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Early Diagnosis Model of Alzheimer's Disease Based on Hybrid Meta-Heuristic with Regression Based Multi Feed Forward Neural Network

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Abstract
Alzheimer Disease is a chronic neurological brain disease. Early diagnosis of Alzheimer illness may the prevent the occurrence of memory cellular injury. Neuropsychological tests are commonly used to diagnose Alzheimer's disease. The above technique, has a limited specificity and sensitivity. This article suggests solutions to this issue an early diagnosis model of Alzheimer's disease based on a hybrid meta-heuristic with a multi-feed-forward neural network. The proposed Alzheimer's disease detection model includes four major phases: pre-processing, feature extraction, feature selection and classification (disease detection). Initially, the collected raw data is pre-processed using the SPMN12 package of MATLAB. Then, from the pre-processed data, the statistical features (mean, median and standard deviation) and DWT are extracted. Then, from the extracted features, the optimal features are selected using the new Hybrid Sine cosine firefly (HSCAFA). This HSCAFA is a conceptual improvement of standard since cosine optimization and firefly optimization algorithm, respectively. Finally, the disease detection is accomplished via the new regression-based multi-faith neighbors' network (MFNN). The final detected outcome is acquired from regression-based MFNN. The proposed methodology is performed on the PYTHON platform and the performances are evaluated by the matrices such as precision, recall, and accuracy.

Keywords Alzheimer's disease · MFNN · Feature extraction · Diagnosis

1 Introduction

A neurologic condition that primarily affects the elderly, Alzheimer Disease (AD) is progressive. There are 3 types: mild, moderate, and chronic. At first, it has an impact on the area of the brain that controls dialect and recollection. The brain shrinks, its ventricles grow larger, and its volume decreases [1]. More than 46.8 million older people, 44 million of whom have Alzheimer's disease, according to current statistics. By

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2050, there could be 131.5 million people on the planet. Among cognitively normal (CN) and dementia, MCI is a stage with a 10% conversion rate to Alzheimer's disease [2]. MCI patients are thought to have a substantially greater chance of acquiring Alzheimer's disease (AD) than those without MCI, with an annual conversion rate of 15–25% [3]. To better diagnose Alzheimer's disease, researchers are using Soft Computing (SC) technology. A novel technique for detecting Alzheimer's disease is carried out using SCs, which employ training (learning) of input–output data sets to establish the design's structure and parameters or hyperparameters [4]. These two steps are feature extraction and classification.

A comprehensive medical history of the patient and the short mental state examination (MMSE) are required for an accurate diagnosis of Alzheimer's disease. Brain MRI has been used by doctors to identify Alzheimer's disease. The ventricles of the brain enlarge as the cerebral cortex and the hippocampus deteriorate. The temporal lobe (entorhinal cortex and hippocampus) is typically first affected by Alzheimer's disease-related brain changes, followed by gradual neocortical impairment [5]. The hippocampus's size has an impact on both spatial and episodic memory. Additionally, it permits communication between the brain and the body. When the hippocampus is reduced, synapses, neuron endings, and cell death are affected. In its very accurate categorization of medical photos, CNN appears to be doing well. There are several models that make use of CNN for classification of AD scans [6]. The SVM is given metrics from the resulting graphs, which have been processed similarly to the graphs in the Brain connection framework [7]. The healthy control (HC) is used by CNN to classify AD [8]. Metaheuristic approaches are used because some HC issues are difficult. It proposes models for combinatorial optimization that address issues with supervised and unsupervised approaches to microarray data processing [9].

The measurement of the hippocampal volume would be challenging. FreeSurfer is a piece of software that measures hippocampus volume automatically or semi-automatically. The amount of time needed may differ greatly depending on the software product's method [10]. The methods for early AD diagnosis require invasive procedures such lumbar puncture, positron emission tomography (PET), cerebrospinal fluid analysis, and the use of radioactive tracers [11]. The volume of the hippocampus, the regional cortical thickness, and the amount of the grey matter are fundamental hypotheses concerning morphological or functional problems in the brain [12]. More clinical and physiological diagnostics should be performed at the genetic level [13]. It is focused on pre-trained or fine-tuned CNN in medical pictures for poly identification and pulmonary embolism detection and also a feed-forward back propagation neural network is used to identify normal and abnormal MRI images [14]. It has gained popularity since it checks the brain's complete vertices in the early detection of AD-related brain areas and subjects. Our goal is to create a tool that will help clinicians [15].

The major contribution of this research work is:

- To select the optimal features using the Sine cosine firefly (HSCAFA), which is an improved version of standard since cosine optimization algorithm and firefly optimization algorithm.
- To detect the disease precisely via the new regression-based multi-faith neighbors' network (MFNN)

Moreover, the details of this work are discussed in further sections, Sect. 2 deals with the findings and an analysis of related existing work of the proposed model are detailed below. Section 3 shows the proposed methodology of the work, the work is experimented with and analysed. Section 4 discusses the work's evaluation results and comparative conversation. Section 5 depicts the work's conclusion.

2 Related Works

"Some of the recent researchdi works related to Alzheimer's disease early detection model were reviewed in this section"

Ghazi et al. [16] (2019) have introduced training recurrent neural networks robust to unfinished data. A generalized training rule for RNN architecture, LSTM network were used, which might manage target values and missing predictors. Six volumetric magnetic resonance imaging (MRI) biomarkers were used to apply the LSTM algorithm to the development of Alzheimer's disease (AD), whole brain, volume of ventricles, entorhinal cortex, hippocampus, middle temporal gyrus and fusiform. Diminished missing values on the LSTM network parameters were achieved.

Raju et al. [17] (2019) suggested about the alzheimer disease inter diagnosis using 3-D convolution neural networks. A cross sectional study was conducted on structural-MRI data from 465 people, including 181 MCI, 132 AD patients, and 152 NC. To classify different stages of AD, 3-dimensional structure with a svm was built. It aided in learning the preferred and distinguishing common characteristics disease, resulting in a supercharged categorization. TensorFlow is used to implement it in the Keras structure in Python. Tedious and time-consuming processes of segmenting and extracting custom characteristics are avoided.

Basaia et al. [18] (2019) developed an A solitary MRI with a deep learning algorithm was used to classify Alzheimer disease and cognitive damage. CNN achievement has been demonstrated distinct AD, s-MCI and c-MCI. All the classifications showed high levels of accuracy. CNN was found to be highly effective in distinctive AD and MCI patients from healthy controls, as well as in predicting conversion to AD within 36 months. It may hasten the adoption of structural MRI into standard practice to aid in patient assessment and management.

Liu et al. [19] (2019) had developed Alzheimer's disease detection by depthwise separable convolutional neural networks. A strong separate and distinct convolutional neural network model was used for AD categorization to boost the efficiency of the DL-algorithm. The depth—wise separate convolution (DSC) replaces the conventional- convolution. AlexNet and GoogLeNet are used for transfer learning to enhance the classification accuracy rate of AD detection, and a good output was obtained.

Ebrahimi et al. [20] (2021) had proposed Deep sequence modeling for Alzheimer's disease detection by MRI. Deep sequence-based networks were used to imitate the sequence of MRI features produced by a CNN for AD detection. The CNN used the ResNet-18 method on an ImageNet dataset. TCN weights with a random Gaussian distribution were generated. Weights generated by pre-trained CNNs are failed to improve in the TCN structure.

Jain et al. [21] (2019) introduced CNN- Centered on magnetic resonance brain images, Alzheimer disease Categorization. Mathematical model *PFSECTL* based on transfer learning was used for CNN architecture. VGG-16 ImageNet dataset adopted for transfer learning and feature extractor. Inception Network and Residual Network failed to develop an alternative neural network.

Francis et al. [22] (2021) investigated Premature detection of Alzheimer's disease using local binary pattern and CNN. A local feature descriptor was used for the detection of (mild cognitive impairment convertible) MCI. A novel interest region descriptor is created by combining the abilities of the LBP texture operator and the SURF descriptor. The feature signifier merged the abilities of the local binary pattern texture operator and quick Hessian sensor to identify main facts and explanations. Accuracy between MCIc and MCInc can be extended later.

Park et al. [23] (2020) suggested the prediction of AD using large-scale gene expression and DNA methylation data with a deep learning model. To improve the prediction accuracy Gene expression and DNA methylation data were applied. Integration and dealing with different omics data with a large number of dimensions and a small sample size were constructed. multi-omics datasets with the same sample group, are failed to access.

Ahmad et al. [24] (2020) suggested the comparison of to detect Alzheimer disease, various machine learning methods such as Fast RCNN, Support Vector Machine (SVM), and Faster RCNN are used. To diagnose the disease by comparing the existed dataset in the software machine learning algorithms are used. In comparison to RCNN and Fast RCNN, the Faster RCNN algorithm will train and test the model much faster than the other object identification algorithms.

Liu et al. [25] (2020) developed a multi-model deep CNN for automatic hippocampus segmentation and classification in Alzheimer's disease. 3D Densely Connected Convolutional Networks (3D DenseNet) The classifier work was built located on the hippocampal-segmentation result. To classify disease status the features from the multi-task CNN and DenseNet models are combined.

3 Proposed Methodology

The main neurological disorder is named Alzheimer's disease, which damages the human brain's memory cells. So, early identification of Alzheimer's disease for effective management and care strategies is critical. A transitional step among the AD and cognitively normal aging is called amnestic MCI, and AD is developed more than age-matched healthy cognition (HC) by patients with MCI. This proposed approach introduces the early diagnosis model of AD on the basis of a hybrid meta-heuristic optimization. It consists of three stages such as, image preprocessing, feature extraction and image classification and detection. Figure 1 demonstrated the schematic block diagram

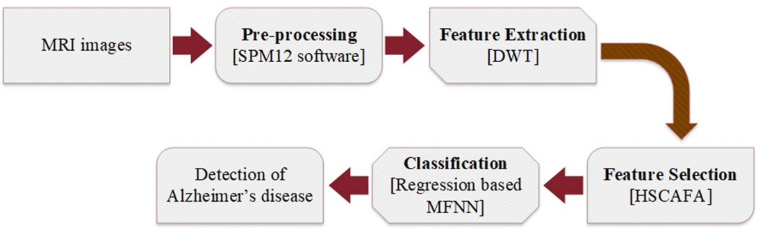

Fig. 1 The proposed methodology's schematic block diagram

of the proposed methodology. The MRI scans are fetched from the ADNI db and processed, with the grey matter amount of ninety ROI being extracted for active characteristics. The classifier was then used to classify the effective features (Fig. 2).

3.1 ADNI Database

3.1.1 ADNI Database

In this work, Alzheimer's Disease Neuroimaging Initiative (ADNI) database is utilized for the experimental datasets (https://www.kaggle.com/datasets/tourist55/alzheimers-dataset-4-class-of-images). The data consists of MRI images. The data has four classes of images both in training as well as a testing set: Mild Demented, Moderate Demented, Non-Demented and Very Mild Demented.

3.2 Image Pre-Processing

In this paper, SPM12 software (http://www.fil.ion.ucl.ac.uk/spm/) was utilized for preprocessing the MRI images. There are 5 steps are included in the preprocessing process such as, (1) skull stripping, (2) spatial standardization and segmentation, (3) modulation, (4) smoothing, and (5) registration. The non-brain tissues are removed in the skull stripping step, then, standardized and segment the cerebrospinal fluid (GSF), white matter (WM) and grey matter (GM). Next, the density feature was converted into a volume feature. Then, the noises are removed from the images. Finally, all subjects' gray matter was registered onto an AAL template.

3.3 Feature Extraction Using DWT

Feature extraction is converting the image to its useful properties. It is very challenging to obtain the useful and optimal numbers of features from MRI images. The DWT feature extraction approach provides local-frequency information and its feature derived

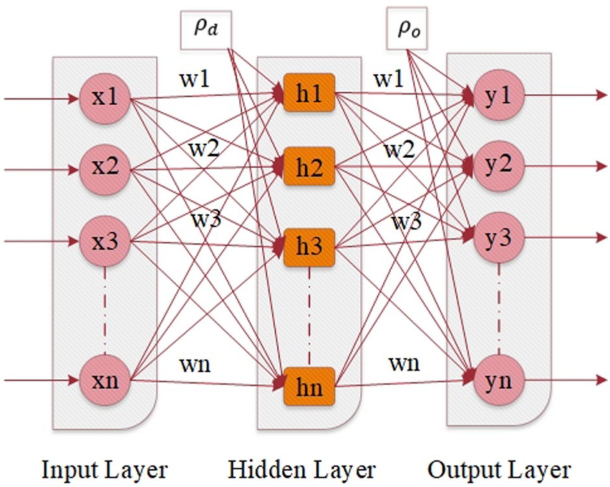

Fig. 2 Network Diagram of MFNN

coefficient. The Daubechies four wavelet can be used for MRI scans because it improves comparison than other feature extraction methods. Wavelets is a perfect measure of patterns because it provides time—frequency information in a localized area. DWT offers enhanced extraction of features, as described below:

$$S = 2^{-u} \tag{1}$$

$$\tau = n2^{-u} \tag{2}$$

where, S denoted the scale and τ defined the translation of the waves utilized in the DWT. In addition, n denotes the count of features.

$$\varphi_{u,v}(t) = 2^{\frac{u}{2}}(2^u t - y) \tag{3}$$

Equation (3) gives the family of a wavelet function, where, the values that fit into an integer set (Z) are described as u, v.

Equations (4) and (5) describe DWT which adds a signal x(t) to a family of synthesis wavelets.

$$x(t) = \sum_u \sum_v C_{u,v} \varphi_{u,v}(t) \tag{4}$$

Were,

$$C_{u,v} = \left(x(t), \varphi_{u,v}(t)\right) \tag{5}$$

Then, the discrete time signal is expressed in Eq. (6).

$$x[n] = \sum_{i=1} toi \sum_{k \in Z} coeff_{i,k} g\left[n - 2^i K\right] + \sum_{k \in Z} d_{i,k} h_i \left[n - 2^i K\right] \tag{6}$$

where, $d_{i,k}$ denoted the signal's scaling coefficients, and $coeff_{i,k}$ represents the wavelet coefficients. The wavelet computation and coefficients of the scaling are shown in Eqs. (7) and (8).

$$coeff_{i,k} = \sum_n x[n] g_i * \left[n - 2^i K\right] \tag{7}$$

$$d_{i,k} = \sum_n x[n] H_i * \left[n - 2^i K\right] \tag{8}$$

where, $g_i * \left[n - 2^i K\right]$ represents the discrete wavelets, $H_i * \left[n - 2^i K\right]$ represents the scaling sequence, and $*$ denoted the complex conjugate. DWT is used to extract feature extracted coefficients from pre-processed MRI images. The wavelet decomposition yields four approximated sub bands: vertical, horizontal, and diagonal. The DWT has the advantage of overcoming the drawbacks of Fourier transform evaluation. It also aids in the detection and recognition of discontinuities in images. The DWT provides the MRI image's local frequency information. After the feature extraction, the elicited features are subjected into feature selection.

3.4 Feature Selection by Hybrid SCAFA

The selection of features is an actual solvable problem that used optimization methods. These methods proposed ways to create a predictive model that reduces the classifier's prediction errors by choosing informative or important features while discarding noisy, redundant, or irrelevant attributes. A new hybrid SCAFA is proposed for the feature selection, which is explained in below:

Recent times, metaheuristic algorithms showed great ability to resolve real world issues. To arrive at the global optimal, the SCA starts with positions at random. The fitness value for each individual is then calculated. It assigns the most notable location to FS as candidate features. The mathematical expression of SCA is expressed in (9).

$$x_{ij}^t = \begin{cases} x_{ij}^t + r_1 * \sin(r_2) * \left| r_3 \left(Xb_j^t \right) - x_{ij}^t \right| R_1 < 0.5 \\ x_{ij}^t + r_1 * \cos(r_2) * \left| r_3 \left(Xb_j^t \right) - x_{ij}^t \right| R_1 \geq 0.5 \end{cases} \tag{9}$$

$$r_1 = \alpha - t\frac{\alpha}{T_{max}} \tag{10}$$

where, t is the current iteration, T is the maximum number of iterations, and a is α constant. When verifying and attaining the least number of specific feature selections together, the SCA's fitness function will improve.

$$F_\theta = \varsigma * \mathrm{E}_r + (1 - \varsigma)\frac{\sum_i \theta_i}{n} \tag{11}$$

where n is the number of features in the dataset, and the fitness function F θ returns a vector of size n with 0/1 elements representing selected or unselected features. E denotes the classifier error rate, and ς is a fixed value (0.05) used to regulate the classification performance in relation to the number of features chosen. After that, probability is calculated by FA to determine which operators will update the solution.

FA is used to improve SCA exploration because it has a high ability to find feasible regions with the best solution. FA is a meta-heuristic method that mimics firefly behaviour. FA algorithm is capable of achieving best results for complicated issues. FA used a series of rules to resemble attractiveness and brightness behaviour.

$$\partial_{ij} = \|\chi_i - \chi_j\| = \sqrt{\sum_{k=1}^{d} \left(\chi_{ik} - \chi_{jk}\right)^2} \tag{12}$$

The following is the firefly movement I which is fascinated to a brighter firefly j: $\chi_i = \chi_i + \rho * \left(\chi_i - \chi_j\right) + \gamma * \varepsilon_i$ (13)

Where, ε_i is the random vector ($\varepsilon_i \epsilon N(\mu, \sigma)$) and γ is the random value ($\gamma \epsilon [0, 1]$).

The probability (Pb) is calculated; within given scenario, if Pbi > 0.5, the SCA operators would upgrade the solution; or else, the FA are used.

$$Pb_i = \frac{F_\theta}{\sum_{i=1}^{N} F_\theta} \tag{14}$$

The main aim is to improve the balancing of exploratory and exploitative within the search phase. For every solution, the fitness function value is computed to decide which solution must be stored for another iteration. The above process repeats till a stopping condition is reached.

3.5 Classification by Regression Based MFNN

In this study, a hybrid approach of regression-based MFNN was proposed for classification purposes. The proposed algorithm achieves best outcomes while avoiding slowdown in local optimum answers and premature convergence in training Feedforward Multi-Layer Perceptron (MLP) ANNs.

Logistic Regression: The linear relation among multiple variables is modelled using linear regression analysis, a statistical technique. Logistic regression is achieved by taking the log odds of probability, which is expressed by:

$$\mathrm{Z}_i = \ln\left(\frac{Pb_i}{1 - Pb_i}\right) \tag{15}$$

where, Pb is the probability. This is used to describe the association between the variables and multiple independent variables in such a way that if the relationship exists, the behaviour of the dependent variable can be estimated from the independent factors. The regression model is given as:

$$y = \beta_o + \sum_{j=1}^{k} \beta_j \chi_j + \varepsilon_j \tag{16}$$

where, the error term is represented as ε, χ denoted the predictor variables, $\beta_o, \beta_1, \ldots .\beta_k$ denoted the partial regression coefficients and y denoted the responsible variable.

MFNN: Networks with more only one layer of artificial neurons, allowing only uni—directional forward links of outputs and inputs, called multilayered feed-forward neural networks or multi-Layer Perceptions (MLP). It is a data-based method which can model nonlinear models through its activation function. Initially, the sum of weights is evaluated by,

$$\delta_j = \sum_{i=1}^{n} \omega_{ij} x_i + \rho_i \tag{17}$$

The input variable was marked by x_i, the weight between xi and neuron j was defined by ω_{ij}, and the bias term of the input variable was determined by ρ_i.

By its differentiable function, the Sigmoid activation function is used in neural network training. The logistic function is denoted by,

$$\varphi_j = \frac{1}{1 + e^{(-s_j)}} \tag{18}$$

where, the sigmoid function's slope parameter is represented as a, the total of all inputs plus term bias is represented as u. Finally, neuron j's output evaluated by,

$$\mathrm{Y}_j = \sum_{i=1}^{k} \omega_{ij} \varphi_j + \rho_j \tag{19}$$

where, Y_j denoted the j^{th} neuron output, ω_{ij} denoted the weight of output and neuron j, and φ_j is denoted as the activation function for j^{th} neuron and ρ_j is the bias term output variable. The network's weights are frequently adjusted so that the fault or objective function is as small as possible. The target function is denoted as

$$E_o = T_o - Y_o \tag{20}$$

where, the predicted (computed) output of i^{th} iteration is represented as Y_o, and the observed (actual) output of i^{th} iteration is represented as T_o.

4 Results and Discussions

This section displays the data and conversation of the suggested method, as well as the executed intrusion detection system. The proposed algorithm's performance is evaluated and compared to the previous algorithm. Accuracy, specificity, recall, precision, False discovery rate (FDR), False negative ratio (FNR), Negative prediction value (NPV), Mathews corelation co-efficient (MCC), False rejection rate (FRR), False positive ratio (FPR), and sensitivity are all measures of matrix performance. Adaptive Network-Based Fuzzy Inference System (ANFIS), Deep Belief Network (DBN) and Artificial Neural Network (ANN), CNN [20], SVM [17] and RNN [16] are used, analysed, and compared to the proposed algorithm. The performance metrics are examined further below.

4.1 Performance Metrics

This portion describes the proposed model's performance measures, some of which have already been validated and checked. The following is a mathematical representation of the analysis of the performance measures included in the scheduled and existing analyses:

i. *Accuracy* The proportion of genuine outcomes inside community, accuracy is defined as whether something is true positive or true negative. It evaluates the precision of a clinical diagnosis on a specific condition. The sensitivity levels indicate how probably a diagnostic is to identify person who do have the disease.

$$Accuracy = Tp + TN * TP + TN + FP + FN \tag{21}$$

ii. *Precision* Precision is described as the number of true positives divided by total of true positives plus false positives.

$$precision = \frac{True\,Positive}{True\,Positive + False\,Positive} \tag{22}$$

iii. *Recall* The number of true positives divided by the number of true positives plus the number of false negatives equals recall.

$$Recall = \frac{Tp}{True\,Positive + False\,Negative} \tag{23}$$

iv. **Negative prediction Value (NPV)—**The negative predictive value is the probability that following a negative test result, that individual will truly not have that specific disease. The number of negative test results for the absence of an outcome (d) divided by the total number of negative test results (b + d).

$$NPV = \frac{b}{(b + d)} \tag{24}$$

v. *False positive rate (FPR)* It is a measure of accuracy for a test: be it a medical diagnostic test, a machine learning model, or something else. In technical terms, the false positive rate is defined as the probability of falsely rejecting the null hypothesis.

$$FPR = \frac{Fp}{Fp + TP} \tag{25}$$

vi. *False Negative Ratio (FNR)* A test result that indicates that a person does not have a specific disease or condition when the person actually does have the disease or condition.

$$FNR = \frac{FN}{FN + TP} \tag{26}$$

vii. *Mathews corelation co-efficient (MCC)* MCC is a statistical tool used for model evaluation. Its job is to gauge or measure the difference between the predicted values and actual values and is equivalent to chi-square statistics for a 2 × 2 contingency table.

$$MCC = \frac{(TP * TN - FP * FN)}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}} \tag{27}$$

viii. *False Rejection Rate (FRR)* FRR is expressed as a percentage of situations in which are user gets a false negative result. To calculate the FRR value, you need to divide the sum of genuine scores falling below the threshold by the total number of genuine scores.

$$FRR = \frac{FR}{Total\, genuine\, matching} \tag{28}$$

ix. *False Discovery Rate (FDR)* FDR is a method of conceptualizing the rate of type I errors in null hypothesis testing when conducting multiple comparisons.

$$FDR = \frac{FP}{Fp + TP} \tag{29}$$

x. *Specificity* Specificity is defined as the proportion of individuals without the disease who test negative (a true negative result) or as an estimated probability that an unaffected individual will test negatively.

$$Specificity = \frac{Fp}{Fp + TN} \tag{30}$$

xi. *Sensitivity* sensitivity of a diagnostic test is expressed as the probability (as a percentage) that a sample tests positive given that the patient has the disease.

$$Sensitivity = \frac{TP}{TP + FP} \tag{31}$$

Table 1 Performance comparison of purposed and existing methods

Algorithms	Performance metrics (%)					
	Accuracy	Precision	Recall	F measure	NPV	FPR
ANN	76.5	53.6	53.08	53.08	84.3	15.6
ANFIS	87.7	75.4	75.4	75.4	91.8	8.565
CNN [20]	88.9	76.54	78.5	79.54	88.54	4.57
SVM [17]	89.45	77.12	74.56	85.45	89.45	2.59
RNN [16]	87.54	68.54	79.54	86.97	89.76	3.24
DBN	96.4	92.8	92.8	92.08	97.6	02.3
Proposed method	98.4	96.5	95.78	94.54	98.9	01.01

Table 2 Performance comparison of purposed and existing methods

Algorithms	Performance metrics (%)					
	FNR	MCC	FRR	FDR	Specificity	Sensitivity
ANN	89.6	90.2	3.0	3.0	84.3	53.08
ANFIS	85.56	91.2	4.6	4.6	91.8	75.4
CNN [20]	88.56	94.3	4.5	4.8	95.4	89.5
SVM [17]	89.54	90.23	3.26	4.25	98.56	78.56
RNN [16]	82.35	91.23	5.6	4.5	97.15	77.54
DBN	84.15	90.25	4.87	3.59	98.56	77.98
Proposed method	90.25	97.58	2.15	3.21	99.23	85.45

4.2 Performance Analysis

This section describes the detailed performance analysis and the comparison of existing and proposed method.

4.2.1 Overall Performance Analysis

In the table below, the suggested and current approaches' performance measures are described. The proposed and current performance measures for accuracy, precision, Recall, Negative prediction value (NPV), False discovery rate (FDR), False negative ratio (FNR), Mathews corelation co-efficient (MCC), False rejection rate (FRR), False positive ratio (FPR), specificity and sensitivity. A confusion matrix is created based on statistical parameters to examine accuracy, precision, Recall, Negative prediction value (NPV), False discovery rate (FDR), False negative ratio (FNR), Mathews corelation co-efficient (MCC), False rejection rate (FRR), False positive ratio (FPR), specificity and sensitivity is shown in the diagrams below. The sensitivity of the data and the time it takes to process it are contrasted. Tables 1 and 2 depicts a performance and comparison of the proposed and existing methodologies' performance indicators and Tables 3 and 4 shows the performance of proposed method with and without feature selection.

Table 3 Performance of proposed method with and without feature selection

	Performance metrics (%)								
	Accuracy	Precision	Recall	Fmeasure	NPV	FPR	FNR	MCC	FDR
With feature selection	98.9	96.9	96.9	96.9	98.9	01.01	03.04	95.9	03.04
Without feature selection	97.4	92.4	92.4	92.4	97.4	02.5	07.5	89.9	07.05

Table 4 Performance of proposed method with and without feature selection

	Performance metrics (%)	
	Specificity	Sensitivity
With feature selection	98.9	96.9
Without feature selection	97.4	92.4

As per the acquired results, the proposed mode has recorded highest accuracy as 98.4%, which is better than ANN = 76.5%, ANFIS = 87.7%, CNN [20] = 88.9%, SVM [17] = 89.45%, RNN [16] = 87.54% and DBN = 96.4%. The major reason behind this improvement is due to the selection of the optimal features. In addition, the proposed model has also recorded the highest Precision as 96.9%, Recall = 95.78%, F measure = 94.54%. Thus, the proposed model is said to be highly significant for AD at the early stage.

In addition, the proposed model has been compared over the existing model in terms of feature selection. The proposed model has also recorded the highest accuracy with feature selection approach.

Tables 1 and 2 clearly elaborates that the comparison of both proposed and traditional methods. Meanwhile the values obtained after attribute selection are efficient than the values obtained using traditional approach for total lines, total number of member functions and member variables. Tables 3 and 4 shows the performance of proposed method with and without feature selection through parameters, Accuracy, Precision, Recall, Fmeasure, NPV and FPR, FNR, MCC, FDR, Specificity and Sensitivity have high value with feature selection.

4.2.2 Performance Analysis

The specificity, sensitivity and accuracy comparison of the proposed and existing methods is shown in Fig. 3. The specificity, sensitivity and accuracy of suggested and current methods such as Artificial Neural Network (ANN), Aptive Network-Based Fuzzy Inference System (ANFIS), Deep Belief Network (DBN) is shown in Fig. 3. The specificity, sensitivity and accuracy for the suggested approach is superior to the other current strategies.

From figure, the sensitivity of proposed method is high when compared to existing method, sensitivity is 96.9% and specificity is 98.9%, performance is better than the existing method. Accuracy is 98.4%, higher than other existing methods.

4.2.3 Precision, F measure and Recall

The Precision, F measure and Recall comparison of the proposed and existing methods is shown in Fig. 4. The Precision, F measure and recall of suggested and current methods

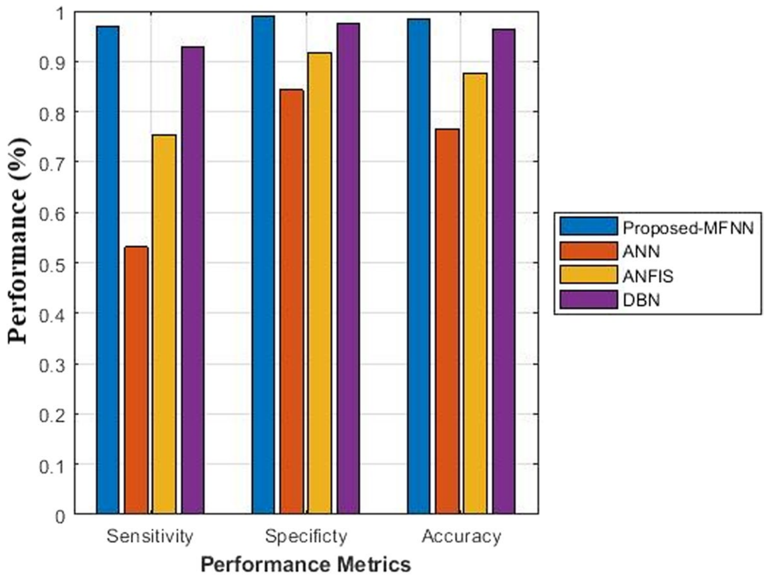

Fig. 3 Comparison of The Proposed and Existing Methods of Specificity, Sensitivity and Accuracy

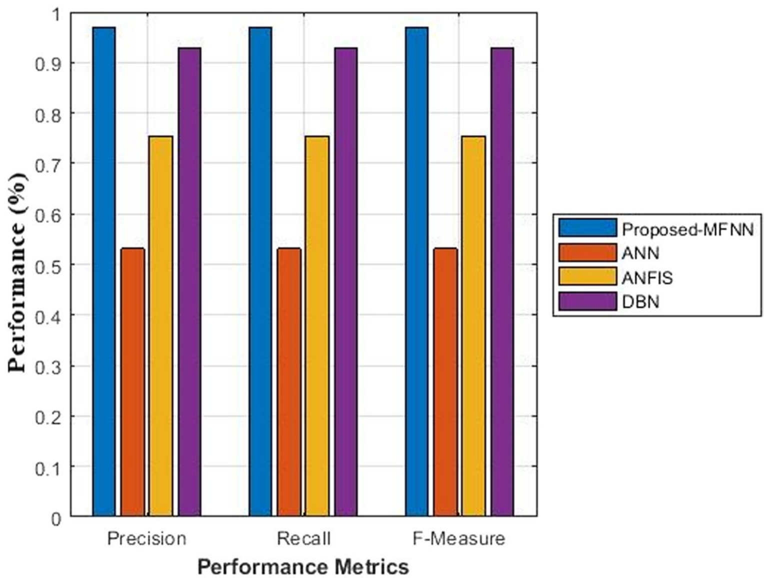

Fig. 4 Comparison of the proposed and existing methods of precision, f measure and recall

such as Artificial Neural Network (ANN), Aptive Network-Based Fuzzy Inference System (ANFIS), Deep Belief Network (DBN) is shown in Fig. 4. The Precision, F measure and Recall for the suggested approach is superior to the other current strategies.

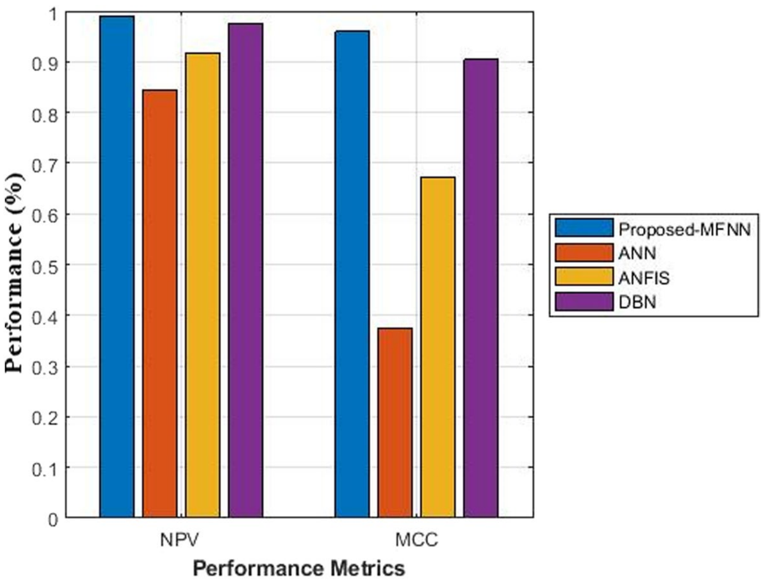

Fig. 5 Comparison of the proposed and existing methods of NPV and MCC

From figure, the Precision of proposed method is high when compared to existing method, F measure is 96.9%, performance is better than the existing method. Recall is 96.9%, higher than other existing methods.

4.2.4 NPV and MCC

The NPV and MCC comparison of the proposed and existing methods is shown in Fig. 5. The NPV and MCC of suggested and current methods such as Artificial Neural Network (ANN), Aptive Network-Based Fuzzy Inference System (ANFIS), Deep Belief Network (DBN) is shown in Fig. 5. The NPV and MCC for the suggested approach is superior to the other current strategies.

From figure, the NPV and MCC of proposed method is high when compared to existing method, NPV is 98.9%, performance is better than the existing method. MCC is 9.5, higher than other existing methods.

4.2.5 FPR and FNR

The FPR and FNR comparison of the proposed and existing methods is shown in Fig. 6. The FPR and FNR of suggested and current methods such as Artificial Neural Network (ANN), Aptive Network-Based Fuzzy Inference System (ANFIS), Deep Belief Network (DBN) is shown in Fig. 6. The FPR and FNR for the suggested approach is superior to the other current strategies.

From figure, the FPR and FNR of proposed method is high when compared to existing method, FPR is 1.01, performance is better than the existing method. FNR is 1.01, higher than other existing methods.

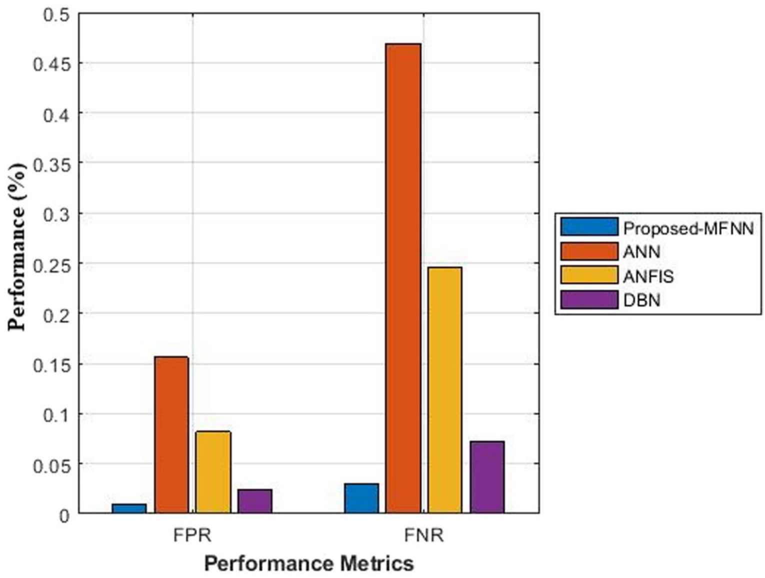

Fig. 6 Comparison of the proposed and existing methods of FPR and FNR

4.3 Performance of Proposed Technique With and Without Feature Selection

This section describes the performance of proposed technique using feature selection and analysed and then compared. Using parameters such as accuracy, precision, Recall, Negative prediction value (NPV), False discovery rate (FDR), False negative ratio (FNR),

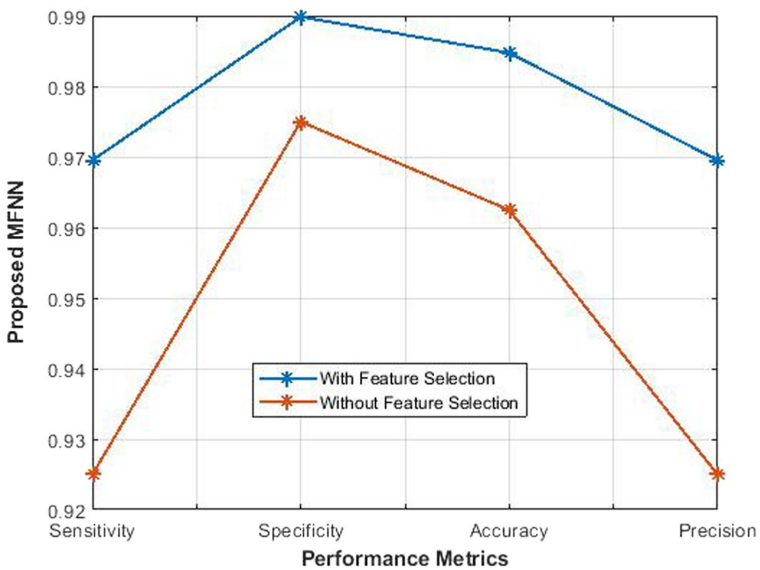

Fig. 7 Performance analysis of proposed method with and without feature selection

Mathews corelation co-efficient (MCC), False rejection rate (FRR), False positive ratio (FPR), specificity and sensitivity, the performance are analysed and plotted in graph and is given below.

4.3.1 Sensitivity, Specificity, Precision and Accuracy

Figure 7, elaborates the performance of proposed method with and without feature selection. Furthermore, the feature selection is done by HSCAFA, using parameters such as accuracy, precision, specificity and sensitivity.

This figure concludes the performance analysis of proposed method with and without feature selection. Moreover, the values formed using feature selection is more than that of output values without feature selection.

4.3.2 Recall, f Measure, NPV, MCC

Figure 8, elaborates the performance of proposed method with and without feature selection. Furthermore, the feature selection is done by HSCAFA, using parameters such as Recall, NPV, MCC, and f measure.

This figure concludes the performance analysis of proposed method with and without feature selection. Moreover, the values formed using feature selection is more than that of output values without feature selection.

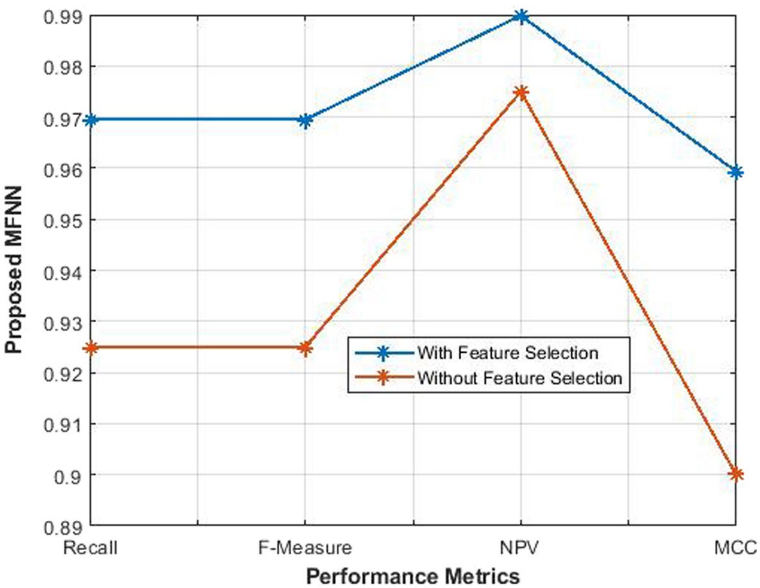

Fig. 8 Performance analysis of proposed method with and without feature selection

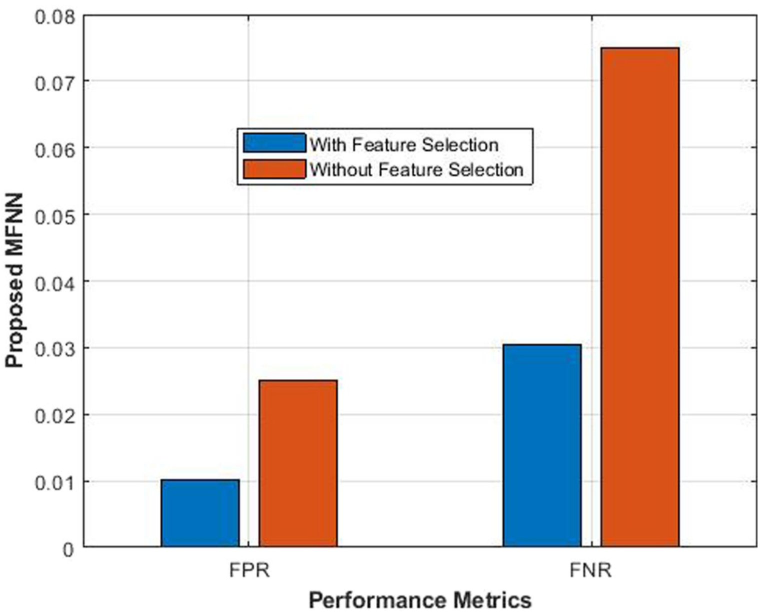

Fig. 9 Performance analysis of proposed method with and without feature selection

4.3.3 FPR and FNR

Figure 9, elaborates the performance of proposed method with and without feature selection. Furthermore, the feature selection is done by HSCAFA, using parameters such as FNR, and FPR.

This figure concludes the performance analysis of proposed method with and without feature selection. Moreover, the values formed using feature selection is more than that of output values without feature selection.

5 Conclusion

This paper has introduced a new AD detection model. The proposed Alzheimer's disease detection model includes four major phases: pre-processing, feature extraction, feature selection and classification (disease detection). Alzheimer's disease detection model (disease detection). The SPMN12 package has been first used to pre-process the collected raw data. The statistical features (mean, median, and standard deviation) and DWT were therefore extracted from the pre-processed data. The best features were also chosen from the extracted features using the new Hybrid Sine Cosine Firefly algorithm (HSCAFA). This HSCAFA is conceptually superior to the firefly and standard sine optimization algorithms, respectively. Finally, the new regression-based multi-faith neighbours' network is used to detect disease (MFNN). The network of multifaith neighbours has been regression-based, and it provides the final detected result. The proposed methodology is performed on the PYTHON platform and the performances are evaluated by the matrices such as precision, recall, and accuracy. As per the acquired results, the proposed mode has recorded highest accuracy as 98.4%, which is better than ANN = 76.5%, ANFIS = 87.7%, CNN [20] = 88.9%, SVM [17] = 89.45%, RNN [16] = 87.54% and DBN = 96.4%. The major reason behind this improvement is due to the selection of the optimal features. In addition, the proposed model has also recorded the highest Precision as 96.9%, Recall = 95.78%, F measure = 94.54%. Thus, the proposed model is said to be highly significant for AD at the early stage.

Author Contributions Author 1: BR. He participated in the methodology, Conceptualization, Data collection and writing the study. He Performed the Analysis the overall concept, writing and editing.

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Data Availability All the data is collected from the simulation reports of the software and tools used by the authors. Authors are working on implementing the same using real world data with appropriate permissions.

Declarations

Conflicts of interest The authors declare that they have no conflict of interest.

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