

Original Article

Ensemble Neuro Evolution of Augmenting Topologies Using Fused Features for Alzheimer's Disease Diagnosis System

S.Chithra¹, R.Vijayabhanu²

^{1,2}Department of Computer Science, Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore, Tamil Nadu, India.

¹Corresponding Author : chithra.kdc@gmail.com

Received: 03 August 2023

Revised: 05 September 2023

Accepted: 04 October 2023

Published: 31 October 2023

Abstract - Alzheimer's Disease (AD) is a neurological condition that makes it difficult for a person to carry out the activities required of them daily. Because of the rapid advancement of Alzheimer's patients and the lack of exact diagnostic techniques, early detection and classification of AD are essential research areas. One of the many researchers' goals is to identify Alzheimer's disease soon and correctly so it can be halted or delayed. Using a wide range of machine-learning algorithms, this study aims to compare the contemporary techniques for diagnosing and categorizing Alzheimer's disease at the early stage. The proposed method effectively compares using the ADNI, which stands for the dataset, which is available to the public. Similarly, it reveals that the multi-feature combination methodology outperforms the single-feature extraction method. This paper proposes an AD diagnosis system that uses ML algorithms such as Support Vector Machine (SVM), Decision Tree (DT), K-Nearest Neighbour (KNN), Neuro Evolution of Augmenting Topologies (NEAT), and Bagging-NEAT (proposed) to diagnose AD in patients accurately. According to the study's findings, the Bagging Neat can efficiently classify the stages of Alzheimer's disease with an accuracy of 95.8% on the test dataset.

Keywords - Alzheimer's Disease, Features extraction, NEAT, Ensemble, Bagging, MR images.

1. Introduction

A typical neurodegenerative brain illness affecting the elderly, AD, has just come to light. The number of people with dementia worldwide is estimated to be 44 million. According to Alzheimer's Disease International, such numbers will rise to 76 million and 135 million by 2030 and 2050. AD is categorized by a slow start and decline of episodic memory, affecting 50% to 75% [1] of these individuals.

The condition known as Moderate Cognitive Impairment (MCI) causes a person's mental ability to gradually deteriorate the risk of developing AD is higher in people with MCI than in the general population. There is no known cure for Alzheimer's disease at this time; however, there are drugs that can assist in delaying the advancement of the illness and minimize the emotional impact it has on individuals. The inability to remember things is one of these indicators [2].

As a result, it's critical to make an early and correct diagnosis of MCI or AD patients. A feature extraction and machine learning classification method for brain disease

diagnosis using neuroimages is being developed. According to studies, structural MRI is the imaging technique used in clinical settings with the highest degree of standardization. It is also beneficial for monitoring the various clinical stages of AD [3]. As a result, structural MR images are used to evaluate our technique.

Grey matter densities, group comparisons of cortical thickness, morphometry, and texture measurements can all be obtained from structural MRI of the complete brain [4]. Compared to techniques that use only one type of feature, combining various feature types can increase the accuracy of the AD diagnosis. This article suggests a new classification scheme for precisely identifying people with multiple stages of AD. We first combine several types of features to extract the more discriminative features.

To be more precise, grey-level analysis and texture analysis may be used to get object information from the brain. By combining these two types of characteristics, performance can be improved. In addition, we use the bagging-based NEAT technique to locate the reliable feature subset and implement it to avoid the overfitting issue associated with feature fusion.



Moreover, the system aims to minimize false positives and negatives in the diagnosis. False positives can lead to unnecessary anxiety and stress for the patient, while false negatives can delay treatment and lead to worse outcomes. The system should be scalable and handle enormous datasets to ensure diagnosis accuracy and reliability.

Bagging NEAT in the Alzheimer's disease diagnosis system improves accuracy and speed, improving patient outcomes. The Alzheimer's disease diagnosis system uses bagging-NEAT to improve the neural network architecture used to diagnose Alzheimer's disease and Moderate Cognitive Impairment (MCI) using medical records. Our method beats comparison methods on the ADNI database.

The proposed technique for diagnosing AD without intrusive procedures employs MRI scans. Efficiency and accuracy both increase with the use of automation. This strategy has the potential to be implemented in clinical settings for prompt intervention and better results. The overall non-invasive, accurate, automated, and accurate detection technique provided by the AD phase diagnosis system employing image classification and ML algorithms is a significant advancement in the field.

The paper's remaining sections are organized: Section 2 reviews AD diagnosis research. Methodology follows. Section 4 describes ML models and experimental setups. The outcomes of the experiments are discussed in Section 5. The conclusion of section 6 includes some recommendations for further study in this field.

2. Literature Survey

Alzheimer's Disease (AD) causes dementia in adults over 65. Every year, more people develop Alzheimer's disease worldwide. Understanding dementia, which is a syndrome, is essential. Alzheimer's disease is responsible for losing long-term declarative memory since it kills brain cells and memories. Appropriate treatment requires an early diagnosis [5]. Therefore, the most significant studies in this area will be presented in this section.

M. Bachute et al. (2021) investigated the hippocampus region using MRI images from 114 healthy people and 127 senior Alzheimer's disease patients. They disassembled the hippocampus and uploaded the resulting dataset to brain suite. The researchers extracted characteristics using texture features, correlation, and decision trees, demonstrating that texture analysis could aid in detecting essential pathogenic alterations in AD and aiding in diagnosis. [6]. Kim et al. (2020) developed a method to predict the start of Alzheimer's disease that is based on machine learning. Researchers could accurately forecast the onset of Alzheimer's disease with an accuracy of 71% by employing

machine learning approaches such as random forest and logistic regression [7].

In their study, Subramanian et al. (2022) advocated using machine learning as an early diagnostic tool for Alzheimer's disease. Using decision trees, k-nearest neighbours, and logistic regression [8], the condition was located with an accuracy of 79%. Subasi et al. explored PET, MRI, and CT-based AD detection approaches, finding MRI the most effective. RBF, ANN, SVM, and PNN were used for classification but had drawbacks like accuracy and instability [9].

Arjaria S.K. et al. (2022) investigated the KNN algorithm on the OASIS dataset to classify the stages of Alzheimer's disease. This work may have limited availability of labelled data and differences in data distribution that affect algorithm performance [10]. Uddin et al. (2023) suggested a voting classifier system to diagnose Alzheimer's disease using the OASIS dataset. The interpretability of the ML model and its ability to handle unbalanced input might be challenging [11].

These limitations include the necessity for hyperparameter optimization, potential limits in collecting complex patterns from 3D brain MR images, overfitting challenges, the impact of inadequate labelled data, and the interpretability and handling of unbalanced data in the ML model. Understanding these limits is critical for future advances in Alzheimer's disease prediction and categorization.

Our proposed model, ensemble neuro evolution of augmenting topologies using fused features, leverages GLCM (Gray-Level Co-occurrence Matrix), GLDM (Gray-Level Dependence Matrix), and GLRM (Gray-Level Run-Length Matrix) features in addition to other relevant features.

By incorporating these advanced texture analysis techniques, our model can effectively extract and utilize information from brain MR images. This allows for a more comprehensive characterization of structural changes associated with Alzheimer's disease.

This integration of GLCM, GLDM, and GLRM features enhances the model's ability to capture intricate patterns and spatial relationships, addressing the limitation of first-order statistical features and improving classification performance.

By applying our proposed model with these advanced features, we aim to achieve more accurate and reliable Alzheimer's disease prediction, contributing to the advancement of early diagnosis and intervention strategies in neurodegenerative disorders.

3. Method to Diagnose AD Stages

The most well-known degenerative illness, AD, develops gradually and kills brain cells. One of the significant causes of dementia, it undermines the patient's ability to operate independently by causing a steady decline in behavioural, social, and cognitive capacities. Compared to conventional ML techniques, the performance of ML models has been good, and they don't need any manually constructed feature extraction.

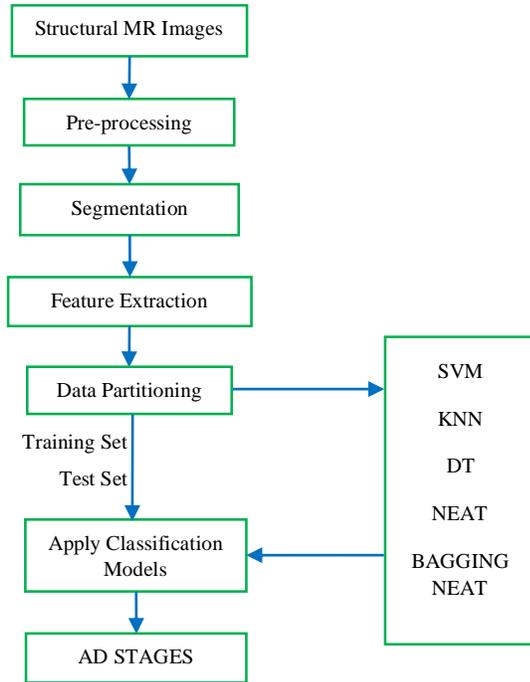


Fig. 1 AD phases classification framework schematic

Recent advances and emerging tendencies in AD identification using machine learning were explored in this paper, with a particular emphasis on AD detection using NEAT. The diagram in Figure 1 illustrates the general layout of a computer-assisted Alzheimer's disease phase diagnosis system based on neuroimaging data.

3.1. Image Preprocessing

The required morphological operations were completed to do the picture preprocessing. The three procedures involved in preprocessing structural MR images are non-uniformity correction, noise filtering, and intensity correction. The skull is removed once these three steps have been completed.

It is the method of eliminating non-cerebral matters from MR brain imaging, like the skull and eye. Based on mathematical morphology, a technique for automatically stripping skulls was developed. A two-stage adaptive denoising algorithm is created in this work. In the first stage, the noise is detected using an adaptive method. Next, the input image is denoised using this and the Hampel filter.

3.2. Segmentation

Segmentation is a crucial task since it affects the outcome of the entire study. The segmentation approach separates the non-brain tissues after the spatial normalization step. In this study, the central slice of the brain in MRI is segmented using the segmentation approach and the proposed morphological operations for skull stripping. Skull stripping is critical in brain imaging processing, improving diagnostic accuracy and speed in medical applications. It removes non-brain tissues, improving segmentation accuracy and lowering brain tissue misclassification [12].

The innovative method was assessed using T1-weighted Magnetic Resonance Imaging (MRI) brain images from the Alzheimer's disease dataset. The visual impression of the skull-bared brain is evidence of the recommended procedure's efficacy. Automated methods for MR image segmentation have been widely employed to assist doctors with qualitative diagnosis.

This is because several processing steps, such as feature extraction and AD stage classification, rely on correctly segmenting anatomical regions. In this study, a TDWT-Fuzzy set theory-based segmentation method for AD-MR images was developed. The suggested segmentation result can be used immediately for a different feature extraction process.

3.3. Feature Extraction

Feature extraction is the process of evaluating image texture to understand better the characteristics that determine the shape and texture of objects. Alzheimer's disease first affects the hippocampus, divided into the head and body. The cortex's grey matter connects the brain's higher order, which governs muscle control, speech, memory, emotions, self-regulation, decision-making, and sensory perception. AD Motor function is slowed by white matter [13].

As employed in this research, the multi-feature combination methodology involves integrating multiple texture feature extraction methods to enhance the characterization of brain images in the context of Alzheimer's disease classification. Specifically, three distinct methods are utilized:

- **Gray-Level Co-occurrence Matrix (GLCM):** This technique computes statistical characteristics based on the spatial connection between the intensities of individual pixels in the image. The results of these calculations provide information about the patterns and structures of texture.
- **Gray-Level Run Length Matrix (GLRLM):** To achieve this, it pulls out run length features, which keep track of how long sequences of pixels with the same intensity value are. These details reveal information about the texture's consistency.

- **Gray-Level Dependence Matrix (GLDM):** It does this by extracting run length features, which capture the lengths of consecutive pixels with the same intensity value. These features provide insights into the continuity of the texture.

Combining these different texture feature extraction methods, this research aims to exploit complementary information from the brain images, capturing various texture and pattern variations that may indicate Alzheimer’s disease. The multi-feature combination allows for a more thorough representation of the visual information, potentially leading to enhanced classification accuracy and better detection of Alzheimer’s disease-related patterns.

4. ML Algorithms for Classification

In this study, the stages of AD are classified using the ADNI dataset using a variety of machine learning algorithms, including K-NN, Decision Trees (DT), Neat, and Bagging Neat.

4.1. Support Vector Machine (SVM)

SVMs can be linear or nonlinear, depending on whether they are used for a binary classification task. SVM can determine the best surface for discriminating between positive and negative training feature samples. Since datasets are often not linearly separable, this minimizes the experimental danger (the total errors in the training and test sets).

SVM accomplishes this by investigating the link between the two datasets. Hyper-planes can describe decision boundaries in high-dimensional feature spaces. This hyperplane classifies vectorized data into two classes for decision-making [14].

4.2. K-Nearest Neighbour (KNN)

This method yields comparable results for comparable training samples. The closest input population value is used to classify all models [15-17]. The K-NN categorization algorithm places objects into groups according to the dominating classes shared by their K nearest neighbours. If K is a positive integer, that’s how many of your neighbours will be reflected in the count.

4.3. Decision Tree (DT)

Quinlan’s DT classifier is one of the most well-known ML techniques. A “DT” is created with leaf and “decision nodes.” Each decision node has several branches containing the test “X” results and related to a test “X” over a particular input data element. Each leaf node represents a group affected by a case’s judgment. A “DT” is created by a split procedure, defeating the goal [18].

The algorithm begins the entire categorization process at the tree’s root node. The feature that divides the feature

space most effectively is the root. To categorize testing (unknown) data, the classes are determined based on the weights computed on the features during the learning phase.

4.4. Neuro Evolution of Augmenting Topologies (NEAT)

NEAT initialization requires a fitness function and user-defined hyperparameters. NEAT hyper-parameters control genome crossover and mutation. Using scheduling decisions, the fitness function evaluates genomic solutions when the population is first initialized in NEAT; only genomes with input and output layers are generated.

Synaptic weights and biases are examples of what might vary during the initial construction of a genome rather than network topologies. NEAT iterations may employ different NNs. Random structures classify NNs. Each generation has subpopulations with comparable node connections. Class genome sizes vary. Each class learns NN weights proportionally to its physical fitness. NN weights are learned without backpropagation [19].

4.5. Proposed Method

In recent years, the subfield of machine learning known as “ensemble learning” has become increasingly popular as a subject of study. Many distinct strategies for training accurate yet heterogeneous component classifiers have been developed to improve the generalization performance of ensemble learning. Three unique categories, each influenced by the approach to classifier training, can be made out of the standard ensemble techniques [20].

This work presents a new ensemble bagging method that we refer to as bagging NEAT. An ensemble classifier’s primary objective is to simultaneously encourage diverse viewpoints and individual precision. Following is a description of each stage of the ensemble bagging algorithm [21].

Algorithm 1: Ensemble Bagging

Input: Training Set $S = \{(x, y)\}; j=1, 2, \dots, m$
 Learning rate L
 Number of ML Classifiers T
 for $I=1, 2, \dots, T$
 Extract n -th sample from S
 Lear L from $S_k: N=L(S_k)$
 Merging classifier $N(x) = \arg \max_{y \neq x} \sum y \in x$
 end for
 Result: Ensemble $N(x)$

4.5.1. Methodology

The strengths of Neuro-Evolution of Augmenting Topologies (NEAT) and bagging can be coupled for improved classification performance in Alzheimer’s disease detection. The following procedures were employed in this work:

Algorithm 2: Bagging -NEAT Algorithm:

Data Preparation:

Input: Data (X) and Labels (Y)

NEAT Evolution:

Initialize NEAT parameters and population

Repeat until convergence criteria are met:

Generate new neural network topologies using NEAT

Evaluate the fitness of each network using the provided dataset.

Select parents and perform genetic operations (mutation, crossover) to create offspring

Replace the population with the offspring

Bootstrap Sampling:

Input: NEAT-evolved networks (NEAT_networks)

For each bootstrap iteration:

Create a bootstrap sample by randomly selecting data points with replacement

For each NEAT network in NEAT_networks:

Train the network on the bootstrap sample

Prediction and Aggregation:

Input: Test data (X_test)

For each NEAT network in NEAT_networks:

Obtain predictions for X_test using the trained network

Ensemble Combination:

Apply an aggregation technique (e.g., majority voting or averaging) to combine the predictions of NEAT networks

Evaluation and Performance Analysis:

Input: Combined predictions and accurate labels for test data (ensemble_predictions, Y_test)

Calculate evaluation measures using ensemble_predictions and Y_test

Output: Evaluation results

In this research, ML approaches for classifying Alzheimer's disease data are analyzed and compared. Classification involves training and assessment. The Bagging-NEAT (proposed) classifier achieves maximum classification accuracy from the results. The experimental findings show that the proposed classifier outperforms

competing classifiers in all classification instances. According to this research, the proposed classifier is the best approach for classifying Alzheimer's disease stages. Table 1 depicts the parameters for applied ML approaches considered for the distinct classification procedures.

5. Result and Discussion

The datasets included in this investigation originated from the ADNI database, which may be viewed at adni.loni.ucla.edu. Food and Drug Administration (FDA), National Institute on Aging (NIA), National Institute of Biomedical Imaging and Bioengineering (NIBIB), private pharmaceutical corporations, and non-profit groups came together in 2003 to form ADNI. The data set consists of 80 samples: 40 standard samples, 40 samples of MCI, and 20 samples of AD. These samples are all represented by T1-weighted MR images in the sagittal plane. There are 49 male samples and 51 female samples altogether. They are between 57 and 95, with 95 being the average age.

MATLAB provides many tools for implementing machine learning algorithms, including libraries for statistical analysis, data preprocessing, and model training and evaluation. Here, the MATLAB R2021b version is used to implement the algorithms. We utilized tools like image processing, statistics, and machine learning for AD stage detection using ML methods. The suggested approach combines bagging with NEAT for AD diagnosis, increasing classification accuracy and resilience. Extensive experiments show that the method is effective, outperforming separate classifiers and fixing their problems. Bagging and NEAT's argument for diagnosing and staging Alzheimer's disease early on is supported by the available data.

5.1. Performance Metrics and Evaluation

The suggested design used ML approaches to more accurately classify Alzheimer's disease. The dataset is split in two, with the more significant portion (80%) used for training and the smaller portion (20%) used for testing. Table 2 shows 3038 examination records are used for training, and 760 are used for testing. Accuracy, sensitivity, specificity, recall, and f1-score are just some of the metrics devised to gauge the efficacy of the proposed layout. Table 3 shows the mathematical method to determine the metrics needed to evaluate the proposed architecture.

Table 1. Parameters for applied ML techniques

Algorithms	Parameters
SVM [22]	Kernel type, C value, Gamma
DT [23]	Maximum depth, minimum samples for a split, minimum samples for a leaf, maximum features, split criterion
KNN [25]	K value, distance metric
NEAT [26]	Population size, mutation rate, crossover rate, compatibility threshold, speciation threshold, number of input and output nodes, activation functions, weight initialization, fitness function, and selection method.

Table 2. Quantity of images utilized for testing and training in total

S. No.	Total Number of Images	Training Set	Testing Set
1	3798	3038	760

Table 3. Formulas for figuring out efficiency ratings [18]

Sl. No.	Performance Metrics	Mathematical Expression
1	Accuracy	$\frac{TP+TN}{TP+TN+FP+FN}$ (1)
2	Sensitivity or Recall	$\frac{TP}{TP+FN}$ (2)
3	Specificity	$\frac{TN}{TN+FP}$ (3)
4	Precision	$\frac{TP}{TP+FP}$ (4)
5	F1-Score	$2X \frac{Precision*Recall}{Precision + Recall}$ (5)

Table 4. Stages prediction of AD with various ML algorithms

Algorithm Details	Performance Analysis with Accuracy			
	Normal	Stage 1	Stage 2	Stage 3
DT	1222	417	23	683
KNN	1273	404	0	723
SVM	1489	767	43	980
NEAT	1568	808	47	1088
Proposed	1616	866	65	1092

Table 5. Performance metrics with GLCM features - k=5 fold cross-validation

Algorithm	Accuracy	Sensitivity	Specificity	Precision	F1-Score
DT	61.7	61.5	54.8	71.4	57.6
KNN	63.2	58.3	45.1	75	63.2
SVM	86.3	85.4	93.5	88.1	85.5
NEAT	92.4	92.3	81	92.5	92.8
Proposed	94.8	95.3	97.5	94.6	94.6

Table 6. Performance metrics with GLCM features - k=10 fold cross-validation

Algorithm	Accuracy	Sensitivity	Specificity	Precision	F1-Score
DT	58.6	61.1	52.4	68	56.4
KNN	60.9	58.1	45.1	73	63.7
SVM	84.2	85.5	92.6	88	85.7
NEAT	89	92	79.2	92.4	92.2
Proposed	90.5	94.7	96.9	94	94.1

5.2. Results and Findings

In this section, we will talk about ways to improve the proposed design and the impact of several existing models (Table 4).

5.3. Performance Analysis with GLCM Features

The Table 5 & 6 represent the results of the k=5 fold and k=10-fold cross-validation procedures, with a focus on the GLCM (Grey Level Co-occurrence Matrix) features:

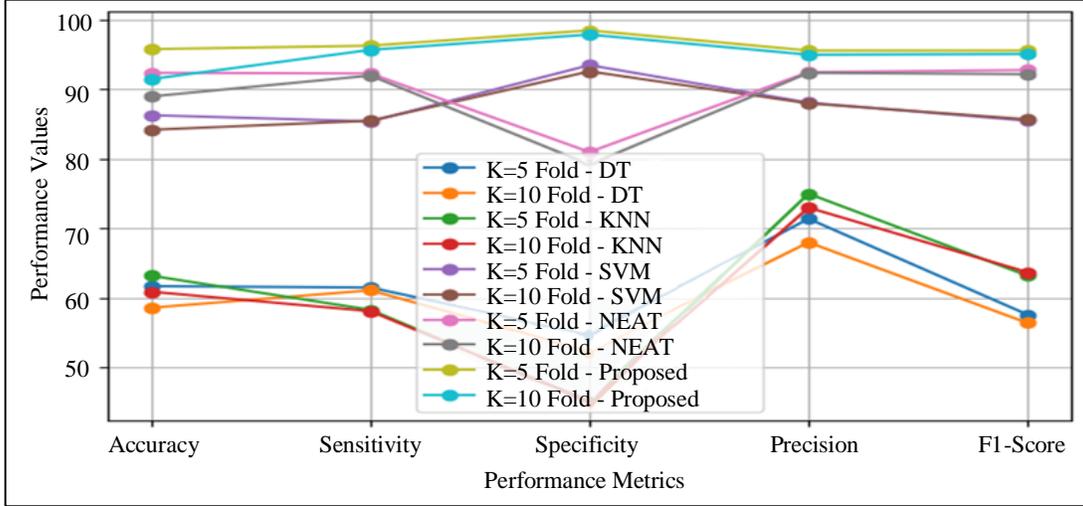


Fig. 2 Performance metrics with GLCM features - k=5 and k=10 fold cross-validation

Table 5 and Table 6 display the accuracy, sensitivity, specificity, precision, and F1-score values for k-fold cross-validation for the DT, KNN, SVM, NEAT, and proposed algorithms, respectively. The findings for a dataset split five ways are shown in the k=5 fold table, and for a dataset split ten ways are shown in the k=10 fold table.

According to the data in Tables 5 and 6, the “Proposed” method achieves the best results in terms of performance metrics. Therefore, for k=5 fold cross-validation, the “Proposed” approach outperforms the other assessed algorithms using GLCM features. When it comes to correctly

identifying instances using GLCM features, it achieves the best overall performance.

5.4. Performance Analysis with GLRLM Features

Tables 7 and 8 represent the performance metrics for five different evaluated using GLRLM features in both k=5 fold and k=10 fold cross-validation. Based on these values, the Proposed algorithm consistently performed better in k=5 fold cross-validation compared to k=10 fold cross-validation, showing higher values in all the performance metrics for k=5 fold. Therefore, the k=5 fold cross-validation appears to be the preferred choice for the proposed algorithm with GLRLM features.

Table 7. Performance metrics with GLRLM features - k=5 fold cross-validation

Algorithm	Accuracy	Sensitivity	Specificity	Precision	F1-Score
DT	89.3	88.1	90.5	87.2	87.9
KNN	87.2	84.5	88.3	85.8	86.2
SVM	90.1	89.6	91.8	89.9	89.8
NEAT	91.8	91.5	92.4	91.6	91.7
Proposed	91.1	90.9	91.3	90.5	91

Table 8. Performance metrics with GLRLM features - k=10 fold cross-validation

Algorithm	Accuracy	Sensitivity	Specificity	Precision	F1-Score
DT	88.4	87.2	89.1	86.3	86.8
KNN	85.9	83.2	87.1	84.5	84.8
SVM	89.2	88.6	90.3	88.9	88.7
NEAT	90.3	90	90.7	89.7	90.1
Proposed	89.7	89.5	89.9	88.9	89.3

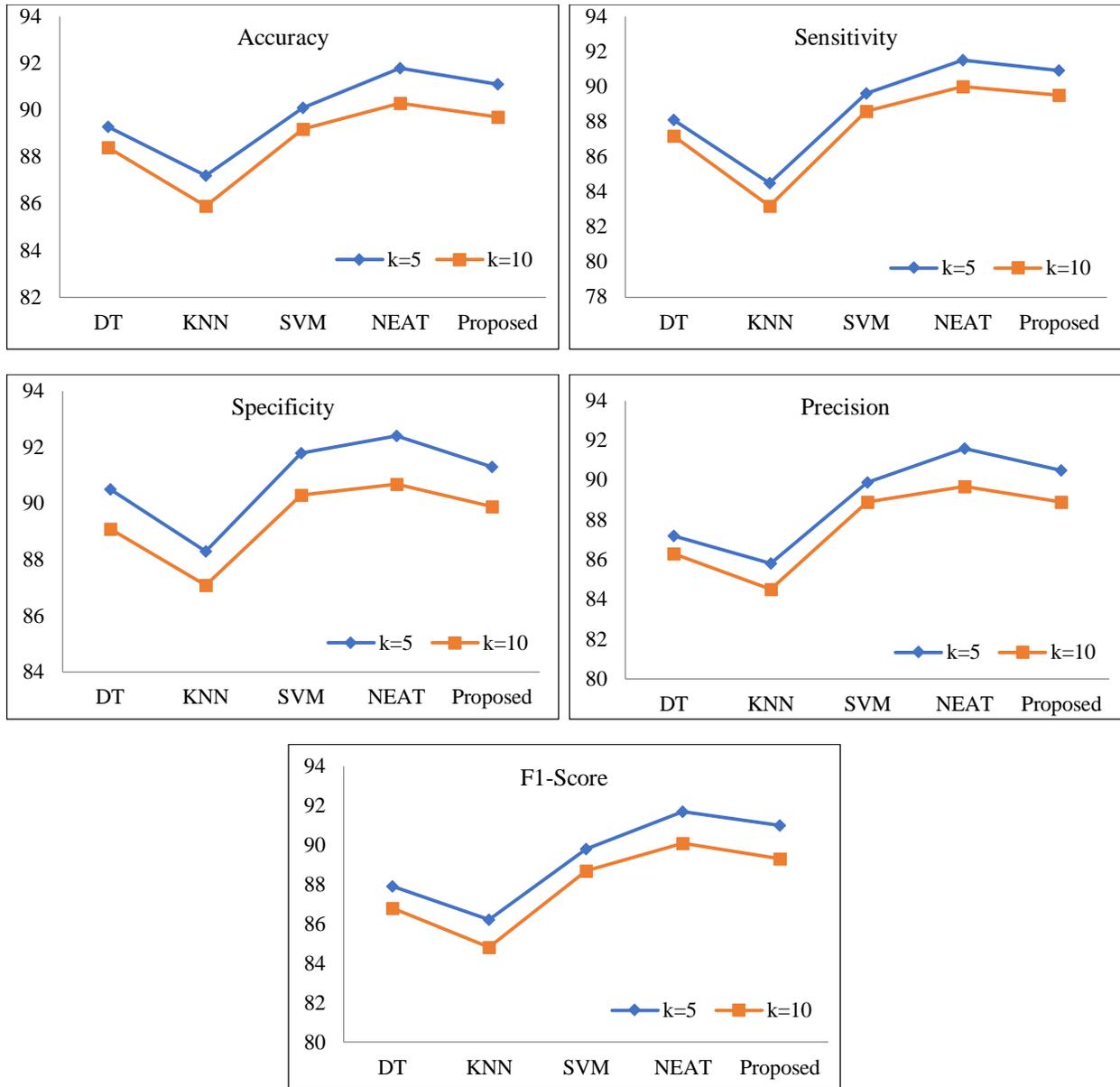


Fig. 3 Performance metrics with GLRLM features - k=5 and k=10 fold cross-validation

5.5. Performance Analysis with GLDM Features

Table 9. Performance metrics with GLDM features - k=5 fold cross-validation

Algorithm	Accuracy	Sensitivity	Specificity	Precision	F1-Score
DT	75.2	72.8	68.5	76.4	73.8
KNN	78.1	75.3	71.8	78.9	76.6
SVM	79.5	77.9	74.6	80.2	78.8
NEAT	76.7	73.9	69.4	77.2	74.5
Proposed	77.8	74.9	70.6	78.5	75.9

Table 10. Performance metrics with GLDM features - k=10 fold cross-validation

Algorithm	Accuracy	Sensitivity	Specificity	Precision	F1-Score
DT	72.5	69.8	66.1	73.1	70.3
KNN	75.3	72.6	68.8	75.9	73.2
SVM	76.4	74.2	70.8	77.2	74.7
NEAT	70.9	68.1	63.5	71.6	68.7
Proposed	74.1	71.3	67.5	74.6	71.9

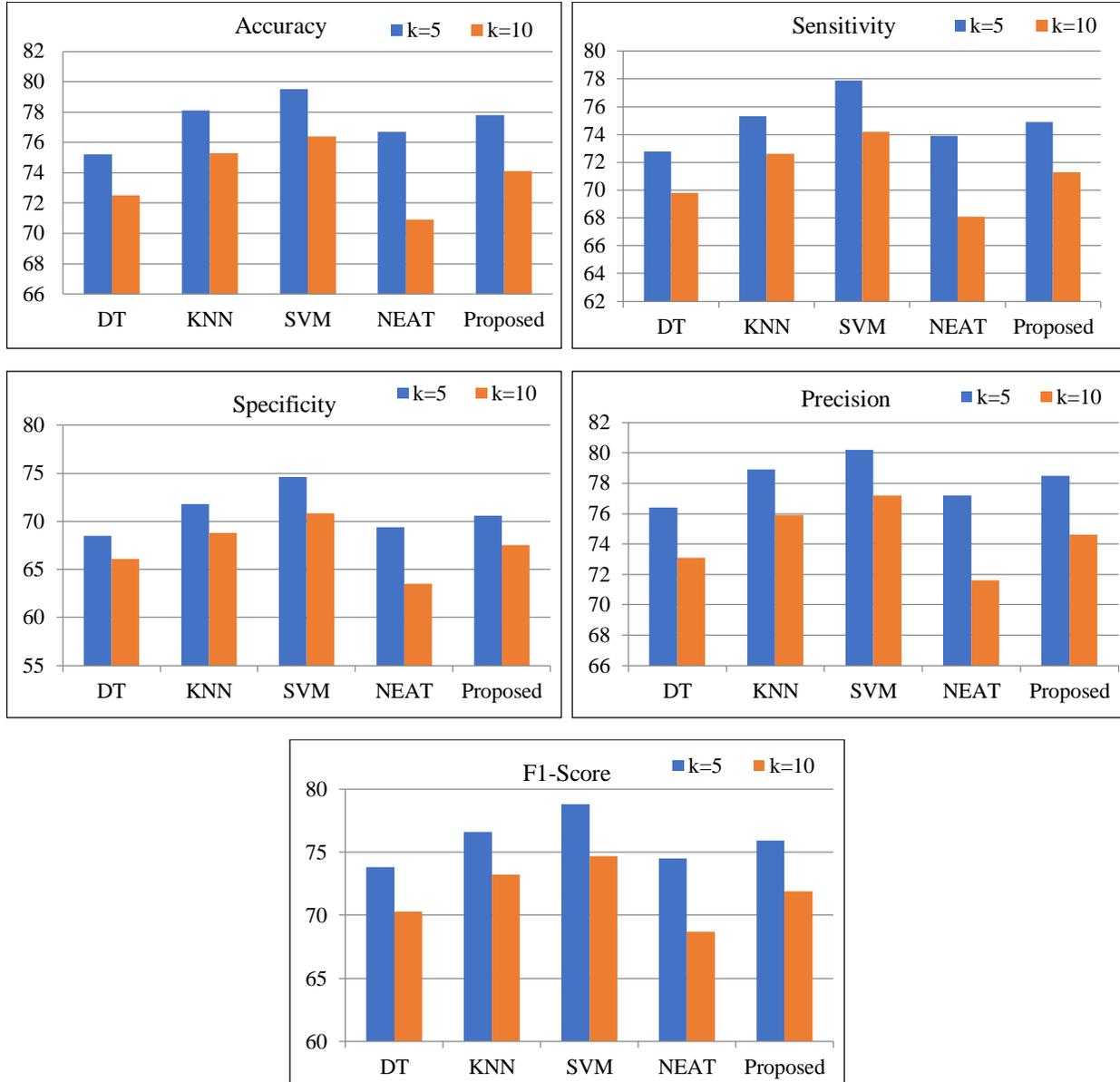


Fig. 4 Performance metrics with GLDM features - k=5 and k=10 fold cross-validation

Table 9, Table 10, and Figure 4 show the performance metrics for five distinct in both k=5 fold and k=10 fold cross-validation using GLDM features. These values indicated that the proposed approach outperformed the k=10 fold cross-

validation algorithm in the k=5 fold cross-validation. All performance indicators (showed higher values for k=5 fold. As a result, it appears that the k=5 fold cross-validation is the best option for the proposed method with GLDM features.

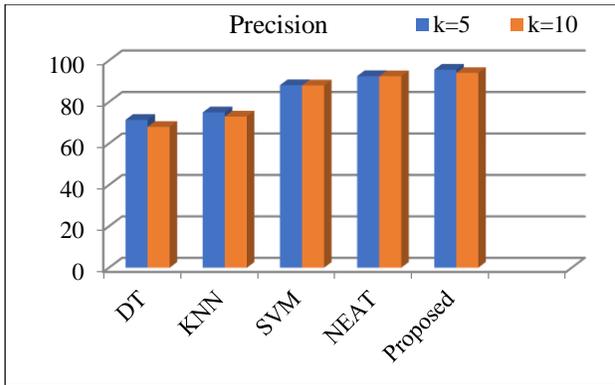
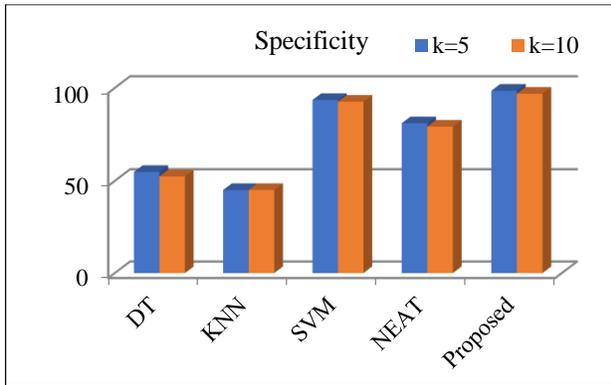
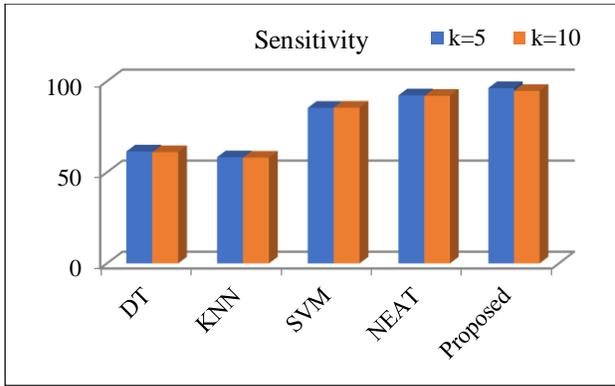
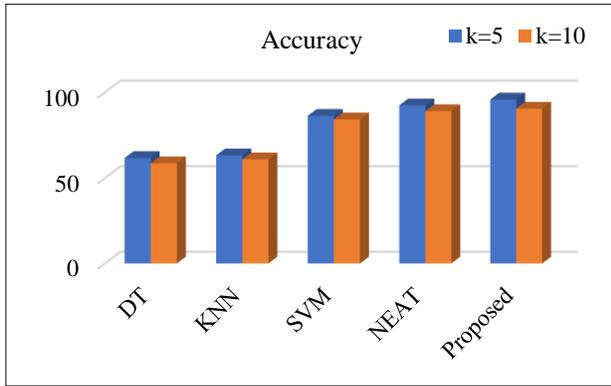
5.6. Fused Features

Table 11. Performance metrics with fused features (GLCM, GLRLM, and GLDM) - k=5 fold cross-validation

Algorithm	Accuracy	Sensitivity	Specificity	Precision	F1-Score
DT	61.7	61.5	54.8	71.4	57.6
KNN	63.2	58.3	45.1	75	63.2
SVM	86.3	85.4	93.5	88.1	85.5
NEAT	92.4	92.3	81	92.5	92.8
Proposed	95.8	96.3	98.5	95.6	95.6

Table 12. Performance metrics with fused features (GLCM, GLRLM, and GLDM) - k=10 fold cross-validation

Algorithm	Accuracy	Sensitivity	Specificity	Precision	F1-Score
DT	58.6	61.1	52.4	68	56.4
KNN	60.9	58.1	45.1	73	63.7
SVM	84.2	85.5	92.6	88	85.7
NEAT	89	92	79.2	92.4	92.2
Proposed	90.5	94.7	96.9	94	94.1



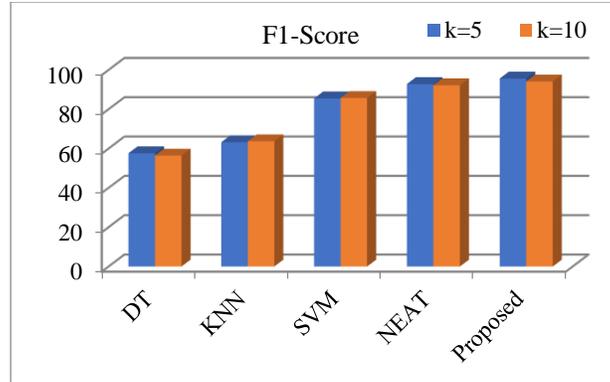


Fig. 5 Performance metrics with fused features - k=5 and k=10 fold cross-validation

Using k=5 and k=10 fold cross-validation, the table and figure display performance metrics for three algorithms using fused features: GLCM, GLRLM, and GLDM. The suggested technique maintains a good level of performance over both k=5 and k=10 fold cross-validation. It has a k=5 accuracy of 95.8% and a k=10 accuracy of 90.5%. Overall, in k=5 fold cross-validation, the proposed approach consistently outperforms existing algorithms across all performance parameters, proving its efficacy in dealing with fused features.

Table 13. Performance analysis with error rate for fused feature with k=5 fold

Algorithms	Error Rate (%)
DT	38.3
KNN	36.8
SVM	13.7
NEAT	7.6
Proposed	4.2

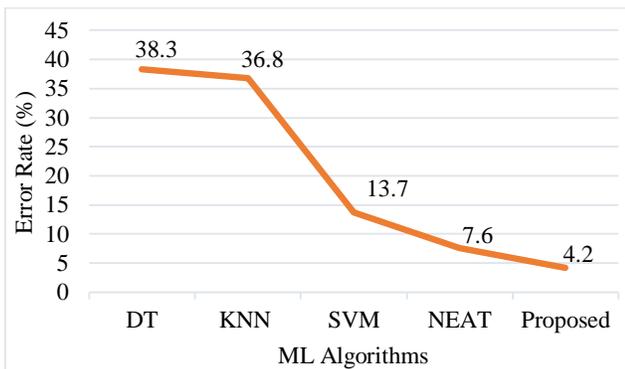


Fig. 6 Performance analysis with error rate

Tables 11 and 12 compare the performance of recommended and current algorithms. According to the Table 11, the proposed method has an accuracy of 95.8%, a sensitivity of 96.3%, a specificity of 98.5%, a precision of 95.6%, and a score of 95.6% in classifying Alzheimer's disease. In terms of performance measures, the above table and figure clearly show that the (proposed) bagging NEAT approach outperforms the other current algorithms. Furthermore, Figure 6 indicates it has the lowest error rate compared to different available techniques.

6. Conclusions and Future Directions

Here, several machine learning techniques are discussed for classifying AD-MRI images, and the classification accuracies of the five classifiers are compared. The experiments are conducted with ADNI database images. From the results, it has come to know that a better performance is reached using the bagging-NEAT (proposed) classifier. Therefore, this research paper concludes that the proposed classifier is the best method for diagnosing AD stages compared to the other classifiers.

Aside from AD diagnosis, the NEAT-based technique can potentially enhance patient outcomes and be applied to other medical tasks. More investigation is required. Furthermore, future improvements to this system can concentrate on refining the data collection method and adopting sophisticated techniques such as deep learning could improve the model's accuracy even further. The proposed approach could also diagnose and detect other neurodegenerative disorders early on. Overall, the ensemble NEAT with fused features for Alzheimer's disease performed well. The diagnosis system is a potentially effective and valuable tool for tackling the challenge of accurate Alzheimer's disease detection and diagnosis.

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