



Enhancing diabetes prediction performance using feature selection based on grey wolf optimizer with autophagy mechanism

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ABSTRACT

Diabetes mellitus, often called a silent killer, is a chronic condition characterized by insufficient insulin production and elevated blood sugar levels, leading to complications in vital organs such as the nerves, eyes, and kidneys. Machine learning is a powerful tool for predicting diabetes; however, noisy features can negatively impact its accuracy, making an effective feature selection essential. This study proposes an improved feature selection approach for diabetes prediction, leveraging the Grey Wolf Optimizer with an integrated Autophagy Mechanism (GWO-AM) on the Pima Indian Diabetes Dataset. The autophagy mechanism, inspired by cellular self-degradation and recycling, is incorporated into GWO to enhance exploration and exploitation. The method was also tested on glioma and lung cancer datasets to assess scalability. Comprehensive experiments demonstrate that GWO-AM significantly improves prediction accuracy while reducing the number of selected features. For the diabetes dataset, GWO-AM achieved an accuracy of 90.91 %, outperforming existing methods. It also excelled in the glioma and lung cancer datasets, highlighting its potential for application to other medical datasets.

1. Introduction

Diabetes mellitus is a long-term health condition that presents a major challenge globally, impacting millions of people. Predicting diabetes early and accurately is essential for prompt intervention and effective management, which may help lower the chances of serious complications linked to the disease. In recent years, machine learning methods have gained prominence in the medical field for their ability to analyze complex datasets and make accurate predictions [1,2]. A vital component of these techniques is feature selection, which focuses on finding the most relevant features in a dataset to improve the performance of predictive models [3,4].

Feature selection is essential for handling high-dimensional data, as it decreases the computational time and enhances the interpretability of the models [5]. There are three common approaches for feature selection: filter, wrapper, and hybrid method. Wrapper methods generally provide higher accuracy compared to filter methods. Besides, they have lower computational costs than hybrid methods and are more straightforward in implementation [5].

Metaheuristic-based wrapper methods have gained significant popularity due to their superior performance in addressing feature

selection problems [3,4,6], including Greylag Goose Optimization (GGO) [7], Waterwheel Plant Algorithm (WPA) [8], Salp Swarm Algorithm (SSA) [9], Grey Wolf Optimizer (GWO) [10], Particle Swarm Optimization (PSO) [11], Genetic Algorithm (GA), Hybrid Whale Optimization Algorithm with Chameleon Hunting Mechanism (HWOA-CHM) [6], Enhanced Salp Swarm Algorithm (ESSA) [12], Grey Wolf Optimizer with Two-phase Mutation (TMGWO) [13], and Particle Swarm Optimization with Adaptive Inertia Weight (PSO-AIW) [14]. The methods have been applied to various cases, such as coronary artery disease [15], gesture recognition [16], cancer disease [17], diabetes disease[3], clinical cancer biomarkers [11], zika virus [18], renewable energy power [19], and classification problems [20,21].

However, metaheuristic-based wrapper methods often face challenges such as local optima and slow convergence. Bio-inspired optimization algorithms have been increasingly explored to address these issues. The GWO has shown promise due to its simplicity and effectiveness in various optimization problems [10,22]. The GWO simulates the natural leadership structure and hunting patterns of grey wolves in nature. Despite its advantages, the GWO can sometimes struggle with premature convergence and get trapped in local optima [23,24]. This paper proposes a Grey Wolf Optimizer with Autophagy Mechanism

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(GWO-AM) to overcome these limitations. Autophagy Mechanism is inspired by the cellular process of autophagy, in which cells degrade and recycle their components [25,26]. This mechanism is integrated into GWO to improve its exploration and exploitation balance, thereby enhancing its performance in feature selection tasks.

In this study, there are several contributions, which are outlined as follows:

1. Enhancing diabetes prediction by introducing a new variant of feature selection through GWO-AM.
2. Presenting a comparison between the GWO-AM with the classical and state-of-the-art metaheuristic-based feature selection methods.
3. Providing an analysis of the influence of GWO-AM on twelve machine learning methods used as classifiers.
4. Evaluating the GWO-AM to other datasets, including glioma and lung cancer datasets.

The rest of this paper is organized as follows: [Section 2](#) covers related work on diabetes prediction and metaheuristic-based feature selection methods. [Section 3](#) then explains the proposed GWO-AM algorithm in detail. [Section 4](#) presents the main results and discussion. Lastly, [Section 5](#) offers the conclusion along with recommendations for future research.

2. Related Work

Diabetes mellitus is a long-term health condition that affects millions of people around the world. Early diabetes prediction is crucial because it allows for timely treatment and management, which can help prevent serious complications. Machine learning techniques have recently become popular in the medical field because they can analyze large amounts of complex data and make accurate predictions. It helps doctors and healthcare professionals identify individuals at risk of developing diabetes, allowing for earlier interventions and better management of the disease.

Several machine learning algorithms have been developed for diabetes prediction using the Pima Indian Diabetes Dataset (PIDD). In 2019, Larabi-Marie-Sainte et al. compared several machine learning algorithms. The results showed that REPTree obtained the best performance with 74.48% accuracy using 10-fold cross-validation [27].

In 2020, Singh et al. proposed the NSGA-II-Stacking method to predict diabetes disease. The results showed that NSGA-II-Stacking outperforms other machine learning algorithms with an accuracy of 83.8% [28]. Alghurair et al. employed several Support Vector Machine (SVM) kernels in the same year. They reported that Linear SVM achieved the best performance with an accuracy of 83% [29]. Moreover, Tigga N et al. compared some machine learning algorithms. They stated that Random Forest (RF) obtained the best performance with an accuracy of 75% [30]. Lastly, Wang M et al. proposed an improved whale optimization algorithm (CMWOA), which combines chaotic and multiswarm strategies to boost SVM. The proposed method was compared with multiple SVM. They said that the proposed method outperformed all the other methods regarding classification performance [31].

In 2021, several studies applied machine learning algorithms like Ensemble-voting [32], Quantum machine learning [33], and Multi-layer Perceptron (MLP) [34] to predict diabetes. These algorithms achieved accuracies of 86%, 79.08%, and 88.57%, respectively. The train-test split method was used for evaluation. Furthermore, Butt et al. also compared different classifiers for diabetes classification. They stated that Long Short-term Memory (LSTM) reached 87.26% accuracy [1].

In 2022, Chang et al. [35] proposed an e-diagnosis system implemented on the Internet of Medical Things (IoMT) using machine learning algorithm, especially for diabetes disease. They compared some machine learning algorithms to obtain the proper algorithm. They employed imputation of zero values on features with invalid zero values using median value. Based on the experimental results, RF obtained promising performance with 79.57% accuracy. At the same time, Madan

P et al. [36] proposed CNN and Bi-LSTM for diabetes prediction in a real-time environment. Using train-test split for evaluation, they stated that CNN and Bi-LSTM achieved 88.37% accuracy.

In 2023, Rupapara et al. presented a Logistic Tree Classifier (LTC) and Feature Fusion for diabetes prediction. Using a train-test split, they showed that the proposed method achieved 85% accuracy [37]. Besides, Reza et al. proposed an improved non-linear kernel for SVM. They employed missing value and outliers handling by leveraging median value. Moreover, a robust synthetic-based over-sampling approach is used to tackle the imbalance class. Based on the experimental results, the proposed method achieved 85.5% accuracy [38].

In 2024, a study [39] proposed En-RfRsk to predict the risk of diabetes disease. Moreover, they compared the proposed method to other machine learning algorithms with train-test split evaluation. The results showed that the proposed method obtained 88.89% accuracy.

Unfortunately, previous studies utilizing machine learning for diabetes prediction have not achieved optimal results, primarily due to the influence of noisy and high-dimensional features. Consequently, implementing feature selection techniques is essential to improve machine learning performance. These techniques can generally be divided into three categories: filter methods, wrapper methods, and hybrid methods [5].

Metaheuristic-based wrapper methods have gained popularity due to their effectiveness in addressing feature selection challenges. In [7], the Greylag Goose Optimization algorithm was introduced as a method for feature selection. The algorithm's performance was evaluated using nineteen datasets from the UCI repository, demonstrating highly promising results for feature selection tasks. Chaudhuri et al. [40] proposed an effective feature selection for detecting of Parkinson's disease using the Binary Whale Optimization Algorithm (BWOA). They stated that the proposed method can significantly improve the accuracy of Parkinson's detection. Moreover, [41] proposed aerial target motion feature selection based on improved GWO. The results presented that the proposed method can improve the accuracy of aerial target motion. Furthermore, [42] compared Naïve Bayes (NB) and SVM with GWO as feature selection for cervical cancer data classification. Based on the experimental results, the proposed obtained promising performance. NB with GWO achieved the best accuracy. Finally, [43] proposed GWO with RF to improve malnutrition classification. The results indicated that GWO can significantly improve machine learning performance.

The application of metaheuristic-based feature selection is proven to improve model performance. Therefore, this study proposes a Grey Wolf Optimizer with Autophagy Mechanism (GWO-AM) as feature selection. Previous studies have demonstrated the effectiveness of GWO in various feature selection tasks, including medical data analysis, image processing, and classification problems. However, despite its strengths, GWO can sometimes suffer from premature convergence and get trapped in local optima. To address these issues, the GWO combined with Autophagy Mechanism (AM) aims to enhance their ability to escape local optima and improve convergence speed. The AM, a cellular process involving the degradation and recycling of cellular components, has recently inspired a new optimization mechanism.

In this context, our work builds on the foundation of GWO and introduces AM to enhance its feature selection performance. The proposed GWO-AM aims to address the limitations of traditional GWO by improving its exploration and exploitation balance. This study represents a novel application of the autophagy mechanism in the context of feature selection for diabetes prediction, providing a comprehensive evaluation of its effectiveness compared to existing methods.

3. Proposed Method

This section provides an overview of the dataset description, pre-processing, GWO algorithm, AM algorithm, Hybrid GWO-AM as feature selection, machine learning, hyperparameter tuning, and experimental framework.

Table 1
Description of the PIMA Indian Diabetes Dataset (PIDD).

Features	Type	Description	No. of missing values
Pregnancies	Numeric	Number of times pregnant	0
Glucose	Numeric	Plasma glucose concentration 2 hours in an oral glucose tolerance test	5
Blood Pressure	Numeric	Diastolic blood pressure (mm Hg).	35
Skin Thickness	Numeric	Triceps skinfold thickness (mm).	227
Insulin	Numeric	2-hour serum insulin (μ)	374
BMI	Numeric	Body mass index (kg/m ²)	11
DPF	Numeric	Diabetes pedigree function	0
Age	Numeric	Age (years)	0
Outcome	Nominal	Diabetes diagnose results (positive:1, negative:0)	0

3.1. Dataset description

The dataset employed in this study is the publicly accessible Pima Indians Diabetes Dataset (PIDD) [44]. The dataset comprises 768 instances, of which 268 correspond to diabetic patients and 500 to non-diabetic individuals. The dataset has eight attributes and one target variable. The attributes include the following: pregnancy, blood pressure, glucose level, skin thickness, insulin level, Diabetes Pedigree Function (DPF), Body Mass Index (BMI), and age. The target variable is the outcome, which indicates the presence or absence of diabetes.

Detailed information regarding the Pima Indians Diabetes Dataset is presented in [Table 1](#).

3.2. Pre-processing

Data pre-processing is an essential stage in transforming data into useful and efficient ones. This study has three stages to data processing: handling missing values, outliers, and z-score normalization. Firstly, addressing missing values is essential for managing incomplete data on certain features, including blood pressure, glucose, insulin, skin thickness, and BMI. In this study, all missing values were addressed using median imputation, a robust method selected due to the presence of skewed distributions and outliers in the dataset, as illustrated in [Fig. 1](#). The median is less sensitive to extreme values compared to the mean, making it a suitable choice for preserving the central tendency of the data while minimizing the influence of outliers [32,38]. This approach ensures the dataset's completeness and reliability for subsequent analysis. Detailed information on the features is provided in [Table 1](#).

Secondly, handling outliers is an essential part of data pre-processing to reduce the influence of extreme values that differ greatly from the rest of the data. Outliers can distort statistical analysis and compromise the accuracy of predictive modeling. This study employed the Interquartile Range (IQR) method to identify outliers within the dataset. Once identified, outliers were replaced with the median value of the respective feature. This approach aims to reduce the influence of outliers while maintaining the integrity of the overall data distribution [32,38].

Lastly, features within PIDD exhibit varying scales, which can impair the performance of certain machine learning algorithms. This is

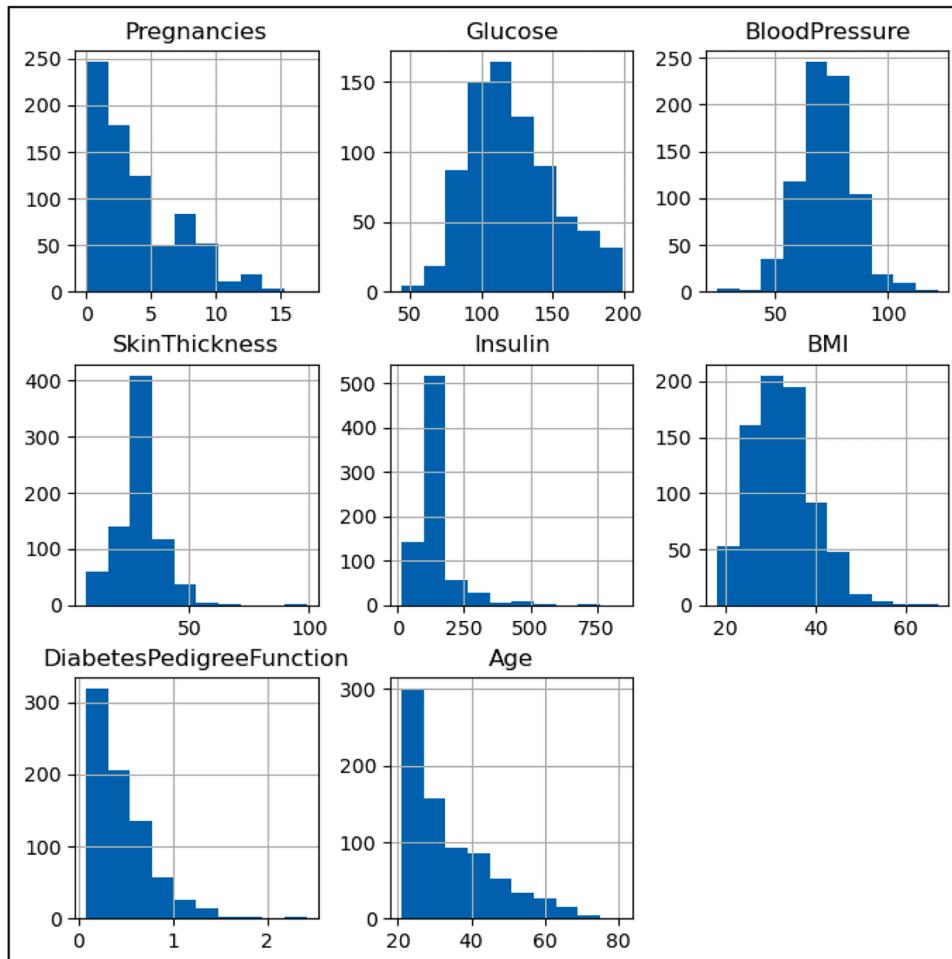


Fig. 1. Histogram plot for each feature in the dataset.

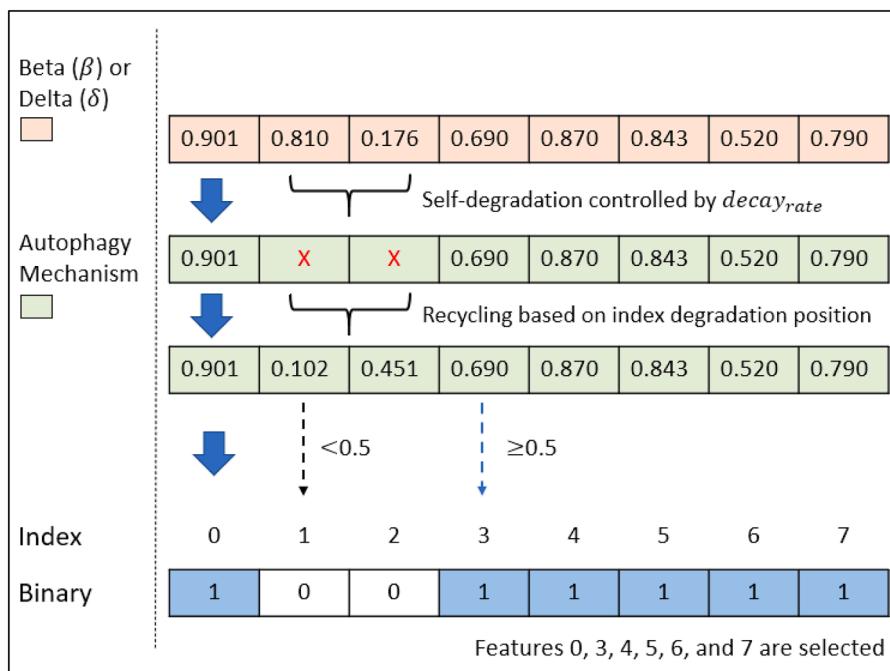


Fig. 2. GWO with first stage Autophagy Mechanism (AM).

particularly true for distance-based methods such as K-Nearest Neighbors (KNN), and gradient-based methods like Logistic Regression (LR). To mitigate this issue, z-score normalization was applied in this study, standardizing the features to a common scale. This process ensures feature comparability, thereby enhancing the effectiveness of the machine learning models. Z-score normalization can be calculated using Eq. (1).

$$Z = \frac{X - \mu}{\sigma} \quad (1)$$

where the X signifies the raw data point. Then, σ is the standard deviation of the dataset measuring the spread of the data. Lastly, μ denotes the mean of the dataset.

3.3. Grey Wolf Optimizer (GWO)

GWO algorithm is a recently developed optimization algorithm by Mirjalili et al. [10]. It imitates grey wolves' leadership structure and hunting behavior in the wild. In this method, alpha (α) is the top solution in the population. Beta (β) and delta (δ) are the second and third-best solutions. The remaining solution is omega (ω). The equation is provided in Eq. (2) to express the encircling behavior mathematically.

$$X(t+1) = X_p(t) - A \cdot |C \cdot X_p(t) - X(t)| \quad (2)$$

where X is the wolf's position vector, X_p is prey's position vector, t is the current iteration, and A and C represent the coefficient vectors, which are computed in Eq. (3) and Eq. (4):

$$A = 2a \cdot r_1 - a \quad (3)$$

$$C = 2 \cdot r_2 \quad (4)$$

where a decreases linearly from 2 to 0 over iterations. r_1 and r_2 are the randomly created vector from $[0,1]$, respectively. The equation is presented in Eq. (5):

$$a(t) = 2 - 2 \cdot \frac{t}{MaxIter} \quad (5)$$

where $MaxIter$ represents the maximum number of iterations.

The other individuals update their positions based on the positions of α , β , and δ wolves, as described in Eqs. (6), (7), (8), and (9):

$$X_1(t) = X_\alpha(t) - A_1 \cdot |C_1 \cdot X_\alpha(t) - X(t)| \quad (6)$$

$$X_2(t) = X_\beta(t) - A_2 \cdot |C_2 \cdot X_\beta(t) - X(t)| \quad (7)$$

$$X_3(t) = X_\delta(t) - A_3 \cdot |C_3 \cdot X_\delta(t) - X(t)| \quad (8)$$

$$X(t+1) = \frac{X_1 + X_2 + X_3}{3} \quad (9)$$

where A_1 , A_2 , A_3 are similar to A , and C_1 , C_2 , and C_3 are similar to C .

3.4. Autophagy Mechanism (AM)

The Autophagy Mechanism is a relatively new concept in optimization algorithms, mimicking the autophagy process in biological systems where cells degrade and recycle components. Below is an implementation of a simplified autophagy mechanism. The AM algorithm involves the following key steps:

- 1) Identification: Identify features or solutions that are potentially irrelevant using statistical or model-based criteria.
- 2) Degradation: Select parts of solutions to degrade based on the degradation rate. To imitate a real-life process, the degradation rate calculated by Eq. (10).

$$Degradation_{rate} = inval \cdot e^{-decay_{rate} \cdot iter} \quad (10)$$

Here, $Degradation_{rate}$ refers to a parameter that controls the number of cells subject to deletion. As the iteration count increases, the degradation rate value decreases. This approach simulates a natural process where a more frequent autophagy mechanism produces fewer damaged cells. In other words, the condition of the cells improves with successive iterations, reflecting enhanced cellular health in the individual. The $inval$ represents the initial value expected during the $Degradation_{rate}$.

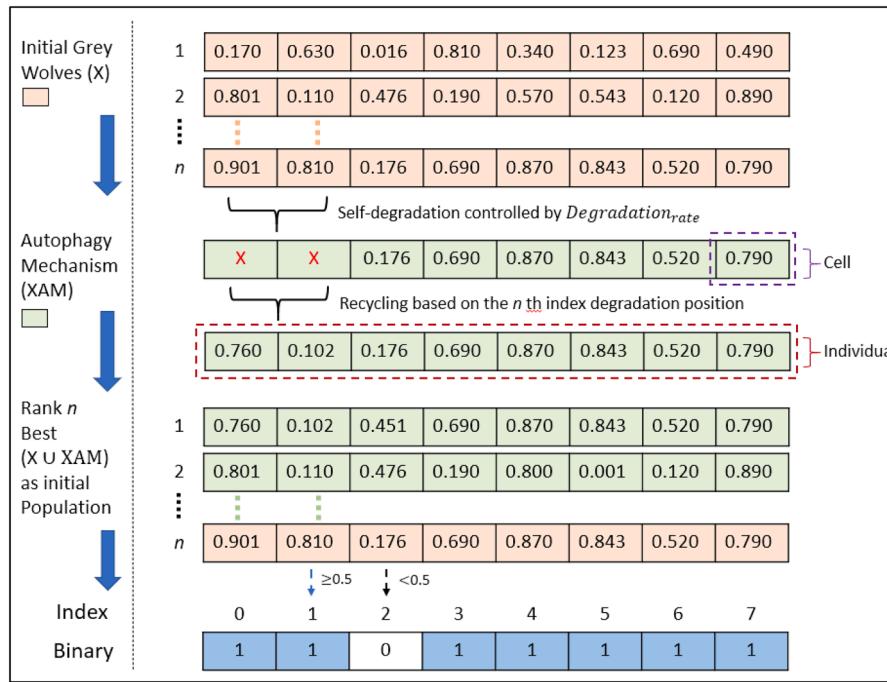


Fig. 3. GWO with the second stage Autophagy Mechanism (AM).

Algorithm 1

The second stage of AM for X_β (Beta Wolf).

```

1 Define indices  $X_\beta = []$ 
2 //Select index position in  $X_\beta$  based on DF value
3 while (len(indices  $X_\beta$ ) < DF)
4     rand_index = random (dim)
5     if (rand_index not in indices  $X_\beta$ )
6         indices  $X_\beta$ .append(rand_index)
7     end if
8 end while
9 // Degradation and Recycling
10 Define  $X_{\beta am} = X_\beta$ 
11 for i in indices  $X_\beta$ 
12      $X_{\beta am}[i] = \text{rand}()$ 
13 end for
14 Convert  $X_{\beta am}$  into binary using Eq. (15)
15 Calculate the fitness of  $X_{\beta am}$ 
16 if  $f(X_{\beta am}) < f(X_a)$ 
17      $f(X_a) = f(X_{\beta am})$ 
18      $X_a = X_{\beta am}$ 
19 end if

```

Algorithm 2

The second stage of AM for X_δ (Delta Wolf).

```

1 Define indices  $X_\delta = []$ 
2 //Select index position in  $X_\delta$  based on DF value
3 while (len(indices  $X_\delta$ ) < DF)
4     rand_index = random (dim)
5     if (rand_index not in indices  $X_\delta$ )
6         indices  $X_\delta$ .append(rand_index)
7     end if
8 end while
9 // Degradation and Recycling
10 Define  $X_{\delta am} = X_\delta$ 
11 for i in indices  $X_\delta$ 
12      $X_{\delta am}[i] = \text{rand}()$ 
13 end for
14 Convert  $X_{\delta am}$  into binary using Eq. (15)
15 Calculate the fitness of  $X_{\delta am}$ 
16 if  $f(X_{\delta am}) < f(X_a)$ 
17      $f(X_a) = f(X_{\delta am})$ 
18      $X_a = X_{\delta am}$ 
19 end if

```

process, which was set to 0.5. Additionally, the $decay_{rate}$ controls how fast the $Degradation_{rate}$ value decreases over time. A higher decay rate means the value decreases faster. $decay_{rate}$ was set 0.008.

$$DF = Degradation_{rate} \cdot TF \quad (11)$$

DF is the number of cells or features deleted, and TF is the total feature. The equation can be seen in Eq. (11). The cells that will be deleted in individuals correspond to the DF value and are selected randomly.

3) Recycling: Recycle cells that have been removed using values from 0-1 to mimic the autophagy process.

3.5. Hybrid GWO with AM as Feature Selection

In this study, the GWO is enhanced by incorporating an AM to improve both exploration and exploitation capabilities. The first stage of AM is employed to enhance exploration by generating new grey wolves

through the autophagy process applied to n initial individuals. These newly created grey wolves are then combined with the initial individuals and sorted according to their fitness values, retaining the top n individuals with the highest fitness. For the first stage, $Degradation_{rate}$ was set to 0.2. This approach is illustrated in Fig. 2.

In the second stage of the AM, the focus is on enhancing the performance of the beta (β) and delta (δ) wolves. These wolves are considered suboptimal compared to the alpha (α) wolf, and thus, the AM is employed to improve their quality through degradation and recycling processes. Following these enhancements, the fitness values of the beta (β) and delta (δ) wolves are compared to the alpha (α) wolf. If either the beta (β) or delta (δ) wolves demonstrate superior fitness, they replace the alpha (α) wolf as the best solution. For the second stage, $Degradation_{rate}$ is set according to decay value (dynamic value) using Eq. (10). The process of this second stage of AM is represented in Fig. 3, and the integrated GWO and AM algorithm is presented in Algorithms 1, 2, and 3.

To update position $X_\alpha, X_\beta, X_\delta$, the equation is presented in Eqs. (12), (13), and (14), respectively.

Algorithm 3

The proposed Method (GWO-AM).

```

1 Initialize the grey wolves position X as  $x_i, i = 1, 2, 3, \dots, n$ 
2 Each grey wolf is represented as a vector with a dimension d that matches the size of the problem
3 Initialize the parameter a, A, and C
4 Compute the fitness of each grey wolf
5 Assign the top three grey wolves to  $X_a, X_\beta, X_\delta$ 
6 Apply the first autophagy mechanism XM as  $\tilde{x}_i, i = 1, 2, 3, \dots, n$  using Fig. 1
7 Define t=0
8 while ( $t < iterations$ )
9   for each grey wolf
10    Update the position of the current grey wolves using Eq. (9)
11  end for
12  Update A, C, and a using Eqs. (2), (3), and (4)
13  Convert the position of wolves into binary form using Eq. (13)
14  Compute the fitness of all grey wolves in the population using Eq. (17)
15  Update grey wolves  $X_a, X_\beta, X_\delta$  using Eqs. (14), (15), and (16)
16  Calculate DF using Eq. (11)
17  Apply Algorithm 1
18  Apply Algorithm 2
19  t=t+1
20 end while
21 return the best of grey wolf of  $X_a$ 

```

$$X_a = X_{t+1}, \text{ if } f(X_{t+1}) < f(X_a) \quad (12)$$

$$X_\beta = X_{t+1}, \text{ if } f(X_{t+1}) < f(X_\beta) \text{ and } f(X_{t+1}) > f(X_a) \quad (13)$$

$$X_\delta = X_{t+1}, \text{ if } f(X_{t+1}) < f(X_\delta) \text{ and } f(X_{t+1}) > f(X_\beta) \quad (14)$$

As feature selection involves binary decisions, the grey wolf position vector is converted into a binary format. This transformation is illustrated in Eq. (15).

$$Binary(X(t+1)) = \begin{cases} 1, & x(t+1) > 0.5 \\ 0, & \text{otherwise} \end{cases} \quad (15)$$

In this study, the fitness value is utilized to reduce the number of selected features while enhancing the model performance [14]. The equation of fitness value is presented in Eq. (16).

$$fitness = a(1 - P) + (1 - a)\left(1 - \frac{\#SF}{\#TF}\right) \quad (16)$$

where the constant $a \in [0,1]$ signifies the weight assigned to the study objective, subset size, and balancing performance. Then, P denotes the accuracy of KNN algorithm. In this study, #TF represents the total number of features and #SF denotes the size of the feature subset being tested. Here, a weight of 0.90 was designated for a . The right side of the equation indicates the percentage of features utilized, whereas the left side represents the accuracy of the proposed method. The code is available at <https://github.com/pulunghendropastyo/GWO-AM>.

3.6. Modeling and Hyperparameter Tuning

Machine learning algorithms are great at handling classification tasks, but their performance can be affected by how their parameters are set. This study used RandomSearchCV to fine-tune machine learning parameters for the best results. The algorithms tested include Linear Regression (LR), K-Nearest Neighbors (KNN), Linear Discriminant Analysis (LDA), Decision Tree (DT), Support Vector Machine (SVM), Gaussian Naïve Bayes (GNB), AdaBoost (AB), Random Forest (RF), Extra Trees (ET), Gradient Boosting (GB), Ensemble-stacking, and Ensemble-voting.

The main goal of using different machine learning algorithms is to see how the GWO-AM affects their performance. The results of the parameter tuning for these algorithms are shown in Table 2.

Table 2

Hyperparameters of machine learning optimized by random search.

Algorithm	Optimal hyperparameter value
LR	{'solver': 'liblinear', 'penalty': 'l1', 'C': 0.1}
LDA	{'solver': 'svd', 'shrinkage': None}
KNN	{'p': 1, 'n_neighbors': 11, 'weights': 'uniform', 'leaf_size': 9, 'algorithm': 'kd_tree'}
GNB	-
DT	{'splitter': 'random', 'min_samples_split': 10, 'min_samples_leaf': 1, 'max_features': None, 'max_depth': None, 'criterion': 'gini'}
SVM	{'shrinking': False, 'probability': True, 'kernel': 'rbf', 'gamma': 'scale', 'degree': 3, 'C': 10}
AB	{'learning_rate': 0.5, 'n_estimators': 150}
GB	{'subsample': 0.8, 'n_estimators': 150, 'min_samples_split': 10, 'min_samples_leaf': 1, 'max_depth': 3, 'learning_rate': 0.1}
ET	{'n_estimators': 50, 'min_samples_split': 2, 'min_samples_leaf': 1, 'max_features': None, 'max_depth': 10, 'criterion': 'gini', 'bootstrap': True}
RF	{'random_state': 20, 'n_estimators': 30, 'min_samples_split': 2, 'min_samples_leaf': 2, 'max_features': 'sqrt', 'max_depth': 40, 'criterion': 'entropy', 'bootstrap': False}

Table 3

Parameter settings of metaheuristic algorithms.

Parameter/Algorithm	Value
Dimension d	Number of features (#TF)
k value of KNN	11
significance level (α)	0.05
Number of population n	10
Number of Iterations	100
Number of runs	20
GWO-AM	degradation rate for first stage=0.2; decay rate=0.008
PSO	inertia weight= 0.9; coefficient1=2; coefficient2=2
GWO	-
GA	mutation rate=0.01; crossover rate=0.8
SSA	-
HWOA-CHM	c=0.7; map1=0.7
ESSA	-
TMGWO	mutation probability= 0.5
PSO-AIW	coefficient1=2; coefficient2=2

3.7. Experimental Setup

In this study, the K-Nearest Neighbors (KNN) algorithm was used to evaluate the effectiveness of selected features during the feature selection process. The study used a hold-out strategy to ensure the results were optimal and test the capabilities of the GWO-AM algorithm. The dataset was randomly divided, with 80% used for training and 20% for testing [45,46]. This process was repeated 20 times to ensure reliable and statistically significant results [47]. The overall performance was measured based on these 20 runs, and accuracy was used to assess how well the model classified the data.

Moreover, the Wilcoxon signed-rank test and ANOVA test were employed to determine the proposed method's performance significance with classical and state-of-the-art metaheuristic algorithms, including PSO, GWO, GA, SSA, HWOA-CHM, ESSA, TMGWO, and PSO-AIW. The parameter settings are described in Table 3, and the flow diagram can be seen in Fig. 5.

Furthermore, this study employed twelve machine learning algorithms to perform classification tasks and assess the effect of the proposed method (GWO-AM). The evaluation metric used to measure performance is accuracy. To ensure a fair comparison with previous research, the experimental protocol involves a train-test split and 10-fold cross-validation. The research process is outlined in the flow diagram presented in Fig. 4. Additionally, to maintain consistency and fairness in comparison, the study utilizes the same programming language (Python 3.10.12) and was conducted on Google Collaboratory.

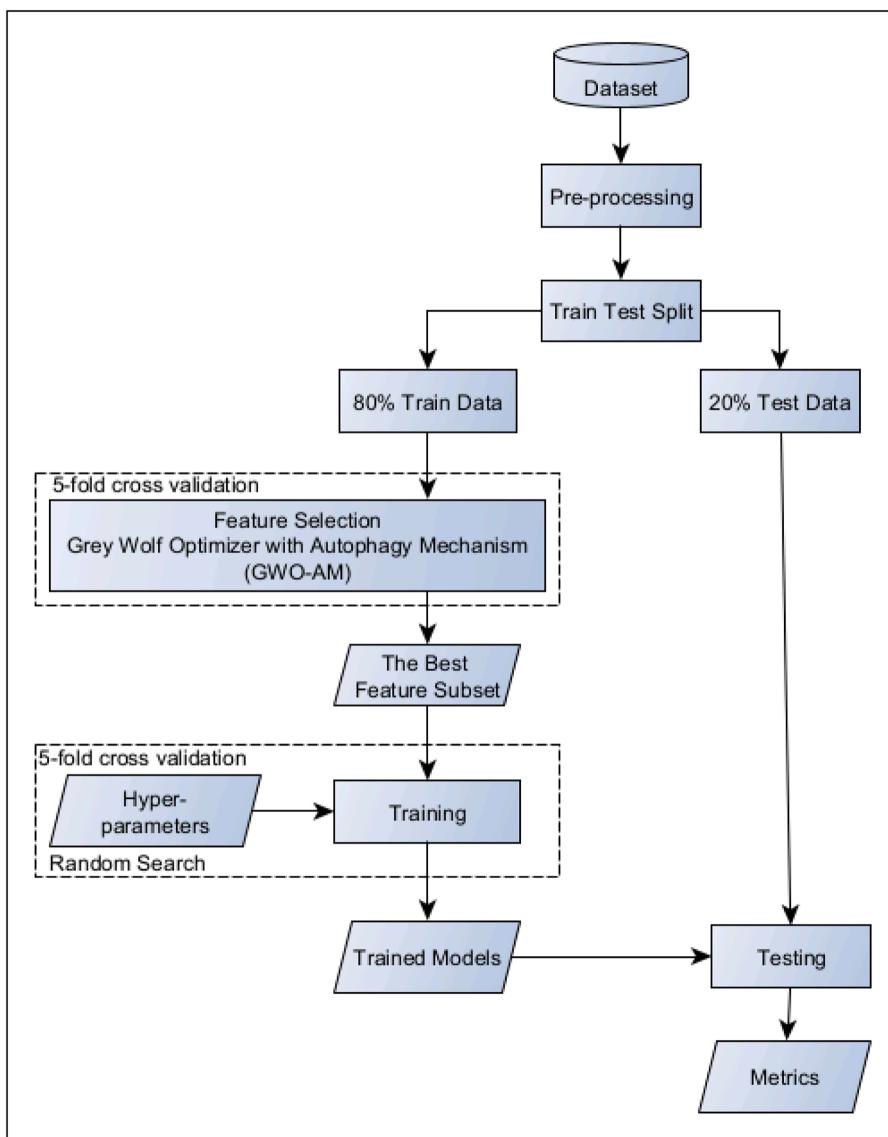


Fig. 4. Flow diagram of the proposed method.

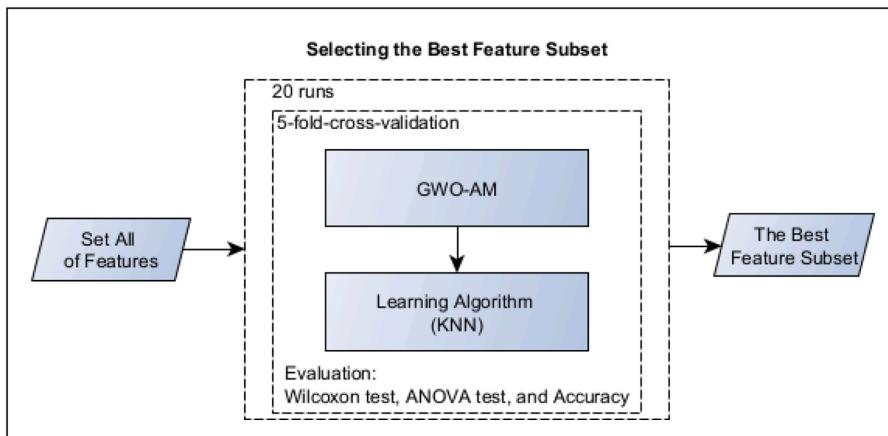


Fig. 5. Flow diagram of the feature selection process.

Table 4

ANOVA test results for the effect of decay rates on GWO-AM's accuracy using the diabetes dataset.

	SS	DF	MS	F (DFn, DFd)	P-value
Treatment (between columns)	0.0039	19	0.00020	F(19,380)= 0.749	P = 0.767
Residual (within columns)	0.1058	380	0.00027		
Total	0.1097	399	-		

Table 5

ANOVA test results for the effect of decay rates on GWO-AM's computational time using the diabetes dataset.

	SS	DF	MS	F (DFn, DFd)	P-value
Treatment (between columns)	2446.79	19	128.77	F(19,380)= 14.07	P<0.0001
Residual (within columns)	3476.97	380	9.14		
Total	5923.77	399	-		

4. Results and Discussion

Firstly, the decay rate is crucial for optimizing the Autophagy Mechanism. It makes the degradation rate adaptive as the iteration process increases, which allows GWO-AM to operate optimally. A sensitivity analysis was performed to find the most effective decay rate, as shown in [Table 13](#). The One-at-a-Time (OAT) sensitivity measure was used for this analysis. OAT is a straightforward approach that evaluates an algorithm's effectiveness by changing only one parameter at a time while keeping others constant [7]. Experiments were conducted using 20 unique decay rates ranging from 0.001 to 0.20, with increments of 0.1%. The algorithm was run 20 times for each value. An analysis of variance (ANOVA) was then performed on the computational time and accuracy to determine if there was a statistically significant difference between the means of the data in [Table 13](#). [Tables 4 and 5](#) present the ANOVA test results for GWO-AM. The p-values for computational time were lower than 0.05, indicating a statistically significant difference between the computational time groups. However, the p-values for accuracy were higher than 0.05, meaning there was no statistically significant difference between the accuracy groups. The significance level for this test was 0.05. These results indicate that the 20 unique decay rates tested do not significantly affect the accuracy of GWO-AM but significantly affect the computation time.

Then, [Figure 6](#) illustrates how the decay rate makes the degradation rate adaptive with each iteration. When the decay rate is smaller, the degradation rate changes slower, and vice versa. A high degradation rate leads to more cells or features being degraded and recycled, resulting in slightly increased computational time. This trend is evident in [Fig. 6\(a\)](#) and the experimental results in [Table 13](#). Besides, the results of the experiment reveal that the decay rate of 0.008 yields the best outcomes in terms of accuracy, number of selected features (#SF), best fitness, and computational time. The superior performance associated with the decay rate of 0.008 suggests that this particular value supports a degradation rate that is neither too rapid nor too slow, thereby ensuring a stable degradation and recycling process within the autophagy mechanism, as seen in [Fig. 6\(b\)](#).

Moreover, the decay rate of 0.008 effectively supports the early and later stages of the search process. In the early stage, it produces a higher degradation rate, which helps aggressively remove less promising regions and encourages broader exploration by replacing more cells. This enables the algorithm to explore the search space quickly. In the later stage, as the algorithm begins to converge, the degradation rate

decreases, helping preserve diverse and potentially good solutions near promising areas. This allows for fine-tuning without losing valuable information. As a result, the decay rate of 0.008 is selected as the optimal setting. Additionally, the Wilcoxon signed-rank test was conducted to determine whether there is a statistically significant difference between the selected decay rate and the other decay rates. The significance level (α) was set at 0.05. Based on the data in [Table 13](#), the selected decay rate significantly affects the computation time (Δ) but does not significantly impact the accuracy of GWO-AM (-). Furthermore, [Fig. 6\(c\)](#) illustrates that the optimal decay rate typically aligns with a degradation rate between 0.2 and 0.3 within the search space. This specific range ensures a balanced degradation process in the feature space, preventing it from being overly aggressive or too minimal. Therefore, a degradation rate 0.2 is used during the first autophagy stage to enhance the initial exploration process.

Secondly, the proposed method was compared with classical and state-of-the-art metaheuristic algorithms to evaluate its robustness and consistency in feature selection. The algorithms were run 20 times, and statistical metrics were gathered to evaluate overall performance and the final outcomes across these 20 independent executions. The optimal parameter values for each algorithm are highlighted in bold. As shown in [Table 14](#), the proposed method surpasses classical methods, achieving an accuracy of 90.91%. A higher accuracy indicates that a more significant proportion of the data has been successfully predicted. At the same time, [Table 15](#) demonstrates that the proposed method outperforms the accuracy of state-of-the-art algorithms such as HWOA-CHM, ESSA, TMGWO, and PSO-AIW. Additionally, the proposed method exhibits a low standard deviation, indicating that it consistently performs well. Moreover, the proposed method uses fewer features (#SF) than other algorithms without decreasing classification performance, demonstrating its effectiveness in selecting relevant features. Unfortunately, the GWO-AM's computation time is relatively slow, with an average time of 53.12 seconds. GWO-AM outperforms GA, TMGWO, and PSO-AIW, which have computation times of 74.79 seconds, 57.18 seconds, and 54.52 seconds, respectively. ESSA is the fastest feature selection algorithm, with a time of 33.32 seconds. The increased computational time in GWO-AM is mainly due to additional mechanisms, particularly the Autophagy Mechanism (AM), which introduces an extra computational complexity of $O(DF^2 + d)$. As a result, the overall computational complexity of GWO-AM becomes $O(t_{max} \cdot (n.d + DF^2 + d))$. This is a notable difference from standard GWO, which has a complexity of only $O(t_{max} \cdot n.d)$. To address this, the study employed an adaptive degradation rate controlled by a decay rate to optimize the value of DF . This degradation rate gradually decreases with each iteration, preventing consistently high values and enabling GWO-AM to operate more efficiently. The adaptive degradation rate is visualized in [Fig. 6](#). It is important to note that this higher computational burden is a trade-off for achieving improved solution quality, robustness, and better model generalization, which can outweigh the drawback in real-world applications. Furthermore, the differences in computation times among the algorithms in this study are relatively minor, differing by only a few seconds.

Next, [Fig. 7 and 8](#) present the proposed method's convergence curves compared with other algorithms. The fitness metric in these figures represents the average fitness value obtained from 20 independent runs. In the figures, the proposed method is indicated by a purple square. According to the experimental results, the proposed method achieves the lowest fitness value, with an average of 0.147, and consistently begins with a low fitness value. Furthermore, the proposed method demonstrates the fastest convergence speed and persistently searches for the global optimum. This performance can be attributed to integrating the Autophagy Mechanism (AM) within the Grey Wolf Optimizer (GWO), significantly enhancing its exploration and exploitation capabilities. Consequently, the proposed method prevents the algorithm from becoming trapped in local optima. In contrast, premature convergence is

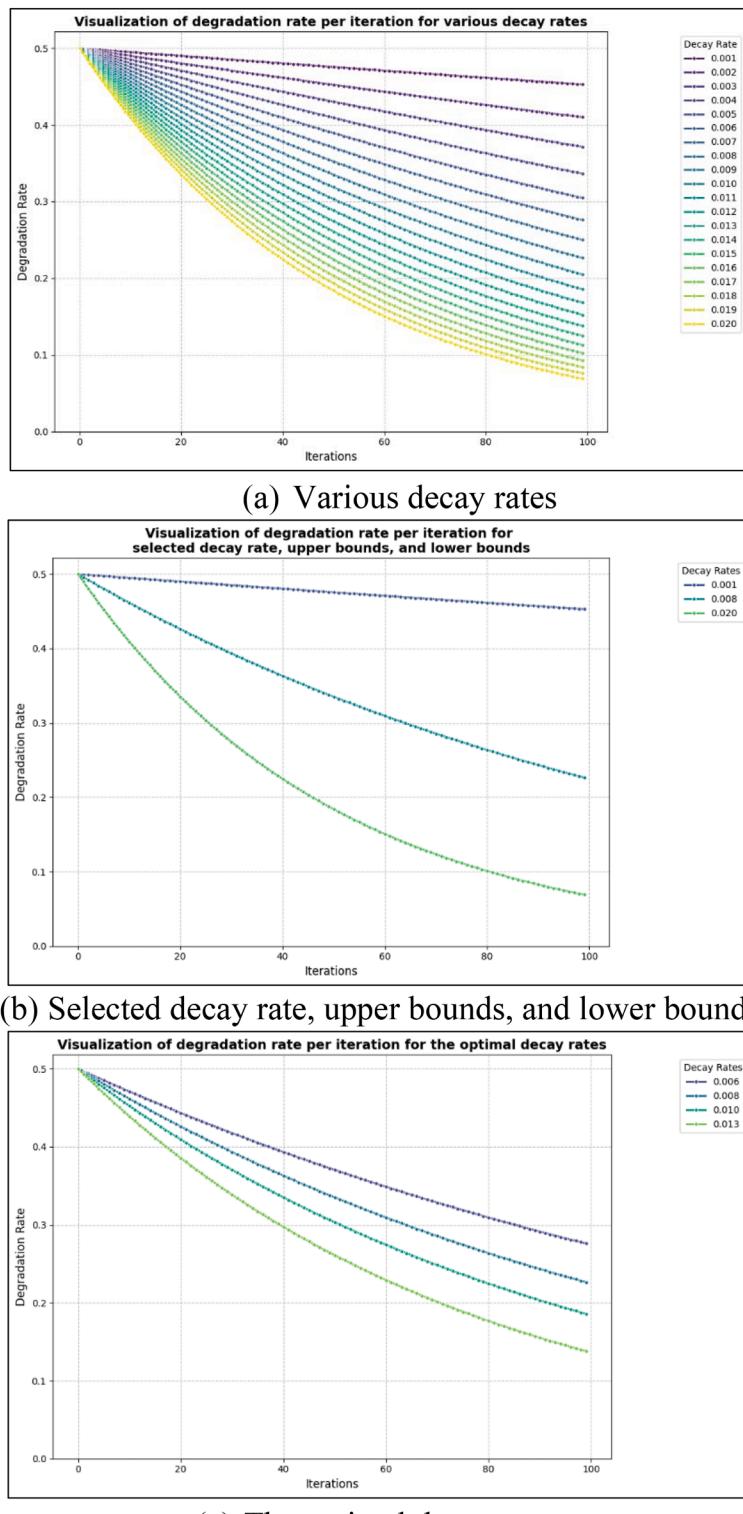


Fig. 6. Visualization of the degradation rate per iteration across different decay rates.

observed in the behaviors of algorithms such as PSO, SSA, GWO, HWOA-CHM, ESSA, and PSO-AIW. Also, GA and TMGWO become slightly trapped in local optima. These results suggest that the GWO-AM algorithm excels in identifying the most valuable feature subset compared to the other algorithms.

Then, the Wilcoxon signed-rank test was performed to assess whether there was a statistically significant difference between the

proposed method and the other algorithms. The significance level (α) for this analysis was set at 0.05. A p-value greater than 0.05 indicates no significant difference between the methods. The results of the Wilcoxon test, as detailed in Tables 14 and 15, show that the proposed method obtains p-values of 0.005, 0.006, 0.011, 0.003, 0.002, 0.001, 0.045, and 0.000 when compared to PSO, GWO, GA, SSA, HWOA-CHM, ESSA, TMGWO, and PSO-AIW, respectively. In addition, an ANOVA test was

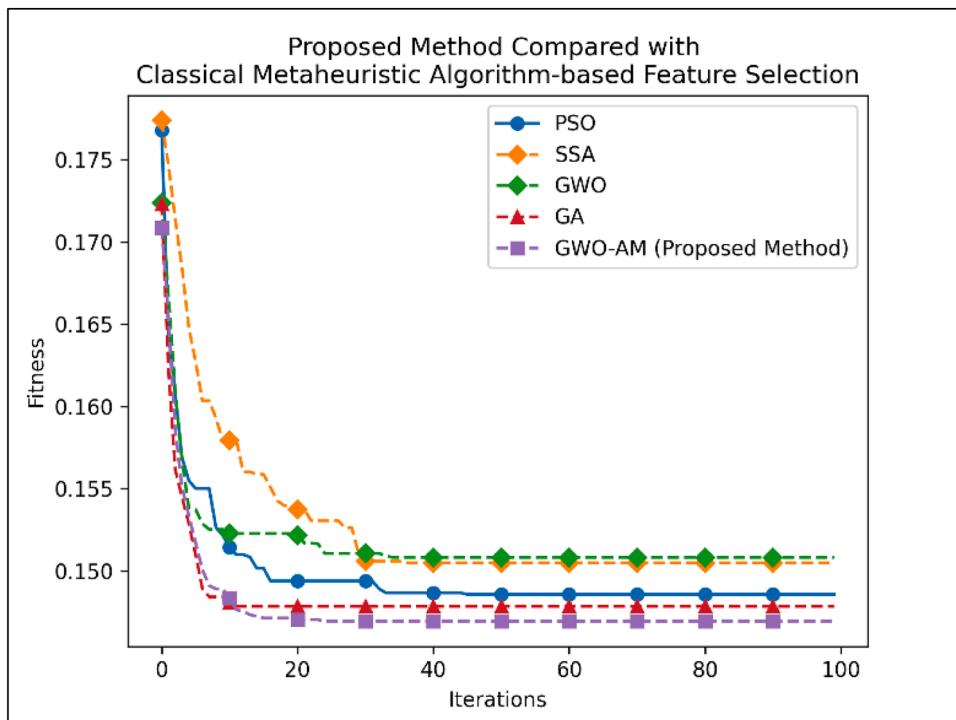


Fig. 7. Convergence curve of the proposed method compared to classical metaheuristic algorithm-based feature selection. The proposed method achieves the lowest fitness value. The curve shows a rapid decrease in error within the first 10 iterations, indicating efficient convergence. After 20 iterations, the performance stabilizes, suggesting that the algorithm effectively reaches an optimal solution.

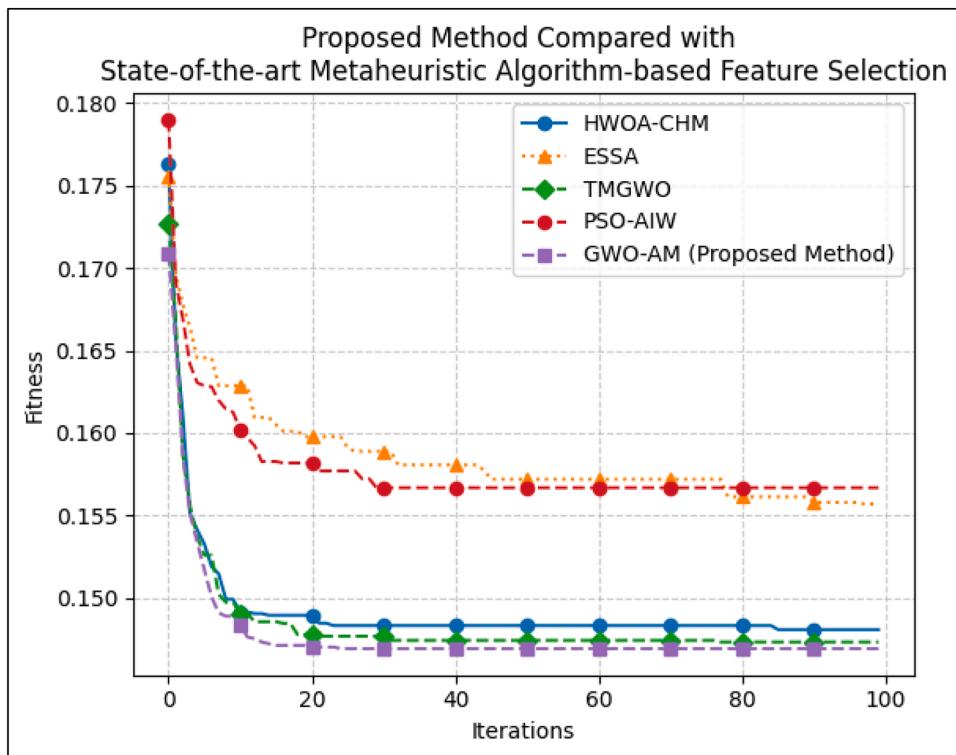


Fig. 8. Convergence curve of the proposed method compared to state-of-the-art metaheuristic algorithm-based feature selection. The proposed method consistently achieves the lowest fitness value, demonstrating the fastest convergence speed and a strong ability to search for the global optimum persistently.

performed to assess whether there were statistically significant differences among the proposed method and the other metaheuristic algorithms. The results, presented in Table 6, confirm the proposed method's

superiority, significance, and effectiveness. These findings indicate that the proposed method consistently outperforms the other algorithms, demonstrating its robust and reliable performance.

Table 6

Analysis of variance (ANOVA) test for assessing the proposed method on the diabetes dataset.

	SS	DF	MS	F (DFn, DFD)	P-value
Treatment (between columns)	0.02829	8	0.0035	F(8,171)= 4.85	P<0.0001
Residual (within columns)	0.12451	171	0.0007		
Total	0.15280	179	-		

Table 7

Effect of GWO-AM on machine learning algorithms using the train-test split protocol.

Protocol: Train-test				
No	Algorithm	Baseline Accuracy (%)	Pre-processing Accuracy (%)	Pre-processing +GWO-AM Accuracy (%)
1	LR	76.62	79.22	86.36
2	LDA	79.87	78.57	87.66
3	KNN	77.27	83.12	90.91
4	DT	70.78	83.12	84.42
5	GNB	78.57	76.62	87.66
6	SVM	77.92	82.47	88.31
7	AB	77.92	85.71	85.06
8	GB	77.27	85.06	88.96
9	RF	77.92	84.42	86.36
10	ET	79.87	84.42	87.66
11	Stacking	78.57	83.12	88.31
12	Voting	79.87	85.06	90.26

Table 8

The effect of GWO-AM on machine learning algorithms using 10-fold cross-validation.

Protocol: K-fold =10				
No	Algorithm	Baseline Accuracy	Pre-processing Accuracy	Pre-processing+ GWO-AM Accuracy
1	LR	76.17±0.03	83.07±0.03	82.81±0.03
2	LDA	77.35±0.03	83.07±0.04	82.55±0.03
3	KNN	73.96±0.03	85.68±0.03	86.72±0.03
4	DT	69.91±0.04	82.17±0.04	83.34±0.03
5	GNB	75.65±0.03	82.15±0.04	81.90±0.04
6	SVM	76.43±0.03	82.42±0.03	85.42±0.02
7	AB	76.57±0.04	87.12±0.03	86.60±0.03
8	GB	76.95±0.04	86.99±0.03	88.03±0.03
9	RF	75.78±0.06	86.85±0.04	86.85±0.04
10	ET	76.82±0.05	85.94±0.03	87.12±0.03
11	Stacking	73.95±0.05	85.94±0.03	85.16±0.04
12	Voting	76.56±0.04	86.98±0.04	86.72±0.04

After comparing the proposed method with other feature selection algorithms, the selected features were used to understand how they affect various machine learning algorithms. The GWO-AM method effectively identified six crucial features: pregnancies, glucose, insulin, BMI, DPF, and age. These are not just statistical picks but deeply significant medically and clinically. Glucose is foundational, as elevated levels directly define diabetes and are the primary diagnostic criterion. BMI highlights the profound impact of body fat, a key driver of insulin resistance, and is a universally recognized clinical risk factor for Type 2 Diabetes. The insulin level, particularly post-challenge, offers a window into the pancreas's ability to cope with insulin resistance, indicating early metabolic strain even before overt diabetes. A history of pregnancies is a critical indicator due to its link with Gestational Diabetes Mellitus, a strong predictor for developing Type 2 Diabetes later in life, and is a standard clinical inquiry. The Diabetes Pedigree Function (DPF) quantifies genetic risk, which is a crucial clinician consideration. Lastly,

Table 9

Comparison of the proposed method with state-of-the-art results using train-test protocol.

Protocol = Train-test				
No	Authors	Year	Techniques	Accuracy
1	[28]	2020	NSGA-II-Stacking	83.80
2	[33]	2021	Quantum	86.00
3	[32]	2021	Ensemble-voting	79.08
4	[34]	2021	MLP	88.57
5	[1]	2021	LSTM	87.26
6	[35]	2022	Machine Learning	79.57
7	[36]	2022	CNN+Bi-LSTM	88.37
8	[37]	2023	LTC (Ensemble) +Feature Fusion	85.00
9	[39]	2024	En-RfRsk	88.89
10	Our Proposed Method	2025	GWO-AM+KNN	90.91

age represents the cumulative exposure to risk factors and the natural physiological changes that increase diabetes susceptibility over time, serving as a fundamental criterion for screening guidelines [48,49]. Our model's consistent selection of these features validates their medical importance, bridging our computational findings with practical clinical insights for more effective diabetes risk assessment.

Subsequently, the study tested 12 different machine learning algorithms, each with unique characteristics, using two evaluation protocols: train-test split and 10-fold cross-validation. The protocols were chosen to compare fairly with previous studies. The results in Table 7 show that the combination of GWO-AM and KNN, using the train-test split, obtains an accuracy of 90.91%. The GWO-AM improved the accuracy of 11 out of 12 machine learning algorithms, except the AB algorithm, which experienced a slight decrease of 0.65%. Significant improvements are seen in the LDA, KNN, and GNB algorithms, which increased by 9.09%, 7.79%, and 11.04%, respectively.

Table 8 shows that the combination of GWO-AM and GB achieves the highest accuracy of 88.03%, outperforming the other 11 algorithms under the 10-fold cross-validation protocol. In this protocol, GWO-AM also improves the performance of eight algorithms, although it causes slight decreases in accuracy for LR, LDA, GNB, and Voting algorithms by 0.26%, 0.52%, 0.25%, and 0.26%, respectively. Additionally, the standard deviation across all algorithms remains very low, indicating that GWO-AM provides consistent results when applied to machine learning algorithms for diabetes prediction. These findings suggest that GWO-AM works particularly well with certain machine learning algorithms. Therefore, choosing the best combination of feature selection and classification algorithms requires thorough experimentation or optimization techniques to find the most effective combination.

Another crucial aspect to consider is the pre-processing techniques employed in this research. The application of missing value handling, outlier detection, and z-score normalization can substantially enhance the performance of machine learning algorithms. This impact is evident in the results presented in Tables 7 and 8.

Table 10

Comparison of proposed method with state-of-the-art results using 10-fold cross-validation.

Protocol = 10-fold-cross-validation				
No	Authors	Year	Techniques	Accuracy
1	[27]	2019	RepTree	74.48
2	[29]	2020	Linear-SVM	83.00
3	[30]	2020	RF	75.00
4	[31]	2020	CMWOAFS-SVM	77.45
5	[34]	2021	MLP	76.00
6	[38]	2023	SVM with Integrated Kernel	85.50
7	Our Proposed Method	2025	GWO-AM+GB	88.03 ±0.03

Table 11

Analysis of variance (ANOVA) test for assessing the proposed method on glioma dataset.

	SS	DF	MS	F (DFn, DFD)	P-value
Treatment (between columns)	0.0584	9	0.0064	F(9,190)= 3.13	P=0.0015
Residual (within columns)	0.03935	190	0.0020		
Total	0.4519	199	-		

After that, the proposed method was evaluated against previous studies for diabetes prediction using both the train-test split and 10-fold cross-validation protocol. Table 9 demonstrates that the proposed method, combined with the KNN algorithm as a classifier, surpasses nine other methods using the train-test split protocol. The comparison includes studies from 2020 to 2024. The proposed method exhibits the most significant performance improvement compared to Kumari S et al. [32], with a difference of 14.56%, and the minor improvement compared to [39], with a difference of 2.02%.

Similarly, Table 10 reveals that the proposed method, when paired with the GB algorithm as a classifier, outperforms several methods from the study [38,34,27,29,30] and [31] using the 10-fold cross-validation protocol. The proposed method shows the highest performance difference compared to study [27], with a difference of 13.55%, and the lowest difference compared to study [38], with a difference of 2.53%. The comparison includes previous studies from 2019 to 2023. The results suggest that the proposed method demonstrates highly promising performance in diabetes prediction.

To evaluate the scalability of the proposed method, we utilized two additional datasets: the glioma dataset (available at <https://jundongl.github.io/scikit-feature/datasets.html>) and the lung cancer dataset (available at <https://www.kaggle.com/datasets/mysarahnabhat/lung-cancer/data>). The glioma dataset consists of 4434 features and 50 samples, while the lung cancer dataset contains 16 features and 284 samples. Both datasets are larger and more complex than the diabetes dataset, making them suitable for testing the scalability of the proposed algorithm. The experiments were conducted using the same configuration as the diabetes dataset but without pre-processing. Additionally, the KNN algorithm was employed as the classifier.

The algorithm was run 20 times on each dataset to assess overall performance, with statistical metrics gathered from these independent runs. The optimal parameter values for each algorithm are emphasized in bold, highlighting the best-performing configurations. As shown in Table 16, the proposed method achieves 77% accuracy on the glioma dataset, marking a 7% improvement over the baseline (without feature selection) and outperforming all other algorithms. Additionally, the Wilcoxon signed-rank and ANOVA test were conducted to evaluate statistical significance, as seen in Tables 11 and 16. The results ($p < 0.05$ for all comparisons) confirm that the proposed method consistently outperforms others, demonstrating its robustness and reliability. Moreover, Fig. 9 further illustrates the convergence curves of the proposed method compared to other algorithms, where a green square represents it. The experimental results indicate that the proposed method attains the lowest average fitness value of 0.148 and consistently starts with a low fitness value. Furthermore, it persistently searches for the global optimum, effectively preventing the algorithm from being trapped in local optima. In contrast, premature convergence is observed in PSO,

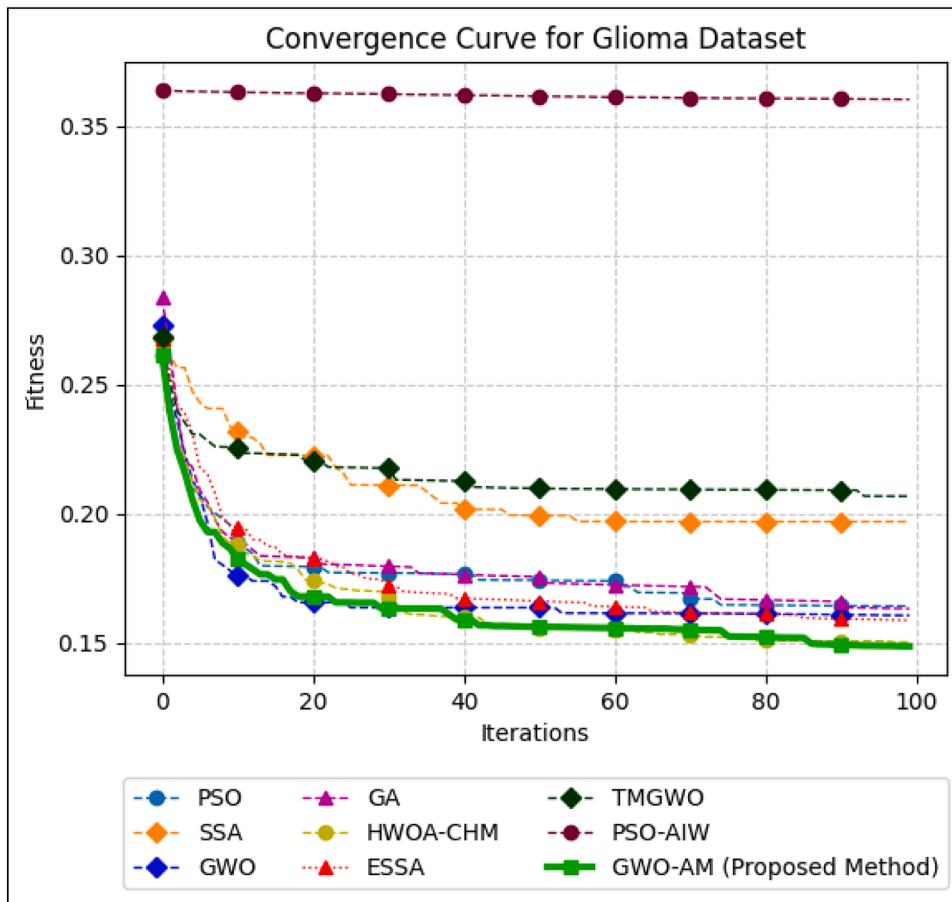


Fig. 9. Convergence curve for the glioma dataset. The proposed method, represented by a green square, is compared to eight metaheuristic algorithms and achieves the lowest average fitness value among all methods.

Table 12

Analysis of variance (ANOVA) test for assessing the proposed method on lung cancer dataset.

	SS	DF	MS	F (DFn, DFd)	P-value
Treatment (between columns)	0.0316	9	0.0035	F(9,190)= 4.52	P<0.0001
Residual (within columns)	0.1478	190	0.0007		
Total	0.1794	199	-		

Table 13

Comparison of performance for different values of the GWO-AM's decay rate.

No	Decay Rate	Performance				
		Avg. Accuracy (%)	Avg. Best Fitness	Avg. Worst Fitness	Avg. #SF	Avg. Time (s)
1	0.001	90.584 ±0.14 (-)	0.147 ±0.0004	0.1748 ±0.0111	6.05 ±0.2179	56.13 (▲)
2	0.002	90.584 ±0.14 (-)	0.147 ±0.0004	0.1678 ±0.0110	6.05 ±0.2179	54.37 (▲)
3	0.003	90.584 ±0.14 (-)	0.147 ±0.0004	0.1684 ±0.0143	6.05 ±0.2179	50.76 (▲)
4	0.004	90.584 ±0.14 (-)	0.147 ±0.0004	0.1682 ±0.0138	6.05 ±0.2179	56.56 (▲)
5	0.005	90.584 ±0.14 (-)	0.147 ±0.0004	0.1641 ±0.0127	6.05 ±0.2179	51.69 (▲)
6	0.006	90.909 ±0.00 (-)	0.146 ±0.0000	0.1752 ±0.0127	6.00 ±0.0000	51.82 (▲)
7	0.007	90.584 ±0.14 (-)	0.147 ±0.0004	0.1724 ±0.0148	6.05 ±0.2179	51.69 (▲)
8	0.008	90.909 ±0.00	0.146 ±0.0000	0.1733 ±0.0128	6.00 ±0.0000	47.04 (▲)
9	0.009	90.584 ±0.14 (-)	0.147 ±0.0004	0.1703 ±0.0139	6.05 ±0.2179	52.57 (▲)
10	0.010	90.909 ±0.00 (-)	0.146 ±0.0000	0.1738 ±0.0140	6.00 ±0.0000	49.55 (▲)
11	0.011	90.584 ±0.14 (-)	0.147 ±0.0004	0.1751 ±0.0145	6.05 ±0.2179	54.83 (▲)
12	0.012	90.584 ±0.14 (-)	0.147 ±0.0004	0.1758 ±0.0134	6.05 ±0.2179	52.57 (▲)
13	0.013	90.909 ±0.00 (-)	0.146 ±0.0000	0.1772 ±0.0146	6.00 ±0.0000	51.48 (▲)
14	0.014	90.259 ±0.19 (-)	0.147 ±0.0006	0.1727 ±0.0140	6.10 ±0.3000	55.68 (▲)
15	0.015	90.584 ±0.14 (-)	0.147 ±0.0004	0.1655 ±0.0142	6.05 ±0.2179	52.07 (▲)
16	0.016	90.584 ±0.14 (-)	0.147 ±0.0004	0.1699 ±0.0149	6.05 ±0.2179	51.12 (▲)
17	0.017	89.935 ±0.23 (-)	0.147 ±0.0007	0.1700 ±0.0145	6.15 ±0.3570	55.58 (▲)
18	0.018	89.935 ±0.23 (-)	0.147 ±0.0007	0.1677 ±0.0175	6.15 ±0.3570	56.18 (▲)
19	0.019	89.935 ±0.23 (-)	0.147 ±0.0007	0.1655 ±0.0120	6.15 ±0.3570	50.77 (▲)
20	0.020	90.259 ±0.19 (-)	0.147 ±0.0006	0.1710 ±0.0178	6.10 ±0.3000	50.72 (▲)

SSA, GWO, GA, ESSA, TMGWO, and PSO-AIW, while HWOA-CHM shows a slight tendency to get trapped. These findings suggest that the GWO-AM algorithm is highly effective in selecting the most valuable feature subset compared to the other algorithms for the glioma dataset.

For the lung cancer dataset, the proposed method obtained an

accuracy of 89.84%, showing an improvement of 5.84% over the baseline and outperforming all other algorithms, as presented in Table 17. Besides, the Wilcoxon signed-rank test was conducted to assess statistical significance. The results indicate that the proposed method consistently outperforms other algorithms, except GA, HWOA-CHM, and PSO-AIW, with p-values of 0.1074, 0.1667, and 0.1015, respectively. In addition, an ANOVA test was performed to assess whether there were statistically significant differences between the proposed method and the other metaheuristic algorithms, as presented in Table 12. The results show that the proposed method confirms the superiority, significance, and effectiveness with a p-value < 0.0001. Moreover, Fig. 10 presents the convergence curves of the proposed method compared to other algorithms, with the proposed method represented by a green square. The experimental results show that the proposed method achieves the lowest fitness value among all algorithms except for PSO-AIW. Although PSO-AIW reaches a slightly better fitness value, its accuracy evaluation results are inferior to the proposed method's, indicating its limited ability to generalize when tested on new data. Additionally, premature convergence is observed in PSO, SSA, GWO, GA, ESSA, TMGWO, and HWOA-CHM. These findings suggest that the proposed method delivers consistently reliable results across various datasets, such as diabetes, glioma, and lung cancer.

5. Conclusion

This study has presented a new feature selection approach that utilizes a hybrid Grey Wolf Optimizer and Autophagy Mechanism (GWO-AM) to enhance diabetes prediction performance. The Pima Indian Diabetes Dataset (PIDD) was used as the dataset. Then, the proposed method was compared to classical and state-of-the-art metaheuristic-based feature selections. The proposed method also employed 12 machine learning algorithms to understand the effect of GWO-AM. The method was further tested on glioma and lung cancer datasets to evaluate its scalability. According to the experimental results, the proposed method can significantly improve the diabetes prediction performance with an accuracy of 90.91%.

Moreover, the proposed method surpassed the other feature selection techniques regarding accuracy, best fitness, worst fitness, and selected features (#SF). This performance can be attributed to integrating the Autophagy Mechanism (AM) within the Grey Wolf Optimizer (GWO), significantly enhancing its exploration and exploitation capabilities. Consequently, the proposed method prevents the algorithm from becoming trapped in local optima. As a result, the GWO-AM significantly improves the performance of machine learning algorithms for diabetes prediction, establishing it as an effective feature selection technique.

Furthermore, the GWO-AM also excels in the glioma and lung cancer datasets, demonstrating its ability to produce consistently dependable outcomes across diverse datasets.

For future research, this method can be applied to other problem domains, combined with different metaheuristic algorithms to achieve diverse outcomes, or integrated with deep learning models to enhance prediction accuracy further. The field of metaheuristic algorithms continues to evolve, as the No Free Lunch (NFL) theorem logically asserts that no single metaheuristic is optimal for solving all optimization problems, particularly in the context of feature selection.

Table 14

Comparison of the proposed method with classical metaheuristic-based feature selections in 20 independent runs.

No	Algorithm	Accuracy (%)	Best Fitness	Worst Fitness	#SF	Wilcoxon Test	Time (s)
1	PSO	88.149±0.030	0.149±0.003	0.177±0.015	6.45±0.497	0.005 Sig. (P<0.05)	50.05
2	GWO	88.766±0.028	0.151±0.007	0.172±0.015	6.20±0.510	0.006 Sig. (P<0.05)	48.61
3	GA	87.987±0.032	0.148±0.001	0.172±0.016	6.45±0.497	0.011 Sig. (P<0.05)	74.79
4	SSA	88.214±0.031	0.150±0.006	0.177±0.015	6.25±0.433	0.003 Sig. (P<0.05)	41.51
5	Proposed Method (GWO-AM)	90.909±0.001	0.147±0.000	0.171±0.012	6.00±0.000	-	53.12

Table 15

Comparison of the proposed method with state-of-the-art metaheuristic-based feature selections in 20 independent runs.

No	Algorithm	Accuracy (%)	Best Fitness	Worst Fitness	#SF	Wilcoxon Test	Time (s)
1	HWOA-CHM	87.759±0.032	0.148±0.001	0.176±0.017	6.50±0.500	0.002 Sig. (P<0.05)	40.50
2	ESSA	87.305±0.027	0.156±0.011	0.176±0.013	6.10±0.768	0.001 Sig. (P<0.05)	33.32
3	TMGWO	89.610±0.026	0.147±0.001	0.173±0.014	6.20±0.399	0.045 Sig. (P<0.05)	57.16
4	PSO-AIW	86.298±0.003	0.157±0.005	0.179±0.012	6.95±0.384	0.000 Sig. (P<0.05)	54.52
5	Proposed Method (GWO-AM)	90.909±0.001	0.147±0.000	0.171±0.012	6.00±0.000	-	53.12

Table 16

Comparison of the proposed method with all metaheuristic-based feature selections on the glioma dataset.

No	Algorithm	Accuracy (%)	Best Fitness	Worst Fitness	#SF	Wilcoxon Test	Time (s)
1	Baseline	70.000±0.000	-	-	4434±0.000	3.1e-4 Sig. (P<0.05)	-
2	PSO	72.999±0.045	0.164±0.026	0.261±0.32	2343.55±33.61	0.0114 Sig. (P<0.05)	60.02
3	GWO	73.500±0.047	0.160±0.019	0.272±0.029	1903.75±89.26	0.0348 Sig. (P<0.05)	61.76
4	GA	73.500±0.047	0.163±0.020	0.283±0.030	2587.00±30.15	0.0348 Sig. (P<0.05)	50.01
5	SSA	73.500±0.048	0.196±0.032	0.268±0.021	2290.70±35.11	0.0196 Sig. (P<0.05)	47.03
6	HWOA-CHM	72.499±0.062	0.150±0.027	0.265±0.033	1166.95±810.77	0.0293 Sig. (P<0.05)	40.41
7	ESSA	73.500±0.047	0.158±0.010	0.267±0.025	1288.80±414.88	0.0348 Sig. (P<0.05)	23.02
8	TMGWO	73.500±0.047	0.206±0.024	0.268±0.040	2452.30±84.33	0.0081 Sig. (P<0.05)	126.62
9	PSO-AIW	72.000±0.040	0.360±0.001	0.363±0.001	2430.25±31.33	0.0038 Sig. (P<0.05)	45.57
10	Proposed Method (GWO-AM)	77.001±0.045	0.148±0.015	0.261±0.028	2134.40±87.412	-	68.07

Table 17

Comparison of the proposed method with all metaheuristic-based feature selections on the lung cancer dataset.

No	Algorithm	Accuracy (%)	Best Fitness	Worst Fitness	#SF	Wilcoxon Test	Time (s)
1	Baseline	84.000±0.000	-	-	16±0.000	1.9e-6 Sig. (P<0.05)	-
2	PSO	86.854±0.024	0.130±0.007	0.164±0.013	9.10±1.479	0.0143 Sig. (P<0.05)	17.75
3	GWO	86.854±0.024	0.128±0.006	0.170±0.016	8.65±1.651	0.0280 Sig. (P<0.05)	27.29
4	GA	87.822±0.040	0.128±0.008	0.167±0.015	9.45±1.071	0.1074 Sig. (P>0.05)	28.25
5	SSA	87.016±0.029	0.139±0.013	0.169±0.012	8.75±1.785	0.0285 Sig. (P<0.05)	16.84
6	HWOA-CHM	88.387±0.025	0.132±0.006	0.168±0.016	9.90±2.808	0.1667 Sig. (P>0.05)	24.21
7	ESSA	86.935±0.025	0.143±0.008	0.173±0.014	6.70±1.791	0.0142 Sig. (P<0.05)	15.09
8	TMGWO	86.693±0.024	0.132±0.012	0.171±0.014	8.10±1.670	0.0154 Sig. (P<0.05)	17.96
9	PSO-AIW	87.741±0.025	0.122±0.012	0.164±0.017	9.30±2.26	0.1015 Sig. (P>0.05)	16.80
10	Proposed Method (GWO-AM)	89.838±0.038	0.123±0.005	0.163±0.013	9.70±1.791	-	20.94

Ethics Statement

This research, centered on feature selection algorithms, was conducted in full compliance with ethical guidelines and standards to maintain integrity, transparency, and responsibility throughout the process.

Informed Consent

Since the study does not involve human participants, informed consent was not applicable. However, any datasets used from external sources were obtained with proper permission, and the use of such data was in compliance with the terms and conditions of the original data providers.

Confidentiality and Anonymity

All proprietary data used in the feature selection algorithms, including case studies and simulation results, have been handled with strict confidentiality. Any data provided by external organizations was anonymized and stored securely to prevent unauthorized access.

Integrity and Transparency

The feature selection algorithms and results presented in this paper are based on verifiable and reproducible methodologies. The research process was transparent, and all relevant parameters, assumptions, and limitations of the models were clearly outlined. The authors guarantee

that the findings are a true representation of the analysis performed.

Fair Use of Data

Any datasets or third-party tools used in this research were properly attributed, and appropriate permissions were obtained. We ensured that no data was used inappropriately or without consent, following ethical standards for data usage.

Ethical Approval

As this research does not involve human participants or sensitive data, it did not require approval from an institutional review board. However, all feature selection algorithms and models were applied with ethical considerations, particularly in ensuring that no harm could come from the algorithm's applications.

Social Responsibility

The feature selection algorithms developed in this research were designed with a focus on practical and responsible applications. The potential social, environmental, and economic impacts of deploying such algorithms were considered, and all results were interpreted with an awareness of their real-world implications.

CRediT authorship contribution statement

Sirmayanti: Writing – review & editing, Writing – original draft,

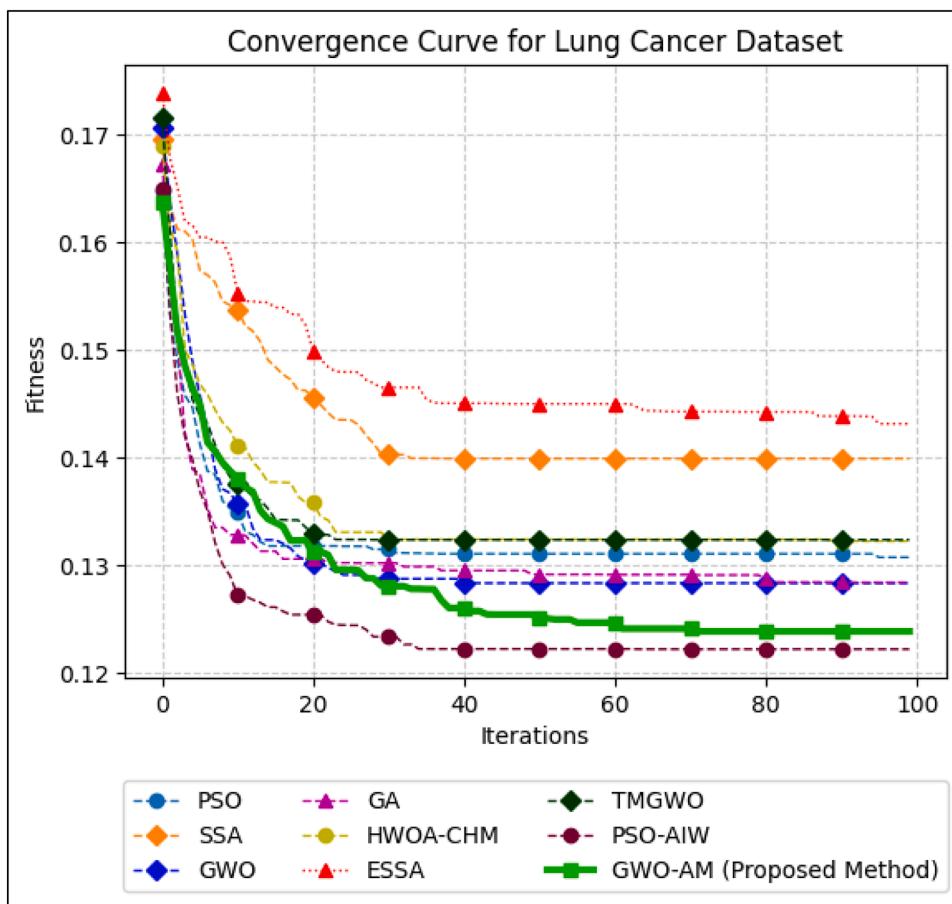


Fig. 10. Convergence curve for the lung cancer dataset. The proposed method, represented by a green square, is compared to eight metaheuristic algorithms. It achieves the lowest fitness value among all algorithms except for PSO-AIW.

Validation, Supervision, Project administration, Methodology, Investigation, Formal analysis, Conceptualization. **Pulung Hendro Prastyo:** Writing – review & editing, Writing – original draft, Visualization, Validation, Methodology, Formal analysis, Data curation, Conceptualization. **Mahyati:** Supervision, Conceptualization.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

Sirmayanti reports financial support was provided by National Research and Innovation Agency Republic of Indonesia. Pulung Hendro Prastyo reports financial support was provided by National Research and Innovation Agency Republic of Indonesia. Mahyati reports financial support was provided by National Research and Innovation Agency Republic of Indonesia. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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