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A Novel Technique for Chronic Kidney Disease Prediction using Glowworm Swarm Algorithm with Adaptive Neuro-Fuzzy Inference System

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ABSTRACT Chronic Kidney Disease (CKD) describes the gradual reduction in kidney function. According to reports published by the World Health Organization (WHO), the prevalence of this disease in Indian adults is comparatively high. The data indicate that 220,000 new patients need renal replacement therapy in India annually. The enhanced precision of Machine Learning (ML) methods in the diagnosis of CKD has made them more significant in medical diagnostics. In recent times, attempts have been made to enhance these methods with the use of effective feature selection algorithms for dataset dimensionality reduction. This research suggests the use of an enhanced feature selection method combining Tabu Search (TS) and Stochastic Diffusion Search (SDS). Following the use of this method, five of the 24 features were removed. In the diagnosis of CKD, the proposed Adaptive Neuro-Fuzzy Inference System (ANFIS) has performed better than other state-of-the-art ML methods. With the aid of an improved diagnostic technique that employs the glowworm swarm optimization (GSO) algorithm, this work enhances the ANFIS model. The GSO method, which models the behavior of glowworms while foraging, is employed to optimize the efficiency of the ANFIS. Additionally, to accelerate convergence during network training, the proposed method employs a hybrid learning algorithm combining the Conjugate Gradient Descent (CGD) with the Least Square Estimator (LSE). Fuzzy logic is employed in the Adaptive Backpropagation Neural Network (ABPNN) classifier for improving its performance. The results demonstrate the efficiency of the ABPNN-GSO-ANFIS algorithm in CKD diagnosis with an accuracy of 99.52%, precision of 99.34%, and recall of 97.82%. The results establish that the proposed algorithm performs better than other state-of-the-art ML algorithms.

INDEX TERMS ABPNN-ANFIS, DL Algorithms, UCI CKD Dataset, GSO, TS, CKD.

I. INTRODUCTION

Diagnosis of CKD is a crucial and complicated issue in healthcare and medical science. CKD has a risk of developing several conditions such as anemia, bone disease, cardiovascular disease, and fluid disturbances. If such technique is implemented early in the course, the risk of these complications is reduced. Clinical diagnosis is crucial through investigation to improve patient outcomes. Early diagnosis allows the physicians to initiate therapy when the kidneys are in a relatively more effective stage, making the treatment effective and improving life. CKD diagnosis is an accurate and efficient tool with remarkable impacts on human health, medical science, and healthcare quality. Data mining is being used extensively in a large number of applications to detect and extract valuable patterns from enormous amounts of data [1]. In the healthcare system, ML methods are widely used to improve the accuracy of disease diagnosis and early diagnosis of medical diseases. The classification methods used in the healthcare system are an important component in the diagnosis of CKD. This study proposes a state-of-the-art feature selection technique combining TS and SDS. To further improve the ANFIS model, this study uses an optimized diagnostic approach using the GSO algorithm. Using the foraging process of glowworms for food as an inspiration, this

global optimization technique significantly improves the efficiency of ANFIS. A hybrid learning algorithm further accelerates the rate of convergence in network training. This algorithm combines the CGD technique with the LSE, enabling efficient and robust learning [2].

In addition, the proposed methodology integrates fuzzy logic into an ABPNN classifier to improve its classification capability. The hybrid use of these innovative methodologies demonstrates the potential of the proposed framework to expedite both diagnostic precision and computational efficiency in diagnosing CKD.

Researchers examined techniques to classify CKD and determined that a Support Vector Machine (SVM) classifier with best subset evaluator and Best-First Search (BFS) strategy resulted in 98.50% accuracy [3]. Other classifiers such as Backpropagation Neural Network (BPNN), radial basis function (RBF), and Random Forest (RF) were also employed in kidney disease classification, with the RBF network resulting in 85.3% accuracy. A comparison study between K-Nearest Neighbors (KNN) and SVM was also performed. A comparison study of Decision Trees (DT), Multilayer Perceptrons (MLP), and Generalized Regression Neural Networks (GRNN) revealed that the DT model provided the highest average prediction accuracy of 90.38% to clinical brain injury data [3]. A comparison trial of four algorithms based on information gain, chi-square and relief: C4.5 DT, Naïve Bayes (NB), K-NN and SVM, revealed that NB provided maximum accuracy in the diagnosis of breast cancer compared to a benchmark dataset.

Under classification of liver disease, K-NN, backpropagation, and SVM were best in terms of accuracy, precision, sensitivity, and specificity for all features. CKD causes the building up of waste products and fluids because the kidneys are unable to remove the waste and control fluids in the normal manner, causing anemia, electrolyte disorders, bone disease, and heart disease [4]. CKD, if not treated, could develop into end-stage renal disease and may have to be placed on dialysis or a transplant. Early detection and treatment will preserve kidney function, slow down the progression of the disease, and enhance outcomes in patients.

Machine learning (ML) has now significantly influenced medical diagnostics, and it is possible to develop effective models for quick and accurate analysis. Deep learning (DL), a form of ML, applies a sequence of operations during training to recognize inherent patterns in data [5]. Multi-layer DL algorithms are particularly effective in managing non-linear data, significantly enhancing medical application. For instance, our DL algorithms are trained using vast amounts of medical data and are specifically created to predict chronic diseases, thus overcoming the limitation of applying standard medical data analysis methods. The approach could reduce the generative model's robustness and generality, resulting in redundant diagnoses and false conclusions. DL thus does not necessarily generate optimal weights or effective models [6]. Ensemble learning mitigates these shortcomings by aggregating multiple models to enhance flexibility as well as generalization. It comprises two core elements: necessary learners and diversity, and begins with a big dataset in a bid to achieve more homogeneous learning.

GSO algorithm is a bio-inspired optimization method that emulates the process of glowworm foraging. Its application in machine learning is mainly in the ability to optimize model efficiency by optimal parameterization and feature selection. GSO is capable of searching the global solution space efficiently, thereby avoiding local minimum traps, which is important in maximizing the accuracy of complex models like ANFIS. The method ensures the model parameters selected are globally optimal for CKD-related prediction problems [7]. Through the emulating of glowworm movement and interaction, GSO optimizes feature selection and therefore minimizes computational complexity without compromising prediction accuracy. ANFIS is a hybrid model with the strength of both neural networks (NN) and fuzzy logic. Its application in CKD detection is its ability to deal with imprecise and uncertain data common in medical diagnosis. ANFIS leverages the learning capability of neural networks during the fine-tuning of fuzzy rules, and thus it is highly effective in modeling complex relationships inherent in CKD data. The two-stage process enables the system to learn from the past but still provides room for uncertainty in clinical variables. The proposed methodology incorporates a hybrid learning algorithm that integrates CGD and the LSE for optimization of training in ANFIS. The integration not only maximizes the convergence rate but also maximizes effective learning from CKD datasets [8].

The contribution of this research can be defined as follows:

1. The suggested method employs a GSO algorithm to increase the ANFIS efficiency.
2. SDS based on TS is used to pick features from the UCI CKD dataset.

The rest of the paper is divided into sections: Section 2 gives a detailed overview of the available literature. In Section 3, the approach and suggested system model are briefly presented. Section 4 covers the experimental results; Section 5 serves as a section for a more generalized research discussion, and Section 6 serves as the conclusion.

II. LITERATURE REVIEW

K-NN, backpropagation and SVM have proven very effective in diagnosing liver diseases, showing substantial accuracy, accuracy, sensitivity and specificity performance. In CKD, problems with waste filtration and fluid balance can lead to waste accumulation and fluid retention, leading to serious complications such as anemia, electrolyte imbalances, bone problems, and cardiovascular problems. If left untreated, CKD may progress to end-stage renal disease, requiring dialysis or a kidney transplant. Early detection and treatment are critical to protecting kidney function and improving patient outcomes. The researchers also used balanced sampling and data standardization to enhance their methods [9].

Artificial intelligence (AI) in medicine has increased dramatically in recent years, especially in early detection and prevention. This review comprehensively reviews current CKD research, analyzing relevant studies, methods, findings,

and limitations. It aims to comprehensively summarize the challenges and developments in CKD research [10]. Additionally, a ML algorithm for early detection of CKD was developed using the UCI CKD dataset.

This study presents a neuro-fuzzy model that leverages ML techniques to detect CKD risk in patients. The model outperforms conventional methods such as SVM and K-NN in terms of accuracy [11].

The researchers used cross-validation and averaging to handle missing data. Although Light GBM has been proven effective, there is limited research on advanced techniques such as data replacement and scaling, feature selection, external testing, and model tuning [12]. ML techniques were used to predict baseline chronic kidney disease, such as mean and mode methods for missing data, principal component analysis, and recursive feature removal for feature selection. However, this study did not include data measurements or hyperparameter optimization.

This research employs a neuro-fuzzy technique combined with hierarchical clustering algorithms to determine the risk levels of CKD in individuals, enhancing early detection and treatment planning [13].

A stacked autoencoder-based deep learning model has been suggested for facilitating early diagnosis of CKD. The SoftMax classifier performed extremely well for class prediction. An improved model with enhanced rare autoencoders (SAE) and SoftMax regression was constructed [14]. The autoencoder imposes penalties on weights for evoking sparsity, and the SoftMax regression model suitable for classification excels in test cases.

The authors in [15] explored the performance of ML models in CKD prediction using a subset of chosen features. Feature selection methods like Pearson correlation, ANOVA, and Cramer's V test were used to select the predictive features. LR, SVM, RF, and gradient boosting (GB) models were employed for modeling subsequently. The results showed that the Gradient Boosting model performed best with the best accuracy, having an F-measure of 99.1%.

The authors in [16] suggest three GSO variants that employ varying mutation operators—Gaussian, Cauchy, and Lévy—aimed at improving the rate of convergence and solution accuracy. The work proves the variants to be efficient at optimizing functionally complex functions.

A machine learning method of predicting the CKD risk based on patient data was suggested in [17]. The authors of that study extracted twenty features from the initial twenty-five, and applied both Random Forest (RF) and Artificial Neural Network (ANN) models. The findings reflected that the best accuracy was reached by the RF model, representing a performance value of 97.12%. This paper provides an overview of GSO-based methods, describing the algorithm's suitability to simultaneous search of multiple solutions with varying objective function values. It also mentions applications of GSO in clustering and other optimization problems [18].

To forecast CKD stages, researchers in [19] have compared various ML algorithms, i.e., Probabilistic Neural Networks (PNN), Multilayer Perceptron (MLP), SVM, and RBF networks. Their work was based on a small dataset consisting of limited attributes. The outcome with 96.7% accuracy indicated that the PNN algorithm had the highest overall classification accuracy.

In [20], the authors presented an Ensemble Deep Learning-based Clinical Decision Support System (EDL-CDSS) for the diagnosis of chronic kidney disease (CKD) in an Internet of Things (IoT) environment. The suggested methodology incorporated the Adaptive Synthetic (ADASYN) method in order to achieve outlier detection. It utilized the ensemble of three models: Deep Belief Network (DBN), Kernel Extreme Learning Machine (KELM), and Convolutional Neural Network with Gated Recurrent Unit (CNN-GRU). Additionally, the Quasi-Oppositional Butterfly Optimization Algorithm (QOBOA) was utilized for the DBN and CNN-GRU model hyperparameter optimization. The authors declared that the EDL-CDSS approach has significant potential for the precise CKD diagnosis in IoT-based medical applications.

[21] considered a number of different ML classifiers like KNN, ANN, SVM, NB, and LR and feature selection methods like Recursive Feature Elimination (RFE) and the Chi-Square test (CST). An available public database including healthy samples and kidney patients was used by the study in training and comparison of predictive models. Their conclusions demonstrated that an LR-based predictive model, in conjunction with an optimum set of features chosen from CST, scored a maximum of 98.75% accuracy.

Comparative study of seven supervised Machine Learning algorithms—KNN, DT, SVM, RF, NN, NB, and LR— were conducted with the intention of finding the most appropriate model for Binary Classification Diagnosis (BCD) [22]. It was compared using a series of metrics, and the outcome indicated that the KNN algorithm was the most optimal on the BCD dataset with a 97% accuracy. Heterogeneous learning often involves using multiple models, with ensemble classifiers created through methods like bagging, boosting, and stacking [23]. We extend the stacked ensemble model to offer a practical and adaptive solution. Research shows that ensemble learning can produce reliable and valuable models.

The reviewed studies highlight that significant research has been conducted on predicting CKD using ML techniques. Various factors, such as dataset size, dataset quality, and the data collection period, play a crucial role in enhancing model performance.

Based on the literature review, several critical research challenges have been identified as essential for advancing predictive capabilities in the field of CKD detection and management:

1. Complexity of CKD Progression: CKD usually hides its presence very well at first and often doesn't show clear symptoms until it's far along. Often the time to get a diagnosis done comes when a condition has progressed quite a bit. To tackle this challenge, the new ML algorithms select very subtle clues from patient information that signal very early stages of CKD. Getting

ahead of the disease and intervening at an early stage can help doctors give better clinical results. The clinician gets a heads up sooner and that leads to better patient management.

2. Integration of Diverse Data Sources: Getting clear diagnoses of CKD ensures looking at all kinds of different aspects like personal information, clinical symptoms someone's reporting, blood check and results from related lab tests and any other medical conditions they might be managing too. This research puts together a really diverse bunch of information and combines it in one consistent framework which allows us to forecast on CKD much better and more accurately than things have been done before. The proposed approach now produces much more sharp predictions about CKD than ever before.
3. Performance of models: The performance of ML models in healthcare applications depends significantly on identifying relevant features and appropriate data preprocessing. Advanced techniques, such as correlation analysis and variance thresholding, are employed in this study to enhance the predictive accuracy of the proposed models.
4. Model Selection and Validation: Choosing the best Machine Learning model to figure out people who have CKD is significantly important for this research. Multiple classifiers are systematically compared and evaluated to identify the model best suited for CKD detection, ensuring high accuracy and reliability.

This research tackles some really big challenges like how to detect and manage CKD. This research altogether puts together new techniques that work super well and that are also very easy to use for noting and managing this condition.

A. PROBLEM STATEMENT

If this problem is not detected and treated promptly, kidney damage can be irreparable. As the illness develops, hazardous electrolytes can build up to dangerously high levels in your blood, making you sick. The advent of CKD is exceptionally concerning since it can damage nearly every organ in the human body. It is a long-term condition with a high morbidity and death rate, costly medical costs, and a substantial risk of developing other illnesses, such as cardiovascular disease. Ten percent of people require medical treatment to survive, although over two million people depend on kidney transplants or dialysis to survive. Approximately 12% of the world's population lives in five wealthy countries, with 2 million people living with primary renal failure [24]. By comparison, less than 20% of the world's population, or more than half of the countries, have access to treatment in more than 100 developing countries. One million people die each year from untreated kidney failure in 112 low-income countries due to the high costs of dialysis and transplantation [24]. Early detection, management and treatment of CKD are crucial given the complexity and varying severity of the disease, which requires accurate prognosis due to patient diversity and often hidden early stages.

III. METHODOLOGY

A. DATASET

The fundamental chronic renal disease dataset for this job is available in the UCI ML repository [25]. Several writers have utilized this dataset to obtain experimental findings. Out of the 400 patients, 150 had CKD negative and 250 had CKD positive, according to the statistics. In the dataset that was utilized, a category label had two values. In other words, 0 and 1 denote negative and positive CKD, respectively. There are 13 category features and 11 numerical features out of the 24 features in the dataset. The link to the dataset is the UCI ML Repository.

B. PREPROCESSING

The UCI dataset contains 25 features (11 numeric features, 11 nominal features, and one categorical feature), provides data from 400 patients, and is used in the proposed model. Of these, 250 were diagnosed with CKD, and 150 were not [25]. Dealing with missing values makes data classification particularly difficult. The dataset contains a categorical response variable called "category," indicating the presence or absence of CKD. This variable has two values: "ckd" for patients with CKD and "notckd" for patients without CKD. Eliminate missing values in the data set before analysis to ensure reliable results.

The purpose of missing value imputation is to maintain the integrity of the data set without reducing the sample size [26]. There are various methods for supplementing missing data, each with unique characteristics designed to solve a specific data problem. The first step in data preparation is to fill in any gaps in the dataset obtained from the UCI ML repository. To account for missing data, average the current values and use the derived average to fill in the gaps [27]. After this pre-processing stage, the dataset is subjected to ML algorithms and the results are evaluated for accuracy and error rate. The dataset is first segmented hierarchically using target features to achieve reliable evaluation.

To preserve a 70/30 ratio, this divides the 280 instances into the training set and the 120 instances into the held-out test set. The appropriate parameters found during the preprocessing and training stages are then validated by evaluating the model's performance using hidden data from the held-out test set [28]. Three threads handle data preparation's numerical, nominal, and ordinal aspects. This covers feature selection, scaling/encoding, and missing data imputation. The preprocessed data is then combined for the training step of five-fold cross-validation. Considering the small size of the dataset (400 examples), 5-fold cross-validation reduces overfitting and improves the model's applicability to classification tasks.

Imputation algorithms are adapted to the dataset's characteristics to handle missing data. Ordinal and nominal variables are imputed using the mode (most common value), and numerical data are imputed using the mean value. Numerical features are scaled using the minimum-maximum scaling technique during the encoding stage. Nominal characteristics are encoded as 0 or 1 depending on their

categories, whereas ordinal features are encoded into numerical categories ranging from 0 to 5 with a step unit of 1.

The steps needed for preprocessing raw data are mentioned below.

1) DATA ENCODING

Utilize the Scikit-learn toolkit's label encoder module to handle the dataset's combination of numerical and categorical attributes. This module transforms categorical data into numerical representation to enhance the performance of ML models.

2) DATA IMPUTATION

When choosing the most appropriate statistical method to handle incomplete data, it is crucial to consider the amount of missing data and the importance of the missing features. If the proportion of missing information is sufficient, traditional mean, maximum, and mode techniques can work well [29]. This study contains many missing data points, as shown in FIGURE 1. We addressed this problem using iterative substitution, a statistical method that fills in missing values and estimates covariate correlations based on observed data. This iterative approach gradually improves the estimate over multiple iterations, resulting in complete and accurate data.

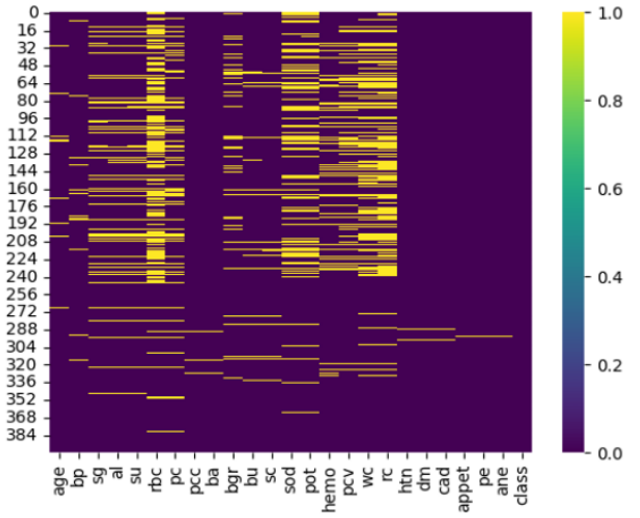

FIGURE 1. Missing Values in the Dataset

3) DATA SCALING

The application of sequential scaling procedures has accomplished data normalization and ideal value resolution. Start the process with considerable improvements to increase resilience and decrease the impact of extreme values. This is accomplished by deleting the median (Q_2) and dividing by the interquartile ranges ($Q_3 - Q_1$). This is depicted in Eq. (1) [6] and Eq. (2) [6] . x denotes the original value in the dataset, σ is the standard deviation of the dataset, representing the spread of data and μ represents the mean (average) of the dataset.

$$Robust\ Scaling\ (x) = \frac{x - Q_2}{Q_3 - Q_1} \quad (1)$$

$$Z - score\ Standardization\ (x) = \frac{x - \mu}{\sigma} \quad (2)$$

Last but not least, min-max scaling is achieved by dividing by the range ($x_{\_max}$, $x_{\_min}$) after the minimal value ($x_{\_min}$) has been removed. To obtain characteristics within a specific range (often 0-1). This is depicted in Eq. (3) [5] . x signifies the original value in the dataset, x_{min} is smallest value in the dataset and x_{max} is the largest value in the dataset.

$$Min - Max\ Scaling\ (x) = \frac{x - x_{min}}{x_{max} - x_{min}} \quad (3)$$

C. TS-BASED SDS FEATURE SELECTION

After the first step of population initialization, SDS starts searching or optimizing. Every agent keeps track of a fresh hypothesis that outlines a fix for the issue. After startup, the testing and propagation procedures are carried out. After assessing the sub-hypotheses in the first scenario, the agent produces a Boolean result. As a result, SDS can evaluate the accuracy of the agent's assumptions and the accuracy of all the data needed for the solution. Each agent completes a Partial Functional Evaluation (pFE) during the testing phase. This demonstrates that the agent believes that pFE is determined by f(h). All agents interact with one another and seek additional agents to spread the idea during the propagation stage [30]. For most search algorithms, locating the perfect response is frequently quite complex. The next challenging step is to find a local minimum or, better yet, a maximum. This job aims to enhance TS functionality and possible solutions. SDS provides various potential solutions to satisfy the TS when the best option is unavailable. It works for all the best solutions and offers broader results for TS candidates by replacing existing solutions with new ones and adding them to the TABU list [31]. This iterative approach (f(j) > f(i)) allows many unmodified transitions from V* to i to j, which helps avoid regional lows. Tabu-SDS is shown in FIGURE 2. The various stages of Tabu-SDS are explained in ALGORITHM 1. The parameters are defined as follows: I represents the solution in the solution set, S represents the maximum number of iterations, V* is the list, and k is the tabu list N, which defines the subset of solutions for i. N(i,k) represents a list containing iteration k and solution i.

ALGORITHM 1.
Selecting Optimal Subsets using a TS approach

Step	Code
1.1	Select a starting point i in S
1.2	Assign i∗=i and k = 0
2.1	Set k = k + 1
2.2	Generate subset V* as a solution N(i,k)
3.1	Select the best j from V*
3.2	Update i = j
4.1	From N(i,k), select the best subset and add it to B
5.1	If no optimal solution is found, request an SDS with the best subset from the TABU list
6.1	From the SDS result, choose the response that best fits the criteria (i.e., highest degree of accuracy)
6.2	Add the selected response to the corresponding TABU list
7.1	If the final state is reached, either return to step 2 or terminate

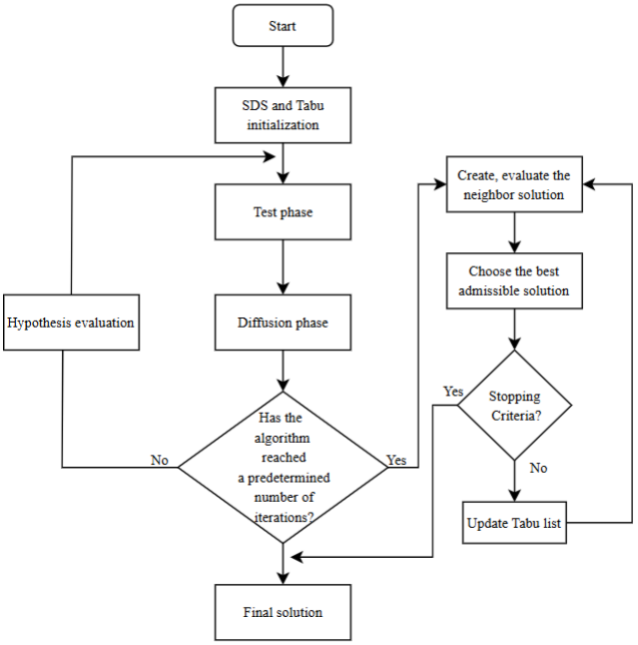

FIGURE 2. Proposed approach showing the TS Algorithm-based hybrid SDS

D. ABNN CLASSIFICATION

This study implemented an ABNN Classification integrated with fuzzy logic to develop a CKD diagnostic system. The training process involves three stages, with 17 input parameters and one output parameter indicating the presence of abnormal or healthy conditions. The preprocessing layer manages missing values and normalizes the data to handle noise. Missing values are addressed using methods like averaging and moving averages of existing values. The ABPNN ML algorithm is trained using the preprocessed data in the application training layer [32].

ANNs have proven effective across diverse fields such as finance, medicine, engineering, geology, physics, and biology. They are particularly intriguing from a statistical perspective due to their potential in prediction and classification tasks. FIGURE 3. illustrates the architecture of an underlying ABPNN, an ANN algorithm utilized effectively for identifying common patterns that differentiate various classes in classification processes. Input is processed via many non-linear hierarchical layer levels in ANNs to learn and categorize features. A robust BPNN with 13 input layers, 36 hidden layers, and three output layers is shown in FIGURE 3. Eq. (4) [31] , which represents the sigmoid function of input x, describes how this network is trained using a supervised learning technique that uses the sigmoid function. Where $\varphi_1(x)$ I s sigmoid function output for the input x, x refers as the input variable to the sigmoid function, a is the scaling factor that adjusts the maximum value of the sigmoid function, b is the parameter that determines the steepness of the sigmoid curve and e denotes the base of the natural logarithm (≈2.718).

$$\varphi_1(x) = \frac{a}{1+e^{-bx}} \quad (4)$$

The evaluation layer assesses the accuracy, precision, and Mean Square Error (MSE) of the ABPNN output. Compliance with the Learning Standards (LC) is therefore validated. If the conditions are satisfied, the data is uploaded to t6.2he cloud; otherwise, redevelopment is required. The proposed approach generally outperforms the other because it combines the outcomes of the two methods with fuzzy logic [33]. A fusion-based training model uses the obtained data to predict chronic renal disease in individuals. This model is saved to a central server when the LC are fulfilled.

The ABPNN comprises a sequence of input, output, and hidden layers that use backward and forward error propagation [34]. During forward propagation, data travels from input to output via hidden layers. In the forward direction, the output layer reduces mistakes and responds to backpropagation faults by modifying weight values to close discrepancies. The suggested ABPNN model uses a supervised learning approach similar to the structure of a Takagi-Sugeno fuzzy inference system [35]. Throughout training, this model continually adjusts its network parameters. A hybrid technique was developed to solve the delayed convergence commonly associated with gradient descent backpropagation algorithms employed in ANFIS training. This hybrid learning technique combines the least squares estimator with the conjugate gradient algorithm.

The least-square algorithm is used as a forward pass to select subsequent parameters in the fourth layer. In contrast, CGD is used as a backward pass to fine-tune premise parameters that correspond to fuzzy sets in the input domain [36]. During training, the network's actual output is compared to the desired output (expected output). Any differences between these outputs cause an error propagating back across the network levels, beginning with the first layer. The primary purpose of this adaptive learning system is to reduce mistakes across the network.

ABPNN with fuzzy logic and ANFIS are combined to produce a denervated classifier in the classification step. Sort and categorize the many forms of chronic renal disease. In this work, we employed ANFIS to classify images of chronic renal disease. Creating a neuro-fuzzy classifier, in which a neural network selects fuzzy system parameters—we integrate ABPNN with fuzzy logic [37]. This work identified brain magnetic resonance imaging anomalies using the Neuropurge classifier. It is an intelligent hybrid system that was created by neural purification. Its main advantage—that this brain cleaning system has the necessary universal load capacity—is that it approaches interpretable If-Then rules. Numerous crucial tasks, such as extraction, application to tangible input variables, and satisfaction computation, are learned by neural network-based learning algorithms. This is why most neural purification systems rely on such purification systems. After the language step measurement, we apply the assumptions and consider the inference parameters of the cleared pairs before clearing the findings [38]. The procedure mentioned above builds the neural network layers one at a time. It is possible to alter the weights in the form of extracted rule parameters thanks to the neural network's design. The weight parameters mentioned above are expressed using the following formula. It complies with a motion constant learning rule. This is depicted in Eq. (5)

[37].In this case, the weights are denoted by w_n and $w(n-1)$.$w_i(n+1)$ symbolizes the updated weight for the i-th parameter at time step n+1, w_n describes the weight at the current time step, $w(n-1)$ denoting the weight at the previous time step $n-1$ and ρ as a learning rate or scaling factor that determines the impact of the weight adjustment.

$$w_i(n+1) = \rho(w_n + w(n-1)) \quad (5)$$

The ABPNN activation function, often known as sigmoid gain, has limited smoothness. The recommended strategy reduces the scaling factor value, which expedites training along the selected path and expands the range of the sigmoid function. The mentioned activation function is depicted in Eq. (6) [37]. $Z_i(t)$ expressed as the output of the activation function for the i-th neuron at time t, Z_n stands for a scaling factor or weight associated with the n-th neuron, d_{in} as an input distance or deviation (possibly related to input features or errors), σ_a is a parameter controlling the spread or smoothness in the numerator (likely related to scaling or variance), σ_b defines a parameter controlling the spread or smoothness in the denominator (affecting scaling or smoothness of the sigmoid function) and e denotes the base of the natural logarithm (≈2.718).

$$Z_i(t) = \sum_{i=1}^{n} Z_n \left(e^{d_{in}^2/2\sigma_a}\right)/e^{d_{in}/2\sigma_b} \quad (6)$$

This is the input distance for each image set displayed by the din variable. The following limitations are relevant when exponential functions describe activation functions. These activation functions are described in Eq. (7) [37]. $activation_i$ is the activation value of the i-th unit, which depends on certain conditions, d_{in} expresses input distance or input value, which serves as part of the calculation for activation, σ_a represents a parameter likely related to the scaling or width of the exponential function, often used to control the spread or sensitivity. $d_{in}^2/2\sigma_a$ symbolizes the argument of the exponential function, which represents a specific transformation of d_{in} and e denotes the base of the natural logarithm (≈2.718).

$$activation_i = \begin{cases} d_{in} = 0 \;\; if \; e^{d_{in}^2/2\sigma_a} > 1 \\ d_{in} = 0 \qquad otherwise \end{cases} \quad (7)$$

Each open connection has a weight and an integer. Weights and numbers regulate the signal between two separate neurons. Therefore, if the network yields consistent results, there's no need to change the weights. As a result, you can generate an error function for unwanted results using the formula mentioned in Eq. (8) [37]. v_i corresponds to the computed value (possibly related to the error or outcome) for the i-th unit or system, $Q_{in}(k)$ as a quantity related to the input i and possibly dependent on a variable k representing probability statistics or a related measure, δ stands for the error function related to the k-th probability statistics and δ^2 is the square of the error function, amplifying its effect in the computation.

$$v_i = \sum_{i=1}^{n} \sqrt{Q_{in}(k)} * \delta^2 \quad (8)$$

A fuzzy logic diagnostic system consists of rules and activation functions. It is helpful in scenarios where data are missing, unclear, or complex, and it isn't easy to draw reliable conclusions [38]. During the cleaning process, raw data is fed into the intelligent system and processed into fuzzy sets or values. Expert systems use fuzzy logic to interpret instructions and map specific inputs to fuzzy outputs based on derived rules. In the refinement stage, the results of the inference process are converted from fuzzy values to discrete values.

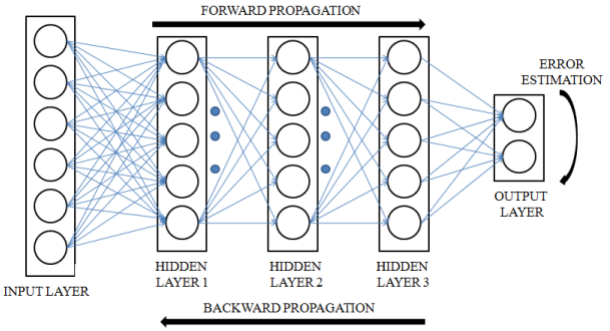

FIGURE 3. Adaptive Backpropagation Neural Network

E. GLOWWORM SWARM ALGORITHM WITH ANFIS

FIGURE 2 of the proposed study presents a novel predictive model for medical diagnostics that improves the ANFIS performance by modifying the GSO algorithm. This method, known as the GSO-ANFIS model, improves the ANFIS model by including GSO algorithms. By maximizing the weights between layers 4 and 5 of the model, the parameters of ANFIS may be modified. A fuzzy C-means (FCM) clustering technique determines how many membership functions are needed. The GSO method, which searches the solution space for ideal weights, is used to modify the ANFIS weights iteratively. After initializing a population, the GSO looks for the optimal weights for ANFIS [39]. The objective function value, which represents the error reduction between observed and predicted values during training, is minimized to find the optimal solution. After that, ANFIS incorporates these adjusted weights to produce predictions. The determined ideal weights are fed into ANFIS during testing to generate precise diagnostic outcomes.

This medical diagnostic method uses the following input factors: age, weight, body mass index (BMI), blood pressure during diastole, blood glucose levels, renal function, and smoking. The stage of chronic renal disease is one output variable. Expert systems have a hierarchical organizational structure. As can be seen in Figure 2, this layer takes seven input components and calculates their CKD stage.

The topmost layer is the purification layer, Level 1, where each input variable undergoes elimination. At this level, inputs to an attribution function are represented by clear-cut values. Each node within this hierarchy functions as a component allocated to its respective function.

Layer 2 houses the rule layer in ANFIS. This tier of ANFIS consists of the rule layer, represented through logarithmic product notation. This layer governs how rules respond to system inputs [40]. Layer 3 is the normalization layer. Each

node is standardized and represented in this structure by the letter "N." This layer uses the effectiveness of rule enforcement in layer 2, often called the normalization layer, to automatically compute normalized weights [41]. Layer 4 is the anti-purge layer. Also known as the inverse purification layer, this fourth layer incorporates multiple linear functions for each input signal. It includes versatile nodes across its structure. At the general level, precisely level 5 in ANFIS, the last layer designated as "∑" is the summation layer. This layer's primary objective is to calculate the overall output by summing all signals from the preceding levels.

IV. RESULTS

Based on our experimentation, Table 1 shows that TP (true positive) is 37, FN (false negative) is 02, FP (false positive) is 03, and TN (true negative) is 38. The performance metrics used for evaluating the model are mentioned in Eq. (9) [38], Eq. (10) [38], Eq. (11) [38], Eq. (12) [38].

$$Sensitivity = \frac{TP}{TP+FN} \quad (9)$$

$$Specificity = \frac{TN}{TN+FP} \quad (10)$$

$$Precision = \frac{TP}{TP+FP} \quad (11)$$

$$Accuracy = \frac{TP+TN}{TP+FP+TN+FN} \quad (12)$$

In TABLE 1, the performance of the proposed model is depicted with selected features. The model's accuracy is 98.5%, the sensitivity is 96.01%, and the specificity is 97.68%.

TABLE 1
The Performance of the Model with Selected Features

Method	Sensitivity (%)	Specificity (%)	Precision (%)	Accuracy (%)
ANN	90.62	92.05	91.02	90.07
OCNN	91.83	94.56	93.69	94.23
RF	95.23	95.45	96.58	96.54
Tabu-SDS	96.01	97.68	97.50	98.5

A heat map is a representation of the Pearson correlation coefficient matrix. The Pearson correlation coefficient represents the linear relationship between two qualities.

Eighty tests were performed with the created fuzzy intelligence system to evaluate chronic renal failure. A group of medical professionals also examined every patient and disseminated their findings. Expert opinion findings and the outcomes produced by the fuzzy inference system were contrasted. By merging these two outcomes, we could accurately categorize 75 out of the 80 tests and create five or more system outputs.

TABLE 2 displays the confusion matrix. Fifteen healthy individuals are shown in the first column; they all fall into the appropriate group (generic category). The second column rates the impact information for ten patients as a concern level. However, as a result, two of the ten patients were classified as having poor health and the other eight as bothersome [42]. Fifteen out of the sixteen patients in the third column with the highest severity were correctly identified, while the last patient was classified as sick. Ten of the eleven identified persons were correctly classified, while one was misclassified in the fourth column. The fifth column further illustrates how well the essential traits of the 14 test patients were identified. Column 6 indicates that one essential patient out of every fourteen is fat or overweight.

TABLE 2
CKD Confusion Matrix

Extremely sick	Very sick	Sick	Very concerning	Concerning	Healthy	Class names
014	000	000	001	000	000	Extremely sick
000	014	000	000	000	000	Very sick
000	000	010	000	000	001	Sick
000	000	001	015	000	000	Very concerning
000	002	000	000	008	000	Concerning
000	000	000	000	000	015	Healthy

Here, the total number of tests = 80, and the number of successes = 75. Using the confidence index analysis technique mentioned in Eq. (13) [42], 93.75% of the fuzzy inference system's outputs were accurately categorized. The proposed fuzzy expert system allows doctors to identify CKD by evaluating the dependent indicators. The results indicate a 6.25% error rate in CKD classification with this fuzzy inference approach. The initial categories of "General," "Concerning," and "Very Concerned" were reclassified as "No." Consequently, additional benign categories were introduced, such as "bad health," "serious disease," and "dangerous disease." TABLE 3 shows the confusion matrix for the 2×2 matrix. Preciseness, specificity, sensitivity, and responsiveness are among the criteria considered in determining the effectiveness of the developed professional healthcare system.

$$Confidence\ indicator = \left(\frac{Success\ number}{Total\ number\ tests} * 100\right) \quad (13)$$

TABLE 3
Matrix With Reduced Dimensionality

Yes	No	Class name
38	002	Yes
003	038	No

In TABLE 4, we have compared the proposed ABPNN-GSO-ANFIS model with certain optimized models namely Gaussian Naïve Bayes (Gaussian NB), K nearest neighbors (KNN), Optimized CNN(OCNN), Optimized ANN(OANN), Deep Belief Networks(DBN), Deep Separable CNN(DSCNN). The table depicts that the proposed ABPNN-GSO-ANFIS achieved an accuracy of 99.52%, while the

traditional DSCNN achieved 99.18%. Balancing the dataset ensures near-perfect accuracy, a crucial metric that all classifiers depend on, indicating the percentage of instances classified correctly. The high accuracy of the proposed model can be attributed to the advantages of GSO-ANFIS, which pre-trains the model by optimizing both local optima and weighting factors in a single step. This approach resolves mismatch issues and optimizes the entire DL model in a single iteration, significantly reducing training time compared to traditional methods such as backpropagation in existing ANFIS. Backpropagation tends to converge towards nearby local minima, potentially missing better solutions at distant points. In contrast, the proposed algorithm navigates around local optima and avoids local maxima through its exploratory behavior, while its exploitative behavior rapidly converges towards global minimum and maximum solutions.

TABLE 4
The performance of the model with classifiers

Gaussian	Accuracy	Precision	Recall	F1-Score
Gaussian NB	89%	79.34%	76.15%	77%
KNN	90.16%	82.53%	78%	78.68%
Optimized CNN	98.4%	97.35%	94.25%	96.24%
Optimized ANN	99.75%	97.97%	95.42%	98.89%
DBN	98.63%	96.655%	97.22%	96.76%
DSCNN	99.28%	97.76	98.08%	97.98%
ABPNN-GSO-ANFIS	99.64%	98.23%	97.73%	99.14%

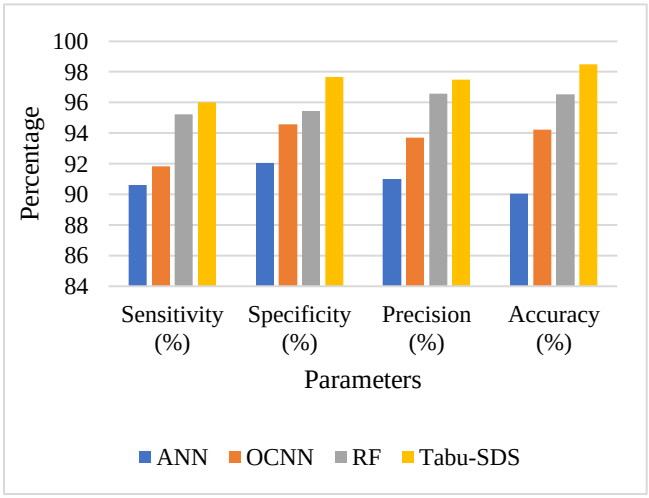

FIGURE 4. **Performance evaluation of various models**

From TABLE 4, ANFIS necessitates a substantial amount of labeled data to produce accurate results. The new attribute, urine microalbumin, contributes significantly to decision-making, resulting in improved precision rates with the proposed ABPNN-GSO-ANFIS model. Existing algorithms often encounter network paralysis when weights fluctuate between low and high values. In contrast, the proposed ABPNN-GSO-ANFIS stabilizes through multiple presentations of input patterns, gradually adjusting weights to achieve an optimal solution. This enhancement notably improves recall percentages in the proposed algorithm. FIGURE 4 describes the performance evaluation of the models. Our model is compared with standard algorithms from the literature. This clearly depicts that our proposed model outperforms all the existing algorithms.

We used the UCI CKD test set to assess how well our pipeline identified nodule development. First, we evaluated the accuracy of illness diagnosis based on physician reports. Given that nodule detectors provide many candidates with related nodule probabilities, our goal was to detect the most significant number of annotated nodules by finding the fewest candidates [43]. Receiver Operating Characteristic curve (ROC) curves were built to assess the sensitivity of identifying annotated (unique) nodules per scan over a range of false positive rates for both the training and test datasets. The confusion matrix showing the model's performance is shown in FIGURE 5. This clearly depicts the True Positives and False Positives for our model.

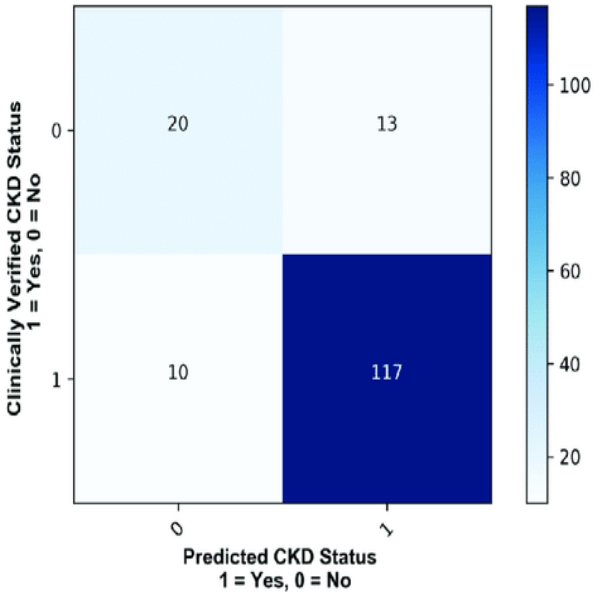

FIGURE 5. **The confusion matrix of the models'**

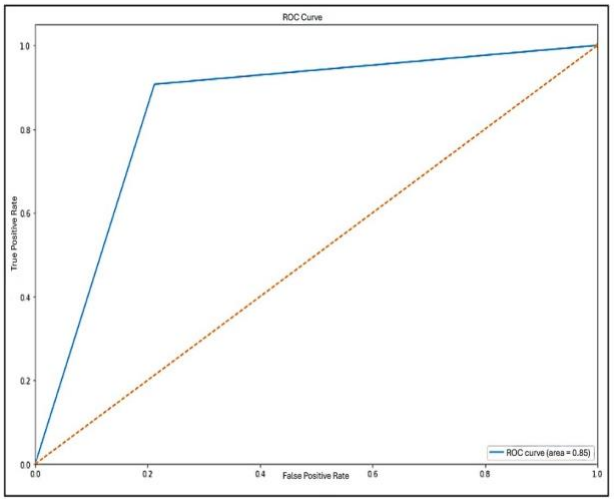

FIGURE 6. **ROC curve of the proposed model**

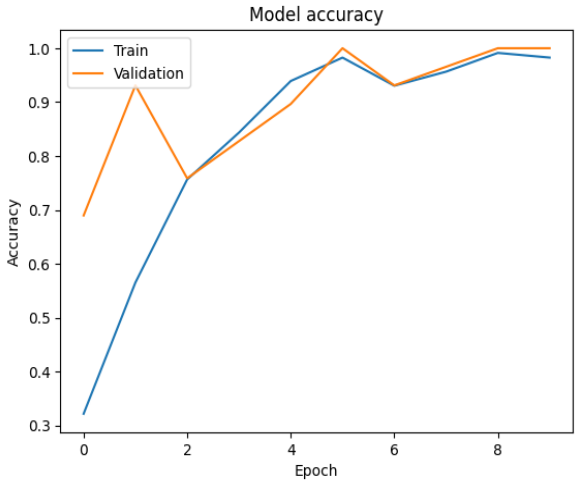

FIGURE 7. Training accuracy vs testing accuracy

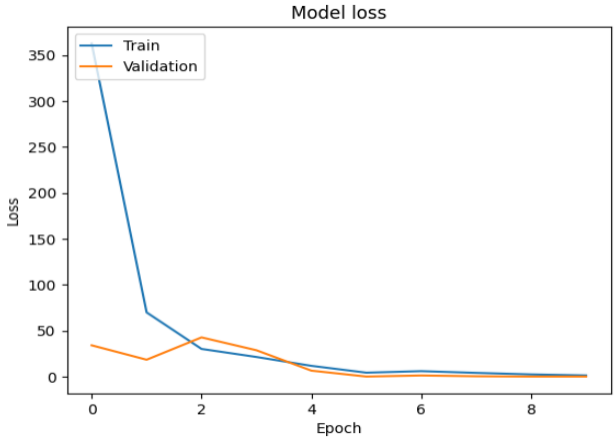

FIGURE 8. Training loss vs testing loss

FIGURE 6 shows the ROC curve of the ABPNN-GSO-ANFIS model, plotting the True Positive Rate (TPR) against the False Positive Rate (FPR) to illustrate the model's ability to differentiate between positive and negative heart disease cases at different thresholds. Lower FPR and higher TPR reflect better performance. The ROC curve of the HDP-DTRF method helps determine the optimal classification threshold, balancing specificity and sensitivity. Points near the upper left corner of the ROC curve indicate superior model performance. FIGURE 7 and FIGURE 8 show the training and testing loss functions and the training and testing accuracy. The prepared training dataset was used to train the proposed algorithm over 100 epochs with a fixed learning rate of 0.1. In current ANFIS models, the backpropagation algorithm is often used, which tends to converge to nearby local minima, which may lead to the loss of superior solutions further away. Far away. The proposed algorithm solves this problem through its exploratory behavior, which helps avoid local optima and local maxima. FIGURE 9 discusses the heatmap for correlation. Furthermore, its exploitative behavior allows fast convergence to minimum and maximum global solutions.

The proposed approach facilitates the identification of early-stage CKD by analyzing non-linear relationships among diverse clinical parameters, enabling timely interventions. These can, in short, bridge healthcare gaps in remote and under-resourced areas by allowing remote diagnosis and telemedicine support.

V. DISCUSSIONS

This research focuses on predicting CKD using a combination of different machine learning techniques. This is mainly done by combining multiple algorithms for feature selection and final selection process. The original dataset initially comprised of 24 features, but due to the introduction of hybrid feature selection algorithms TS-SDS, the number of features were reduced drastically to 19. During the preprocessing phase, missing values present in the dataset were addressed appropriately. When diagnosing stages of CKD, the proposed new hybrid technique outperforms all the standard state-of-the-art algorithms. This study enhances the predictability of the model by combining GSO. By replicating the behaviors of glowing beetles when they scavenge for food, this novel method helps in predicting faster.

TABLE 5
State of art techniques of the proposed model

Study and Year	Sampling Strategy	Accuracy (%)
[44]	- 70% training and 30% testing	96.00
[45]	- 10-fold cross-validation	96.12
[46]	- 10-fold cross-validation	91.40
[47]	- 70% training and 30% testing	96.00
Proposed Model	- 80% training and 20% testing	99.52

The high accuracy achieved by the proposed model is due to the GSO-ANFIS framework, which trains the model by simultaneously optimizing local optima and weighting factors in a single step. This method greatly reduces training time compared to standard methods. To measure the model's performance, 10-fold cross validation was used. The confusion matrix was designed to classify the correct and incorrect instances, which ultimately depicted the model's efficiency. TABLE 5 indicates the comparison of the proposed model with few recent literatures, who have tried deploying varieties of hybrid models. The results depict that the proposed model has better performance in terms of all the metrics than the recent works. Thus, the integration of GSO with ANFIS significantly improves the model's classification performance, making it a valuable tool for CKD diagnosis. By optimizing local optima and weighting factors in a single step, the proposed model achieves efficiency in training, reducing computational time compared to traditional methods like backpropagation [42]. This makes it more practical for real-time applications. The hybrid TS-SDS feature selection technique reduces dimensionality while preserving relevant information, improving model interpretability and robustness.

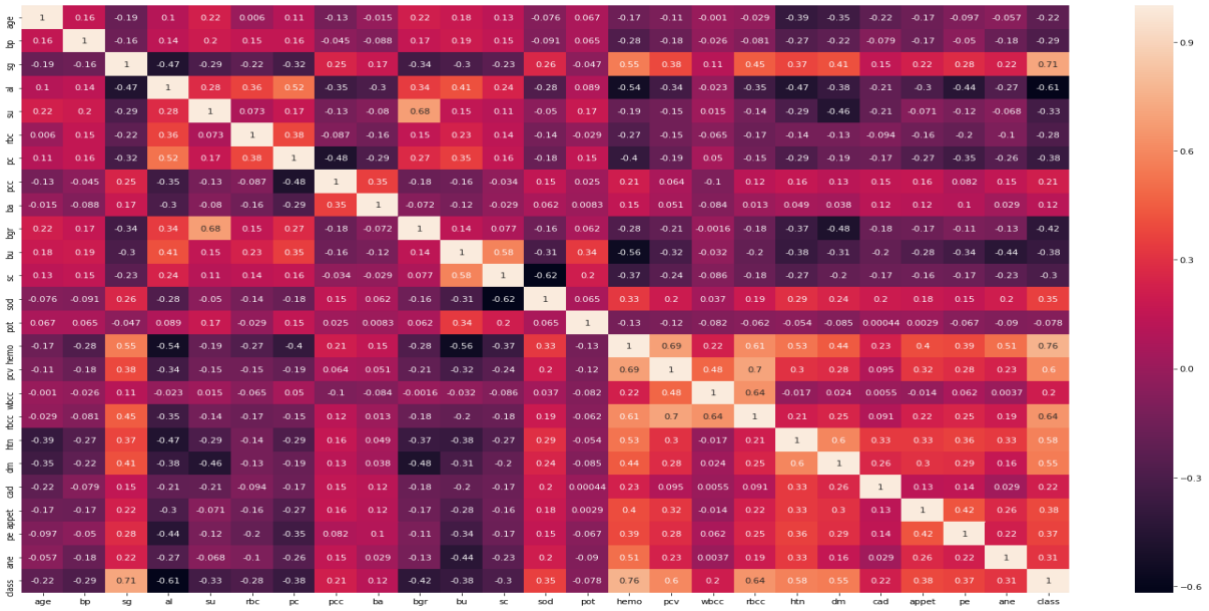

FIGURE 9. **Correlation heat map**

The model's high accuracy and efficiency also suggest it could be integrated into clinical decision-support systems, assisting healthcare professionals in diagnosing CKD more effectively [44].

VI. CONCLUSIONS

CKD stands as a leading cause of renal disease-related deaths worldwide. According to the 2024 World Kidney Day report, kidney-related diseases account for at least 2.4 million deaths annually, making them the sixth fastest-growing cause of mortality worldwide. In this study, we introduced the ABPNN-GSO-ANFIS technology to enhance the automated classification of CKD. Utilizing the TS-SDS algorithm, we identified optimal relationships between each feature and the target features, prioritizing them based on their correlation percentages. The proposed ABPNN-GSO-ANFIS model achieved an accuracy of 99.52%, surpassing the conventional models. It would be inaccurate to suggest that the developed fuzzy expert system could replace specialist doctors or the collective expertise of medical teams. Instead, it is intended to serve as a supportive tool for doctors, aiding decision-making without supplanting their valuable contributions. Moreover, implementing this medical expert system requires only computers and software, making it feasible for use in hospitals with limited resources and in geographic areas where hospital access is limited or unavailable. A limitation of this research was that the data size was small (400 records). Better analysis can be performed when this data size increases and we receive balanced data. Moreover, AI models trained on datasets from specific regions or demographic groups may not generalize well to other populations with different genetic, environmental, or lifestyle factors. Ensuring patient data confidentiality and compliance with regulations like GDPR and HIPAA is a significant challenge. This needs to be considered when we work with real-time records. This study employed supervised ML algorithms and feature selection techniques to identify the optimal subset of features for model development. Future work could explore the performance differences achieved using unsupervised or DL algorithms. Developing a mobile-based system would further enhance its utility by enabling experts to monitor patients' status remotely and allowing patients to assess their condition independently.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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