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A MACHINE LEARNING APPROACH FOR EARLY RENAL RISK PREDICTION USING IMPROVED SSA AND ANNGO

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Abstract -Chronic kidney disease (CKD) is a general term encompassing a number of diverse kidney diseases with increasing frequency and prevalence as well as harmful side effects includes renal failure, cardiovascular disease, and early death. It is sometimes referred to as Chronic Renal Disease a stage of advanced renal function loss. Unfortunately, there is no cure for this ailment, but it is possible to halt its growth and mitigate the harm by diagnosing it early. As a result, it is now of utmost importance to identify such illnesses at an early stage. If the risk factors for chronic kidney disease are identified early on, timely treatment and the proper course of action may be performed. Along with mining tools, machine learning is crucial in overcoming this obstacle. In this research, we used a hybrid model and feature selection technique to construct an hybrid machine learning model to forecast CKD. With an accuracy of 99.87%, the results demonstrated that the proposed classifier performed best in the renal diagnosis method.
Keywords -Chronic Renal Disease, Renal failure prediction, machine learning, kidney disease, classification.

INTRODUCTION

End-stage kidney disease (ESKD), commonly known as renal failure, is a pathological state of partial or complete loss of renal function brought on by the progression of chronic kidney disease (CKD) to a more advanced stage. Uremia or possibly fatal consequences would soon affect patients with renal failure, and the only options for therapy are dialysis or kidney transplantation. Renal failure is becoming more common, and its overall mortality rate is rising [1]. Chronic kidney disease (CKD) is a non-growing, rapidly spreading illness that greatly increases mortality and causes health problems. According to the statistics, there were 755 million individuals in the globe in 2019, with about 418 million of them being female and 337 million male. With 17.5% of the world's population, India's healthcare problems are extremely important [2].

This chronic illness has a number of symptoms including hypertension, bone thinning, lessening erve damage, blood count level, and causes blood vessel and heart disease [3]. Predicting CKD at an early stage and monitoring on risk factors may assist to stop the illness from spreading further and reduce its impact on a person's health. Glomerular filtration rate (GFR) is a remarkable indicator of renal function for assessing severity. The patient's GFR determine the kidney function. The GFR value will fall as the function of kidney get worse. Age, blood count, gender, race, and additional considerations including patients' sufferings are taken into consideration while calculating the GFR[2]. Figure 1 illustrates the some of the cause of CKD.

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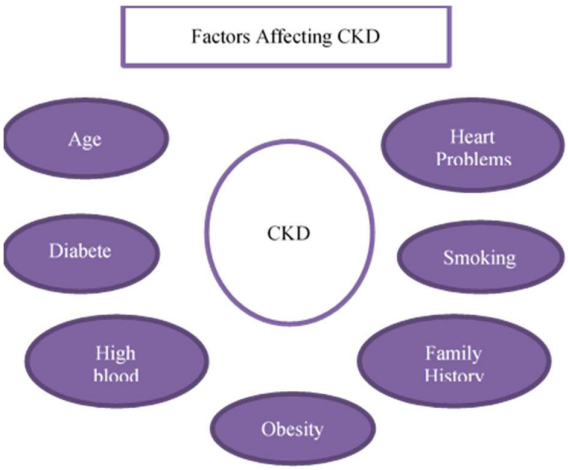

Figure 1 Factors Affecting CKD

It is impossible to create a risk model using conventional cohort research methodologies without a significant number of patient samples and adequate laboratory test data encompassing all studied disciplines. The extensive use of electronic medical record systems, particularly the development of regional health information platforms for data exchange and sharing, has resulted in the accumulation of substantial amounts of clinical medical data [4]. These platforms provide a strong data foundation for medical health research. Big data platforms make it quicker and cheaper to compile huge population datasets than traditional cohort research methods, which especially improves the effectiveness of observational studies.

Yet, machine learning techniques are increasingly being used for clinical analysis because of their superior ability to employ complex mathematical operations to calculate enormous volumes of data. By extracting and analyzing retrospective population data from electronic health record (EHR) big data systems, many clinical investigations would become noticeably more practical in terms of data accessibility. This will also be shown in our study on renal failure.

In this study, we aimed to demonstrate the viability of general chronic illness populations to renal risk prediction from CKD patients. From the UCI data repository, 361 patient records with 25 attributes (11 numerical and 14 nominal) were chosen. The risk models for renal failure were created using five machine learning methods, of which the integrated approach performed best on the test set.

In this work, a hybrid model and feature selection technique is adopted to construct an hybrid machine learning model to forecast CKD. The traditional squirrel search is improved with good point asset and global optimum position and introduced the hybrid classification model with artificial neural network with grasshopper optimization. The contribution of this research is as follows:

To design and develop a robust diagnosis system to discover the chronic kidney disease.

Most impactful features are extracted with improved squirrel search based feature selection

A replicable hybrid machine learning model is proposed to successfully detect CKD and non-CKD.

RELATED WORKS

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Prediction of CKD is a popular study topic. In order to develop a reliable and effective prediction system, many researchers applied several machine learning algorithms.

In order to reduce the dataset's dimensionality and strongly select the features associated with CKD, Sara et al [5] applied two strategies: feature selection (FS) and hybrid wrapper and filter-based FS (HWFFS). After the features from the two methodologies were combined, an SVM classifier was used to identify the hybrid traits.

Almansour et al [6] suggested using machine learning approaches to detect CKD at an early stage. For the classification techniques, the authors employed a dataset of 400 patients and 24 factors connected to the diagnosis of chronic renal illness. The accuracy of ANN and SVM, which the researchers used to diagnose CKD, was 99.75% and 97.75%, respectively.

SVM, MLP and Radial Basis Function (RBF), and Probabilistic Neural Networks (PNN) approaches were utilized by Rady et al [7] to diagnose a CKD dataset. With an accuracy of 96.7%, the authors found that the PNN approach was outperformed by the SVM, MLP, and RBF algorithms.

Aditya Khamparia et al [8] provides a unique deep learning architecture for classifying chronic kidney illness using multimedia data and stacked autoencoder models with softmax classifiers. A softmax classifier is then used to forecast the final class after the stacked autoencoder assists in extracting the dataset's important characteristics.

For the purpose of diagnosing CKD, Kim et al [9] suggested a genetic algorithm (GA) based on neural networks (NN). The weight vectors used to train the NN were optimized genetic algorithm. 741 ultrasound images total—251 of normal kidneys, 328 of mild- to moderate-CKD, and 162 of severe-CKD—were used by the researchers. The authors achieved a classification rate of 95.4% using an artificial neural network (ANN).

Table 1: Prior CKD prediction method and their performance metrics.

Author	Dataset	Modality	Feature selection	Classification	Accuracy
Sara et al.	UCI CKD dataset	Diagnose of CKD	HWFFS	SVM	90%
Rady *et al*	361 Indian CKD patient	CKD Detection	-	PNN	96.7%
Almansour et al.	UCI CKD dataset	CKD or not-CKD detection	-	SVM	99.75%
Elkholy et al	UCI CKD dataset	CKD Detection	-	MDBN	98.5%
Khamparia et al.	UCI dataset	CKD or not-CKD	Stacked Autoencoder	Stacked Autoencoder	99%
Kim et al.	ultrasound images	Normal, mild and moderate CKD, severe CKD	GLCM	ANN	95.4 %

Elkholy et al [10] Provides a robust model for classifying the kidney disease and prediction. It employs a modified Deep Belief Network (DBN) classification algorithm to forecast kidney-related disorders. In comparison to existing models, the proposed model achieved the accuracy of 98.5% and a sensitivity of 87.5%. The study of the results demonstrates the present model is

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suitable for clinical decision making. These approaches can help in the early detection of CKD and its associated stages, which slows the course of kidney damage.

METHODS

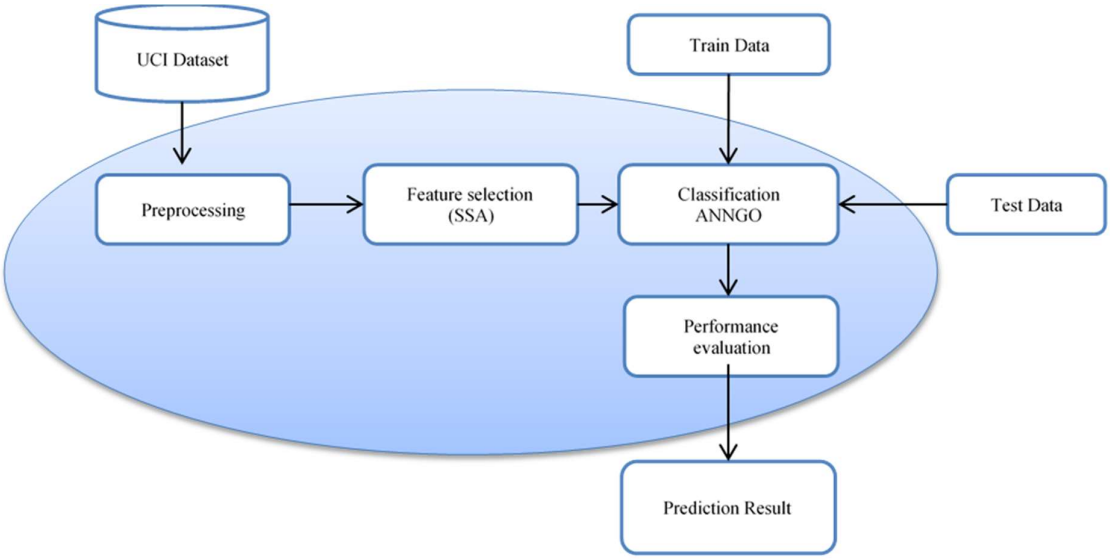
The applied methods are extensively discussed in this section. Techniques for preparing datasets, feature selection, and hybrid approach to classification used to diagnose are described and examined. Inspecting the CKD dataset is the primary phase of the proposed study. The proposed methodology architecture is given in figure1. The data collected from the UCI repository is further processed with label encoding and applied SSA to select the most significant features for the classifier. Finally the hybrid ANNGO approach classifies the CKD effectively on the selected features.

Dataset

UCI Dataset is used in the proposed model. It has 25 attributes, 14 nominal, 11 numerical, and 1 class attribute, and it has information on 400 patients, 250 of whom have CKD and 150 of whom do not.

Preprocessing

It can be difficult to classify data with missing values. Before conducting data analysis, the dataset must be modified because it contains missing values, which decrease efficiency. The difficulties of scenarios with missing values are thought to be avoided with imputation. For numerical characteristics, the median imputation is used, which uses the attribute's midpoint value.



The mode imputation is used for nominal attributes, which uses the most frequent value per column. Further label encoding process is performed for the selected dataset.

Feature selection

Squirrel search algorithm is the latest and powerful method utilized for feature selection process. Yet, the SSA's limited capacity for exploration could cause an early convergence to the local optimum. In order to address this issue, SSA has been improved in two ways. The first involves applying the good point set method to improve the starting location. The other is expanding the influence of the ideal location on the population as a whole rather than employing the original algorithm's sole guidance of global optimal position.

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Squirrel search algorithm

Mohit et al. presented the SSA in 2018. This algorithm mimics the southern squirrel's dynamic foraging behaviour [13]. The SSA makes the assumption that there is only one hickory nut tree, a few of oak trees, and the majority of other trees in a forest, each of which is home to a squirrel. The ideal, suboptimal, and general solutions are represented by the hickory nut tree, oak tree, and normal tree, in that order. In search of the best food supply, the hickory nut tree, which denotes the best solution, squirrels would hop between other trees. Squirrels move about as they search for food, updating their positions to reflect new information. A squirrel's location is mathematically represented by an n-dimensional vector, with each of its values denoting a different position variable.

to establish a starting point with a standardized random distribution in SSA [13], apply Eq (1). These places are sorted in descending order after the population location's fitness has been evaluated.

$$Sq_i = Sq_L + R(0,1) \times (Sq_a - Sq_b) \quad (1)$$

In Eq. (1), Sq_a is the upper limit of the squirrel search, while Sq_b denotes the lower limit. Sq_i represents the ith squirrel's position as an n-dimensional vector.

Location update

The position updated formula is separated into three categories as represented in Eq (2-4) during the iterative process. One squirrel will walk towards the hickory nut tree while perched on an oak. On typical trees, squirrels are separated into two groups: one for the oak tree and the other for the hickory nut tree. Mohit introduced the requirement of a hunter showing up in order to enhance the ability of the global search [13]. When this circumstance occurs, a squirrel will run into a hunter and be forced to turn around. The squirrel will then find a safe position in the search area at random.

Category 1

Oak tree squirrel moving towards the hickory nut tree.

$$Sq_{ot}^{z+1} = \begin{cases} Sq_{ot}^{z} + k_d \times K_c \times (Sq_{ht}^{z} - Sq_{ot}^{t}); & F_1 \geq P_p \\ Random\ location & otherwise \end{cases} \quad (2)$$

Oak tree squirrel moving towards the hickory nut tree.

$$Sq_{ot}^{z+1} = \begin{cases} Sq_{ot}^{z} + k_d \times K_c \times (Sq_{ht}^{z} - Sq_{ot}^{t}); & F_1 \geq P_p \\ Random\ location & otherwise \end{cases} \quad (2)$$

Category 3

Normal tree squirrel moving towards the hickory nut tree.

$$Sq_{nt}^{z+1} = \begin{cases} Sq_{nt}^{z} + k_d \times K_c \times (Sq_{ht}^{z} - Sq_{nt}^{t}); & F_3 \geq P_p \\ Random\ location & otherwise \end{cases} \quad (4)$$

P_p stands for the probability of a predator's presence in Equations (2)–(4). Within the range [0, 1], F_1, F_2, and F_3 are all random numbers. K_c is a gliding constant and 1.9 is the value it as mentioned in [13]. k_d is the squirrel's glide distance when it jumps between trees. The normal gliding distance is adjusted to obtain a perturbation range of k_d spanning [0.5, 1.11] in order to prevent the equation from being too perturbed. The algorithm's capacity for local search is significantly enhanced by the fact that k_d undergoes a sliding modification with each iteration

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[13]. A flying squirrel reaches the hickory nuts tree at position Sq_{ht}^{z}, the oak tree in position Sq_{ot}^{z}, and the normal tree in position Sq_{nt}^{t}, where t is the number of iterations.

Seasonal Monitoring Condition

Seasonal changes have a big impact on flying squirrels' foraging habits [43]. In order to keep the algorithm from being stuck in local optimal solutions, a seasonal monitoring condition is added. The seasonal constant must first be determined using Eq (5).

$$Sq_{c}^{z} = \sqrt{\sum_{x=1}^{d}\left(Sq_{ot,x}^{z} - Sq_{ht,k}\right)^{2}} \quad (z = 1,2,3) \quad (5)$$

Then, the status of the seasonal monitoring is examined. S_m is computed as per Eq (6)

$$S_m = \frac{10E - 6}{(365)^{t/(t_{max/2.5})}} \quad (6)$$

When $Sq_{c}^{z} \geq S_m$ occurs, the winter is ended, likewise, flying squirrels that lose the ability to travel through the forest will haphazardly change the locations where they are looking for food sources: formula for relocating is as follows

$$Sq_{nt}^{j} = Sq_a + L(n) \times (Sq_a - Sq_b) \quad (7)$$

L(n) can be calculated by Eq(8)

$$L(w) = 0.01 \times \frac{t_p \times \mu}{\left|t_q\right|^{1/\beta}} \quad (8)$$

μ is computed by Eq (9)

$$\mu = \left(\frac{\Gamma(1+\beta) \times \sin(\pi\beta/2)}{\Gamma\left((1+\beta)/2\right) \times \beta \times 2^{\left(\frac{(\beta-1)}{2}\right)}}\right) \quad (9)$$

Where $\Gamma(w) = (w-1)$

Where is β constant of 1.5 and t_p and t_q are two normally distributed random values in the range [0, 1].

Improved SSA

The SSA has been enhanced in two ways. The first involves applying the good point set approach to improve the starting location. The original evolutionary algorithm simply followed the global optimal position; the second is broadening the influence of the ideal location on the population as a whole.

Good-point set (GPS)

The initial population strategy used by the majority of optimization algorithms is based on an even distribution of random numbers. It is well known that the outcomes of each optimization algorithm iteration are related in some way to the population's preceding generation. The algorithm can function more effectively in terms of convergence speed by improving the starting population's dispersal. Therefore, the solution space cannot be equally covered by initial population locations that are uniformly dispersed at random. The good-point sets technique, however, can meet this condition.

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Choose the GPS according to Eqn (10) to initialize the SSA population

$$G_p = \left\{w_1^{(n)} \times d, w_2^{(n)} \times d, \cdots w_x^{(n)} \times d\right\} d = 1,2, \ldots, n \qquad (10)$$

Global optimal position(GOP)

Moreover, we incorporate chaotic principles into the SSA and apply chaotic perturbation to the optimal point following each update. The global optimal point in the original algorithm merely helps to guide the evolution of other points; it does not change itself over each iteration. In the first combination, a new position is produced by chaotic mapping in each iteration using the global best solution. The survival of the fittest selection process is used to choose both this new position and the overall ideal position. As the approach is enhanced, the optimal solution acquires local search capability, which aids the solution in avoiding the local optimal one.

Typically, logistic mapping is the chaotic map utilized in chaos optimization, as seen in the equation below.

where the system constant is used. The system is in a chaotic state when = 4.

$$d = \epsilon \times d \times (1 - d) \qquad (11)$$

Classification

Classification plays a critical role in renal risk prediction by helping to categorize patients into different risk groups based on their clinical characteristics, laboratory test results, and imaging studies. This information can then be used to determine the appropriate course of treatment and management strategies to prevent or slow the progression of renal disease. By accurately classifying patients into different risk groups, clinicians can tailor treatment plans to each individual patient's needs and optimize outcomes.

Grasshopper optimization algorithm

Meta-heuristic algorithms are built on the idea of simulating nature. Global optimization issues are typically solved using these strategies. The different types of meta-heuristic algorithms include those that are based on evolution), swarm intelligence, physical & chemical, and human-based.

The organic activities of grasshopper swarms are similar to GOA. The two stages of nature-inspired optimization algorithms are exploration and exploitation. Throughout the exploration, the search agents of the optimization process move abruptly. But while being abused, they typically relocate nearby. The following equations describe how the grasshopper behaves and how optimization search works.

$$P_{gi} = r_1 S_{gi} + r_2 GF_{gi} + r_3 WA_{gi} \qquad (12)$$

Where P_{gi} denotes the location of the gi th grasshopper, and gi stands for each individual grasshopper. S_{gi} is a metaphor for the grasshoppers' social interactions represented by Eq (13). Similar to this, GF_{gi} and WA_{gi} are used to represent the forces of gravity and wind advection, respectively.

$$S_{gi} = \sum_{\substack{j}}^{Num} sf\left(d_{gi,j}\right) \widehat{d_{gi,J}} \qquad (13)$$
$$j \neq gi$$

Where sf denotes the social forces strength$sf = fe^{-r/1} - e^{-r}$, value 1 represents the attractive length scale, f refers intensity of attraction and Num denotes number of grasshopper. $d_{gi,j}$ represents the absolute distance among gi th and j th grasshopper$\left(d_{gi,j} = \left|P_j - P_{gi}\right|\right)$, and $\widehat{d_{gi,J}}$

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denotes the vector among two grasshopper $\widehat{d_{gi,J}} = \left(P_j - P_{gi}\right) \Big/ d_{gi,j}$. Artificial grasshoppers' social interactions are influenced by the s function. This function divides the distance between each pair of grasshoppers into three regions (attraction region, comfort zone, and repulsion region). In their investigation of distances from 0 to 15, Saremi et al. [22] found that there was repulsion between [0 2.079]. They suggested calculating the comfort distance as the separation of two plastic grasshoppers by 2.079 units. Repulsion or attraction does not function well in a safe environment. But the s function returns to zero if this distance exceeds 10. As a result, this function is unable to exert powerful pressures over considerable distances between grasshoppers. GF_i (gravitational force) is another element of P_{gi}.

$$GF_i = -g\widehat{e_g} \tag{14}$$

where g stands for the gravitational constant and $\widehat{e_g}$ for the unity vector pointing at the center of the earth. Finally, Ai (wind advection) is the final part of P_{gi}.

$$WA_i = u\widehat{e_w} \tag{15}$$

Where u and $\widehat{e_w}$ represent continuous drift and a unity vector in the wind's direction respectively. Traditional swarm-based algorithms imitate the swarm as it explores and takes use of the search space surrounding a solution. The GO model of P_{gi} replicates the interactions of a swarm of grasshoppers since the mathematical equations are in free space. Equation (1) is expanded to produce Equation (5). it models the behavior of the grasshopper in many spatial dimensions, including 2D, 3D, and hyper dimensional environments,

$$P_{gi}^d = dc\left(\sum_{j=1}^{Num} c\frac{ub_d - lb_d}{2} s\left(\left|P_j^d - P_{gi}^d\right|\right)\frac{P_j - P_{gi}}{d_{gi,j}}\right) + \widehat{T_d} \tag{16}$$

Td is the optimal (goal) solution, as the ease, repulsive, and attraction zones are reduced in size by the lowering constant c. The upper as well as lower bounds in the Dth dimension are denoted as ub_d and lb_d, respectively. Each search agent in GOA has a single position vector, which is used to calculate each search agent's next position. Equation (5)'s first component, the summation, replicates grasshopper interaction by taking into account the positions of other grasshoppers. $\widehat{T_d}$ is a symbol for their propensity to go to source of food. In Eq (17), c simulates the slowdown of grasshoppers as they approach the food source.

$$c = cmax - l\frac{cmax - cmin}{L} \tag{17}$$

Where the current iteration and the maximum number of iterations, L and l, respectively. Cmin and Cmax are the least and maximum values greatest values. We utilized the same settings as Saremi et al. [22], who used cmax = 1 and cmin = 0.00001. In summary, the swarm eventually approaches a stationary target as the comfort zone is reduced by the c parameter. Additionally, the swarm correctly pursues a moving object by $\widehat{T_d}$. The grasshoppers will approach the objective throughout several repetitions.

Artificial Neural Network (ANN)

The ANN is a machine learning technique that investigates the link between phenomena (input-output data pairs) by comparing the way the human brain solves problems [9]. The ANN approach has three layers: input, hidden, and output, and connections between them allow for the potential of linking every single neuron in one layer to every conceivable neuron in the other layer. The

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choice and design of meta-parameters including learning rate, output function, number of nodes in the hidden layer, and inputs have a significant impact on the ANN's accuracy and performance. The dataset is divided into three groups using this method: tests, validation, and training The ANN picks up on interactions discovering the patterns between input and output pairs in the training stage, methods like back-propagation and optimization models are used. The datasets must be validated in order to make adjustments and boost learning process accuracy. The developed ANN model's prediction ability is also evaluated using the testing dataset following the training stage.

ANNGO

First, GO trains the ANN to improve the initial weight and biases in the grasshopper optimization of neural networks (ANNGWO). The back-propagation method will next train the neural network to fine-tune the weights and biases determined in the earlier step in order to discover the most global optimal model.

Result and Discussion

The present model is evaluated before and after applying the improved SSA feature selection. The classifier is evaluated using the performance metrics like accuracy, precision, recall, f1 score, rmse, mcc and kappa. UCI chronic kidney disease dataset is adopted for the experiment. The performance metrics are evaluated before and after applying the feature selection approach and their result are showed in following figures.

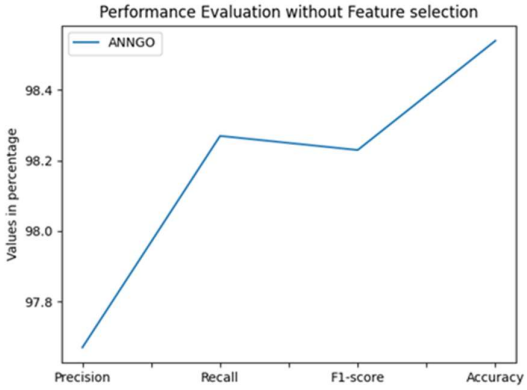

Figure 3. Performance comparison of different metrics before feature selection

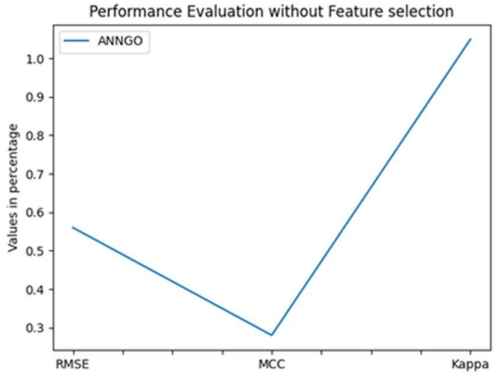

Figure 4. Performance comparison of different metrics before feature selection

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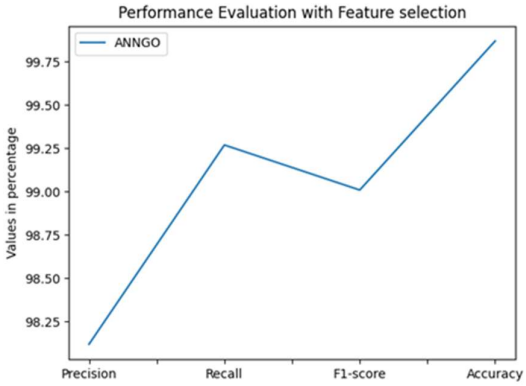

Figure 5 Performance comparison of different metrics after feature selection

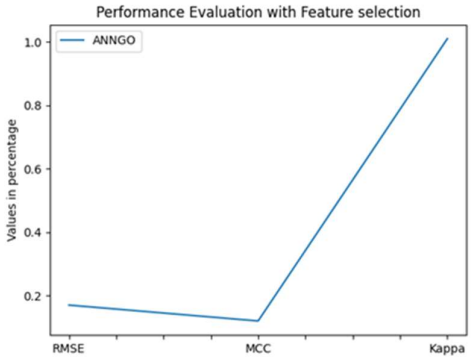

Figure 6 Performance comparison of different metrics after feature selection

Figures 3 to 6 depict the proposed model's performance. The four widely used conventional algorithms SVM, KNN, ANN, and RF came in second with comparable performance, while the suggested technique ANNGO with improved SSA feature selection earned the best performance on the test set with accuracy of 99.87%.

The efficacy if the present model is compared with traditional machine learning model as shown in figure 7. It shows that the combination of improved SSA feature selection with hybrid ANNGO provides the highest CKD detection accuracy compared to other four methods.

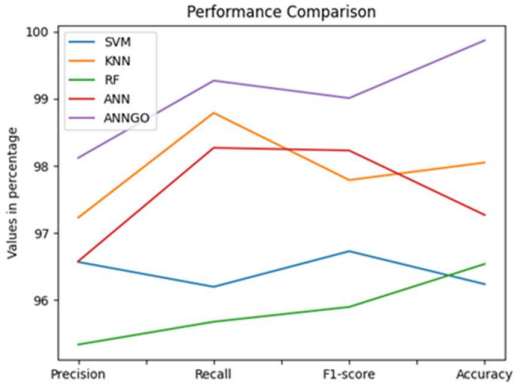

Figure 7. performance comparison of ANNGO with four existing method

Conclusion

This research has established an efficient, simple, and reliable strategy for CKD classification and attributions selection. The following processes were used to complete the current work: data collection, pre-processing, model training, relevant attribute selection, and model assessment on

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chosen attributes. With an accuracy of 99.87, the suggested classifier achieves the best performance. The findings of this investigation showed that the key characteristics that the ISSA discovered were in line with prevalent clinical thought. It was also demonstrate that the proposed ANNGO achieve high classification accuracy with improved SSA feature selection.

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