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Enhancing Alzheimer's disease diagnosis through metaheuristic feature selection and advanced classification techniques

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ABSTRACT

A diverse array of diagnostic and detection methods has been developed as a result of the advent of Alzheimer's disease (AD) as a significant global health issue. This study employs bio-inspired algorithms, such as the parrot optimization algorithm (POA), grey wolf optimizer (GWO), and differential evolution (DE), to identify the most effective feature selection techniques for AD diagnosis. The predictive accuracy of these algorithms was improved by the simple keywords: Alzheimer's disease optimization classification machine learning metaheuristic mentation of the Alzheimer's disease Dataset. This was achieved by integrating a personalized fitness function and optimizing parameter settings with decision tree classifiers. To evaluate the algorithms' effectiveness in machine learning models with population sizes of 30 and 60, precision, recall, accuracy, and F1-score were evaluated at 5, 15, and 30 iterations. The gradient boosting and XGBoost classifiers consistently obtained the highest results, while DE, GWO, and parrot optimization (PO) achieved maximal accuracy rates of 0.94, 0.93, and 0.94, respectively. These findings underscore the efficacy of integrating metaheuristic algorithms with robust classifiers to enhance the predictive accuracy of AD diagnosis. Furthermore, they illustrate that artificial intelligence (AI) algorithms that are operated by biological processes can accurately forecast AD, with the success rates and stability of the proposed methods serving as metrics for evaluating their efficacy.

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1. INTRODUCTION

To accelerate the identification of biomarkers during the initial phases and progression of Alzheimer's disease, the Alzheimer's disease neuroimaging initiative (ADNI) was established by the National Institute on Aging. The successful automation and optimization of design processes that utilized data from cerebrospinal fluid (CSF), positron emission tomography (PET), and magnetic resonance imaging (fMRI) were the primary focus of researchers [1]–[3]. Initially, this project develops machine-learning models that incorporate the most critical attributes of the style selection to identify an optimal solution to the critical binary classification of VCI to control subjects [4], [5]. The research concludes by identifying the components assessed for statistical inter-group variations in all models. As a result, we analyzed classification success, which is the degree to which these components accurately represent the severity of a

mental illness in a life-threatening manner and the degree to which they facilitate the understanding of the progression of Alzheimer's disease. Our proposed method was shown to be robust across a range of study parameters by utilizing a variety of machine learning models that included eigenvectors of feature selection procedures, as well as by selecting over 150 ADNI VCI and controlling moderate to medium VCI, gender-matched peers from the ADNI [6], [7].

The potential of machine learning in revolutionizing disease identification is a beacon of hope for the future of medical research. This application of automated algorithms, based on historical data, is particularly promising in the accurate identification of maladies. The strides in machine learning could significantly benefit Alzheimer's Disease, a condition that poses a significant challenge for clinicians due to its varied characteristics and the progression of these characteristics in its initial stage.

Feature selection is a critical component of data analysis and machine learning, as it enhances the interpretability and efficacy of predictive models. By selecting the most relevant features from a dataset, feature selection techniques are intended to improve the accuracy of models, prevent overfitting, and reduce computational complexity [8], [9]. These techniques can be broadly classified into three categories: filter methods, wrapper methods, and embedded methods [10]. Filter methods operate independently of the learning algorithm, while statistical measures are implemented to evaluate the relevance of features. The most frequently employed filtering techniques are chi-square tests, correlation coefficients, and mutual information. These methods are computationally efficient and provide a rapid method for removing irrelevant or redundant features before model training [11], [12]. Conversely, wrapper methods evaluate feature subsets by the efficacy of a specific learning algorithm. Recursive feature elimination (RFE) and forward or backward selection methods are included in this category. Even though wrapper methods are often more precise than filter methods, they are computationally intensive because they require multiple model training and evaluation phases [13], [14].

In addition to conventional feature selection methods, metaheuristic algorithms have gained popularity due to their ability to efficiently investigate the feature space and identify optimal feature subsets [15]. Metaheuristic algorithms are high-level problem-independent techniques that employ mechanisms to investigate the global search space and circumvent local optima. Among the most frequently employed metaheuristic algorithms in feature selection are genetic algorithms (GA), particle swarm optimization (PSO) [16], [17], ant colony optimization (ACO), and differential evolution (DE) [18], [19]. Applying metaheuristic algorithms in conjunction with feature selection techniques provides a powerful approach to managing high-dimensional data and intricate feature spaces [20]. The flexibility and robustness of these algorithms enable a wide range of applications in various domains, including medical diagnosis, image processing, and bioinformatics [21], [22]. By leveraging the benefits of both traditional and metaheuristic methodologies, researchers and practitioners can develop predictive models that are more precise and efficient.

The primary contributions of this research are as follows: i) Optimal feature selection was achieved by applying four bio-inspired algorithms differential evolution (DE), grey wolf optimizer (GWO), and parrot optimization algorithm (POA) to the Alzheimer's disease dataset. ii) A fitness function designed explicitly for a decision tree classifier is employed to reduce the number of features. iii) We have integrated various classification algorithms (Decision *et al.*) with specific features. iv) We investigated parameters, including population size and iterations, to identify the most effective configurations. And v) We meticulously evaluated the performance of DE, GWO, and POA using the F1-score, precision, recall, and accuracy, ensuring a robust analysis.

2. RELATED WORKS

Martinez-Murcia *et al.* [23] employ deep convolutional autoencoders to analyze Alzheimer's disease data. Their method entails the decomposition of magnetic resonance imaging (MRI) images and retrieving MRI features correlated with cognitive symptoms, thereby facilitating the comprehension of neurodegenerative processes. The impact of the brain on each autoencoder manifold coordinate is determined through regression and classification analyses, which involve the examination of the extracted features in various combinations. The accuracy of Alzheimer's disease (AD) diagnosis is greater than 80% when imaging-derived markers are used in conjunction with MMSE or ADAS11 scores.

The classification of AD has been substantially enhanced by applying machine learning (ML) and data mining. The classification of Alzheimer's disease stages using datasets such as the ADNI and the TADPOLE challenge has been the subject of numerous studies that have employed algorithms such as K-nearest neighbors (K-NN), decision trees, naive Bayes, generalized linear models (GLM), and deep learning. These methods have demonstrated promising results, with GLM attaining an 88.24% accuracy in classifying AD stages. Nevertheless, the challenges of data sparsity and comprehensive feature selection persist. It is imperative to improve the representation of underrepresented classes and enhance feature

selection to improve the accuracy and effectiveness of AD classification. Key characteristics include the clinical dementia rating sum of boxes (CDRSB) cognitive test, patient age, and overall brain volume [24].

The study "early-stage Alzheimer's disease prediction using machine learning models" was conducted by Kavitha et al. [25]. The study utilized datasets from the open access series of imaging studies (OASIS) and Kaggle to predict early AD. Using precision, recall, accuracy, and F1-score metrics, they assessed the performance of decision tree (DT), random forest (RF), support vector machine (SVM), gradient boosting, and voting classifiers. The potential of ML techniques for early AD diagnosis was demonstrated by the maximum validation accuracies of 86.92% and 85.92% attained by the RF and extreme gradient boosting (XGBoost) models, respectively. The mortality rates of Alzheimer's disease are reduced as a result of the more effective treatment that is facilitated by early detection. The study emphasizes the importance of machine learning (ML) in providing clinicians with the necessary tools to enhance patient outcomes and implement timely interventions. Future research will concentrate on refining feature selection and exploring new features to improve diagnostic accuracy.

Salvatore *et al.* [26] employed machine learning techniques to analyze MRI data from the ADNI in order to identify early biomarkers for AD. The subjects were categorized as cognitively normal (CN), AD, mild cognitive impairment converters (MCIc), and non-converters (MCInc) using principal component analysis (PCA) for feature extraction and support vector machines (SVM) for classification. We found significant MRI biomarkers in the following areas: The hippocampus, basal ganglia, entorhinal cortex, and cerebellum were all identified as sites of substantial MRI biomarkers. 76% for AD vs. CN, 72% for MCIc vs. CN, and 66% for MCIc vs. MCInc were the classification accuracies. The potential of ML to improve the early diagnosis and management of Alzheimer's disease is underscored by these findings, which will enable the development of more effective treatments and reduce the duration and cost of clinical trials.

In the detection and classification of AD, Kishore *et al.* [27] examined the efficacy of a diverse array of machine learning algorithms, including logistic regression, DT, RF, naive Bayes (NB), and SVM. Cross-validation, feature selection, and data preprocessing were implemented using clinical data and MRI scans to surmount the constraints of conventional methods. The SVM with a linear kernel (C=2) achieves the highest accuracy of 95%, followed by naive Bayes and logistic regression with 93%. These results underscore the significant potential of these algorithms to improve the early detection of Alzheimer's disease and to provide the requisite interventions.

Sivakani and Ansari [28] utilized the OASIS longitudinal MRI dataset to examine the effectiveness of machine learning algorithms in the early identification and classification of Alzheimer's disease. Their research underscored the significance of feature extraction and selection in enhancing the accuracy of Alzheimer's disease predictions. The expectation-maximization (EM) technique was utilized for clustering, best-first search was performed for feature selection, and the dataset was preprocessed to address missing values. To do classification, linear regression and Gaussian process models were employed. The Gaussian process approach exhibited high efficiency and accuracy in Alzheimer's disease classification, with a receiver operating characteristic (ROC) accuracy of 94.65%. The research finds that the effectiveness of machine learning models in identifying Alzheimer's disease is significantly improved with the application of efficient feature extraction and selection techniques

3. BACKGROUND

3.1. Overview of metaheuristic optimization

Metaheuristic optimization is one of the numerous methods for resolving intricate optimization problems. It is divided into three categories: evolutionary computation, nature-inspired algorithms, and swarm intelligence [29]. Even when unscheduled phenomena occur during the search, metaheuristic algorithms can search for dispersed solution spaces and focus logic to achieve a global minimum solution [30].

3.1.1. Differential evolution

Differential evolution is a population-based metaheuristic process that initializes its population in the search space and updates this population with the best offspring from the competition between a population member and a synthesized mutant vector generation after generation (or iteration after iteration) based on the three principles described here [31]. A continuous ring-switching differential evolution algorithm (DE jDE) that is collectively determined by the alternative dispute resolution main clause (ADM) or optimizing control and intelligence (OCI) in order to synthesize a mutant vector controls the population strategy. DENN ensembles have developed a variety of evolutionary strategies to achieve this. The strategy for evolving the new parameters for the forthcoming denotation of DE may be determined by the dynamics of those rings [32], [33]. The rings of DENN that will be employed are then determined by a meta-analysis.

The fundamental concepts that DE deals with include:

a. Population-Based Search: DE operates on a population of potential solutions. Each member of the population has the potential to solve the optimization problem.
b. Selection: The objective function serves as a guiding light in DE. It assesses the trial vector and if the experimental vector produces a superior objective function value it replaces the target vector in the population for the next generation.
c. Crossover: DE values diversity and this is evident in its crossover operation. This operation involves the combination of elements from the mutant vector and the target vector to generate an experimental vector.
d. Mutation: Mutation is the fundamental mechanism of DE in which new candidate solutions (mutant vectors) are generated by combining existing solutions.

3.1.2. Grey wolf optimizer

To resolve global optimization issues the GWO emulates the social hierarchy and predatory behavior of grey wolves. It assigns wolves to alpha, beta, and omega roles with alphas being the leaders of the pursuit. The algorithm is recognized for its competitive performance and rapid convergence distinguishing it from other optimization algorithms. It is effective for both constrained and unconstrained problems [34].

The fundamental concepts that GWO deals with include:

a. Leadership hierarchy: GWO models the social hierarchy of grey wolves dividing them into four categories:
   - Alpha: The best solution in the population representing the leader.
   - Beta: The second-best solution assisting the alpha in decision-making.
   - Delta: The third-best solution following the alpha and beta.
   - Omega: The remaining wolves following the leaders.
b. Hunting mechanism: The hunting process of grey wolves is mathematically modeled to guide the search for optimal solutions. This process includes three main phases: encircling prey, hunting, and attacking prey (exploitation).

$$D = |C\ X_{prey} - X| \quad (1)$$

$$X(t+1) = \frac{X_1 + X_2 + X_3}{3} \quad (2)$$

3.1.3. Parrot optimization

Parrot optimization is a literature-based algorithm predicated on parrots' exceptional learning capabilities [35]. PO is a population-based optimization algorithm of exceptional quality that seeks the optimal solution in a real-valued search space. Parrots' learning is governed by their action orientation which motivates this algorithm to track the search movements by maintaining a balance between exploration and exploitation to identify the optimal location.

Algorithm Steps:

a. Initialization: Generate an initial population of candidate solutions randomly. Evaluate the fitness of each individual using the objective function.
b. Leader selection: Identify a subset of the best individuals in the population as leaders. These leaders influence the movement of other individuals.
c. Communication and movement: The position of each individual is updated in accordance with the information it receives from leaders and neighboring parrots.

$$X_i(t+1) = X_i(t) + r_1\left(X_{leader} - X_i(t)\right) + r_2\left(X_{neighbor} - X_i(t)\right) \quad (3)$$

3.2. Overview of classification

3.2.1. Decision tree

A decision tree (DT) is a non-parametric supervised learning algorithm for classification and regression tasks. It generates a tree structure of decisions and their potential repercussions by recursively dividing the dataset into subsets based on the most significant attribute [36]. Each internal node in classification represents a "test" on an attribute, each branch represents the test result, and each leaf node represents a class label or a continuous value in regression. The dividing process continues until a halting criterion is met, such as completing all samples in a node that belongs to the same class, attaining a maximal tree depth, or lacking any additional information gain. Decision trees are simple to understand and interpret, require minimal data preprocessing, and can be employed to analyze numerical and categorical data [37]. Nevertheless, they are prone to overfitting if not pruned, and they may be unstable due to the potential for a completely different tree to emerge from modest data changes.

3.2.2. Random forest

Random forest is an ensemble learning method that determines the class based on the mode of the classes (classification) or the mean prediction (regression) of the individual trees during training [38]. It constructs a decision tree for each subset and generates numerous subdivisions of the original dataset through bootstrap sampling (random sampling with replacement). A random subset of features is chosen at each node, and the most appropriate feature from this subset is used to divide the node [39]. The correlation between trees is diminished as a result of this variability. The predictions from all individual trees are combined to produce the final prediction. Compared to individual decision trees, random forests are more accurate, can handle large datasets efficiently, and can handle thousands of input variables without variable deletion, all of which reduce overfitting [40]. However, they are more computationally intensive, complex, and less interpretable than individual decision trees. The optimization of engineering designs, the training of neural networks, the clustering and data mining of data, the processing of images and signals, the development of control systems, and the simulation of financial data are all areas in which they are extensively employed.

3.2.3. Gradient boosting

Gradient Boosting is a valuable machine-learning technique for solving regression and classification problems. It entails the incremental development of a model from an ensemble of poor learners, typically decision trees [41]. It functions by initiating with an initial prediction, often the mean of the objective variable in regression problems, and subsequently incorporating decision trees into the model. Each new tree predicts the previous model's residual errors (differences between actual and predicted values) [42]. The algorithm minimizes the loss function through gradient descent, which ensures that the new model is in alignment with the negative gradient of the loss function about the predictions of the current model. The learning rate reduces the contribution of each new tree, thereby accelerating the learning process and improving generalization. Regularization techniques such as subsampling, L1/L2 regularization, and tree pruning are implemented [43] to prevent overfitting. Gradient boosting is a highly accurate and robust method that can perform regression and classification tasks. It is capable of accommodating a wide variety of loss functions. However, it is prone to overfitting if scrupulously calibrated, and training can be efficient for large datasets. It is widely used in optimizing engineering designs, neural network training, clustering and data mining, image and signal processing, control systems, and financial modeling.

3.2.4. XGBoost

Extreme gradient boosting is a sophisticated machine learning algorithm based on the gradient boosting framework and engineered to achieve high efficiency and performance [44]. It sequentially constructs an ensemble of decision trees, with each subsequent tree rectifying the errors of the preceding trees. Additionally, it implements L1 and L2 regularization to prevent overfitting. XGBoost is efficient with sparse data, supports parallel processing for performance, and internally manages missing values [45]. It can scale to large datasets, employs pruning to prevent overfitting, and permits the use of custom objective functions and evaluation metrics. The high accuracy and scalability of XGBoost have made it a preferred choice in fields such as finance and biology, and it is widely used in various machine learning competitions and applications.

4. METHOD

4.1. Approach

Figure 1 depicts the primary stages of the proposed approach implemented in this investigation. This methodology includes three phases. Four bio-inspired algorithms were implemented to identify the most advantageous attributes during the initial phase. Four machine learning classifiers were implemented for training during the second phase. Ultimately, the algorithms were validated using the performance metrics.

4.1.1. Dataset

A single dataset was used to assess the proposed characteristic-choice set of rules: the Alzheimer's disease dataset [46]. This dataset is frequently utilized to analyze factors associated with Alzheimer's, construct predictive models, and conduct statistical analyses. It is publicly accessible. The Alzheimer's Disease dataset contains the comprehensive health statistics of 2,149 patients, each individually identified by an ID number between 4751 and 6900. Demographic information, lifestyle factors, scientific records, and medical, cognitive, and functional variables comprise the Alzheimer's disease dataset.

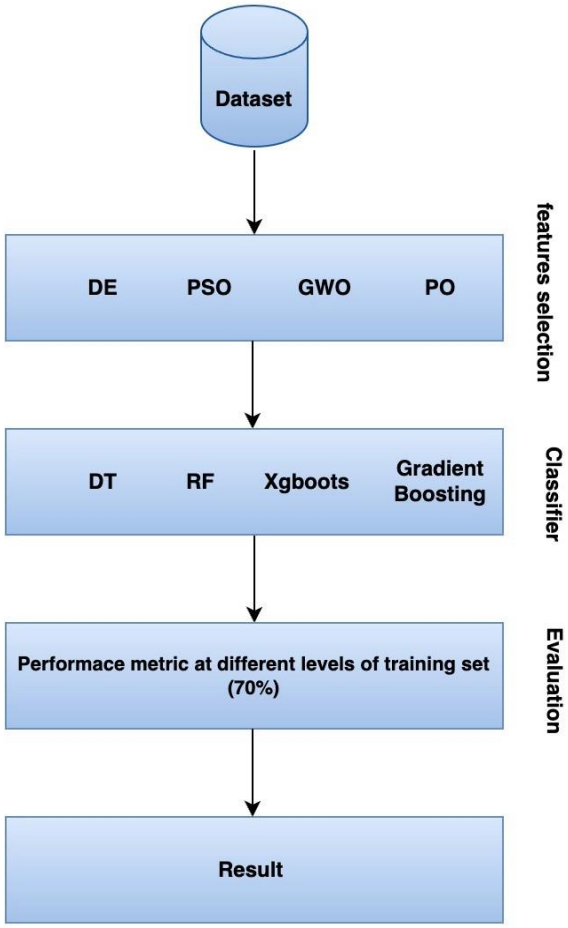

Figure 1. Proposed approach

4.1.2. Feature selection

Various attributes and features are incorporated into a copious increase in medical data. Most attributes do not contribute to predictive application outcomes, increasing computation time and resources. Therefore, to attain high accuracy rates, selecting a subset of features is necessary. Differential evolution (DE), grey wolf optimizer (GWO), and parrot optimization algorithm (POA) were employed in this study to identify the optimal subset of features based on the Alzheimer's disease dataset. By employing a fitness function that was developed explicitly for a decision tree classifier, the dataset's features were diminished in order to optimize the model's accuracy.

In order to assess each subset of features, the fitness function trains a decision tree classifier on the training set (70% of the data) and calculates the accuracy on the test set (30% of the data). Accuracy is the proportion of correct predictions the classifier makes, and the fitness score is calculated as 1 − accuracy. The fitness function can be mathematically represented as (4):

$$Fitness(S) = 1 - \frac{1}{N_{test}} \sum_{i=1}^{N_{test}} \delta(y_i, y\hat{}i) \quad (4)$$

where S is the subset of selected features, N_{test} is the number of test samples, y_i is the true label of the i-th test sample, $y\hat{}i$ is the predicted label of the i-th test sample, and $\delta(y_i, y\hat{}i)$ is the Kronecker delta function, which is 1 if $y_i = y\hat{}i$ and 0 otherwise. For the Alzheimer's disease dataset, DE, GWO, and POA were applied to the training set.

4.1.3. Classification

The subsequent step is to commence the classification process, which entails training the set of features using a variety of classifiers. This is because we have successfully identified the most suitable features in the Alzheimer's disease dataset and have purified all potentially noisy data as a result of the feature selection process in the previous step. We conducted experiments with a variety of parameters in DE,

GWO, and POA, such as the number of iterations (the replication of a process to produce an outcome) and population size (the arbitrary construction of populations to determine the optimal population size based on the problem). We conducted experiments on populations of 30 and 60 and iterations of 5, 15, and 30 to determine the most effective configuration for feature selection and classification.

4.1.4. Evaluation

Four performance metrics were employed to assess the parrot optimization (PO), differential evolution (DE), and grey wolf optimizer (GWO) algorithms: precision, recall, F-score, and accuracy. Accuracy is a statistical bias metric that quantifies the percentage of a test's success rate. Low accuracy values suggest a discrepancy between the actual and result sets. Table 1 illustrates the confusion matrix for classification, which represents the classification of the potential outcome of recommending an item to a user. Accuracy employs four test measures.

Table 1. Confusion matrix for classification

	Recommended	Not recommended
Preferred	True positive (TP)	False negative (FN)
Not preferred	False positive (FP)	True negative (TN)

4.1.5. The F-score

The F-score, a solitary digit, concisely evaluates a system or model's ability to generate precise optimistic predictions and identify every positive instance. The algorithm integrates two fundamental metrics, namely recall (the capacity to identify all positive cases) and precision (the accuracy of optimistic predictions). By achieving an equilibrium between these two variables, the F1-score offers a unified metric for evaluating performance. Elevated values on a scale of 0 to 1 indicate superior performance. It serves as a practical instrument for assessing the efficacy of classification systems. Defined by this formula is the F-score:

$$F\,1 \;=\; 2 \cdot \frac{\text{Precision} \cdot \text{Recall}}{Precision + Recall} \tag{5}$$

4.1.6. Precision

Indicates the proportion of positive cases predicted by the model that turned out to be true. It quantifies the precision with which the model generates affirmative predictions. The formula for precision is:

$$Precision \;= \frac{TP}{TP + FP} \tag{6}$$

4.1.7. Recall

As with sensitivity, recall quantifies the accuracy with which the model detects true positives. It provides the number of accurate optimistic predictions the model makes relative to the total number of positive cases. The formula for recall is:

$$Recall \;= \frac{TP}{TP+FN} \tag{7}$$

5. RESULTS AND DISCUSSION

The Alzheimer's disease dataset was employed to evaluate the DE, GWO, and POA algorithms. In this context, these metaheuristic algorithms have not been extensively compared for feature selection, to the best of our knowledge. Four classifiers were employed to evaluate the feature selection algorithms: gradient boosting, XGBoost, RF, and DT. In order to guarantee the impartiality of the outcomes, the algorithms were trained with identical methodologies. The scikit-learn library in Python, which includes built-in libraries for feature selection algorithms, had the classifiers available. Tables 2 to 4 list numerous input parameters that are employed in the execution of these feature selection algorithms. The parameters' values were determined through experimentation and are contingent upon the unique characteristics of each algorithm.

Table 2. Input parameters for parrot optimizer

Parameter	Description
lb	Lower bound for the search space
ub	Upper bound for the search space
dim	Dimensionality of the search space
N	Population size
Max_iter	Maximum number of iterations

Table 3. Input parameters for differential evolution (DE)

Parameter	Description
lb	Lower bound for the search space
ub	Upper bound for the search space
dim	Dimensionality of the search space
PopSize	Population size
iters	Number of iterations
mutation factor	Mutation factor (controls the amplification of the differential variation). Default is 0.5. crossover ratio
crossover ratio	Crossover ratio (controls the probability of crossover). Default is 0.7

Table 4. Input parameters for grey wolf optimizer (GWO)

Parameter	Description
lb	Lower bound for the search space
ub	Upper bound for the search space
dim	Dimensionality of the search space
SearchAgents no	Number of search agents
Max iter	Maximum number of iterations

6. DISCUSSION

Two tables, Tables 5 and 6, present the DE algorithm's evaluation results on the Alzheimer's disease dataset. The tables evaluate population sizes of 30 and 60 across various iterations (5, 15, and 30). The gradient boosting classifier consistently achieved the highest accuracy for a population size of 30, as depicted in Table 5, with a maximum of 0.935866 at five iterations. XGBoost also demonstrated satisfactory performance, attaining its maximum accuracy of 0.935556 after 30 iterations. In contrast, the DT and RF classifiers exhibited lower accuracy but were still dependable. The DT achieved 0.897468 after 30 iterations, while the RF reached 0.923204 after five iterations.

Table 5. DE algorithm using 30 population

Iterations	Classifier	Accuracy	Precision	Recall	F1-score
5	Decision tree	0.89	0.88	0.84	0.85
	Gradient boosting	0.93	0.94	0.88	0.9
	Random forest	0.92	0.95	0.84	0.89
	XGBoost	0.94	0.95	0.88	0.91
15	Decision tree	0.9	0.88	0.84	0.85
	Gradient boosting	0.93	0.94	0.88	0.91
	Random forest	0.92	0.95	0.84	0.88
	XGBoost	0.94	0.94	0.88	0.9
30	Decision tree	0.9	0.89	0.84	0.87
	Gradient boosting	0.93	0.93	0.88	0.91
	Random forest	0.92	0.95	0.84	0.89
	XGBoost	0.94	0.95	0.88	0.91

The gradient boosting classifier again attained the highest accuracy of 0.936693 at 30 iterations when the population size was increased to 60 in Table 6. XGBoost closely matched this result. The DT and RF classifiers yielded reliable outcomes, with the DT attaining an accuracy of 0.898036 after 30 iterations and the RF reaching 0.923721 after 30 iterations. These findings indicate that the gradient boosting classifier consistently outperformed others in accuracy, particularly at higher iterations and larger population sizes.

Additionally, XGBoost exhibited high accuracy and robustness across various configurations. When combined with robust classifiers such as gradient boosting and XGBoost, the DE algorithm demonstrated efficacy in improving predictive accuracy for Alzheimer's disease diagnosis. The gradient boosting classifier achieved the highest accuracy of 0.936693 at 30 iterations and a population size of 60.

Table 6. DE algorithm using 60 population

Iterations	Classifier	Accuracy	Precision	Recall	F1-score
5	Decision tree	0.89	0.87	0.84	0.86
	Gradient boosting	0.93	0.94	0.88	0.91
	Random forest	0.91	0.95	0.83	0.88
	XGBoost	0.93	0.95	0.88	0.91
15	Decision tree	0.9	0.88	0.84	0.86
	Gradient boosting	0.93	0.94	0.88	0.9
	Random forest	0.92	0.95	0.84	0.89
	XGBoost	0.94	0.95	0.88	0.91
30	Decision tree	0.9	0.88	0.84	0.86
	Gradient boosting	0.93	0.94	0.88	0.9
	Random forest	0.92	0.95	0.84	0.89
	XGBoost	0.94	0.95	0.88	0.91

Tables 7 and 8 illustrate the accuracy, precision, recall, and F1-score evaluation results of the GWO algorithm on the Alzheimer's disease dataset. In a series of iterations (5, 15, and 30), the GWO algorithm was assessed with population sizes of 30 and 60. At 30 iterations, the gradient boosting classifier consistently demonstrated superior accuracy for the GWO algorithm with a population size of 30 in Table 7, with a maximal accuracy of 0.935142. XGBoost also exhibited satisfactory performance, achieving the highest accuracy of 0.935039 after five iterations. Conversely, the DT and RF classifiers maintained their consistency while exhibiting a marginally lower level of accuracy. At 30 iterations, the DT obtained its highest accuracy of 0.896021, while the RF achieved 0.923979 during the same period. The efficacy of the GWO algorithm with a population size of 30 is demonstrated in Table 7. This table compares the efficacy of the algorithm at different iterations and classifiers. The gradient boosting classifier attained a high accuracy of 0.934057 at 30 iterations when a population size of 60 was used, closely following XGBoost's 0.935659 accuracy at 15 iterations Table 8. Both the DT and RF classifiers produced findings that were fairly remarkable in their respective categories. When compared to the RF, which was able to reach an accuracy of 0.924961 in the same length of time, the DT was able to attain an accuracy of 0.897519 over the course of thirty iterations. According to the data, it would appear that the Gradient Boosting and XGBoost classifiers consistently beat other approaches in terms of accuracy. This was especially true when the number of iterations was raised and the population size was increased. The GWO algorithm's ability to improve the expected accuracy of Alzheimer's disease diagnosis is notably apparent when it is applied in conjunction with these effective classifiers. This is because the GWO algorithm is able to improve predicted accuracy. The XGBoost classifier attained the highest accuracy for the GWO method with a population size of 60 and 15 iterations (accuracy = 0.935659). Table 8 demonstrates the effectiveness of the GWO method with a population size of 60 across various classifiers and iterations.

Tables 9 and 10 illustrate the evaluation results of the PO algorithm on the Alzheimer's disease dataset in terms of precision, recall, accuracy, and F1-score. The PO algorithm was evaluated with population sizes of 30 and 60 in various iterations (5, 15, and 30). The gradient boosting and XGBoost classifiers consistently achieved higher accuracy for the PO algorithm with a population size of 30 in Table 9. At 30 iterations, gradient boosting attained a maximal accuracy of 0.928062, while XGBoost achieved 0.929199. On the other hand, the DT and RF classifiers demonstrated slightly lower accuracy but continued to operate consistently. The DT achieved its highest accuracy of 0.883618 at 30 iterations, while the RF achieved 0.917313 at 15. The performance of the PO algorithm with a population size of 30 across various classifiers and iterations is illustrated in Table 9.

Table 7. GWO algorithm using 30 Population

Iterations	Classifier	Accuracy	Precision	Recall	F1-score
5	Decision tree	0.89	0.87	0.84	0.86
	Gradient boosting	0.93	0.94	0.88	0.91
	Random forest	0.92	0.95	0.84	0.89
	XGBoost	0.94	0.94	0.88	0.91
15	Decision tree	0.89	0.87	0.84	0.86
	Gradient boosting	0.93	0.94	0.88	0.91
	Random forest	0.92	0.95	0.84	0.89
	XGBoost	0.93	0.94	0.88	0.91
30	Decision tree	0.9	0.88	0.84	0.86
	Gradient boosting	0.93	0.94	0.88	0.91
	Random forest	0.92	0.95	0.84	0.89
	XGBoost	0.94	0.95	0.88	0.91

Table 8. GWO algorithm using 60 population

Iterations	Classifier	Accuracy	Precision	Recall	F1-score
5	Decision tree	0.89	0.87	0.84	0.86
	Gradient boosting	0.93	0.94	0.88	0.91
	Random forest	0.92	0.95	0.84	0.89
	XGBoost	0.93	0.94	0.88	0.91
15	Decision tree	0.9	0.88	0.84	0.86
	Gradient boosting	0.93	0.94	0.88	0.91
	Random forest	0.92	0.95	0.84	0.89
	XGBoost	0.94	0.95	0.88	0.91
30	Decision tree	0.9	0.88	0.84	0.86
	Gradient boosting	0.93	0.94	0.88	0.91
	Random forest	0.92	0.95	0.85	0.9
	XGBoost	0.93	0.94	0.88	0.91

Table 9. PO algorithm using 30 population

Iterations	Classifier	Accuracy	Precision	Recall	F1-score
5	Decision tree	0.87	0.84	0.82	0.83
	Gradient boosting	0.92	0.94	0.85	0.89
	Random forest	0.91	0.95	0.81	0.88
	XGBoost	0.92	0.94	0.85	0.89
15	Decision tree	0.88	0.86	0.83	0.84
	Gradient boosting	0.93	0.94	0.87	0.9
	Random forest	0.92	0.95	0.83	0.88
	XGBoost	0.93	0.94	0.86	0.9
30	Decision tree	0.88	0.86	0.83	0.84
	Gradient boosting	0.93	0.94	0.87	0.9
	Random forest	0.92	0.95	0.82	0.88
	XGBoost	0.93	0.94	0.87	0.9

Table 10. PO algorithm using 60 population

Iterations	Classifier	Accuracy	Precision	Recall	F1-score
5	Decision tree	0.89	0.87	0.84	0.85
	Gradient boosting	0.93	0.94	0.88	0.91
	Random forest	0.92	0.95	0.82	0.88
	XGBoost	0.94	0.95	0.88	0.91
15	Decision tree	0.89	0.87	0.84	0.85
	Gradient boosting	0.93	0.94	0.88	0.91
	Random forest	0.92	0.95	0.82	0.88
	XGBoost	0.94	0.95	0.88	0.91
30	Decision tree	0.89	0.87	0.84	0.85
	Gradient boosting	0.93	0.94	0.88	0.91
	Random forest	0.92	0.95	0.83	0.88
	XGBoost	0.93	0.94	0.88	0.91

With a population size of sixty, the gradient boosting and XGBoost classifiers achieved a substantial level of accuracy, as shown in Table 10. Gradient boosting was able to achieve a maximum accuracy of 0.934935 after 15 iterations, whilst XGBoost was able to achieve an accuracy of 0.935556 after the same number of rounds. A great performance was displayed by both the RF and DT classifiers. The RF classifier attained an accuracy of 0.918398 after 30 iterations, while the DT classifier reached an accuracy of 0.890698 under the same conditions. The results of the study reveal that the gradient boosting and XGBoost classifiers displayed consistently higher accuracy, particularly when the population sizes were raised, and the number of iterations was increased. When combined with reliable classifiers, the PO method results in a considerable improvement in the predicted accuracy of Alzheimer's disease diagnosis. With a population size of sixty and fifteen iterations, the XGBoost classifier was able to achieve an accuracy of 0.935556 for the PO method. Table 10 provides a comprehensive analysis of the performance of the PO method, which utilizes a population size of sixty with a number of different classifiers and iterations included.

7. CONCLUSION

This study highlights the significant enhancement of predictive accuracy in classifiers applied to the Alzheimer's disease dataset through the critical role of feature selection. This highlights the effectiveness of employing metaheuristic optimization algorithms, specifically PO, GWO, and DE, to attain this objective. The gradient boosting and XGBoost classifiers demonstrated enhanced accuracy, precision, recall, and

F1-scores across various population sizes and iterations, as supported by the research findings. The DE algorithm, combined with Gradient Boosting, attained a maximum accuracy of 0.935866 following five iterations with a population size of 30. This is particularly significant. Similarly, GWO achieved an optimal accuracy of 0.935659 using XGBoost after 15 iterations with a population size of 60. Following 15 iterations, the PO algorithm achieved an accuracy of 0.94 with a population size of 60. This study underscores the significance of feature selection in enhancing diagnostic models for Alzheimer's disease. The study underscores the efficacy and robustness of metaheuristic algorithms in this context. Future research may investigate the incorporation of additional classifiers to enhance diagnostic accuracy and the application of these algorithms across various medical datasets. A potential approach to enhance the detection of Alzheimer's disease and other complex medical disorders involves the integration of metaheuristic optimization algorithms with robust classifiers. Examples of these classifiers include Gradient Boosting and XGBoost.

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This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
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R : **R**esources
D : **D**ata Curation
O : Writing **O**riginal Draft
E : Writing Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

INFORMED CONSENT

Informed consent is not applicable to this study as it does not involve human participants or identifiable personal information.

ETHICAL APPROVAL

Ethical approval is not applicable to this study as it does not involve human participants or animals.

DATA AVAILABILITY

The data that support the findings of this study are openly available on Kaggle

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