Journal of Theoretical and Applied Information Technology
31st January 2025. Vol.103. No.2

ISSN: 1992-8645 www.jatit.org E-ISSN: 1817-3195

CHRONIC KIDNEY DISEASE PREDICTION USING AN ENSEMBLE OF SVM, LR, AND MLP MODELS

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ABSTRACT

Chronic kidney disease (CKD) is a global issue, and it needs to be detected as early as possible for the effective treatment. Many studies applied Machine learning (ML) techniques for predicting the CKD in early stages. Different approaches were used in building models using ML algorithms. The algorithms were trained individually, and ensemble approach were used to build the model. Different datasets were used for different studies. The accuracy of the model is the main concern in the prediction of diseases. It is important to build a model which can produce the highest accuracy. In this study we aim to build a model using different machine learning approaches to predict the CKD in early stages. The ML algorithms such as K Nearest Neighbor (KNN), Random Forest (RF), Multilayer Perceptron (MLP), Logistic Regression (LR) and Support Vector Machine (SVM) were used to do the experiment. RF and KNN were applied individually on CKD dataset and SVM, MLP and LR were ensembled using Voting Classifier. The performance of the models was analysed in terms of accuracy, precision, F1-score and recall. The ensembled method showed the highest accuracy of 100% compared to other individual models. This proves that the ensemble model performed better than each individual models.

Keywords: *CKD Prediction, Machine Learning, SVM, LR, MLP, Ensemble model, Voting Classifier*

1. INTRODUCTION

Chronic kidney disease (CKD) is considered as a health condition where kidneys cannot filter toxins from the blood. If it is untreated, leads to kidney failure [1]. CKD is a major health concern which affects about 10 million people worldwide [2]. Kidney diseases are found mostly in people who have diabetes, hypertension, obesity and ageing [3]. In 2021, European Renal Association, American Society of Nephrology, and International Society of Nephrology stated that above 850 million people struggle by some sort of kidney disease and this figure is almost double the number of people suffering from diabetics. In 2017 CKD took around 1.2 million people's lives and CKD was responsible for 1.43 million people's deaths in 2019 [4]. As CKD is one among the major diseases that results in the death of people, important measures should be taken for early detection. Early detection helps to decrease the high burden of death as well as other associated disabilities, supporting health system to achieve economically viable prevention, especially in countries with low and medium income [5].

Artificial Intelligence (AI) is a important field in Computer Science. Artificial intelligence is significant in many sectors, especially in education, health, industry and business. Machine Learning, a sub field of AI is applied in many fields in which different algorithms are trained based on some datasets and models are developed. In machine learning, the two main classifications of algorithms are supervised and unsupervised learning. Machine learning techniques are widely utilized in the prediction of diseases. Supervised machine learning methods are mostly used in studies conducted for the prediction. Few studies reported that stand-alone machine learning models has been used to predict the disease while in other ensemble machine learning techniques are applied for the same. Based on the study conducted by [6], Support Vector Machine algorithm (SVM) is the most often used algorithm in the research and Naïve Bayes algorithm

fall in the second position. On the other hand, Random Forest (RF) algorithm had the highest accuracy in the prediction followed by SVM. In the previous studies the highest accuracy for the CKD prediction was 99.6%.

Earlier predictions of chronic kidney disease help to avoid dialysis and kidney transplantation. The challenges associated with the kidney disease prediction: (i) Availability of limited datasets and (ii) Identifying the appropriate AI model. To address these challenges, study propose a novel model for kidney disease prediction. Recently Artificial Intelligence has played a major role in the medical domain to automate the process of diagnosis and prognosis of diseases. The main contribution of our study is as follows as:

1. Proposing a novel ensemble model which combines Logistic regression (LR), Support Vector Machine (SVM), and Multilayer Perceptron (MLP) classifiers for chronic kidney disease prediction.

2. Conducted performance evaluation experiments that demonstrate the advantage of using ensemble methods over traditional AI models on chronic kidney disease prediction.

The paper is structured as follows: Section 2 demonstrates the related works applied on the kidney disease prediction. Section 3 details the methodology of our proposed model. Section 4 explains about the dataset and experimental analysis. Section 5 discusses the results obtained. Section 6 discusses the limitations of our study. Section 7 concludes the paper and suggests future research directions.

2. RELATED WORK

To identify the related works on chronic kidney disease prediction using AI. We conducted a study using Scopus database, it has been noticed that there are numerous publications addressing kidney disease prediction between 2010 and 2024. These studies focus on various aspects of kidney related conditions such as chronic kidney disease, kidney failure, kidney stones, kidney injury, and renal cancer. The significant number of publications in this domain indicates the importance of research being conducted to improve the prediction of kidney diseases.

Anantha Padmanaban & Parthiban [7] used ML classification techniques to identify Kidney disorder at the early stages. There were thirteen attributes in the dataset. The Decision tree algorithm showed 91% accuracy and Naïve Baye achieved 86% of accuracy on prediction. Yildirim [8] compared some sampling algorithms to handle imbalanced data while predicting chronic kidney disease. The basic artificial neural network with Multilayer perceptron model which learns the features using back propagation algorithm was applied to predict chronic kidney disease. To address the challenges of imbalanced dataset, they have employed different sampling algorithms such as resample, SMOTE and Spread Sub Sample to increase the performance of the model. Different learning rate ranging from 0.1 and 0.8 were applied. The study was conducted using the software, WEKA 3.7 for the analysis. Spread Sub Sample algorithm performed well at a learning rate of 0.1 as it took the shortest execution time. Resample method achieved better accuracy result compared to others. Zhang et al., [9] proposed a novel model that integrates Least Absolute Shrinkage and Selection operator (LASSO) for feature selection and a Multi-Layer Perceptron (MLP) model to predict the survival of the chronic kidney disease patients. The research utilised total 5617 records of data from a hospital from 1st January 2000 to the 27th of July 2017. The performance of both models was comparable, and they achieved high accuracy. However, to achieve the greatest performance, the hyperparameters required for the model were chosen manually. Also, imbalanced dataset resulted into lower sensitivity which affected models' overall performance. Devika et al. [10] assessed the efficiency of datamining classifiers such as Naïve Bayes, Random Forest and KNN, based on execution time, accuracy, precision, for the chronic nephritic sickness prediction. Random Forest attained the greatest score of 99.844% accuracy and 0.99 F-measure compared to other classifiers. Wang et al. [11] applied different AI techniques such as XGBoost , Random Forest and ResNet to assess the risk of CKD. From the available dataset of 23 features, a model based on regression is built for predicting the creatine level. The creatine value along with the features are used for the prediction of CKD risk. To solve the issue of unbalanced data while predicting the creatine level, under sampling method have been used. The result of creating prediction is improved by using an ensembled learning and achieved R squared value of 0.5590. While categorising samples for CKD, an area under the Receiver Operating Characteristic curve (AUC) of 0.76 is obtained using the predicted value of creatinine. Haemoglobin, age, sex, waist, smoking habit and urine protein were the most

influenced features for predicting creatinine. Chittora et al. [12] applied seven machine learning classifiers, such as Chi-square Automatic interaction detector, random tree, C5.0, logistic regression, linear support vector machine (LSVM) and artificial neural network (ANN) to the UCI dataset for chronic kidney disease. For each classifier, the results have been found using six different feature selection techniques. LSVM with penalty L2 using synthetic minority over-sampling technique with full features shows the highest accuracy of 98.86%. Additionally, one deep neural network was used on the same dataset, achieving the best accuracy of 99.6%. Barah and Mehrotra [13] examined machine learning (ML) algorithms in order to find kidneys that are at the danger of being discarded, during the match run and following biopsy and machine perfusion outcomes. The ML models were developed based on AdaBoost, Random Forests (RF), Neural Networks, Support Vector Machines, and K-nearest Neighbors using data from decaying donor kidneys from 2014 to 2019. These models were compared with Logistic Regression (LR) model. Out of this comparison, RF showed the best performance by correctly categorising 4762 eliminated kidneys compared to LR's performance of 3422. Both models were improved by adding biopsy and machine perfusion variables and RF outperformed LR on all metrics by attaining 0.904 AUC and 0.775 balanced accuracy, outperforming LR across all metrics. Debal & Sitote, [14] applied Extreme Gradient Boosting (XGBoost), RF, Decision Tree (DT) and SVM algorithms to predict both binary and multistage classification of CKD. The feature selection has been done using Univariate Feature Selection and Recursive Feature Elimination with Cross-Validation (RFECV). For the binary classification, SVM as well as RF with RFECV achieved best accuracy which is 99.8%. Also, XGBoost performed best with 82.56% accuracy for dataset of five classes. Bai et al. [15] evaluated the effectiveness of five models using ML algorithms such as random forest, naïve Bayes, logistic regression (LR), K-nearest neighbors and decision tree, against the Kidney Failure Risk Equation (KFRE). The study exhibited three models, naïve Bayes, logistic regression, and random forest, have the same predictability and higher sensitivity score than KFRE. Islam et al. [16] built a collection of predictive models using several ML techniques for CKD prediction. The classifier algorithms: Ada boost, Naïve Bayes, Random Forest, KNN, Decision tree, XgBoost, CatBoost, Light gradient boosting machine (LGBM), Stochastic gradient boosting, Gradient boosting, Extra tree, SVM, Artificial Neural Network (ANN) and Hybrid machine learning have been used to create models and found all the models have accuracy of more than 97% by utilizing the different variables in the dataset. Among the models XgBoost algorithm achieved the greatest performance metrics, with testing accuracy of 98.3%. Using ML techniques, such as RF, KNN and Decision Tree, for analysis, Kaur et al. [17] implemented a model using a dataset of 400 samples from UCI machine learning repository for CKD prediction. They have implemented Ant Colony Optimization (ACO) algorithm to find the most significant prediction variable. The decision tee has achieved the highest accuracy of 95% and by using ensembled bagging method, its performance enhanced to 97%. Md. Mustafizur Rahman et al. [18] implemented eight ensemble ML techniques including gradient boosting decision tree (GBDT), light gradient boosting (LightGBM), xtreme gradient boosting (XGBoost), adaptive boosting, random forest (RF), bagging, voting and stacking, on two datasets. Multivariate Imputation by Chained Equations (MICE) imputation method was used to handle missing values, and unbalanced data is dealt with SVMSMOTE method. The measures: 99.75% accuracy, 99.40% precision, 99.41% recall, 99.61% F-measure, and 99.57% AUC-ROC were achieved by the suggested method.

3. METHOD

K Nearest Neighbor (KNN)

The K-Nearest Neighbors (KNN) classifier is one of the ML techniques, a lazy learning algorithm mainly used for classification, regression, and imputing missing data. A KNN determines the similarity of a target data point to other data points by calculating the Euclidean distance between these points, which represents the straight-line distance between two points A and B. The KNN selects neighbors from the set of objects that share similar properties often considered for training the model. The pre-processing steps will be applied on the dataset before employing the KNN techniques to improve the performance of the model.

Random Forest

The Random Forest (RF) algorithm is an ensemble method which shares similarities with the nearest neighbour predictor in different ways. It improves the performance by applying a divide-and-conquer approach which follows the principle of combining several weak learners to form a reliable learner. In RF, the Decision Tree (DT) algorithm serves as the weak learner, which is aggregated across many trees. Each decision tree iteratively

splits the dataset based on a criterion that maximizes data separation, resulting in a tree-like structure [20].

Support Vector Machine

Support vector machine (SVM) falls under supervised learning algorithm, which is commonly used for classification tasks. It is also used for regression problems. It is applied in several domains including bioinformatics, image recognition, disease prediction and stock market analysis [21]. Many machine learning algorithms struggles in terms of accuracy when the dataset has more features and limited examples. But SVM works well with the limited number of data samples. SVM uses the concept of hyperplane to classify the data points into separate classes. The hyperplane is a line in two-dimensional space and a multi-dimensional plane in other higher dimensional spaces. The support vectors are the nearest data points to the hyper plane. SVM tries to maximise the distance between the support vectors of both the classes in the classification tasks. SVM uses soft margin concepts to deal with data point which may not classified perfectly by a hyperplane, especially dataset contains noise and outliers [22].

SVM uses kernel function to classify non-linearly separable data by transforming the data into a higher dimensional space. The different types of kernel functions are linear kernel, polynomial kernel, Radial Basis Function (RBF) Kernel (Gaussian Kernel) and sigmoid kernel.

Logistic Regression

Logistic Regression (LR) is a simple classification algorithm which is mainly used for binary classification of categorical variable. Logistic regression is used commonly in the sectors of health care and banking for the prediction. The algorithm models the relation between the independent variables and probability of binary outcome. If the probability is greater than 0.5 it falls under yes category, otherwise under no category [23]. Sigmoid curve is used to calculate the probability.

Multilayer Perceptron

An artificial neural network approach known as a Multilayer Perceptron (MLP) includes several layers of neurones, including input, hidden layers, and output layers. Neurons process the data sequentially by doing some computation such as weighed sum and applying nonlinear transformations. MLP are applied to solve different types of complex problems. They are trained by utilising the backpropagation algorithm, which calculates the gradients of a loss function in relation to the model's parameters and adjusts these parameters incrementally to reduce the loss [24].

In this research, we have employed an ensemble approach consisting of SVM, LR, and MLP using a voting classifier as shown in figure 1. The ensemble method helps to improve the accuracy of CKD prediction by utilising each classifier's unique strength and minimising their weaknesses. The base learners, SVM, LR, and MLP, are trained individually on the same dataset. The voting classifier combines the predictions from these base learners to produce a final prediction. Soft voting is the method used here in which each model predicts the probability of each class, and the final prediction is made by finding the class with highest average probability. The diversity in models helps to improve the ensemble's generalisation capability.

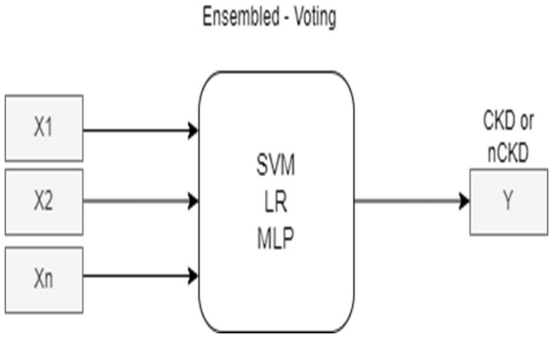

Figure. 1. The proposed ensemble model

Ensemble Methodology: Data Processing and Model Development Steps:

We follow a strategy for prediction as shown in figure 2:

(i) Data acquisition and pre-processing: Data acquisition and pre-processing are very important steps for preparing the dataset for model training. After acquiring dataset from the repository, necessary steps have been taken for the data processing. The column which was irrelevant to the dataset has dropped. Otherwise, it will negative impact the performance of model. The datatype and null values in the dataset were examined and null values were imputed by mean value for continuous variables and mode value for categorical variables. Label Encoding was used to convert categorical columns into numerical format so that machine learning models can interpret categorical variables. These processes ensure that the resultant data is clean.

(ii) Feature Selection: The important features influencing the prediction of CKD were selected. This helps to identify the features which are more influential in predicting whether a patient has CKD or not. It reduces the dimensionality and improves model's performance by avoiding overfitting. After the feature selection, the dataset is divided into independent variables as x, and dependent variable as y, which represents the outcome of the prediction.

(ii) Model Development: The dataset has split into train data and test data. It is very important to split the data into test and train set. The training data is used by the model to learn the relationship and pattern between the independent variables and dependent variable. The model has trained based on the train data using different ML classifiers. These classifiers adjust the internal parameters to reduce the errors and improve accuracy. The model is evaluated against the test data after training has done. Using the test data model's prediction capabilities are assessed using relevant metrics.

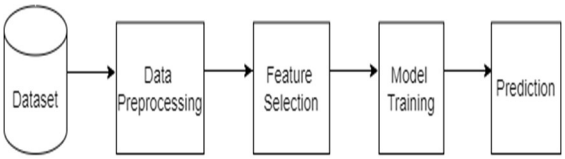

Figure. 2. Proposed Methodology

4. EXPERIMENTAL ANALYSIS

Dataset

The dataset used in this study was downloaded from UCI Machine learning repository [25], a well-known machine learning and data science community repository. The dataset consisted of medical record of 400 different people in which 24 features are independent variable and one feature is targeting variable. The independent variables include blood pressure, sugar, serum creatinine, hypertension and other relevant medical factors. The following figure 3 depicts the 25 features, descriptions and data types in the dataset.

The analysis has done using Jupyter Notebook and different algorithms were used for building model. The experiment has done in two ways. The ML algorithms, KNN and Random Forests were used and built different models for the prediction. Then another ensemble approach, SVM, LR and MLP using Voting Classifier, has been implemented.

Initially we carried out with the following process such as after the preprocessing and feature selection, the dataset has split into training and testing data using 70:30 ratio. Using the training data, A KNN classifiers with two neighbours were trained. Then a confusion matrix and classification report were used to evaluate the model's performance on test data. Also, an RF classifier has applied to the same train data and the performance is evaluated using the test data. Here we were able to evaluate the performances of these models.

Variable Name	Role	Type	Description	Units	Missing Values
age	Feature	Integer	Age	year	yes
bp	Feature	Integer	blood pressure	mm/Hg	yes
sg	Feature	Categorical	specific gravity		yes
al	Feature	Categorical	albumin		yes
su	Feature	Categorical	sugar		yes
rbc	Feature	Binary	red blood cells		yes
pc	Feature	Binary	pus cell		yes
pcc	Feature	Binary	pus cell clumps		yes
ba	Feature	Binary	bacteria		yes
bgr	Feature	Integer	blood glucose random	mgs/dl	yes
bu	Feature	Integer	blood urea	mgs/dl	yes
sc	Feature	Continuous	serum creatinine	mgs/dl	yes
sod	Feature	Integer	sodium	mEq/L	yes
pot	Feature	Continuous	potassium	mEq/L	yes
hemo	Feature	Continuous	hemoglobin	gms	yes
pcv	Feature	Integer	packed cell volume		yes
wbcc	Feature	Integer	white blood cell count	cells/cmm	yes
rbcc	Feature	Continuous	red blood cell count	millions/cmm	yes
htn	Feature	Binary	hypertension		yes
dm	Feature	Binary	diabetes mellitus		yes
cad	Feature	Binary	coronary artery disease		yes
appet	Feature	Binary	appetite		yes
pe	Feature	Binary	pedal edema		yes
ane	Feature	Binary	anemia		yes
class	Target	Binary	ckd or not ckd		no

Figure. 3. Features in the dataset

In this experiment, the kidney dataset has been pre-processed to prepare it for building the

model. The irrelevant column names 'id' was removed. The missing values were replaced by the mean or mode value for numerical and categorical variables respectively. Using a label encoder, categorical variables were encoded into numerical format. The dataset has been split into x as features and y as target variable. Then the dataset has divided into train data and test data using 80:20 ratio. StandardScaler was applied to both training and testing dataset to standardise the data.

After the data preprocessing, SVM, LR and MLP classifiers were initialised. An ensemble model was created using voting classifier with soft voting method. The soft voting method ensures that the prediction is based on the average probability of all classifiers. The class which is having the highest average probability is selected for prediction. A standardised training data set was used to train the model. The test data set was used to evaluate the model performance. The performance of the model was measured using the classification report. The given ensembled method aggregated the strength of each classifier to provide robust kidney disease prediction. Also, the similar experiment using the same ensemble method has been carried out by splitting the same dataset into 70:30 train-test ratio.

5. RESULT

The classification report obtained during the model evaluation provides report provides the details like precision, recall, f1-score, support, accuracy, macro average and weighed average. These metrics are explained below.

$$Precision = \frac{TP}{TP+FP} \quad (1)$$

$$Recall = \frac{TP}{TP+FN} \quad (2)$$

$$F1\text{-}score = 2 \times \frac{Precision \times Recall}{Precision+Rec} \quad (3)$$

$$Accuracy = \frac{TP+TN}{TP+TN+FP+F} \quad (4)$$

Here, TP (True Positive) is the number of Truly predicted positive cases, FP (False Positive) is the number of cases incorrectly predicted as positive, TN (True Negative) is the number truly predicted negative cases, and FN (False Negative) is the number of cases incorrectly predicted as negative.

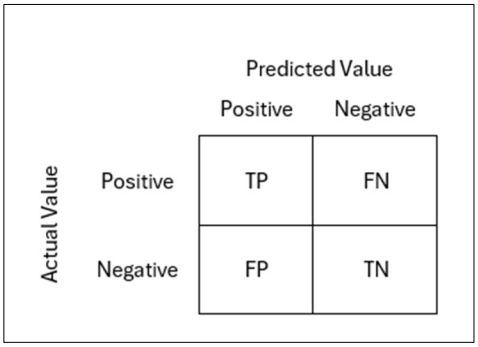

Figure. 4. Confusion Matrix

The below table depicts the result of the experimental work for individual models, RF and KNN and ensemble method using SVM, LR and MLP with Voting Classifier. The training and testing set split ratio 70:30, the accuracy achieved was 99%. The train and test data split ratio were modified to 80% for training and 20% for testing dataset. The proposed ensemble model performance was improved by achieving 100 % in accuracy, precision, recall and f1-score metrics.

Table 1. The performance of different ML models during the experiment

Model	Prec	Recall	F1-score	Acc
KNN (70:30 split)	0.89	0.89	0.89	0.89
RF (70:30 split)	0.99	0.98	0.98	0.98
Ensemble-SVM, LR and MLP (70:30 split)	0.99	0.99	0.99	0.99
Ensemble-SVM, LR and MLP (80:20 split)	1.00	1.00	1.00	1.00

From the above table, we observed KNN obtained a precision, recall, F1-score, and accuracy of 0.89. This represents an average performance in CKD prediction. Even though the model achieved consistent results in all the metrics, it showed some limitation in this specific task. It showed a consistent matric of 0.89 in all measures but needs improvement. Random Forest (RF) shows better performance, attaining 0.99 precision value, 0.98 recall value, 0.98 F1-score, and 0.98 accuracy. The improved accuracy and recall metrics show that

RF effectively balances true positives while reducing false positives. The precision value of RF indicated that 99% of the observations classified as positive were correct. According to the recall value, the model identified 98% of the actual CKD cases.

Ensemble Method (Support Vector Machine, Logistic Regression, Multi-Layer Perceptron): The ensemble model, using a voting classifier, outperformed both KNN and RF. It attained nearly best performance compared with all other models. The ensemble technique attained a precision, recall, F1-score, and accuracy of 0.99 with a 70:30 split. Applying an 80:20 train-test split yielded an overall score of 100% for all metrics: F1-score, recall, precision, and accuracy. This 100% accuracy shows that the model is highly effective in classifying positive and negative CKD cases. There was no false positive ad false negative while calculating the metrics. These highly performing ensemble model can significantly help in the early detection and accuracy of CKD diagnosis.

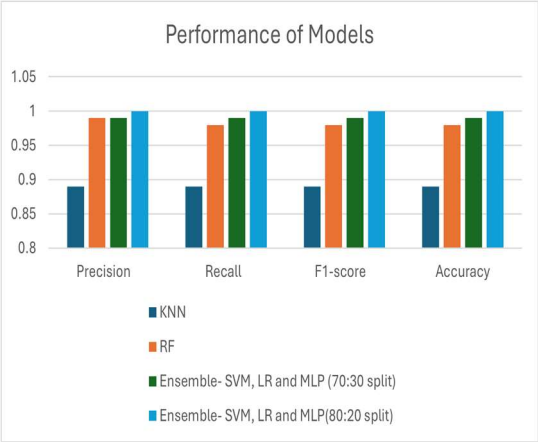

Figure. 3. Comparison of models performance

Table 2: Comparison of our proposed model with the state-of-the-art:

Model	Acc	F1-score
[8]	**≈98.5%**	**0.99**
[10]	**99.84%**	**0.99**
[16]	**98.3%**	**.98**
[18]	**99.75**	**0.99**
[26]	**99%**	**1**
Our Proposed Study	**100%**	**1**

Table 2 shows the performance comparison between our proposed model and the existing models on the same dataset. Our proposed model shows promising results compared with all other models.

Limitation:

In this study, the main challenge is the availability of datasets. We have used the dataset from the single hospital within a 2-month period. Although, our model predicts 100% accuracy on this dataset, concerns arises on the generalizability of the proposed AI model. In future, we can address it by using the multi-institutional dataset to avoid the bias of the model.

6. CONCLUSION

In this study, we built an ensemble method to predict CKD in a more accurate way. The models such as KNN and RF were tested, and their performance was compared with an ensemble model which comprises of SVM, LR and MLP. This ensemble model outperformed all the individual algorithms by obtaining 100% accuracy when the dataset is split into 80:20 ratio for training and testing. The highest accuracy which is obtained using this approach shows that how ensemble model can utilise the strengths of individual models to improve accuracy of the prediction. Our result proves that the ensemble model can be an effective tool for the prediction of CKD compared to the state-of-the art. Even though, our model has achieved the perfect accuracy, it should be validated using different CKD datasets. In the future work, we recommend integrating additional algorithms into the ensemble model and examine the model across different patient demographics.

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