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Optimization of Support Vector Machine Classifier Using Grey Wolf Optimization Algorithm for Chronic Kidney Disease Prediction

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Abstract

The massive generation of medical data from smart health-care applications in recent years necessitates the development of big data classification strategies. Medical data classification can be used to visualize patterns in the data and detect the presence of the disease in medical data. We present an efficient support vector machine (SVM) hybridized with a grey wolf optimization (GWO) algorithm for chronic kidney disease (CKD) data classification in this work. Initially, infinite feature selection (IFS) algorithm is used to select the best features from a set of available features. The dataset's selected features are processed and fed into the GWO optimized SVM algorithm. The proposed CKD classification strategy has been simulated in MATLAB. CKD dataset from UCI machine learning repository is utilized for testing the developed strategy. The performance of the proposed CKD classification strategy is examined by accuracy and root mean square error (RMSE) values. According to the investigational findings, the proposed CKD classification system achieved accuracy and RMSE value of 97.58% and 0.1581, respectively, for classifying subjects into the CKD and non-CKD categories. The performance of GWO optimized SVM algorithm is outstanding, according to the experimental observations.

Keywords: Chronic kidney disease, Infinite feature selection, Grey wolf optimization, Support vector machine, Classification

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Introduction

Chronic diseases, according to the World Health Organization, appear to pose a substantial concern to developing countries.[1] Chronic kidney disease (CKD) has garnered considerable attention, because of its fatal outcome. CKD is a kidney illness that can be treated in its early phases but eventually leads to renal failure. In 2016, CKD claimed the lives of 753 million individuals globally, with males accounting for 336 million deaths and females accounting for 417 million.[2]

The kidney disease is called "chronic" because it develops gradually and lasts a long time, impairing the urinary system's function. The build-up of by-products in the blood resulted in the emergence of many other health complications. Diabetes, high blood pressure, and heart disease are all significant risk factor for CKD patients.[3] Patients with CKD experience adverse effects, particularly in the end phase, that impair the neurological and immunological systems. The glomerular filtration rate (GFR) primarily depicts kidney function and is used by doctors to diagnose kidney disease.[4] CKD is divided into five phases based on the GFR level. Table 1 depicts the progression of kidney disease as measured by GFR.

The preferred technique to manage CKD is to diagnose it early on; but, waiting until it is too late might lead to kidney failure, which necessitates dialysis or kidney transplantation to live normally. As a result, early diagnosis, control, and management of the disease are extremely important. Furthermore, because of its dynamic and covert characteristic in the initial phases, as well as patient heterogeneity, it is critical to be able to accurately predict the occurrence of CKD.[6]

CKD prediction has traditionally relied on basic statistical approaches as well as a doctor's judgment and expertise. These techniques frequently lead to unintended biases, inaccuracies, and high expenses, as well as a negative influence on patient care quality. More reliable and sophisticated computational technologies such as machine learning became more realistic to adopt and explore in the CKD prediction domain as the availability of electronic health data has increased.[7,8] Support vector machines (SVMs) are one of the most extensively utilized machine learning algorithms.[9] Recent research work done by various researchers in the prediction of CKD using SVM is as follows:

Polat *et al*.[10] used wrapper and filter strategies to minimize the dimension of the CKD dataset. The SVM classifier was also used to identify the disease. The study found that the SVM classifier using the filtered subset of the best first search engine feature selection method appears to have a greater accuracy rate of 98.5% in the diagnosis of CKD particularly as compared to other chosen methods.

Tekale *et al*.[11] processed 14 CKD attributes and predicted the accuracy for the decision tree (DT) and SVM algorithm. Experimental results showed that the SVM outperformed with an accuracy of 96.75%.

Shetty *et al*.[12] employed clinical data to predict chronic renal disease using SVM and K-nearest Neighbor (KNN) algorithm. As

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Table 1: Classification of CKD[5]

Stage	*Description*	*GFR (ml/min/1.73m²)*
1	Kidney damage with normal or increased GFR	≥90
2	Kidney damage with mild decreased GFR	60–89
3	Moderate decreased GFR	30–59
4	Severe decreased GFR	15–29
5	Kidney failure	<15

evidenced by the higher values of the selected performance indicators, the SVM classifier outperformed the KNN with an accuracy, recall, and precision of 90.09%, 1, and 0.5000.

Kumar and Thangaraj[13] analyzed the CKD dataset obtained from the UCI machine learning repository. Pre-processing techniques such as missing value replacement, unsupervised discretion, and standardization were used to improve the accuracy. After each filter, three classifiers, namely, Naive Bayes, multilayer perceptron, and SVM, were used for the pre-processed data set. The findings showed that SVM outperformed all the other classifiers in terms of accuracy.

Using synthetic kidney function test dataset, Vijayarani and Dhayanand[14] utilized SVM and artificial neural network (ANN) to categorize kidney disorders. The results of the classifier performance showed that SVM outperformed ANN, with an accuracy of 76.32%.

For predicting CKD, Kaur and Sharma[15] investigated the effectiveness of the KNN and SVM algorithms. The results revealed that the SVM classifier outperformed KNN classifier with an accuracy of 78.09% and an error rate of 21.9%.

Using the UCI machine learning repository CKD dataset, Charleonnan *et al*.[16] discussed DTs, logistic regression, SVM, and KNN as CKD detection classifiers. The SVM technique outperformed the others in regards of identification accuracy and sensitivity, according to the findings. The average accuracy of four classifiers was assessed 5 times. The SVM classifier had the higher accuracy of 98.3%, whereas the logistic, DT, and KNN classifiers had average accuracy of 96.555%, 94.8%, and 98.1%, respectively, as per the experimental observations.

Chen *et al*.[17] used three multivariate models, namely, KNN, SVM, and soft independent modeling of class analogy (SIMCA), to assess patient risk using clinical data from the UCI machine learning repository. Different types of composite data were also used to assess the feasibility and robustness of these models in CKD risk assessment, in which proportional disturbances were introduced to simulate measurement variances caused by environmental and instrument disturbances. For the original data set, the three proposed multivariate models distinguished between CKD and non-CKD patients with overall accuracies of more than 93%. In this study, KNN and SVM performed better than SIMCA.

However, the researchers are skeptical of SVM's performance due to issues such as over-fitting, pair-wise categorization, and parameter regularization. A set of algorithms known as meta-heuristic algorithms can achieve a solution for such regularization by dynamically adjusting the candidate solution and finding an optimized solution to problems by optimizing the objective function. In light of the foregoing, the parameters of the SVM are optimized in this study using the grey wolf optimization (GWO) algorithm for identifying CKD and non-CKD patients.

Materials and Methods

The data for this study were collected over a 2-month period in 2015 from CKD patients at Apollo Hospital in Managiri, Madurai, Karaikudi, Tamil Nadu, India. Data are accessible at the University of California, Irvine (UCI) data repository known as Chronic_kidney_disease Dataset.[18]

IFS Method

It is a graph-based method that permits power series matrices' convergence qualities to determine the relevance of a feature in respect to all others. Each characteristic is expressed by a node on to an affinity graph in the IFS formulation, with weighted connections representing relationships among them.

Each l-length path throughout the graph is considered a significant feature selection. As a consequence, the significance of each possible subset of features can indeed be examined by altering these pathways and letting those to approach to an infinite number.

Every feature in the initial set is given a final score, with the score reflecting how much the feature fits the categorization task. As a consequence, rating the IFS output in descending order allows subsets feature selection to be performed at the model selection step to determine the number of features to be chosen.[19]

GWO

Mirjalili *et al*.[20] introduced GWO, a modern meta-heuristics strategy inspired by grey wolves. In terms of search agent movement strategy, the GWO algorithm resembles the grey wolf hierarchy's leadership behavior and hunting process.[21] The GWO algorithm was chosen for this study because, according to the multiple studies, it generates superior outcomes than other meta-heuristic approaches.

The most appropriate option for describing the grey wolf leadership hierarchy will be alpha (α), followed by beta (β) and delta (δ). Omega (w) will be the last solution to be examined. The optimization model that will be created is a depiction of the grey wolf hunting behavior alpha, beta, and delta, with omega solely following these groups.[22]

The grey wolves are encircling their prey during the hunt. Equations (1) and (2)[23] are numerical models of surrounding behavior:

$$\vec{D} = \vec{C}.\vec{X}_p(t) - \vec{X}(t) \quad (1)$$

$$\vec{X}(t+1) = \vec{X}_p(t) - \vec{A}.\vec{D} \quad (2)$$

where,

t = current iteration

$\vec{D}$ = surrounding prey vector

$\vec{A}, \vec{C}$ = Co-efficient vector

$\vec{X}$ = a grey wolf's position vector

$\vec{X}_p$ = the prey's position vector.

The following equations (3) and (4) show the determination of vectors $\vec{A}$ and $\vec{C}$:[20]

$$\vec{A} = 2\vec{a}.\vec{r}_1 - \vec{a} \quad (3)$$

$$\vec{C} = 2.\vec{r}_2 \quad (4)$$

where $\vec{r}_1$ and $\vec{r}_2$ are random vectors between [0, 1] and $\vec{a}$ components are linearly reduced from 2 to 0 during the iterations.[20]

Assume alpha (the most acceptable candidate solution), beta, and delta are experts in prey locating knowledge to imitate the hunting behavior of grey wolves in mathematics. As a result, the three best responses will be documented during the repetitions, and the computation for the next iteration will be modified based on the prior three best responses. The formulas defined by equation (5), (6), and (7):[20,22]

$$\begin{aligned}
\vec{D}_\alpha &= \left|\vec{C}_1.\vec{X}_\alpha - \vec{X}\right| \\
\vec{D}_\beta &= \left|\vec{C}_2.\vec{X}_\beta - \vec{X}\right| \\
\vec{D}_\delta &= \left|\vec{C}_3.\vec{X}_\delta - \vec{X}\right| \quad (5) \\
\vec{X}_1 &= \vec{X}_\alpha - \vec{A}_1.\left(\vec{D}_\alpha\right) \\
\vec{X}_2 &= \vec{X}_\beta - \vec{A}_2.\left(\vec{D}_\beta\right) \\
\vec{X}_3 &= \vec{X}_\delta - \vec{A}_3.\left(\vec{D}_\delta\right) \quad (6)
\end{aligned}$$

$$\vec{X}(t+1) = \frac{\vec{X}_1 + \vec{X}_2 + \vec{X}_3}{3} \quad (7)$$

The convergence of the needed best solution determines the repetition termination of the GWO computation. Computing the alpha value yields the best solution and the value of the resulting alpha position is the variable that will be used in the next computation or phase. If the issue has no constraints, the solution can be obtained by terminating the iterative procedure by setting the maximum iteration (t) at the start of the computing process.[24]

SVM

In 1992, Boser, Guyon, and Vapnik proposed the SVM as a classification approach. Because of its excellent accuracy and ability to manage data with large dimensions, the SVM approach is widely employed in bioinformatics.[25] SVM seeks to optimize the margin by finding a hyper-plane between two specific categories in the data.[26] The hyper-plane linear model is represented by equation (8):[27]

$$f(x) = sign(w^T x + b) \quad (8)$$

Where,
w = weight vector
b = bias term
x = input vector

Given a dataset $\{(x_i, y_i)\}, x_i \in X^n, y_i \in \{-1,+1\}, i=\{1,2,1a\ D\}$, equation (9) describes the SVM optimization problem (9):[27]

$$\min \frac{1}{2}w^2 \quad (9)$$

$$\text{subject } y_i\left[w_i^T x_i + b\right] \geq 1 \quad (10)$$

The SVM optimization is based on equation (11),[27] if the classification appears to have an error tolerance:

$$min.\frac{1}{2}w^2 + C\sum_{i=1}^{D}\zeta_i \quad (11)$$

subject to

$$\left\{\begin{matrix} y_i\left[w_i^T x_i + b\right] \geq b\zeta_i \\ \zeta_i \geq 0 \end{matrix}\right\} \quad (12)$$

When a problem cannot be split linearly in the input space, a kernel function in SVM is used. The kernel function defined in equation (13).

$$K(x_i,x_j)=(\varnothing(x_i),\varnothing(x_j)) \quad (13)$$

Where $\varnothing(x_i)$ signifies the input data x_i s mapped feature space and in the high-dimensional feature space, $K(x_i, x_j)$ is the kernels' function that is equal to the inner product of two vectors.[28] As a result, the kernel SVM formula is in the equation (14):[29]

$$min_{w,\zeta}\frac{1}{2}w^T w + C\sum_{i=1}^{D}\zeta_i \quad (14)$$

Subject to

$$\left\{\begin{matrix} y_i\left[w^T\varphi(x_i) + b\right] \geq +-\zeta_i \\ \zeta_i \geq 0 \forall i \end{matrix}\right\} \quad (15)$$

In terms of variables λ_i, we may achieve the SVM kernel optimization: [30]

$$max_\lambda\left(\sum_{i=1}^{D}\lambda_i - \frac{1}{2}\sum_{i=1}^{D}\lambda_i\lambda_j y_i y_j K(x_i, x_j)\right) \quad (16)$$

Subject to

$$\left\{\sum_{i=1}^{D}\lambda_i y_i, 0 1\lambda_i \leq C\right\} \quad (17)$$

In the next algorithm, the radial basis kernel function will be used, for which,

$$K(x_i, x_j)=exp(-\gamma||x_i - x_j||)^2 \quad (18)$$

Optimizing SVM Parameters Using GWO Algorithm

SVM has been used to solve a variety of classification issues with great success. The kernel function selected and its parameter values have an impact on SVM efficiency.[31] As we all aware, the accuracy of the SVM model's prediction is dependent on the correct parameters. The error penalty C and the kernel parameters must both be set to maximize SVM efficiency. The training data were utilized to change the parameters (C,). As a result, as noted on review by Faris, Aljarah, Al-Betar, and Mirjalili,[32] this meta-heuristic technique can be used to identify the acceptable SVM parameters.

Results and Discussion

The methods provided in Section 3 were used to evaluate the UCI dataset. There are 400 observations in the dataset that have missing or noisy values. It contains 250 CKD patient records and

Table 2: CKD dataset description

S. No.	Attribute	Description	Type	Permissible values
1.	Age	Patient's age	Numerical	in years
2.	Bp	blood pressure	Numerical	in mm/Hg
3.	Sg	specific gravity	Nominal	(1.005,1.010,1.015,1.020,1.025)
4.	Al	Albumin	Nominal	(0,1,2,3,4,5)
5.	Su	Sugar	Nominal	(0,1,2,3,4,5)
6.	Rbc	red blood cells	Nominal	normal, abnormal
7.	Pc	pus cell	Nominal	normal, abnormal
8.	Pcc	pus cell clumps	Nominal	present, not present
9.	Ba	Bacteria	Nominal	present, not present
10.	Bgr	blood glucose random	Numerical	in mgs/dl
11.	Bu	blood urea	Numerical	in mgs/dl
12.	Sc	serum creatinine	Numerical	in mgs/dl
13.	sod	Sodium	Numerical	in mEq/L
14.	pot	Potassium	Numerical	in mEq/L
15.	hemo	Hemoglobin	Numerical	in gms
16.	pcv	packed cell volume	Numerical	in cells/cumm
17.	Wc	white blood cell count	Numerical	in cells/cumm
18.	Rc	red blood cell count	Numerical	millions/cmm
19.	Htn	Hypertension	Nominal	yes, no
20.	Dm	diabetes mellitus	Nominal	yes, no
21.	Cad	coronary artery disease	Nominal	yes, no
22.	appet	Appetite	Nominal	good, poor
23.	Pe	pedal edema	Nominal	yes, no
24.	Ane	Anemia	Nominal	yes, no
25.	class	Class	Nominal	CKD, non-CKD

Table 3: Ranks and weights of the features

S. No.	Feature	Description	Rank	Weight
1.	Sc	serum creatinine	12	2.1276
2.	Htn	Hypertension	19	0.9515
3.	Bu	blood urea	11	1.9008
4.	Al	albumin	4	1.8975
5.	Su	Sugar	5	1.5060
6.	Wc	white blood cell count	17	1.5051
7.	age	Patient's age	1	1.3367
8.	cad	coronary artery disease	21	1.3214
9.	ane	anemia	24	1.2615
10.	bgr	blood glucose random	10	1.2495
11.	Pe	pedal edema	23	1.2164
12.	pcc	pus cell clumps	8	1.1858
13.	Ba	Bacteria	9	0.9964
14.	Bp	blood pressure	2	0.9515
15.	pot	potassium	14	0.6289
16.	Pc	pus cell	7	0.0788
17.	Dm	diabetes mellitus	20	0.788
18.	sod	Sodium	13	-0.4497
19.	Rbc	red blood cells	6	-0.4772
20.	Rc	red blood cell count	18	-0.7983
21.	appet	Appetite	22	-0.9822
22.	Pcv	Packed cell volume	16	-1.1657
23.	Sg	specific gravity	3	-1.1681
24.	Hemo	Hemoglobin	15	-1.2123

150 non-CKD patient records. As a result, 62.5% of people in each class have CKD, while 37.5% do not. These observations were made on people ranging in age from 2 to 90 years old. The CKD dataset contains 24 characteristics, including 11 numeric and 13 nominal features, as well as a 25th feature that denotes the CKD classification or status. Table 2 contains a description of the CKD dataset.

The purpose of the data pre-processing in this work was to clean the data. To begin, the proposed method identified both empty cells and NaN values. These values were replaced with the mean values of the rest of the data set column once they were discovered. The string input with two categories was converted to numerical class in the second phase of pre-processing so that the classifier could comprehend and use it for training.

Table 4: Parameter settings

Parameter	Value
Population size (no. of grey wolves	05
No. of iterations	50
α (alpha), β (beta), and δ (delta)	Random values
Kernel function	Linear

The unsupervised infinite feature selection strategy examined the data in the feature extraction phase and calculated the weights of each feature, as shown in Table 3, using the alpha-factor, which in the proposed model was 0.82. The more informatics data columns were chosen based on weights. This was accomplished by specifying a weight threshold against which the weights were tested and the selected features were segregated. The mean of the weights of all features was used to define the threshold in the proposed work. The ranks and weights of 24 features are shown in Table 2. Out of the 24 features available, 15 were chosen for CKD prediction.

In the next step, a GWO-SVM classifier was developed using 70% training features and 30% testing features. Table 4 shows the various parameters and settings for the GWO-SVM algorithm that was determined after preliminary experimentation.

A high value of accuracy of 97.58% and a low value of root mean square error (RMSE) of 0.1581implies that predicted results are close to the actual results and the model is well fitted.

Conclusion and Future Scope

The main objective of this study was to develop a hybrid algorithm for classifying the subjects into CKD and non-CKD category. This was carried out using the GWO algorithm for generating a much better accuracy (97.58 %) and RMSE (0.1581) after optimizing the SVM parameters. This work could be useful for researchers and engineers who used hybrid machine learning algorithms to

predict the presence or absence of a disease. Our future research will focus on testing the proposed approach with a larger set, other feature extraction, and optimization methodologies for predicting the presence or absence of a disease.

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