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A hybrid of Grey Wolf (GWO) and Particle Swarm Optimization (PSO) to predict chronic kidney disease

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ABSTRACT

Chronic kidney illness represents one of the greatest chronic ailments, with a considerable rate of mortality around the globe. It is also one of the most critical illnesses nowadays, where an accurate diagnosis must be made as soon as feasible. Several studies have recently focused on creating computer-aided techniques to identify CKD in the early stages. In medical science, machine learning methods are now a valuable tool, contributing significantly to disease predictions. The primary purpose of the present research is to construct a reliable prognostic model using a hybrid of Grey Wolf and Particle Swarm Optimization for the choice of features to support classifiers on the CKD dataset. This approach helps reduce dimensionality and enhance model performance. In CKD data analysis, four ML algorithms are applied: KNN, NB, DT, and SVM. The experimental findings were implemented on the CKD dataset, and the results show that the suggested approach achieved exceptional matching performance (100%, 98.75%, 100%, and 100%), respectively. In this aspect, machine learning algorithms have proven to be promising and point towards the future of disease diagnosis.

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1. Introduction

Chronic kidney disease (CKD) is described as an impairment of kidney structure or function, and is also a non-communicable disease that has dramatically increased morbidity and mortality. It is rapidly spreading and rising to the top of the list of deaths all over the world. According to the 2019 annual World Kidney Disease Day of awareness assessment, a minimum of 2.4 million individuals die every year from kidney disease [1]. Diabetic nephropathy causes a slow reduction in kidney function and may lead to end-stage renal failure, which is associated with a much higher risk of cardiovascular problems. This pathological process accelerates the evolution of chronic renal disease while also increasing the risk of cardiovascular disease. As a result, diabetes, together with hypertension, is a major global risk factor for chronic renal disease, as both contribute to an interdependent and independent increase in cardiovascular risk [2]. Early diagnosis of renal failure is critical. Detecting kidney illness early reduces the danger of permanent kidney damage. To decrease the significant potential risks associated with chronic kidney damage and associated diseases, patients ought to undergo frequent tests and early diagnosis [3]. ML algorithms enable quick

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diagnosis and management, as well as the prediction of CKD progression in high-risk people, which enables earlier preventive steps. Integrating machine learning into medical databases will enable medical professionals to make educated judgments and safeguard public safety [4]. Artificial intelligence has significantly improved healthcare by automating medical operations. Advances in hardware, big data technologies, and software have made it easier to diagnose kidney disease. Experts in computer technology are looking for techniques to simulate kidney biological processes and provide reliable diagnostic results. The desire for massive data storage, greater machine learning, and deep learning capabilities drives the rise of image collections [5].

Feature selection is a quick and effective method for condensing features into a manageable subset by removal unnecessary ones. It shortens computing time by extracting the most data from a dataset with a finite number of attributes. FS enhances prediction outcomes in a variety of applications, such as data mining, machine learning, and recognition of patterns [6]. Encapsulation, inclusion, and filtering are three techniques for validating feature selection. To evaluate as a subset of features in a filtering technique, the encapsulation techniques employ a learning strategy as a sub-process of assessing whether the feature set is better than before.

This is an article describes a proof-of-concept study in which a dataset is used to build machine learning models for predicting chronic kidney illness. The machine learning models were created and tested using readily available datasets. The findings demonstrate both the viability of machine learning models for this critical clinical job and their potential to help in personalized treatment. This current study investigates the application of the use of machine learning techniques to perform early CKD diagnosis, following the preprocessing step, with an emphasis on missing values and iterative computation. Grey Wolf and Particle Swarm Optimization are used to find key traits and forecast CKD automatically. ML methods such as KNN, SVM, DT, and NB are utilized to diagnose chronic kidney disease. The research assesses testing accuracy by matching it to the findings of previous research.

This paper is divided into parts organized as follows manner: Section 2 provides a comprehensive assessment of the current literature, as well as emphasizes the distinctiveness of our findings. Section 3 describes the approaches used and introduces the suggested system model. In section 4, we will focus on the data categorization process. In Section 5, we analyze the experimental results, engaging in a discussion and comparing our suggested model with other research. Lastly, in Section 6, the study discusses potential further study areas.

2. Related Work

The following section will provide a review of the latest studies that show the successful use of algorithms based on DL and ML strategies in identifying chronic kidney disease (CKD) issues across several domains. It will also discuss several machine learning and deep learning strategies that use the prediction card.

Shahinda Elkholy et al.[3]. This paper provides DFS-ODBN, an optimized deep belief network for the identification of chronic kidney illness. It depends on the Grasshopper Optimization Algorithm classifier and the density-based feature selection approach. The DFS-ODBN architecture has three phases: initial processing, selecting features, and classification. The enhanced DBN outperforms existing approaches in the context of accuracy, sensitivity, and specificity, achieving 99.75 % accuracy while employing fewer characteristics.

And Muhammad Shoaib Arif et al [6]. A novel machine learning technique for diagnosing CKD was suggested, which included preprocessing procedures, feature selection, hyperparameter optimization, and ML algorithms. The model overcomes problems with healthcare data by applying iterative imputation for values that are missing and a sequential method for data scaling. The model was evaluated on the UCI CKD dataset, obtaining 100% accuracy and confirming its ability to diagnose early-stage CKD.

While Debabrata Swain et al [7]. In this work, a series of data preparation steps was conducted on the dataset to create a generic model that included the proper imputation of the missing items, in addition to data balancing, applying the SMOTE method, and feature scaling. A statistical approach, especially the chi-squared test, was utilized to determine the smallest number of attributes that are both acceptable and strongly correlated with the outcome. Several supervised learning algorithms were also used to build a strong machine learning classifier. Regardless of the numerous implemented learning approaches, the random forest, as well as the support vector machine models, showed the lowest rates of false negatives along with testing accuracy, at 99.33% and 98.67%, accordingly. When evaluated using 10-fold cross-validation, SVM excelled RF.

And Ernest et al [8]. The researchers' study employed ML techniques, combined with those from DL, to detect chronic kidney disease early, where researchers used a dataset from the campus of the University of California at Irvine to train a variety of algorithms, including DT, gradient boosting, RF, and SVM. Also, the CNN model showed the most remarkable prediction accuracy of 97% after feature selection was applied. The study also examined the top K- features for CKD prediction.

Elif Nur Yildiz et al. [9]. Using a two-class dataset, this study presents a hybrid approach that utilizes a convolutional neural network, combined with long short-term memory, to classify CKD automatically. This dataset contained thirteen features and a single output. Assume the features showed that CKD was diagnosed. The suggested CNN-LSTM-based model outperformed many well-known machine learning methods, achieving an accuracy rate for classification of 99.17%.

R.H. Aswathy et al.[10]. This research presents the Flower Pollination Algorithm-based Deep Neural Network model, which is an IOT and cloud-based CKD testing model. It involves collecting information, data preparation, selecting features, and classification using IOT gadgets. The model uses the Oppositional Crow Search (OCS) algorithm to select the optimal features from preprocessed data. The FPA-DNN technique demonstrated superior performance, having the most incredible sensitivity of 98.80 %, accuracy of 98.75%, F-score of 99%, specificity of 98.66%, and kappa of 97.33%.

Walaa N. Ismail [11]. This paper employs machine learning and autonomous choosing features approaches to help graders in identifying relevant and informative subsets in a dataset. Snake optimization methods were created to find optimal solutions by replicating snake behavior throughout the hunting phase. A new framework, named CKD-SO, has been developed for kidney disease data. Five machine learning algorithms and the snake optimization technique are used to develop a precise prediction model, achieving 99.7% accuracy in detecting kidney disease.

PANKAJ CHITTORA et al [12]. The article compares seven classification algorithms for chronic kidney failure, leveraging data from the repository maintained by UCI. Results show that LSVM with L2 penalty achieved the maximum accuracy of 98.86% when employing a simulated minority oversampling approach with total characteristics. In comparison, a deep neural network that was trained had the best accuracy of 99.6%. Other classification techniques include correlation-based feature selection, wrapper approach element choosing, the least absolute shrinking and select operator (LASSO) method of regression, and synthetic minority oversampling.

Chamandeep Kaur [5]. This research uses a dataset of 400 chronically ill kidney samples from the ML Repository at UCI. The research was performed using three machine Learning classification methods: LR, DT, and SVM, with the bagging ensemble approach utilized to improve model performance. Machine learning classifiers are trained on the dataset's clusters for chronic renal illness. This Kidney illness dataset is then organized into nonlinear characteristics and categories. The decision tree gives the best outcomes overall, with an accuracy rate of 95%. In the end, we get the highest accuracy of 97% with the bagging ensemble technique.

Vijendra Singh [13].The research aims to develop a deep neural network to evaluate its performance with various machine learning approaches. The network parameters were fixed using Recursive feature elimination (RFE), and chosen attributes were forwarded to machine learning algorithms for categorisation. The recommended deep neural network models passed all four classifications, achieving 100% accuracy and surpassing SVM, KNN, RF, logistic regression, and NB. The structure of the network optimal parameters was established and tested multiple times.

Preet Kamal Kaur [14]. The study aims to predict patient diseases while preventing privacy breaches by utilizing a meta-heuristic firefly optimizing algorithm for generating random noise. A classifier based on random forest was used on both the original and disturbed datasets, preserving the significance of prediction results even after perturbation. This approach for applications in healthcare that require both safeguarding privacy protection and reliable prediction, with outcomes of 97% accuracy on the original data and 95% accuracy on the perturbed data.

Ebrahime Mohammed Senan [15]. This study evaluated a dataset of 400 patients that had 24 characteristics. The missing numerical and nominal data were replaced using statistical analysis approaches such as mean and mode. To select among the most essential characteristics, Recursive Feature Elimination was used. This study used four

classification algorithms: KNN, SVM, RF, and DT. The random forest approach surpassed all different algorithms, reaching 100% accuracy, recall, precision, and F1 score for all metrics.

3. Methodology

The following section offers an exhaustive description of the suggested methodology that presents a precise strategy to the diagnose CKD, where the framework of the current study contains five phases, which are (i) the step of dataset prior to processing, (ii) selecting of features, (iii) executing the classification implementation, and (iv) examining how well the classifier performed. We first employ preparation of data methods to create sets that are used for training before implementing them in testing data. Categorical attributes have been encoded, and values that are missing are estimated. The next stage involves attempting to normalize and balance the data into categories, and the model in the current research uses a mix of Grey Wolf Optimization and Particle Swarm, which was utilized in the model constructed in this investigation. The efficiency of the model has been evaluated across all properties of the specified characteristics. Also, using ML classifiers such as KNN, SVM, DT, and NB was used to train the model to graphically explain many of the steps of the suggested methodology, as demonstrated in the Figure.1

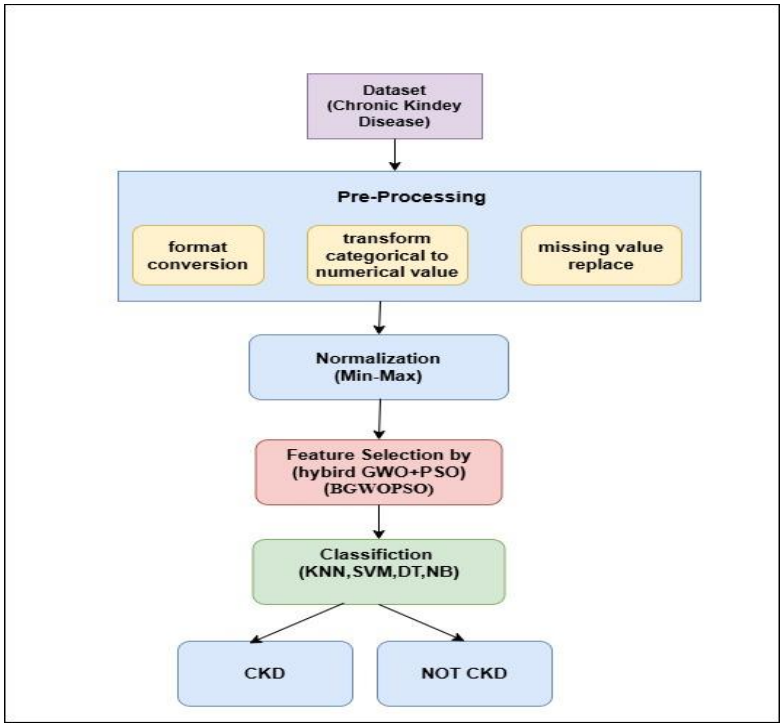

Fig 1: Proposed Methodology of CKD

3.1. Dataset collection

The data are acquired from the ML repository at UCI, where the CKD dataset used in this study comprises 400 points of data in total, with 24 different characteristics, of which 11 are numerical, and 14 are nominal in nature. Of the total number of 400 instances, 250 have been allocated to the CKD class, with the remaining 150 given to the non-CKD class. This contains attributes such as age, blood pressure, specific gravity, albumin, sugar, red blood cells, plus cell, pus cell clumps, bacteria, blood glucose random, blood urea, serum creatinine, sodium, potassium, hemoglobin, packed cell volume, white blood cell count, red blood cell count, hypertension, diabetes mellitus, appetite, pedal edema, and anemia [7]. The dataset is publicly available at http:// archive.ics.uci.edu/dataset/336/ chronic+kidney+disease. The following figure is shown as a sample for the dataset in Fig. 2 , which presents attributes of the CKD dataset.

age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	bu	sc	sod	pot	hemo	pcv	wbcc	rbcc	htn	dm	cad	appet	pe	ane	class
48	80	1.02	1	0	?	normal	notprese	notprese	121	36	1.2	?	?	15.4	44	7800	5.2	yes	yes	no	good	no	no	ckd
7	50	1.02	4	0	?	normal	notprese	notprese	?	18	0.8	?	?	11.3	38	6000	?	no	no	no	good	no	no	ckd
62	80	1.01	2	3	normal	normal	notprese	notprese	423	53	1.8	?	?	9.6	31	7500	?	no	yes	no	poor	no	yes	ckd
48	70	1.005	4	0	normal	abnorma	present	notprese	117	56	3.8	111	2.5	11.2	32	6700	3.9	yes	no	no	poor	yes	yes	ckd
51	80	1.01	2	0	normal	normal	notprese	notprese	106	26	1.4	?	?	11.6	35	7300	4.6	no	no	no	good	no	no	ckd
60	90	1.015	3	0	?	?	notprese	notprese	74	25	1.1	142	3.2	12.2	39	7800	4.4	yes	yes	no	good	yes	no	ckd
68	70	1.01	0	0	?	normal	notprese	notprese	100	54	24	104	4	12.4	36	?	?	no	no	no	good	no	no	ckd
24	?	1.015	2	4	normal	abnorma	notprese	notprese	410	31	1.1	?	?	12.4	44	6900	5	no	yes	no	good	yes	no	ckd
52	100	1.015	3	0	normal	abnorma	present	notprese	138	60	1.9	?	?	10.8	33	9600	4	yes	yes	no	good	no	yes	ckd
53	90	1.02	2	0	abnorma	abnorma	present	notprese	70	107	7.2	114	3.7	9.5	29	12100	3.7	yes	yes	no	poor	no	yes	ckd
50	60	1.01	2	4	?	abnorma	present	notprese	490	55	4	?	?	9.4	28	?	?	yes	yes	no	good	no	yes	ckd
63	70	1.01	3	0	abnorma	abnorma	present	notprese	380	60	2.7	131	4.2	10.8	32	4500	3.8	yes	yes	no	poor	yes	no	ckd
68	70	1.015	3	1	?	normal	present	notprese	208	72	2.1	138	5.8	9.7	28	12200	3.4	yes	yes	yes	poor	yes	no	ckd
68	70	?	?	?	?	?	notprese	notprese	98	86	4.6	135	3.4	9.8	?	?	?	yes	yes	yes	poor	yes	no	ckd
68	80	1.01	3	2	normal	abnorma	present	present	157	90	4.1	130	6.4	5.6	16	11000	2.6	yes	yes	yes	poor	yes	no	ckd
40	80	1.015	3	0	?	normal	notprese	notprese	76	162	9.6	141	4.9	7.6	24	3800	2.8	yes	no	no	good	no	yes	ckd
47	70	1.015	2	0	?	normal	notprese	notprese	99	46	2.2	138	4.1	12.6	?	?	?	no	no	no	good	no	no	ckd
47	80	?	?	?	?	?	notprese	notprese	114	87	5.2	139	3.7	12.1	?	?	?	yes	no	no	poor	no	no	ckd
60	100	1.025	0	3	?	normal	notprese	notprese	263	27	1.3	135	4.3	12.7	37	11400	4.3	yes	yes	yes	good	no	no	ckd
62	60	1.015	1	0	?	abnorma	present	notprese	100	31	1.6	?	?	10.3	30	5300	3.7	yes	no	yes	good	no	no	ckd
61	80	1.015	2	0	abnorma	abnorma	notprese	notprese	173	148	3.9	135	5.2	7.7	24	9200	3.2	yes	yes	yes	poor	yes	yes	ckd
60	90	?	?	?	?	?	notprese	notprese	?	180	76	4.5	?	10.9	32	6200	3.6	yes	yes	yes	good	no	no	ckd
48	80	1.025	4	0	normal	abnorma	notprese	notprese	95	163	7.7	136	3.8	9.8	32	6900	3.4	yes	no	no	good	no	yes	ckd
21	70	1.01	0	0	?	normal	notprese	notprese	?	?	?	?	?	?	?	?	?	no	no	no	poor	no	yes	ckd
42	100	1.015	4	0	normal	abnorma	notprese	present	?	50	1.4	129	4	11.1	39	8300	4.6	yes	no	no	poor	no	no	ckd
61	60	1.025	0	0	?	normal	notprese	notprese	108	75	1.9	141	5.2	9.9	29	8400	3.7	yes	yes	no	good	no	yes	ckd
75	80	1.015	0	0	?	normal	notprese	notprese	156	45	2.4	140	3.4	11.6	35	10300	4	yes	yes	no	poor	no	no	ckd
69	70	1.01	3	4	normal	abnorma	notprese	notprese	264	87	2.7	130	4	12.5	37	9600	4.1	yes	yes	yes	good	yes	no	ckd

Fig 2:Dataset of CKD prediction

3.2. Preprocessing Phase :

This section discusses the many stages of preprocessing, which is an essential stage in machine learning that involves three operations :

First, after data collection, the completeness of information was confirmed, indicating that 158 records were complete. To guarantee data integrity, missing numerical values were substituted via linear interpolation. This preserved statistical consistency and avoided bias caused by the elimination of incomplete entries.

Second, to enable the algorithms to process qualitative data, categorical variables were converted to binary numerical representations (such as 1 and 0). Ten categories of attributes were encoded in this manner, ensuring their compliance with the requirements of mathematical models without compromising classification meaning.

Third, data scaling. As a final step before modelling, all numerical features underwent scaling using the Min-Max Normalization method to convert their values to a standardized range between zero and one, using the equation [6]

$$max - min_{scaling(x)} = \frac{x - x_{min}}{x_{max} - x_{min}} \quad (1)$$

3.3. Feature selection Phase

The primary objective of choosing attributes is to determine the best features (a useful selected group of features) among all the features. It improves classifiers and reduces time complexity (dimensionality) by removing superfluous features.

- **Particle Swarm Optimization :**

The swarm intelligence algorithm PSO was developed by Kennedy, who first published the PSO algorithm in 1995. In PSO, solutions can be represented through particles, each with two vectors indicating their developmental status in the process of searching the environment: a location vector and the velocity vector. For a problem in D-dimensional space, particles hold the location vector, $X_i = x_{i,1}, x_{i,2}, \dots x_{i,d}$, and the velocity vector $V_i = v_{i,1}, v_{i,2}, \dots v_{i,d}$ during the algorithm iteration[16]

$$v_d^i = w \times v_d^t + c_1 \times v_1 \times (Pbest_d - x_d^t) + c_2 \times v_2 \times (gbest_d - x_d^t) \quad (2)$$

$$x_d^{t+1}=x_d^t+v_d^{t+1} \quad (3)$$

Where v_i and x_i stand for the ith particle's movement and its position, correspondingly, and pbesti and (Pbest)d for the ith particle's current historically optimum solution and the global optimal solution, respectively. In addition, r1 and r2 are two random values taken from [0,1], and c1 and c2 represent the position constants. Additionally, t and w stand for the current iteration number and inertia weight, respectively [17]. The PSO algorithm is enhanced by using a swarm of particles that change their positions from iteration to iteration. To identify the optimum solution, every particle travels to its global and personal best locations [18]. At the final stage of each cycle, the swarm particles are assessed for their fitness values, with each particle having a distinct fitness value [19].

- **Grey Wolf Optimization :**

The Grey Wolf Optimizer (GWO) mechanism, inspired by grey wolves, was developed in 2014 using the Mirjalili optimization algorithm. The GWO social hierarchy is broken down into four phases: Alpha, Beta, Gamma, and Omega [20]. Alpha wolves lead, omega wolves hunt first, and beta wolves consult with the alpha. The intelligent social structure model includes three primary phases: chasing, surrounding, and attacking. Equations are employed for modeling circular behavior [21].

$$X^{\rightarrow}(t+1) = X_P{}^{\rightarrow}(t) + A^{\rightarrow} \times D^{\rightarrow} \quad (4)$$

$$D \rightarrow = \left|\overrightarrow{C} \times X_P{}^{\rightarrow}(t) - X^{\rightarrow}(t)\right| \quad (5)$$

In which t is the number of iterations $D^{\rightarrow}$ is as defined in 2 $XP^{\rightarrow}$ represents the prey location $A^{\rightarrow}$,$D^{\rightarrow}$ represents the vectors of coefficients, and $X^{\rightarrow}$ indicates the grey wolf's position.

$$\overrightarrow{C} = 2r_2^{\rightarrow} \quad (6)$$

$$A^{\rightarrow} = 2 \times \alpha^{\rightarrow} \times r_1^{\rightarrow} - \alpha^{\rightarrow} \quad (7)$$

The vectors $C^{\rightarrow}$ and $A^{\rightarrow}$ They are found using equations 5 and 4. While r1 and r2 are Random vectors in [0,1], the various elements of $\alpha^{\rightarrow}$ They are lowered linearly from (2.0 - 0.0) during the span of the iterations. Alpha is the optimal candidate for grey wolf hunting, and three of the best solutions are maintained up to a specific iteration, forcing other solutions, such as omega, to move to the optimal location in the decision space. The following formula can be used to calculate the updating positions mechanism.

$$X^{\rightarrow}(t+1) = \frac{(\overrightarrow{x_1 + x_2 + x_3})}{3} \quad (8)$$

where the following are x_1,x_2, and x_3 are defined and computed [22]

$$\overrightarrow{x_1} = \overrightarrow{X_\alpha} - A_1(\overrightarrow{D_\alpha}) \quad (9)$$

$$\overrightarrow{x_2} = \overrightarrow{X_\beta} - A_2(\overrightarrow{D_\beta}) \quad (10)$$

$$\overrightarrow{x_3} = \overrightarrow{X_\delta} - A_3(\overrightarrow{D_\delta}) \quad (11)$$

Symbols denote the swarm's three optimal choices at a particular iteration t, and are denoted by symbols ($\overrightarrow{x_1}$), $\overrightarrow{x_2}$, and $\overrightarrow{x_3}$ Computed using equations (7) and (21) , respectively.

- **Hybrid Binary of Grey Wolf and Particle Swarm Optimization**

This section presents the hybrid method of PSOGWO, which combines the PSO and GWO algorithms to enhance the algorithm's ability to utilize the strengths of both optimizers. The hybrid PSOGWO is used for feature selection in a binary form, allowing agents to move continuously across the search space. The update procedure promotes every individual to the top three remedies, requiring the agents to operate in the binary space[23]. Which can be created by modifying the position updating (8)

$$X_d^{t+1} = \left\{ \begin{array}{cc} 1 & if\ sigmoid\left(\frac{x_1+x_2+x_3}{3}\right) \\ 0 & otherwise \end{array} \right\} \geq rand \qquad (12)$$

The random number rand is chosen from a uniform distribution, and X_d^{t+1} which is the binary number that indicates the updated place at cycle t in dimension d, represented by the sigmoid function (a).

$$sigmoid(a) = \frac{1}{1+e^{-10(x-0.5)}} \qquad (13)$$

where x_1, x_2, x_3 have been altered and derived using the formulae below.

$$X_1^d = \left\{ \begin{array}{cc} 1 & if\left(X_\alpha^d + b\ step_\alpha^d\right) \geq 1 \\ 0 & otherwise \end{array} \right\} \qquad (14)$$

$$X_2^d = \left\{ \begin{array}{cc} 1 & if\left(X_\beta^d + b\ step_\beta^d\right) \geq 1 \\ 0 & otherwise \end{array} \right\} \qquad (15)$$

$$X_3^d = \left\{ \begin{array}{cc} 1 & if\left(X_\delta^d + b\ step_\delta^d\right) \geq 1 \\ 0 & otherwise \end{array} \right\} \qquad (16)$$

$$b\ step\ {}^{d}_{\alpha,\beta,\delta} = \left\{ \begin{array}{cc} 1 & if\ c\ step\ {}^{d}_{\alpha,\beta,\delta} > rand \\ 0 & otherwise \end{array} \right\} \qquad (17)$$

Where d denotes dimension (c step $^{d}_{\alpha,\beta,\delta}$), d is also a continuous value, and the Rand is a randomised value derived from an evenly distributed occurrence $\in[0,1]$. The following formula is used to calculate this component.

$$c\ step\ {}^{d}_{\alpha,\beta,\delta} = \frac{1}{1+e^{-10(A\ {}^{d}_{1}\ D\ {}^{d}_{\alpha,\beta,\delta}-0.5)}} \qquad (18)$$

In BGWOPSO, both exploration and exploitation are controlled by means of an inertia constant weight that stays constant. This is scientifically modelled in the following order, depending on the top three solutions' positions, positioning changed in (16)

$$D_\alpha^{\rightarrow} = |C_1^{\rightarrow}.X_\alpha^{\rightarrow} - w * X^{\rightarrow}| \qquad (19)$$

$$D_\beta^{\rightarrow} = \left|C_1^{\rightarrow}.X_\beta^{\rightarrow} - w * X^{\rightarrow}\right| \qquad (20)$$

$$D_\delta^{\rightarrow} = |C_1^{\rightarrow}.X_\delta^{\rightarrow} - w * X^{\rightarrow}| \qquad (21)$$

As a result, the positions and velocities have been updated accordingly.

$$v_i^{k+1} = w * (v_i^k + c_1 r_1(x_1 - x_i^k) + c_2 r_2(x_2 - x_i^k) + c_3 r_3\left(x_1 - x_i^k\right) \qquad (22)$$

The top three solutions, x1, x2, and x3, are revised in accordance with (11)

$$x_i^{k+1} = x_d^{t+1} + v_i^{k+1} \qquad (23)$$

Where Eqs. (12) and (22) are used to calculate x_d^{t+1} and v_i^{k+1}

4. Classification

A key component of supervised learning is the classification method. To identify the target attribute, classifiers apply what they have learned from the training dataset to the testing dataset. This section describes four different classifiers that are used to predict diseases.

4.1 K-*Nearest Neighbours*

K-nearest neighbours is a popular supervised machine learning technique that predicts Observations to belong to classes with the most significant percentage of K-nearest neighbours rather than training a dataset. Distance is used to assess similarity, with the closest data point being considered the most similar [24]

$$d(a,b) = \sqrt{(b_i - a_i)^2} \tag{24}$$

Euclidean vectors represent the Euclidean distance between points a and b, a_i and b_i

4.2 Support Vector Machine

SVM is a widely used supervised learning technique for classification and regression tasks. It partitions n-dimensional space into classes using a choice limit, creating a hyperplane for future classification[19]. SVM is available in two varieties: Linear SVM, which divides data into two classes using a straight line, and Nonlinear SVM, which handles data not directly isolated [25].

4.3 Naive Bayes

Naive Bayes is a highly effective inductive learning algorithm for machine learning and data mining, despite its assumption of attribute independence[26]. It is a probability-based prediction technique that uses Bayes' theorem to calculate the posterior probability for each class or group of the target variable. Naive Bayes uses an independent feature model and relies on the Bayes Theorem to base its predictions [27]

$$P(X|Y) = \frac{P(Y|X) * P(X)}{P(Y)} \tag{25}$$

B is sample data with unknown class, X is the Hypothesis that Y is class data, P(X|Y) is the Hypothesis probability based on the condition, and P(X|Y) is the probability of sample Z data based on X conditions.

4.4 Decision Tree

It represents one of the most widely used supervised ML techniques for classification. DT tackles the difficulty of applying ML by converting data into a tree layout based on arranged values that represent features. Each of the nodes in a tree of decision indicates the characteristics of each instance to be divided into classes, and every node in the leaf structure provides the label for the class to which the particular instances correspond [28]

5. Model evaluation

Performance evaluation is an essential stage in developing an ML model. The prediction model must be tested to confirm that it matches the collection of information and performs well with new data. In this work, the assessment of performance is used for determining the model's generalization accuracy on previously unknown data. Various performance evaluation metrics have been computed, including accuracy, precision, recall, and the F1-score[29].

$$accuracy = \frac{TP + TN}{TP + TN + FP + FN} * 100 \tag{26}$$

$$precision = \frac{TP}{TP + FP} \tag{27}$$

$$Recall = \frac{TP}{TP + FN} \tag{28}$$

$$F - score = \frac{precision * \ sensitivity}{precision + sensitivity} \tag{29}$$

True Positive (TP) denotes properly classified positive data, whereas True Negative (TN) displays correctly categorized negative information, False Positive (FP) denotes false positive data, and False Negative (FN) symbolizes false data that is negative [30].

5.1. Results

The suggested model, which employs a hybrid BPSOGWO feature selection technique to reduce the total number of attributes and eliminate redundant data into (6) features, was compared to various machine learning classifiers to produce the results. Choose the capacity to forecast chronic kidney disease (CKD) 80% of the dataset was utilized for training, and 20 % was used for testing. The classifiers used in this study were KNN, SVM, Naive Bayes, and Decision Tree. Furthermore, the dataset used for the proposed model yielded results as illustrated in Fig. 3

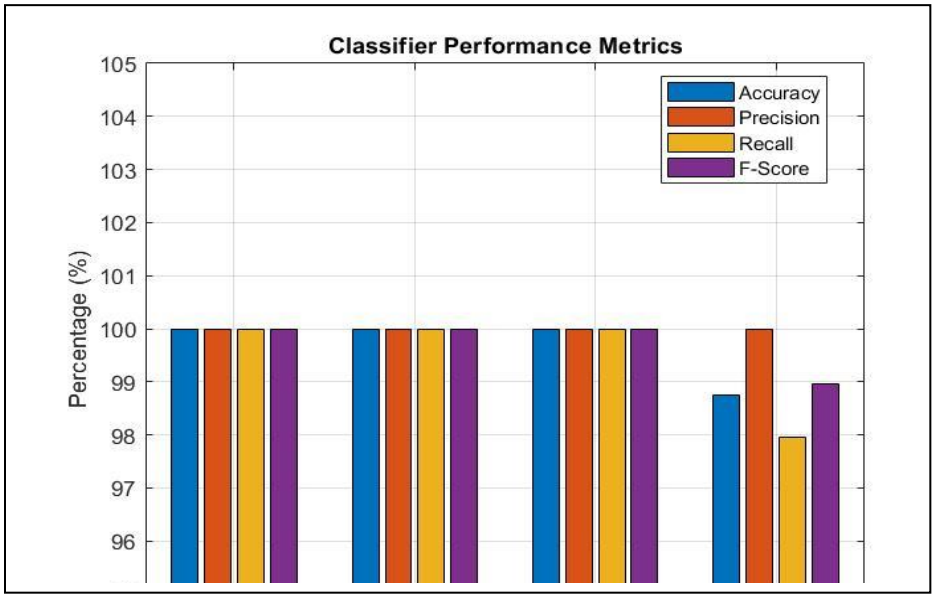

Fig. 3. Performance Comparison Graph

In this algorithm, the population size is 15, the number of iterations is 50, and the algorithm is based on the SVM classifier, Table 1 indicates the hyper parameter values selected for the suggested approach.

Table 1 : Hyperparameters for Model Suggested

Hyper parameter	values
Weight cost (W)	0.01
Accerleration coefficients(c_1, c_2, c_3)	0.5
Max number of split in DT	20
Threshold	0.5
Number of Neighbor of KNN	5
Distance Metric	Euclidean
Iterations (t)	50
Populalion size (N)	15

Where a calculated fitness function as shown in Feature Selection Convergence in Fig.4 .

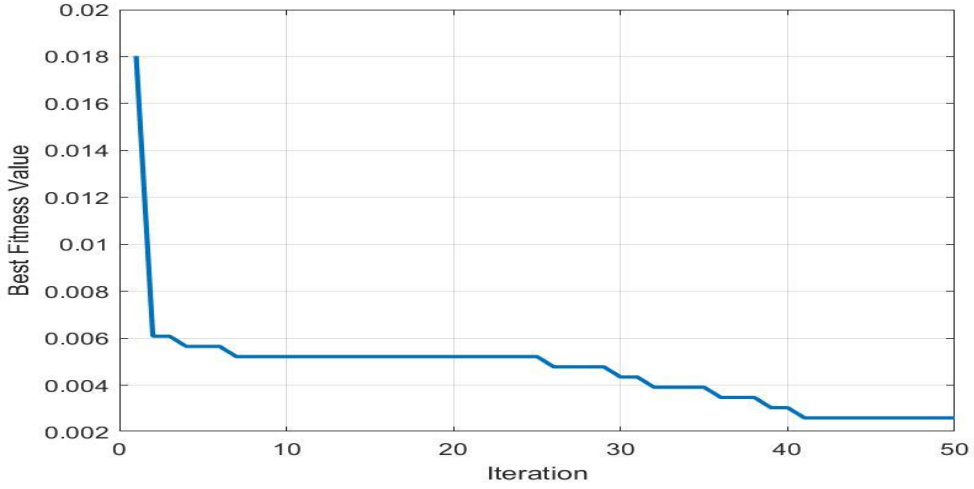

Fig. 4 Feature Selection Convergence

5.2 Discussion

In this study, the CKD dataset was utilized to assess the likelihood of chronic renal failure. The datasets consist of 24 attributes, including both numeric and nominal attributes, in addition to the category to which each occurrence corresponds. The set of data contains values that are missing, which were addressed during the preparation stage. Then, the feature choosing approach using the BGWOPSO algorithm is employed to pick the most important characteristics, and certain features have often been chosen in iteration set selections, which indicates that they are among the most accurate features and have a robust prognostic relationship to the class. The most commonly chosen attributes using the selection technique on which our proposed model is based reduce diagnostic time to 8.09804 seconds and cost by limiting the number of features to 6.

Additionally, a binary vector is used to initialize a solution in this study, which is a one-dimensional array of bits. The length of this vector equals the number of features. In this binary vector, 0 and 1 have the following: where zero signifies that the feature is not chosen, while one indicates that the feature is selected. Four ML models were utilized in this study: SVM, KNN, NB, and DT. The model evaluation was conducted using a hold-out validation approach with an 80-20 training-testing division, as well as a random seed that was determined to guarantee reliability. In order to preserve and evaluate fairness and reduce data leakage, test results remained totally secret through the feature choice and training the classifier phases, and other performance evaluation criteria include accuracy, recall, f1-score, sensitivity, and specificity. According to the results, our model consistently performed better than the previous research, highlighting the importance of our feature selection and preparation technique in raising prediction accuracy. The accuracy metrics employed to evaluate the quality of the suggested model show that when compared to the work, the proposed technique was more accurate than the other methods that used the same dataset inside [9], [3], [6], [11], and [7]. The suggested model was made in MATLAB 2021a. Testing and assessment take place on a Core i7 machine with an NVIDIA graphics card.

Table 2: Comparison investigation of the suggested approach with present models from the literature using the UCI data set.

Authors	Year	Model Suggest	Accuracy
Shahinda Elkholy et al. [3]	2023	DFS-ODBN	99.75
Muhammad Shoaib Arif et al [6]	2023	Boruta algorithm	KNN=100 , NB=97.5%
Debabrata Swain et al [7]	2023	SMOTE + chi-squared	SVM =99.33 , RF =98.67
Walaa N. Ismail [11]	2023	Snake - SVM	SVM= 97.16
Elif Nur Yildiz et al [9]	2023	CNN and LSTM	99.17
Proposed Model	**2026**	**BGWOPSO**	**KNN = 100% , SVM=100 , DT=100% , NB=98.75 %**

6. Conclusions

This study shows how important it is to find and treat chronic kidney disease (CKD) as soon as possible because it can lead to serious and even deadly problems. Chronic kidney disease is one of the illnesses that ML algorithms can now predict. This is because machine learning techniques are becoming more and more common in the medical field for diagnosis. The study aims to determine the most effective method for obtaining accurate results compared to other CKD detection methods by combining the Grey Wolf and Particle Swarm Optimization feature selection algorithms. The 400 people separated into those with and without chronic kidney disease were used to test the suggested model. Using advanced algorithms and a set of data from the educational institution of California at Irvine (UCI), where KNN, DT, SVM, and Naive Bayes have proven to be able to achieve 100%, 100%, 100%, and 98.75% prediction accuracy. This investigation successfully addresses the missing values in the data. Further studies will include domain experience in outlier detection in the study, which would improve the techniques. Furthermore, algorithms for DL can determine groupings of patients with CKD who have a greater probability of responding well to specific treatments. This method may result in more customized and effective treatment for those with chronic kidney failure.

References

[1] M. M. Nishat et al., "A Comprehensive Analysis on Detecting Chronic Kidney Disease by Employing Machine Learning Algorithms," EAI Endorsed Trans. Pervasive Heal. Technol., vol. 7, no. 29, Nov. 2021, doi: 10.4108/eai.13-8-2021.170671.

[2] M. Evans et al., "A Narrative Review of Chronic Kidney Disease in Clinical Practice: Current Challenges and Future Perspectives," Advances in Therapy, vol. 39, no. 1. Adis, pp. 33–43, Jan. 01, 2022. doi: 10.1007/s12325-021-01927-z.

[3] S. Elkholy, A. Rezk, A. A. El, and F. Saleh, "Enhanced Optimized Classification Model of Chronic Kidney Disease.", International Journal of Advanced Computer Science and Applications 14.2 (2023) doi: 10.14569/IJACSA.2023.0140239.

[4] P. Düsing et al., "Vascular pathologies in chronic kidney disease: pathophysiological mechanisms and novel therapeutic approaches," 2037, Journal of molecular medicine 99.3 (2021): 335-348., doi: 10.1007/s00109-021-02037-7/Published.

[5] C. Kaur, M. S. Kumar, A. Anjum, M. B. Binda, M. R. Mallu, and M. S. Al Ansari, "Chronic Kidney Disease Prediction Using Machine Learning," J. Adv. Inf. Technol., vol. 14, no. 2, pp. 384–391, 2023, doi: 10.12720/jait.14.2.384-391.

[6] M. S. Arif, A. Mukheimer, and D. Asif, "Enhancing the Early Detection of Chronic Kidney Disease: A Robust Machine Learning Model," Big Data Cogn. Comput., vol. 7, no. 3, Sep. 2023, doi: 10.3390/bdcc7030144.

[7] D. Swain et al., "A Robust Chronic Kidney Disease Classifier Using Machine Learning," Electron., vol. 12, no. 1, Jan. 2023, doi: 10.3390/electronics12010212.

[8] P. Ramanaiah, "Feature Selection AI Technique for Predicting Chronic Kidney Disease," Am. J. Artif. Intell., vol. 8, no. 2, pp. 32–40, Jul. 2024, doi: 10.11648/j.ajai.20240802.11.

[9] E. N. Yildiz, E. Cengil, M. Yildirim, and H. Bingol, "Diagnosis of Chronic Kidney Disease Based on CNN and LSTM," Acadlore Trans. AI Mach. Learn., vol. 2, no. 2, pp. 66–74, Jun. 2023, doi: 10.56578/ataiml020202.

[10] R. H. Aswathy et al., "Optimized tuned deep learning model for chronic kidney disease classification," Comput. Mater. Contin., vol. 70, no. 2, pp. 2097–2111, 2022, doi: 10.32604/cmc.2022.019790.

[11] W. N. Ismail, "Snake-Efficient Feature Selection-Based Framework for Precise Early Detection of Chronic Kidney Disease," Diagnostics, vol. 13, no. 15, Aug. 2023, doi: 10.3390/diagnostics13152501.

[12] P. Chittora et al., "Prediction of Chronic Kidney Disease - A Machine Learning Perspective," IEEE Access, vol. 9. Institute of Electrical and Electronics Engineers Inc., pp. 17312–17334, 2021. doi: 10.1109/ACCESS.2021.3053763.

[13] V. Singh, V. K. Asari, and R. Rajasekaran, "A Deep Neural Network for Early Detection and Prediction of Chronic Kidney Disease," Diagnostics, vol. 12, no. 1, Jan. 2022, doi: 10.3390/diagnostics12010116.

[14] P. K. Kaur, K. P. S. Attwal, and H. Singh, "Firefly Optimization Based Noise Additive Privacy-Preserving Data Classification Technique to Predict Chronic Kidney Disease," Rev. d'Intelligence Artif., vol. 35, no. 6, pp. 447–456, Dec. 2021, doi: 10.18280/ria.350602.

[15] E. M. Senan et al., "Diagnosis of Chronic Kidney Disease Using Effective Classification Algorithms and Recursive Feature Elimination Techniques," J. Healthc. Eng., vol. 2021, 2021, doi: 10.1155/2021/1004767.

[16] F. Wang, H. Zhang, and A. Zhou, "A particle swarm optimization algorithm for mixed-variable optimization problems," Swarm Evol. Comput., vol. 60, Feb. 2021, doi: 10.1016/j.swevo.2020.100808.

[17] A. G. Gad, "Particle Swarm Optimization Algorithm and Its Applications: A Systematic Review," Arch. Comput. Methods Eng., vol. 29, no. 5, pp. 2531–2561, Aug. 2022, doi: 10.1007/s11831-021-09694-4.

[18] E. H. Houssein, A. G. Gad, K. Hussain, and P. Nagaratnam, "Major Advances in Particle Swarm Optimization : Theory , Analysis , and Application," Swarm Evol. Comput., vol. 63, no. February, p. 100868, 2021, doi: 10.1016/j.swevo.2021.100868.

[19] A. Roy and S. Chakraborty, "Support vector machine in structural reliability analysis: A review," Reliability Engineering and System Safety, vol. 233. Elsevier Ltd, May 01, 2023. doi: 10.1016/j.ress.2023.109126.

[20] F. Al Thobiani, S. Khatir, B. Benaissa, E. Ghandourah, S. Mirjalili, and M. Abdel Wahab, "A hybrid PSO and Grey Wolf Optimization algorithm for static and dynamic crack identification," Theor. Appl. Fract. Mech., vol. 118, Apr. 2022, doi: 10.1016/j.tafmec.2021.103213.

[21] S. N. Makhadmeh et al., "Recent Advances in Grey Wolf Optimizer, its Versions and Applications: Review," IEEE Access, vol. 12, pp. 22991–23028, 2024, doi: 10.1109/ACCESS.2023.3304889.

[22] A. K. Abasi, A. T. Khader, and M. A. Al-betar, "An Improved Text Feature Selection for Clustering Using Binary Grey Wolf An Improved Text Feature Selection for Clustering Using Binary Grey Wolf Optimizer," no. January, 2021, doi: 10.1007/978-981-15-5281-6.

[23] Q. Al-Tashi, S. J. Abdul Kadir, H. M. Rais, S. Mirjalili, and H. Alhussian, "Binary Optimization Using Hybrid Grey Wolf Optimization for Feature Selection," IEEE Access, vol. 7, pp. 39496–39508, 2019, doi: 10.1109/ACCESS.2019.2906757.

[24] M. Bansal, A. Goyal, and A. Choudhary, "A comparative analysis of K-Nearest Neighbor , Genetic , Support Vector Machine , Decision Tree , and Long Short Term Memory algorithms in machine learning," Decis. Anal. J., vol. 3, no. May, p. 100071, 2022, doi: 10.1016/j.dajour.2022.100071.

[25] A. Kurani, P. Doshi, A. Vakharia, and M. Shah, "A Comprehensive Comparative Study of Artificial Neural Network (ANN) and Support Vector Machines (SVM) on Stock Forecasting," Annals of Data Science, vol. 10, no. 1. Springer Science and Business Media Deutschland GmbH, pp. 183–208, Feb. 01, 2023. doi: 10.1007/s40745-021-00344-x.

[26] I. Romli, T. Pardamean, S. Butsianto, T. N. Wiyatno, and E. Bin Mohamad, "Naive Bayes Algorithm Implementation Based on Particle Swarm Optimization in Analyzing the Defect Product," in Journal of Physics: Conference Series, IOP Publishing Ltd, Mar. 2021. doi: 10.1088/1742-6596/1845/1/012020.

[27] S. S. Reddy, N. Sethi, R. Rajender, and G. Mahesh, "Forecasting Diabetes Correlated Non-alcoholic Fatty Liver Disease by Exploiting Naïve Bayes Tree," EAI Endorsed Trans. Scalable Inf. Syst., vol. 10, no. 1, 2023, doi: 10.4108/eai.29-4-2022.173975.

[28] H. Dabiri, V. Farhangi, M. J. Moradi, M. Zadehmohamad, and M. Karakouzian, "Applications of Decision Tree and Random Forest as Tree-Based Machine Learning Techniques for Analyzing the Ultimate Strain of Spliced and Non-Spliced Reinforcement Bars," Appl. Sci., vol. 12, no. 10, May 2022, doi: 10.3390/app12104851.

[29] K. M. Sujon, R. Hassan, K. Choi, and A. Samad, "empirical evidence from advanced statistics , ML , and XAI for evaluating business predictive models," 2025, doi: 10.1186/s40537-025-01313-4.

[30] I. Ariawan et al., "Extraction of Morphometric Features the shape of mangrove leaves based on digital images and classification using the Support Vector Machine Extraction of Morphometric Features the shape of mangrove leaves based on digital images and classification using", Karbala International Journal of Modern Science 10.2 (2024): 5,doi: https://doi.org/10.33640/2405-609X.3349.