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Detection of chronic kidney disease using binary whale optimization algorithm

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ABSTRACT

Chronic kidney disease (CKD), a medical illness, is characterized by a steady deterioration in kidney function. A disease's ability to be prevented and effectively significantly treated depends on early diagnosis. The addition of filter feature selection to the machine learning algorithm has been done to detect CKD. However, the quality of its feature subset is not optimal. Wrapper feature selection can improve the quality of these feature subsets. Therefore, we proposed wrapper feature selection and binary whale optimization algorithm (BWOA) to enhance the accuracy of early CKD detection. We also make data improvements to improve accuracy, namely the preprocessing process with the median and modus techniques. We used a public dataset of 250 medical records of kidney sufferers and 150 completely healthy people. There are 24 features in this dataset. The test results showed that adding BWOA feature selection can increase accuracy. The proposed method produced an accuracy of 100%. Further research on these methods can be used to develop expert systems for early detection of CKD.

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1. INTRODUCTION

Chronic kidney disease (CKD) is characterized by a steady deterioration in kidney function [1]. Millions of individuals worldwide are affected by this serious global health issue. The prevalence of this disease continues to increase significantly, and this can lead to severe complications such as kidney failure, heart disease, and an increased risk of death. Early diagnosis of CKD has a vital role in prevention and effective treatment. However, there are frequently no noticeable symptoms in the early stages, making a rapid diagnosis challenging [2]. Traditional diagnosis is based on analysis of clinical parameters such as serum creatinine level, glomerular filtration rate, and albuminuria level. This approach may not be sensitive or specific in early detection.

Machine learning (ML) has been a potent tool in healthcare in recent years. Examples include breast cancer recognition [3], detection of lung cancer [4], parkinson disease classification [5], diagnosis of hepatitis disease [6], prediction of cardiac illness [7], chronic and infectious diseases [8], the severity grading and identifying of diabetic retinopathy [9], [10], and the prediction of infected COVID-19 [11]–[14]. The accuracy of diagnosis can be significantly increased by using ML in the early identification of CKD. Many ML methods were utilized by Qin *et al.* [2] to identify CKD. Logistic regression (LR) and random forest (RF) fusion produced the best accuracy.

Artificial neural network (ANN) and RF techniques were employed in [15]. According to the test findings, the RF algorithm generated superior accuracy, at 97.12%. Decision tree (DT), K-nearest neighbors (KNN), and LR were the three ML algorithms that Ifraz *et al.* utilized [16]. According to test findings, LR has the highest accuracy (97%). Venkatesan *et al.* [17] compared five ML algorithms namely support vector machine (SVM), KNN, RF, LR, and DT. In addition, extreme gradient boosting (XGBoost), another technique, was contrasted with this one. According to the test findings, XGBoost has the highest accuracy (98%). Additionally, Anggoro and Mukti [18] adjusted the XGBoost hyperparameters.

To improve accuracy, some researchers added feature selection techniques. Typically, feature selection has two kinds: filter and wrapper [19]. Poonia *et al.* [20] added the chi-square filter feature selection to several ML algorithms. The test results showed that adding this feature selection can increase accuracy. However, some studies showed that the quality of its feature subset is not optimal because it does not use a learning algorithm [21]. This weakness can be replaced by using wrapper feature selection. Therefore, we proposed a wrapper feature selection method, the binary whale optimization algorithm (BWOA), to increase the accuracy of CKD early detection.

2. METHOD

This section outlines the processes of the suggested CKD detection system, as shown in Figure 1. The dataset from CKD serves as the study's input. In contrast, the performance assessment of the suggested model serves as its output. Preprocessing, feature selection, and classification are the primary procedures.

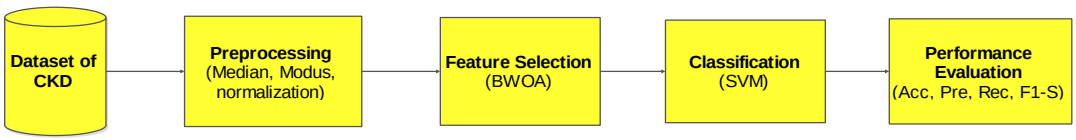

Figure 1. Proposed system for early detection of CKD

2.1. Dataset of chronic kidney disease

This work utilized a public dataset of 250 renal disease patients and 150 healthy patients' medical information [22]. This dataset has 25 variables comprised of 24 features and a target (two classes: CKD and not CKD patients). The features are as in Table 1.

Table 1. Feature of the CKD dataset

Feature abbreviation	Feature	Data type
f-1	Age	Number
f-2	Blood pressure	Number
f-3	Specific gravity	Number
f-4	Albumin	Number
f-5	Sugar	Number
f-6	Red blood cells	Categorical
f-7	Pus cell	Categorical
f-8	Pus cell clumps	Categorical
f-9	Bacteria	Categorical
f-10	Blood glucose random	Number
f-11	Blood urea	Number
f-12	Serum creatinine	Number
f-13	Sodium	Number
f-14	Potassium	Number
f-15	Hemoglobin	Number
f-16	Packed cell volume	Number
f-17	White blood cell count	Number
f-18	Red blood cell count	Number
f-19	Hypertension	Categorical
f-20	Diabetes mellitus	Categorical
f-21	Coronary artery disease	Categorical
f-22	Appetite	Categorical
f-23	Pedal edema	Categorical
f-24	Anemia	Categorical

2.2. Preprocessing

Preprocessing consists of 2 stages, namely handling lost data and normalization. The handling of lost data was used to populate missing feature values. The techniques used were median in numeric data and modus in categorical data. The modus strategy replaced the missing feature value with the dataset's most significant number of categories, whereas the median technique replaced it with its median value [15].

The normalization stage consists of 2 processes. The first process was to convert categorical features into numeric ones. Normalizing with the same range of feature values between 0 and 1 was necessary. The method used was a min-max normalization, as in (1):

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

where x_{norm} is the normalized feature, x is the feature, x_{min} is the most minor feature, and x_{max} is the most significant feature.

2.3. Feature selection

2.3.1. Whale optimization algorithm

An optimization technique known as the whale optimization technique (WOA) was developed after observing how whale groups behave when looking for food in the ocean [23]. The two stages of this method are exploitation and exploration [24]. This algorithm updates the solution using (2) and (3) in the exploitation phase.

$$\vec{D} = \left|\vec{C}.\overrightarrow{X^*}(t) - \vec{X}(t)\right| \quad (2)$$

$$\vec{X}(t+1) = \overrightarrow{X^*}(t) - \vec{A}.\vec{D} \quad (3)$$

The t variable is the iteration, X^* is the best solution, and X is the solution. A and C represent vector coefficients calculated by (4) and (5):

$$\vec{A} = 2\vec{a}.\vec{r} - \vec{a} \quad (4)$$

$$\vec{C} = 2.\vec{r} \quad (5)$$

The variable of a is calculated using (6); r represents a random vector between [0,1].

$$a = 2 - t\frac{2}{t_{max}} \quad (6)$$

The variable of t_{max} is the maximum iteration. A spiral equation is constructed between the present and ideal solutions using (7):

$$\vec{X}(t+1) = \overrightarrow{D'}.e^{bl}.\cos(2\pi l) + \overrightarrow{X^*}(t) \quad (7)$$

$\overrightarrow{D'} = |\overrightarrow{X^*}(t) - \vec{X}(t)|$, l represents a random value between [-1, 1], and b represents the spiral's form. The whale's position is updated as in (8):

$$\vec{X}(t+1) = \begin{cases} \overrightarrow{X^*}(t) - \vec{A}.\vec{D}, & if\ p < 0.5 \\ \overrightarrow{D'}.e^{bl}.\cos(2\pi l) + \overrightarrow{X^*}(t), & if\ p \geq 0.5 \end{cases} \quad (8)$$

Exploration to improve exploration in WOA is the focus of the second phase. Vector A is utilized with random numbers higher than one or less than 1 to drive solutions away from the most well-known search agents. In (9) and (10), which are mathematical models, can be used to describe this procedure.

$$\vec{D} = |\vec{C}.\overrightarrow{X_{rand}} - \vec{X}| \quad (9)$$

$$\vec{X}(t+1) = \overrightarrow{X_{rand}} - \vec{A}.\vec{D} \quad (10)$$

The variable of $\overrightarrow{X_{rand}}$ represents a random positional vector. The explanation of the WOA algorithm is as in Pseudocode 1 [23].

Pseudocode 1. The WOA algorithm

```
Initialize the whales population Xi (i = 1, 2, ..., n)
Calculate the fitness of each search agent
X*=the best search agent
while (t < tmax)
    for each search agent
    Update a, A, C, l, and p
        if (p<0.5)
            if (|A| < 1)
              Update the position of the current search agent by Eq. (3)
            else if (|A|≥1)
              Select a random search agent (Xrand)
              Update the position of the current search agent by Eq. (10)
            end if
        else if (p ≥ 0.5)
            Update the position of the current search by Eq. (7)
        end if
    end for
    Check if any search agent goes beyond the search space and amend it
    Calculate the fitness of each search agent
    Update X* if there is a better solution
    t=t+1
end while
return X*
```

2.3.2. Binary whale optimization algorithm

The BWOA, which converts solutions into binary form, modifies the WOA. The WOA search space is continuous, whereas WOA is only 0 and 1. For this reason, this value is converted into binary form with a threshold of 0.5. If the continuous value exceeds the point, the conversion result is 1, and the others are 0.

A vector of N items serves as a representation of the BWOA feature selection solution. The original dataset's feature count is N. The vector's cells all have a value of 0 or 1. A value of 1 means the associated option has been chosen, whereas a value of 0 means that nothing has been decided. As in (11), the fitness function evaluates each resulting solution.

$$Fitness = \alpha\gamma_R(D) + \beta\frac{|R|}{|C|} \quad (11)$$

where $\gamma_R(D)$ is the misclassification, $|R|$ is the number of subset features, $|C|$ is the number of features, α is the weight of classification error, and β is the weight of the selected one. Most studies used the KNN classifier [24]–[27]. We used SVM classifier. The α value is 0.99, and the β value is 0.01 [25].

2.4. Classification of support vector machine

Finding the ideal separator function from an unlimited number to distinguish between two data classes is the fundamental goal of SVM [28]. This separator function is called the hyperplane. To get the best hyperplane, SVM conducts a learning process. The separator function used is linear defined as in (12), and f(x) is formulated in (13).

$$g(x) = sgn\big(f(x)\big)g(x) \quad (12)$$

$$f(x) = w^T x + b \quad (13)$$

where x, $w \in R^n$ and $b \in R$ (R in scalar space, R^n in vector space).

The SVM optimization problem formula for linear classification cases can be formulated mathematically as in (14).

$$\min_{w,b} \frac{1}{2}\|w\|^2 \text{ to } y_i(wx_i+b)\geq 1,\ i=1,\ldots m \quad (14)$$

where x_i represents the input value, y_i represents the output value of 1 or -1, and the w and b parameters are the parameters to look for. From the above formulation, it will minimize the objective function of $\frac{1}{2}\|w\|^2$ or maximize the quantity of $\frac{1}{\|w\|}$ or w^Tw with the limiter $y_i(wx_i+b)\geq 1$. The delimiter will be $(wx_i+b)\geq 1$ if the data output is y_i=+1, and the delimiter will be $(wx_i+b)\leq$ -1 if y_i= -1.

2.5. Performance evaluation

Evaluation of this research used the accuracy, precision, recall, and F1-score, as defined by (15)-(18), respectively [29]. The training and test portions of the dataset were split by a ratio of 75% to 25%, respectively.

$$Accuration = \frac{T_{pos}+T_{neg}}{T_{pos}+T_{neg}+F_{pos}+F_{neg}} \quad (15)$$

$$Precision = \frac{T_{pos}}{T_{pos}+F_{pos}} \quad (16)$$

$$Recall = \frac{T_{pos}}{T_{pos}+F_{neg}} \quad (17)$$

$$F1-score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (18)$$

The confusion matrix is used to calculate the values of T_{pos} (true positive), T_{neg} (true negative), F_{pos} (false positive), and F_{neg} (false negatives), as seen in Table 2.

Table 2. Confusion matrix of CKD early detection

		Actual values	
		CKD	Not CKD
Predicted values	CKD	Tpos	Fpos
	Not CKD	Fneg	Tneg

3. RESULTS AND DISCUSSION

The experiment in this study was carried out with two scenarios: without and with BWOA feature selection. The goal is to find out the influence. Every scenario was evaluated against the linear, radial basis function (RBF), and polynomial SVM kernel types.

3.1. Experiment without binary whale optimization algorithm

Test results using SVM classifiers without BWOA, as seen in Table 3. The best accuracy and F1-score results use polynomial kernels, which are 98% and 98.39%, respectively. Meanwhile, the precision value is lower than others.

Table 3. The experiment result without BWOA feature selection

Kernel	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
Linear	96	**100.00**	93.65	96.72
RBF	97	**100.00**	95.24	97.56
Polynomial	**98**	98.39	**98.39**	**98.39**

3.2. Experiment with binary whale optimization algorithm

Test results with BWOA are shown in Table 4. Linear and RBF kernels produce perfect accuracy of 100%, while polynomial kernels produce 99% accuracy. The best fitness value reaches 0.005833 using the RBF kernel with 14 features. A comparison of accuracy between without and with feature selection (BWOA) is shown in Figure 2. Adding BWOA to SVM causes its accuracy to increase by 4% in linear kernels, 3% in RBF kernels, and 1% in polynomial kernels. In addition, adding this feature selection results in perfect recall values. For this reason, it can be concluded that adding BWOA feature selection can improve system performance.

Finally, we compared the proposed method with other research on the same dataset, as shown in Table 5. Qin *et al.* [2] used an integrated model (combination of LR and RF), Venkatesan *et al.* [17] used XGBoost, and Poonia *et al.* [20] used LR with chi-square filter feature selection. We can see that the proposed method is superior. For this reason, it can be concluded that the BWOA feature selection can increase performance by selecting features relevant to the early detection of CKD.

Table 4. The experiment result of BWOA feature selection

SVM kernel	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	Fitness	Feature number	Selected feature
Linear	100	100.00	100	100.00	0.007500	18	f-1, f-2, f-3, f-4, f-5, f-6, f-8, f-9, f-10, f-12, f-13, f-14, f-15, f-16, f-18, f-19, f-23, f-24
RBF	100	100.00	100	100.00	0.005833	14	f-3, f-4, f-6, f-7, f-9, f-10, f-14, f-15, f-16, f-17, f-19, f-21, f-22, f-23
Polynomial	99	98.44	100	99.21	0.014483	11	f-2, f-3, f-6, f-7, f-9, f-10, f-13, f-14, f-15, f-20, f-22

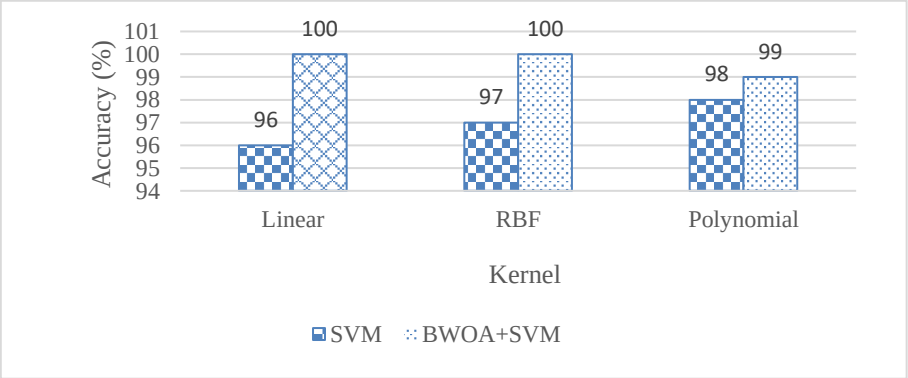

Figure 2. Comparison of without and with BWOA

Table 5. Performance of the proposed method and other research

Authors	Accuracy (%)	F1-score (%)
Qin *et al.* [2]	99.83	99.86
Venkatesan *et al.* [16]	98.00	98.90
Poonia *et al.* [19]	98.75	-
Proposed method	100.00	100.00

4. CONCLUSION

In this study, we propose an early detection method of CKD using BWOA feature selection. We also make data improvements to improve accuracy, namely the preprocessing process with median and modus methods. The test results showed that adding BWOA feature selection can increase accuracy. Important features selected from the proposed method are specific gravity, albumin, red blood cells, pus cell, bacteria, blood glucose random, potassium, hemoglobin, packed cell volume, white blood cell count, hypertension, coronary artery disease, appetite, and pedal edema. Further research on these methods and features can be used to develop expert systems for early detection of CKD.

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