through piecewise constant function. The segmented image is determined through recognizing least Mumford–Shah function, efficiently outlining the ROI. A series of pixels attained from this area defines the segmented border, precisely isolating the ROI. This technique improves segmentation as well as minimizes computational time.

3.4 Feature extraction

The DILMIE-boost method continues through feature extraction, a vital stage that transforms segmented brain areas into quantitative descriptors. These aspects indicate structural as well as textural characteristics of the brain, which are influenced by AD.

Texture aspects explain how pixel intensities are spatially dispersed across an image**.** In texture study, contrast and correlation are computed to estimate the association among neighboring pixel intensities. Contrast imitates the degree of dissimilarity in intensity values, especially differences between pixels where intensity stages are not equivalent. A high contrast value suggests significant local intensity variation, which is often indicative of complex or irregular textures.

$$CS = \sum_{i,j}(i-j)^2 P_{ij} \tag{8}$$

Where, CSrepresents a contrast, $(i,j\ )$ denotes occurrence of a pixel pairs with intensities within an image. Correlation measures the linear relationship between the gray levels of neighboring pixels, helping to evaluate how intensity values change regarding one another across an image. It indicates the degree to which pixel intensities are statistically dependent or consistently vary together.

$$CC = \sum \frac{P_{ij}\,(i-M_i)(j-M_j)}{D^2} \tag{9}$$

Where CC represents the correlation of an image, M_i and $M_j$represents mean of the pixels intensity$P_i\ and\ \ P_j$, D represents the deviation of the pixels.

In the multi-modal MRI images, RGB color histograms are employed to capture the distribution of pixel intensities across each color channel. These histograms provide global distributions of the color composition in the image. To further describe these distributions, color moments are computed for each channel.

First, the input face-segmented ROI grayscale image is converted into its mean, variance, and skewness.

$$\mu_c = \frac{1}{m}\sum_{j=1}^{m} I_j \tag{10}$$

Where,μ_c symbolizes a mean, I_j' indicates intensity of pixels 'P', 'm' indicates total numeral of pixels at image. Based on mean value, the variance is measured as given below,

$$\sigma^2{}_c = \frac{1}{m}\sum\left(I_j - \mu_c\right)^2 \tag{11}$$

Where, $\sigma^2{}_c$ indicates a variance, I_j denotes an intensity of pixel, μ_c symbolizes a mean, finally, the skewness is calculated as follows,

$$SK_c = \frac{\frac{1}{m}\sum\left(\left(I_j-\mu_c\right)\right)^3}{\left(\frac{1}{m}\sum\left(\left(I_j-\mu_c\right)\right)^2\right)^{3/2}} \tag{12}$$

Where SK_c denotes the skewness. Based on the above-said mean, variance, and skewness, the color features are extracted.

The shape is represented by its contour (i.e., boundary) that encircles the entire structure. The Orthogonal Radial-Angular Shape Descriptor is widely used in image analysis. The shape feature extraction process is expressed as follows:

$$X = \tau_{nm}(d).e^{jm\theta_{PC}} \tag{13}$$

$$d = \sqrt{x^2 + y^2} \tag{14}$$

$$\theta_{PC} = arc\tan\left(\frac{y}{x}\right) \tag{15}$$

Where, X denotes a feature extraction output, $\tau_{nm}(r)$ denotes a radial polynomial of order n and repetition$m$, θ_{PC} denotes angle in polar coordinates,d denotes a distance from the origin. Followed by, Feature fusion are performed as follows

$$FV = \{texture, color, shape\} \tag{16}$$

After that,FV denotes a Feature fusion vector. The extracted features are given as input to the classifier.

The justification for selecting texture features is that they capture structural variations in brain tissues caused by Alzheimer's disease. Intensity features describe changes in RGB color histogram distribution, reflecting tissue degeneration, while shape features describe morphological brain changes such as atrophy and structural deformation. These features collectively enhance discriminative ability for accurate Alzheimer's disease diagnosis.

3.5 Margin-infused Emphasis Boost Classifier

Once features are extracted from the Region of Interest (RoI) in MRI images, the next step involves classifying these images for accurate disease diagnosis. To achieve this, the proposed DILMIE-boost technique utilizes the Margin-infused Emphasis Boost classifier model with a set of RoIs. The Emphasis Boosting technique is an ensemble machine learning approach that enhances disease diagnosis accuracy by combining several weak classifiers. It operates by training these weak classifiers in parallel. While a weak classifier provides slightly better results, a strong classifier achieves highly accurate classification for distinguishing different classes of Alzheimer's disease. In this context, the proposed model utilizes this ensemble approach to effectively classify the multiple classes of Alzheimer's disease, thereby improving overall performance. In contrast to other ensemble methods, Emphasis Boosting is employed for achieving higher accuracy, especially when dealing with complex or larger datasets and classes.

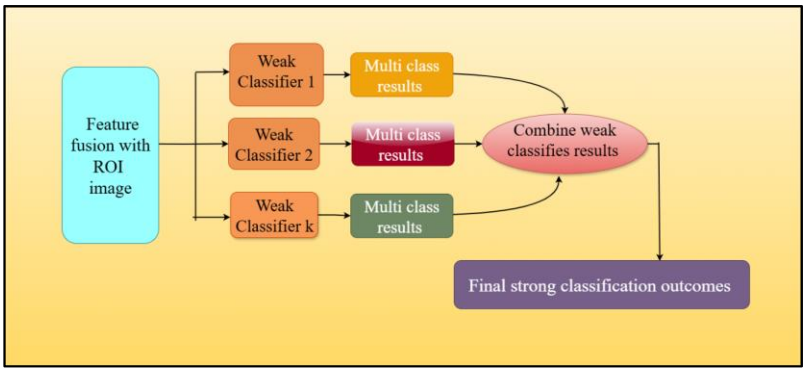


Figure 3. Schematic structure of ensemble classifier

Figure 3 depicts the schematic structure of an ensemble classifier for diagnosing different classes of Alzheimer's disease with higher accuracy. The ensemble boosting classifier considers the training set $\{FV_i, Y_b\}$ where FV_i indicates the feature vector from the segmented ROI image with training samples, and Y_b indicates the ensemble classification output or strong classifier output. First, the ensemble learning model constructs 'k' number of weak learners $H_1, H_{2,} H_{3,} \ldots . H_k$as Margin-infused Relaxed Classification Classifier

The Margin-Infused Relaxed Algorithm (MIRA) is a ML method for multiclass categorization tasks. It updates model parameters incrementally by examining each training sample. The algorithm ensures that each image is correctly classified with a margin. Let us consider the input segmented images $SI = \{SI_1, SI_2, \ldots, SI_b\}$ withFV_i. For each image, the similarity score between the testing and training image is measured by applying a Marczewski-Steinhaus coefficient.

$$SC = \frac{FV_i \cap T_k}{\sum FV_i + \sum T_k - FV_i \cap T_k} \tag{17}$$

Where, SC indicates a similarity coefficient, FV_i denotes a feature vector from the training image, andT_k denotes a feature vector from testing image, the intersection symbol '$\cap$' indicates mutual dependence between the images,$\sum FV_i$ is the sum of FV_i score, $\sum T_k$ is the sum of $T_k$score. The similarity function provides the output values from 0 to 1$[0 \leq SC \leq 1]$. After computing these scores, the algorithm chooses a class through the maximum score, indicating closest match between the input image and that class. The input is then classified into this most similar class.

$$W = \arg\max SC \tag{18}$$

Where, W denotes a weak learner result, $\arg\max SC$ denotes an argument of maximum similarity score. This process allows the model to make diagnosis of multiple classes. In this way, the weak learner categorizes the images into different classes. In order to obtain the strong classification output, the weak classification results are combined as follows,

$$Y = \sum_{i=1}^{k} W_i \tag{19}$$

Y denotes strong categorization output, W_i represents weak categorization result. For every output, weights are randomly assigned.

$$Y = \sum_{i=1}^{k} W_i \, \vartheta_i \tag{20}$$

Where, '$\vartheta_i$represents weights. The proposed boosting approach employs a weighted emphasis mechanism to evaluate the classification errors 'CR' produced by individual weak learners.

$$CR = \exp\left[\left(\sum_{i=1}^{k} W_i \, \vartheta_i - Y\right)^2\right] \tag{21}$$

Based on the computed error rate, the weight assigned to each weak learner is adjusted accordingly. In MIRA, dissimilarity among actual as well as forecasted classification, called error margin, is used to adjust the weights of the weak learners. This helps improve accuracy while making only small changes to the model's weights. The weight adjustment is performed using a gradient-based approach, which updates the model in the direction that reduces the classification error.

$$\vartheta_{t+1} \quad = \vartheta_t - \eta M_t \tag{21}$$

$$M_t = \varphi v_{t-1} + \ (1 - v)\frac{\partial CR}{\partial \vartheta_t} \tag{22}$$

Where, ϑ_{t+1}denotes updated weight, $\vartheta_t$indicates previous weight, ηrepresents learning rate, '$\frac{\partial CR}{\partial \vartheta_t}$, represents a partial derivative of 'CR'with current weight 'ϑ_t', φindicatesdefault value 0.9 . In this way, a weight's value gets updated using the Gradient method. This process is repeated iteratively until the classification error is minimized. By continuously refining the weight in this way, the ensemble classifier becomes more accurate at distinguishing between different stages or types of AD. Each iteration improves the method's ability to correctly classify new MRI inputs based on learned patterns. Finally, the weak learner results with minimum error are considered the final strong classified result. The Emphasis Boost classification algorithm is given below,

Algorithm 3: Margin-infused emphasis boost classifier

Input: segmented MRI images $SI_1, SI_2, \ldots, SI_b$, Feature vector FV_i
Output: Improve the disease diagnosing accuracy
Begin
// **Initialize the classes** $c_1 -$ Mild Demented , $c_2 -$ Moderate Demented, $c_3 -$ Non Demented $c_4 -$ Very Mild Demented
Step 1: **For each** segmented ROI image with feature sector 'FV_i '
Step 2. Construct 'k' number of weak classifiers
Step 3. Compute the similarity 'SC'
Step 4:*if* $\arg\max SC$' **then**
Step 5: Classify the input image into different classes
Step 6: **End if**
Step 7: **End for**
Step 8: Combine the set of weak learner results ' $Y = \sum_{i=1}^{k} W_i$ '
Step 9: **for each** weak classifier results 'W_i'
Step 10: Initialize the weight ' ϑ_i'
Step 11: Compute the error by applying emphasis function using (20)
Step 12: **Update the weight using (21)**
Step 13: ***if*** $\arg\min CR$'
Step 14: **Obtain final** classification results
Step 15: **else**
Step 16: **Go to step 12**
Step 17: **End if**
Step 18: **End for**
Step 19: **Return** (accurate disease classification output)
End

Algorithm 3 details the procedure for diagnosing Alzheimer's disease with improved accuracy using a Margin-infused Emphasis Boost classifier. This method builds an ensemble of weak learners using segmented MRI images with extracted feature vectors. Initially, these weak learners classify different stages of Alzheimer's disease. The outputs from all weak learners are aggregated, and corresponding weight values are initialized. An emphasis function is applied to assess the classification error of each weak learner. Based on this classification

error, the weight is updated using a gradient function. This process is repeated until the minimal error is found. Finally, the weak learner with the lowest error is selected as providing the final classification results. This approach enhances Alzheimer's disease diagnosing accuracy.

4. Experimental Setup

4.1 Dataset Introduction and Data Exploration

The significant proposed DILMIE-boost technique involves collecting high-quality multiple MRI brain images to serve as input for the disease prediction process. An Augmented Alzheimer MRI Dataset, employed for disease diagnosis, is extracted from Kaggle [25]. The Alzheimer's disease database comprises around 33,984 MRI images, classified into four separate categories in both training and testing sets. The information consists of two folders: "single," including original images, and "other," including augmented images used for AD analysis. Therefore, the augmented images folder is collected for AD diagnosis. Experimental assessments of the DILMIE-boost technique and existing PCA+ANN [1], and DPSM with weighted voting [2] are implemented in a MATLAB-based graphical programming environment for accurate Alzheimer's disease diagnosis. To conduct the experiment, an Augmented Alzheimer MRI Dataset is employed for disease diagnosis. The Multi-Class Alzheimer MRI database is a comprehensive and diverse gathering of images representing diseases with four classes. For experimental purposes, the number of MRI images ranges from 3,000 to 30,000.

Table 1. AD multiclass images

S. No	MRI Image Classes	Original Images	Augmented Images
1	Mild-demented	896	8960
2	Moderate-demented	64	6464
3	Non-demented	3200	9600
4	Very Mild-demented	2240	8960
Total Images		6400	33984

5. Results and Discussion

Result analysis of the DILMIE-boost technique and existing PCA+ANN [1], and DPSM with weighted voting [2] are compared using various metrics

PSNR: This metric is utilized to assess the excellence of a pre-processed MRI image by comparing it with the original image. This evaluation relies on the MSE, which computes the average of squared dissimilarity among corresponding pixel values in both images. A smaller MSE value signifies a higher degree of similarity, indicating that the preprocessing has better preserved the image quality.

$$PSNR = 10 * \log_{10}\left[\frac{255^2}{MSE}\right] \tag{24}$$

$$MSE = [I_O - I_P]^2 \tag{25}$$

Where '$PSNR$'designates a peak signal to noise ratio, MSE denotes mean square error,I_P indicates preprocessed image size, $I_O$indicates original image size. It is measured in decibels (dB).

Accuracy: it refers to the proportion of correctly identified multiple stages of Alzheimer's disease diagnosis. Accuracy is mathematically represented as given below.

$$Acc = \frac{TP+TN}{TP+TN+FP+FN} * 100 \quad (26)$$

From equation (20) accuracy 'Acc', is calculated depend on 'TP', 'TN', 'FP' and 'FN'.

Precision: The precision is defined a method's capability to correctly recognize a specific stage of Alzheimer's disease among all images predicted as belonging to that stage. In multi-class classification, precision is calculated separately for each class using the following formula:

$$Pre = \left(\frac{TP}{TP+FP}\right) * 100 \quad (27)$$

Where, Pre denote a precision,TPindicates true positive, FPsymbolize false positive.

Recall: It also referred to as sensitivity, is a performance parameter that evaluates method effectiveness at correctly identifying specific classes of Alzheimer's disease. In disease classification, recall measures the proportion of true cases for a given stage of Alzheimer's disease that are correctly detected by the model.

$$Rec = \left(\frac{TP}{TP+FN}\right) * 100 \quad (28)$$

Where, Rec denote a recall,TP indicates true positive, FN symbolize false negative.

F1 score: It is a widely employed assessment parameter at categorization tasks, including disease diagnosis. It represents the harmonic mean of precision and recall**,** giving a balanced measure of a method's capability to properly identify positive cases while reducing FP and FN.

$$F1\ score = \left(2 * \frac{Pre*Rec}{Pre+Rec}\right) \quad (29)$$

Pre-processing Time: This is defined as the amount of time required by the proposed framework to perform image pre-processing method, including image enhancement, noise removal, normalization, and resizing, for all input MRI images. It is computed as follows:

$$T_{Pre} = \sum_{i=1}^{n} I_i * time_{pre}(I_i) \quad (30)$$

Where, T_{Pre}denotes the total preprocessing time based on the input images 'I_i', 'n' is the total number of MRI images and $time_{pre}(I_i)$ is specified as pre-processing time required for the i^{th} MRI input image.

Segmentation Time: The segmentation time is defined as the time required to identify and extract the ROI from preprocessed MRI images using the proposed segmentation algorithm. It is measured as follows,

$$S_{Time} = \sum_{i=1}^{n} I_i * T_{Seg}(I_i) \quad (31)$$

Where, S_{time}denotes the total segmentation time based on the input images 'I_i', 'n' is the total number of MRI images and $T_{Seg}(I_i)$ is denotes the segmentation time required for the i^{th} MRI input image.

Classification Time: It is defined as the time required by the DILMIE-boost classifier to classify the segmented MRI images into different stages of Alzheimer's disease. It is mathematically expressed as:

$$Clss_T = \sum_{i=1}^{n} I_i * CT(I_i) \quad (32)$$

Where, $Clss_T$denotes the total classification time based on the input images 'I_i', 'n' is the total number of input MRI images and $CT(I_i)$ is denotes the classification time required for the i^{th} MRI input image.

Execution Time: This is defined as the total time required by the proposed method to diagnose Alzheimer's disease from the input MRI images. The execution time of each stage is measured separately, and the total execution time is obtained by summing the individual processing times. The overall execution time is measured as follows,

$$ET = \sum_{i=1}^{n} I_i * (T_{Pre} + S_{Time} + Clss_T) \quad (33)$$

Where, ET denotes a Disease diagnosis time based on the input images 'I_i' and the actual time consumed in diagnosing the different stages of Alzheimer's disease using Pre-processing, segmentation and classification denoted by '$(T_{Pre} + S_{Time} + Clss_T)$'. It is calculated in milliseconds (ms).

Computational Complexity: Computational complexity is the amount of memory required by the algorithm during each stage of the preprocessing, segmentation, and classification process for Alzheimer's disease detection. Each stage of preprocessing, segmentation, and classification is measured as follows.

The Overall Computational Complexity is measured as,

$$Total_{CC} = \sum_{i=1}^{n} I_i * memory[Pre + Seg + class] \quad (34)$$

From the Equation 34, computational complexity is represented by $Total_{com}$, number of memory is represented by I_i and memory instances is required by the algorithm during the pre-processing, segmentation and classification processes for Alzheimer's disease detection is represented by $memory[Pre + Seg + class]$. It is measured in terms of MB.

Specificity: It is measured to correctly identify the negative sample images.

$$Spec = \frac{T_n}{T_n + F_n} \quad (35)$$

Where, '$Spec$' is Specificity.

Table 2. Quantitative analysis of PSNR

Image size (KB)	PSNR (dB)		
	Proposed DILMIE-boost	**PCA+ANN [1]**	**DPSM with weighted voting [2]**
10.73	55.46	45.02	49.96
11.12	54.32	45.71	49.14
10.97	50.98	44.78	48.39

11.78	52.86	45.98	47.79
9.1	49.34	44.04	47.62
11.24	51.35	46.61	48.21
10.2	52.14	46.91	49.34
12.12	53.16	46.05	48.85
10.91	50.17	46.76	49.09
10.57	50.40	44.84	47.14

Table 2 illustrates a comparison of PSNR against MRI brain image sizes (KB). The PSNR values are evaluated for three different methods: the proposed DILMIE-boost technique, and the existing PCA+ANN [1], and DPSM with weighted voting [2]. Across all image sizes, the DILMIE-boost technique consistently improved the overall performance compared to the other two existing methods by achieving higher PSNR values and lower Mean Square Error (MSE). For each approach, ten different image sizes were analysed. The results expose that the DILMIE-boost technique improves PSNR by approximately 14% and 7% compared to [1] and [2], respectively. This enhancement is attained due to the use of Discrete Laplacian Filter-based image denoising, which examines the relationship between each pixel and the average intensity of its surrounding pixels. Pixels close to the standard are measured as normal, while considerably dissimilar ones are recognized as noise. This filtering procedure efficiently smoothes out noise, leading to clearer images, minimum MSE, and an overall enhanced PSNR result.

Table 3. Quantitative analysis of Acc

Number of MRI images	**Accuracy (%)**		
	Proposed DILMIE-boost	**PCA+ANN [1]**	**DPSM with weighted voting [2]**
3000	96	91.33	93.33
6000	96.78	91.42	94.23
9000	96.05	91.48	93.65
12000	96.86	91.23	94.08
15000	96.88	91.22	93.98
18000	96.36	91.26	93.22
21000	96.65	91.56	93.45
24000	96.32	91.65	93.62
27000	96.45	91.82	93.89
30000	96.78	91.9	93.47

Table 3 presents the identification rates of disease diagnosis accuracy using three different models: the proposed DILMIE-boost technique, and the existing PCA+ANN [1] and DPSM with weighted voting [2]. Outcomes demonstrate that the DILMIE-boost method consistently attains superior accuracy compared to the other two models. For example, with 3000 images, DILMIE-boost achieves 96% accuracy, while the conventional methods [1] and [2] achieved 91.33% and 93.33%, respectively. Overall, these outcomes denote that the DILMIE-boost method shows an enhancement of 5% and 3% over [1] and [2]. This noteworthy improvement is mainly due to the combination of the Margin-infused Emphasis Boost classifier. This ensemble classifier classifies dissimilar phases of AD by segmented MRI images through an extracted aspect vector. An emphasis function is utilized to review categorization error. This procedure improves the accuracy of latent fingerprint recognition.

Table 4. Quantitative analysis of Pre

Number of MRI images	**Precision (%)**		
	Proposed DILMIE-boost	**PCA+ANN [1]**	**DPSM with weighted voting [2]**
3000	96.74	92.23	93.98

6000	96.56	92.22	93.84
9000	96.48	92.15	93.69
12000	96.89	92.08	93.88
15000	96.05	92.33	93.75
18000	96.47	92.45	93.65
21000	96.96	92.48	93.63
24000	96.22	92.69	93.78
27000	96.05	92.08	93.12
30000	96.12	92.36	93.66

Table 4 illustrates a comparative study of precision in AD diagnosis across a varying number of images, ranging from 3,000 to 30,000 MRI brain images. This study compares the outcome of DILMIE-boost against [1] and [2]. Results demonstrate that DILMIE-boost consistently attains superior precision (Pre) than conventional methods. For instance, with 3,000 images, DILMIE-boost, [1], and [2] attained precision of 96.74%, 92.23%, and 93.98%, respectively. Similarly, different results were examined with diverse counts of input images. The average of ten outcomes shows that DILMIE-boost demonstrates an average Pre-enhancement of 4% and 3% compared to [1] and [2]. This improvement is attributed to the combination of a sophisticated ensemble learning approach where a gradient-based plan is used to regulate weights, efficiently minimizing categorization errors. These processes improve the technique's capability to precisely differentiate between dissimilar phases of AD diagnosis, minimizing false positives (FP) and considerably enhancing overall Precision.

Table 5. Quantitative analysis of Rec

Number of MRI images	**Recall (%)**		
	Proposed DILMIE-boost	**PCA+ANN [1]**	**DPSM with weighted voting [2]**
3000	97.65	95.73	96.66
6000	97.69	95.23	96.75
9000	97.56	94.56	96.36
12000	98.05	94.89	96.23
15000	97.23	94.74	96.39
18000	97.63	94.58	96.48
21000	97.88	94.78	96.74
24000	97.36	94.33	96.33
27000	97.74	94.15	96.85
30000	97.23	94.61	96.12

Table 5 presents a graphical comparison of recall performance in identification across different dataset sizes, ranging from 150 to 1500 images. DILMIE-boost is evaluated against [1] and [2]. The DILMIE-boost method consistently delivers maximum recall. For example, with 3000 images, DILMIE-boost achieved a recall of 97.65%, compared to 95.73% for [1] and 96.66% for [2]. The DILMIE-boost technique shows a recall enhancement of 3% and 1% over [1] and [2], respectively. This improved result is mainly due to the amalgamation of an ensemble learning classifier through a weight emphasis function. This permutation effectively reduces false negatives (FN) and improves true positives (TP) by enhancing accuracy through feature analysis. As a result, the overall recall capability of DILMIE-boost is considerably improved.

Table 6. Quantitative study of F1 score

Number of MRI images	**F1 score (%)**		
	Proposed DILMIE-boost	**PCA+ANN [1]**	**DPSM with weighted voting [2]**
3000	97.19	93.94	95.30
6000	97.12	93.70	95.27

9000	97.01	93.33	95
12000	97.46	93.46	95.04
15000	96.63	93.51	95.05
18000	97.04	93.50	95.04
21000	97.41	93.61	95.15
24000	96.78	93.50	95.03
27000	96.88	93.10	94.94
30000	96.67	93.47	94.87

Table 6 illustrates the F1-score evaluation across different images, comparing the results of the DILMIE-boost technique with existing PCA+ANN [1] and DPSM with weighted voting [2]. The F1-score, which balances precision and recall, serves as a key indicator of each technique's overall efficiency in disease analysis. Outcomes show DILMIE-boost consistently attains superior F1-scores compared to the other two DL techniques. This enhancement emphasizes DILMIE-boost's ability to improve both precision and recall concurrently. Higher results are mainly attained because of the incorporation of an ensemble classifier, which improves the accuracy of disease analysis. On average, across ten experimental runs, the DILMIE-boost technique shows a 4% increase in F1-score compared to [1] and 2% compared to [2], highlighting its efficiency in Alzheimer's disease diagnosis.

Table 7. Quantitative analysis of pre-processing time

Number of MRI images	**Pre-processing time (ms)**		
	Proposed DILMIE-boost	**PCA+ANN [1]**	**DPSM with weighted voting [2]**
3000	60	68	64
6000	67.8	73.4	69.4
9000	69.4	75.7	73.2
12000	71.6	79.8	75.7
15000	75.3	83.4	78.5
18000	79.7	87.2	81.3
21000	83.2	90.3	85.6
24000	88.3	95.7	90.9
27000	91	115.4	100.8
30000	97.5	118.7	110.3

Table 7 above illustrates the pre-processing time of the DILMIE-boost method and the existing methods [1] and [2] for different numbers of MRI images. The pre-processing time gradually increases for all methods as the number of MRI images increases, due to larger datasets requiring more image enhancement, normalization, and noise removal operations. The DILMIE-boost method consistently requires less pre-processing time than the existing methods. For 3,000 MRI images, the proposed method completes the pre-processing stage in 60 ms, whereas PCA+ANN and DPSM with weighted voting require 68 ms and 64 ms, respectively. Similarly, for 30,000 MRI images, the proposed method records a pre-processing time of 97.5 ms, which is lower than 118.7 ms for PCA+ANN and 110.3 ms for DPSM with weighted voting. These results show that the proposed method performs the pre-processing stage more efficiently while maintaining stable performance as the dataset size increases.

Table 8. Quantitative analysis of segmentation time

Number of MRI images	**Segmentation time (ms)**		
	Proposed DILMIE-boost	**PCA+ANN [1]**	**DPSM with weighted voting [2]**
3000	62	70	68
6000	69.2	75.5	72.5
9000	71.5	79.3	75.4
12000	73.8	81.4	79.6

15000	78.6	85.4	81.4
18000	82.6	91.2	84.5
21000	85.7	95.4	87.2
24000	90.2	99.8	91.3
27000	93.4	111.3	92.4
30000	100.3	120.4	110.5

Table 8 describes the segmentation time of the DILMIE-boost method and different existing methods for varying numbers of MRI images. The segmentation time increases as the number of MRI images increases for all methods. The proposed DILMIE-boost method takes 62 ms for 3,000 MRI images, whereas PCA+ANN and DPSM with weighted voting take 70 ms and 68 ms, respectively. Similarly, for 30,000 MRI images, the proposed method records 100.3 ms, while PCA+ANN and DPSM with weighted voting require 120.4 ms and 110.5 ms, respectively.

Table 9. Quantitative analysis of classification time

Number of MRI images	**Classification time (ms)**		
	Proposed DILMIE-boost	**PCA+ANN [1]**	**DPSM with weighted voting [2]**
3000	64.5	73	70
6000	71	78.2	74.3
9000	73.2	81.4	79.5
12000	75.9	85.6	82.4
15000	82.3	89.3	85
18000	84.6	94.5	90
21000	88.4	98.6	91
24000	91.7	103.4	95.6
27000	95.3	110.8	99.4
30000	101.9	115.7	110.3

Table 9 shows the classification time of the proposed DILMIE-boost method and existing methods for varying numbers of MRI images. The classification time increases gradually with the number of MRI images for all methods. The proposed DILMIE-boost method takes 64.5 ms for 3,000 MRI images, while PCA+ANN and DPSM with weighted voting take 73 ms and 70 ms, respectively. For 30,000 MRI images, the proposed method records 101.9 ms, whereas PCA+ANN and DPSM with weighted voting require 115.7 ms and 110.3 ms, respectively. These results demonstrate that the proposed DILMIE-boost method requires less classification time than the existing methods. Therefore, the proposed method classifies MRI images more efficiently and provides a faster diagnosis of Alzheimer's disease.

Table 10. Quantitative analysis of *ET*

Number of MRI images	***ET* (ms)**		
	Proposed DILMIE-boost	**PCA+ANN [1]**	**DPSM with weighted voting [2]**
3000	66	75	72
6000	72.5	80.5	77.6
9000	75.8	85.7	80.3
12000	78.6	90.2	84.3
15000	82.5	93.8	86.9
18000	86.9	96.7	90.4
21000	90.2	103.6	95.8
24000	93.6	110.8	103.6
27000	97.5	117.6	109.6
30000	106.8	121.7	116.7

DILMIE-boost technique consistently demonstrates faster disease diagnosis compared to the other two approaches. For example, with 3000 images, the DILMIE-boost technique

recorded a disease diagnosis time of 66 ms, while [1] and [2] recorded 75 ms and 72 ms, respectively. Finally, across ten trials, the DILMIE-boost technique achieved a time reduction of about 13% and 7% compared to [1] and [2]. This enhancement in speed is primarily due to the segmentation and feature extraction. In DILMIE-boost, the Piecewise Linear Mumford–Shah functional method is utilized to segregate the ROI area. Afterward, dissimilar aspects, namely texture, color, and shape, are effectively extracted. This updated procedure minimizes computational demands, resulting in earlier and more precise disease analysis.

Table 11. Quantitative analysis of C_{com}

Number of MRI images	C_{com}(MB)		
	DILMIE-boost	PCA+ANN [1]	DPSM with weighted voting [2]
3000	45	66	75
6000	51.2	70.2	80.4
9000	63.9	75.4	83.7
12000	71.7	71.5	88.7
15000	75.6	80.3	97.3
18000	79.8	85.9	103.4
21000	83.2	93.4	108.7
24000	88.5	98.7	115.8
27000	91.7	102.8	120.3
30000	99.6	110.6	131.4

DILMIE-boost technique consistently demonstrates faster disease diagnosis compared to the other two approaches. For instance, with 3000 images, DILMIE-boost recorded a diagnosis time of 66ms, whereas [1] and [2] recorded 66ms and 75ms, respectively. Across ten trials, the DILMIE-boost technique achieved a time reduction of approximately 12% and 26% compared to [1] and [2]. This enhancement in speed is primarily attributed to its efficient pre-processing, segmentation, and classification stages. In DILMIE-boost, a Margin-Infused Emphasis Boost classifier is used to classify MRI images into multiple classes for disease diagnosis. Each weak learner processes the feature set once, contributing to its computational efficiency. Since the number of boosting iterations is fixed, the classification stage also exhibits near-linear computational growth.

Table 12. Quantitative study of specificity

Number of MRI images	Specificity (%)		
	DILMIE-boost	PCA+ANN [1]	DPSM with weighted voting [2]
3000	97.9	94.8	94
6000	97.2	94.2	92.5
9000	96.8	93.2	91.1
12000	96.5	92.2	90.6
15000	95.8	92.8	90.8
18000	96.3	93.2	91.1
21000	96.7	93.3	91.3
24000	97.5	94.3	92.4
27000	96.3	93.8	91.6
30000	96	93.3	91.1

The outcome of the DILMIE-boost technique with 3000 images taken showed, the specificity was found to be 97.9, 94.8, and 94 by existing PCA+ANN [1], and DPSM with weighted voting [2] respectively. As a result, the NRGOCDBN of precision was enhanced up to 3%, and 6%, over [1], and [2].

5.1 ROC and AUC Performance Analysis

The ROC (Receiver Operating Characteristic) curve and AUC (Area under the Curve) are commonly used to evaluate the performance of binary classification models. The ROC curve is a graphical representation of the true positive rate (TPR) against the false positive rate (FPR). Therefore, the ROC curve is plotted with TPR on the y-axis and FPR on the x-axis.

Table 13. ROC results

False positive rate	True positive rate		
	DILMIE-boost	PCA+ANN [1]	DPSM with weighted voting [2]
0	0	0	0
0.1	0.28	0.2	0.18
0.2	0.55	0.38	0.29
0.3	0.64	0.56	0.47
0.4	0.73	0.67	0.59
0.5	0.82	0.71	0.63
0.6	0.88	0.75	0.7
0.7	0.91	0.83	0.79
0.8	0.93	0.9	0.85
0.9	0.94	0.92	0.9
1	0.96	0.93	0.91

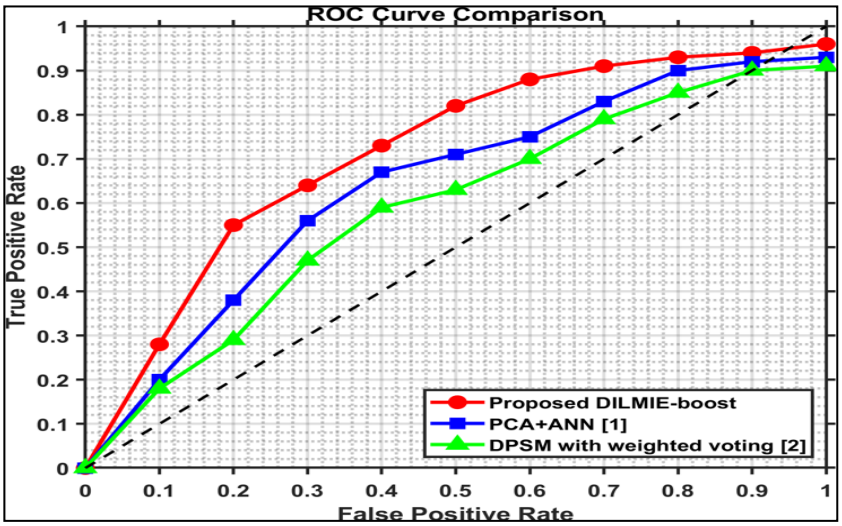


Figure 4. Graphical designs of ROC results

Figure 4 denotes the AUC graph for proposed and existing methods. From the results, AUC values are 0.96 using the DILMIE-boost technique, 0.93 using PCA+ANN [1], and 0.91 using DPSM with weighted voting [2]. The proposed DILMIE-boost technique provides a higher AUC for the best classifier performance.

5.2 Confusion Matrix for Colorectal Cancer

To compute the performance of the DILMIE-boost technique, the confusion matrix is a statistical method for classification. It depends on true positives (TP), false positives (FP), true negatives (TN), and false negatives (FN).

	Total number of sample images 3000	Actual value		
		Positive	Negative	
Predicted value	Positive	TP=2750	FP=150	2900
	Negative	FN=40	TN=60	100
	Total	2790	210	

Figure 5. Confusion matrix for DILMIE-boost technique

In Figure 5, the confusion matrix for the proposed DILMIE-boost technique is demonstrated. From this figure, 3000 data samples are considered. The DILMIE-boost technique properly classified 2750 TP, 80 TN, 150 FP, and 40 FN samples.

6. Implementation and Results Analysis

The qualitative analysis of the proposed DILMIE-boost technique and its effectiveness in Alzheimer's disease diagnosis is discussed in this section. First, a number of multiclass input MRI images are gathered from the database at the acquisition stage. The multi-image acquisitions from the database are illustrated in Figure 6.

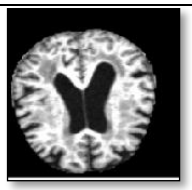
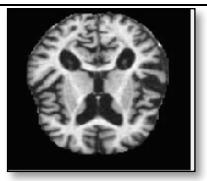
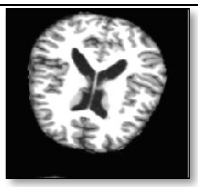
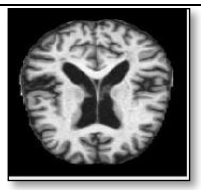
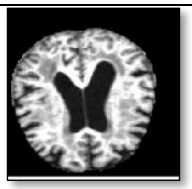
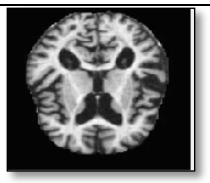
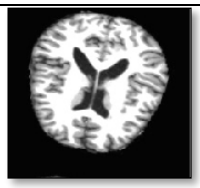
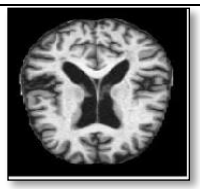
Mild	Moderate	non-demented	very mild demented
			

Figure 6. Multi image acquisitions from database

	Mild	Moderate	Non-demented	Very mild demented
Original images				

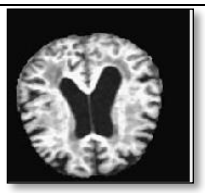
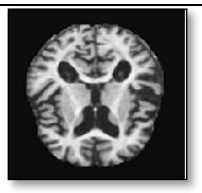
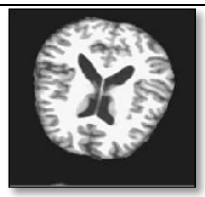
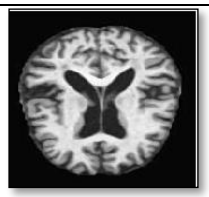
Preprocessed images				

Figure 7. Image preprocessing

After collecting the MRI brain images from the dataset, a Discrete Laplacian Filter is employed for image contrast enhancement by reducing noise while preserving important structures Figure 7 represents image preprocessing.

After preprocessing, segmentation is carried out using the Fuzzy Piecewise Linear Mumford–Shah functional method to analyze and differentiate visual patterns in images for disease diagnosis. Figure 8 shows the image segmentation process, which is described as follows:

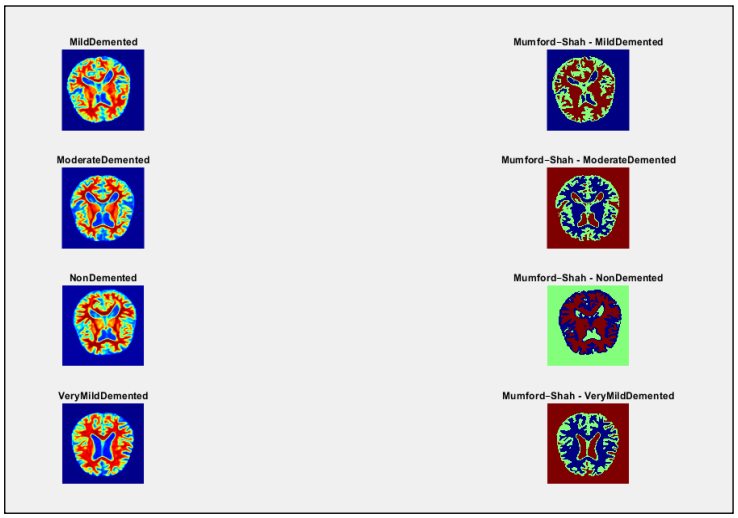


Figure 8. Image segmentation

Followed by, feature extraction is carried out in the image analysis, aimed at identifying and isolating relevant information from segmented ROI to improve the performance of classification. From Figures 9, 10, and 11, the feature extraction by Mild Demented is listed as,

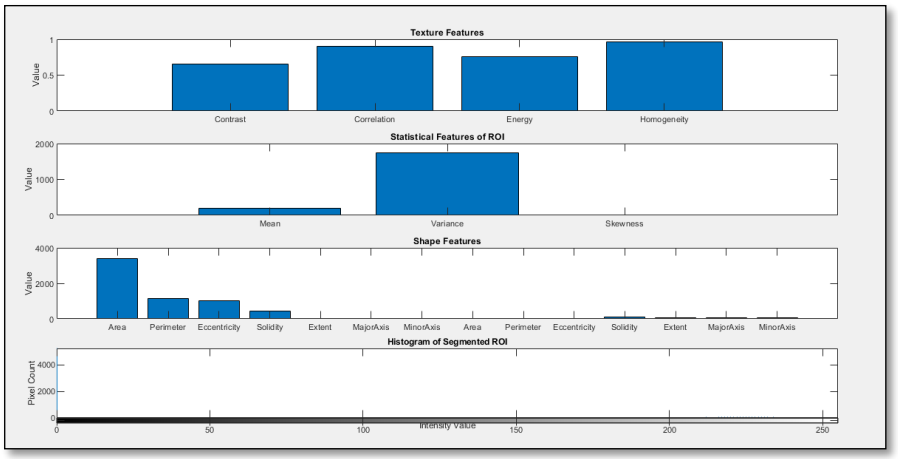


Figure 9. Feature extraction by mild demented

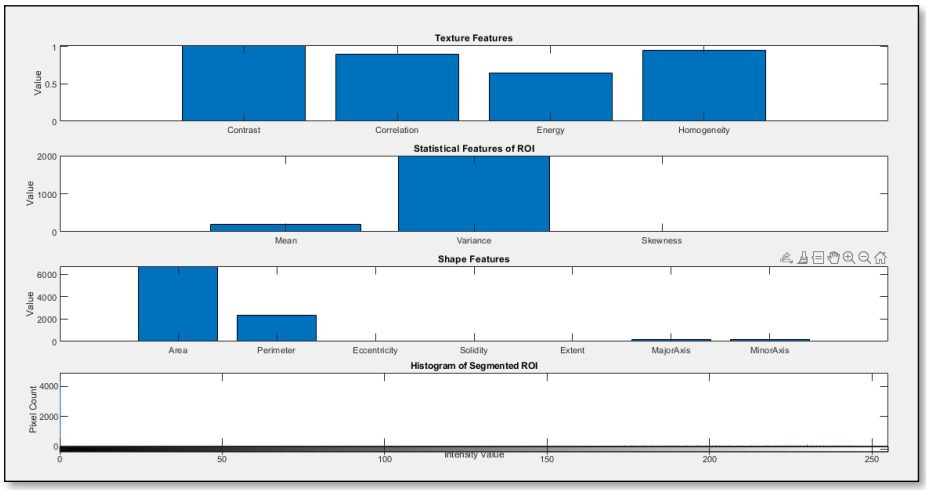


Figure 10. Feature extraction by moderate demented

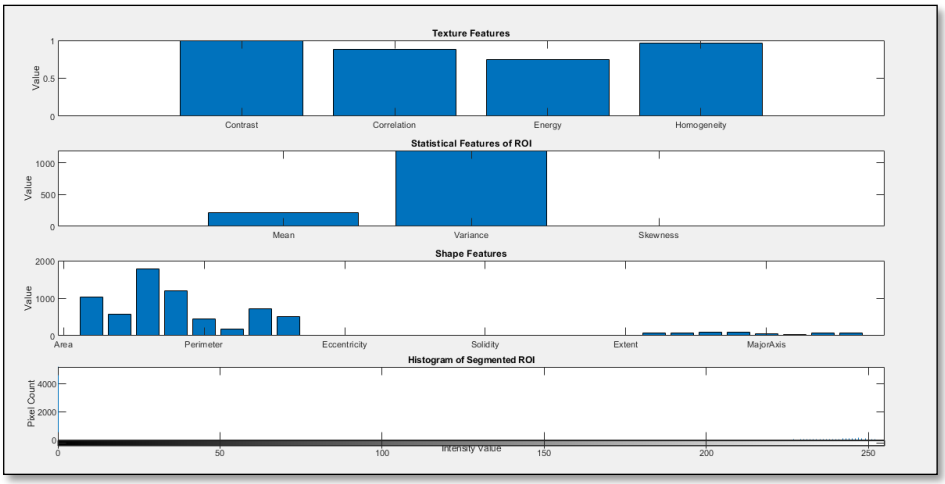


Figure 11. Feature extraction by non-demented

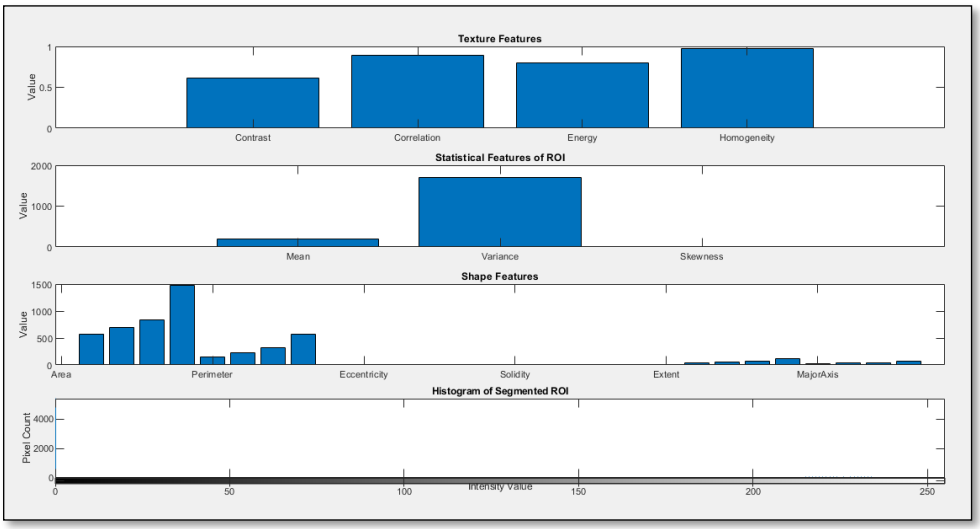


Figure 12. Feature extraction using very mild demented

Finally, the classification-based Alzheimer's disease detection involves dividing an image into four classes using Margin-Infused Emphasis Boost classifier, allowing for more

precise identification. Figure 13, illustrates the classification using Alzheimer's disease detection as follows,

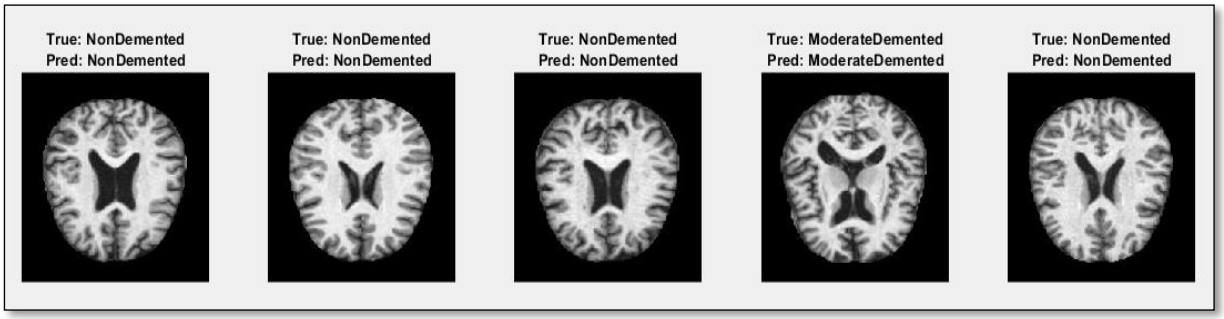


Figure 13. Classification based Alzheimer's disease detection

This study compares the proposed DILMIE-boost technique with the existing PCA+ANN [1] and DPSM with weighted voting [2] using an Augmented Alzheimer MRI Dataset. The comparison is based on different parameters, namely accuracy, precision, recall, F1-score, and disease diagnosing time. In this approach, brain MRI images are collected from the dataset in the acquisition phase. This is followed by Discrete Laplacian Filter Pre-processing, designed to eliminate noisy pixels from the input MRI images. The Discrete Laplacian operator is a finite-dimensional graph used for increasing image quality. Next, segmentation using the Piecewise Linear Mumford–Shah functional algorithm is carried out to partition the improved image into several sub-divisions. For every segmented region, RoI features are extracted for efficient classification to perform disease diagnosis. With the extracted features, the Margin-Infused Emphasis Boost classifier utilizes margin-infused relaxed classification as a weak learner to classify the MRI images into multiple classes for performing disease diagnosis. In this way, Alzheimer's disease diagnosis is carried out with MRI images. The results of the quantitative analysis described that the DILMIE-boost technique offers improved accuracy in disease prediction with reduced time when compared to existing approaches.The results confirm that the proposed DILMIE-boost technique improves PSNR by 10%, accuracy by 4%, recall by 3%, and F1-score by 3%, with a 12% reduction in disease diagnosis time, when compared to different existing PCA+ANN [1] and DPSM with weighted voting [2] methods.

7. Conclusion

The DILMIE-boost technique shows significant potential for AD diagnosis, thus supporting more dependable and complete analysis necessary for early recognition and intervention. However, conventional ML methods for disease diagnosis are more vulnerable to error. DILMIE-boost provides a dependable method for early recognition and analysis of AD and timely intervention for patients. DILMIE-boost begins with image pre-processing to improve contrast, which leads to a decrease in MSE and an improvement in PSNR. Fuzzy-based image segmentation is used to recognize ROIs and extract more pertinent aspects for the detection of AD. This procedure minimizes disease diagnosis time. Classification is carried out to categorize different phases of AD. Comprehensive result assessment is performed with different parameters across multiple images. Outcomes of the quantitative study show the DILMIE-boost method is better than existing techniques by attaining superior PSNR, enhanced accuracy, precision, and recall scores, and earlier DDT.

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