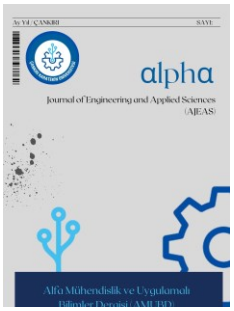

Alpha Journal of Engineering and Applied Sciences
(2023) 1/ 1: 50 – 61
Alfa Mühendislik ve Uygulamalı Bilimler Dergisi
(2023) 1/1: 50 – 61

Research Article

Received	*Accepted*	*Published*
28/11/2023	*26/12/2023*	*31/12/2023*

Chronic Kidney Disease Prediction with Stacked Ensemble-Based Model

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Abstract
Chronic kidney disease (CKD) is viewed as a significant health issue worldwide. Treating this disease early is crucial to prevent it from causing further problems. Researchers have been using different machine learning-based approaches to predict this disease in recent years. The focus of this paper is on a stacked ensemble model that can be used to predict CKD. The proposed model is applied to an open-access CKD dataset. The dataset is made suitable for classification by undergoing several pre-processing steps. The proposed model comprises two phases. First, the prediction process was performed using base classifiers. Then, the stacked ensemble model is used to combine these base classifiers in the best way. The recursive feature elimination technique is used to select the most discriminative features. The optimal hyperparameters for classification algorithms are determined using the hyperparameter optimization technique. When compared to other base classifiers, the suggested stacked model achieves 100% accuracy. Furthermore, the proposed model is compared to various approaches in the literature and achieved a high classification rate.

Keywords: *Chronic kidney disease, machine learning, stacked ensemble, hyperparameter tuning*

Yığılmış Topluluk Tabanlı Model ile Kronik Böbrek Hastalığı Tahmini

Özet
Kronik böbrek hastalığı (KBH) dünya genelinde önemli bir sağlık problemi olarak kabul edilmektedir. Daha fazla soruna yol açmasını önlemek için bu hastalığın erken dönemde tedavi edilmesi çok önemlidir. Araştırmacılar son yıllarda bu hastalığı tahmin etmek için farklı makine öğrenimi tabanlı yaklaşımlar kullanmaktadır. Bu makalenin odak noktası, KBH'yi tahmin etmek için kullanılabilecek yığılmış bir topluluk modelidir. Önerilen model açık erişimli bir CKD veri setine uygulanmıştır. Veri kümesi, çeşitli ön işleme adımlarından geçirilerek sınıflandırma için uygun hale getirilmiştir. Önerilen topluluk modeli iki aşamadan oluşmaktadır. İlk olarak, tahmin işlemi temel sınıflandırıcılar kullanılarak gerçekleştirilmiştir. Ardından, bu temel sınıflandırıcıları en iyi şekilde birleştirmek için yığılmış topluluk modeli kullanılır. En ayırt edici öznitelikleri seçmek için özyinelemeli öznitelik eleme tekniği kullanılmıştır. Hiperparametre optimizasyon tekniği kullanılarak sınıflandırma algoritmaları için en uygun hiperparametreler belirlenmiştir. Diğer temel sınıflandırıcılarla karşılaştırıldığında, önerilen yığılmış model %100 doğruluk elde etmektedir. Ayrıca, önerilen model literatürdeki farklı yaklaşımlara karşı değerlendirilmiş ve yüksek bir sınıflandırma oranına ulaşmıştır.

Anahtar kelimeler: *Kronik böbrek hastalığı, makine öğrenmesi, yığılmış topluluk, hiperparametre optimizasyonu*

1. Introduction

The loss of kidney function over a period is called chronic kidney disease (CKD). This disease can be considered a progressive situation, affecting approximately 10% of the total population. The number of deaths caused by CKD annually is nearly 2 million. In this respect, it is considered a significant health problem. Diabetes, hypertension, cardiovascular disease, smoking, and obesity are all known to increase the risk of CKD. Identifying risk groups and early diagnosis is crucial to stop the disease's progression and reduce the risk of death [1–2].

Identifying a disease's status through symptoms and signs is known as a disease diagnosis. Machine learning (ML) can help predict disease diagnosis using pre-existing datasets. These algorithms can build models that can predict disease diagnosis and treatment. Therefore, there have been multiple ML models developed by researchers to diagnose this disease. Traditional ML algorithms such as Logistic regression (LR), Decision tree (DT), Support vector machine (SVM), Naive Bayes (NB), Artificial network (ANN) and K-nearest neighbors (KNN) are frequently used in the literature for predicting CKD [3, 4]. Since these algorithms have weaknesses and advantages over each other, choosing a single classifier may not give a high classification rate. Instead of using a single classifier, ensemble learning algorithms build models with multiple classifiers. Ensemble learning (EL) techniques aim to unify the predictions from different models to improve classification performances. These techniques can also reduce the error rate of the forecasting model when the underlying models are distinct and independent. These techniques can increase the classification rate of the model by combining weak classifiers to create a robust classifier. [5]. At the same time, ML algorithms utilize the discriminative abilities of the features present in datasets. However, not all of these features may be of equal importance. In this case, the use of feature selection (FS) methods can be beneficial. These methods can enable classifiers to learn data more efficiently by eliminating redundant features from the dataset. Thus, the cost of model building is reduced, and the classification rate of the model may increase [6]. Meanwhile, unbalanced class distributions in datasets can also affect the performance of classifiers. Class imbalance occurs when the class distributions are not close to each other. The prediction model converges to the majority class, leading to the under-classification of the minority class [7]. For an effective CKD prediction, this study suggests a prediction model based on ensemble learning algorithms that can remove the class imbalance in the dataset, choose the most discriminative features and improve the performance of classifiers. This research has the main contributions and limitations listed below.

- The three phases of the study to effectively predict CKD are data preprocessing, hyperparameter tuning, and the combination of individual ML with stacked ensemble models.
- The experimental results of this framework demonstrate that ensemble methods are more effective in predicting CKD compared to individual ML algorithms.
- The study demonstrates that combining ML algorithms through ensemble methods can effectively predict the early stages of diseases like CKD.
- The superiority of the suggested model is that it achieves a better classification result than other ML algorithms known in the existing literature.
- The study's findings are limited in generalizability due to their testing on an open-access dataset.

2. Related Works

ML algorithms have been used in many studies to predict CKD in recent years. Some recent studies are summarized in this section. Pal [8] suggested a bagging model for the prediction of CKD. The suggested model was compared with LR, SVM, and DT algorithms. As a result of the experiments,

the suggested model yielded an accuracy of 97.23%. However, the limitations of the study include the lack of data imputation, data balancing, and FS methods. Debal and Sitote [9] presented a comparative analysis to predict CKD. RF, SVM, and DT were selected as ML algorithms. The recursive feature elimination (RFE) technique was employed as the FS method. As a comparative result, the RF algorithm gave better results than the other algorithms. Priyanka et al. [10] tried five different classifiers to predict this disease. K-NN, SVM, DT, ANN, and NB algorithms were preferred as classifiers. As a consequence of the benchmarking, the NB algorithm outperformed with an accuracy of 94.6%. The data set used in the study was subjected to the classification process without going through preprocessing stages. Islam et al. [11] attempted to predict this disease by using multiple classifiers and performing a comparative analysis. The RFE method was used as the FS algorithm, and various preprocessing methods were employed to make the data suitable for classification. The XGBoost algorithm obtained the maximum classification rate of 98.06% of accuracy, compared to the other algorithms. Chittora et al. [12] utilized seven ML algorithms for the classification process. The SMOTE algorithm is utilized for the data balancing process Correlation-based feature selection and least absolute and shrinkage and selection operator regression algorithms were used to select the significant features. As a result of the comparisons, the deep neural network (DNN) algorithm achieved the highest accuracy with an accuracy rate of 99.6 %. However, hyperparameter tuning and data imputation were not utilized in this study. Rajeshwari and Yogish et al. [13] tried to predict CKD utilizing different machine learning algorithms in their study. NB, RF, DT, and SVM algorithms were preferred for the classification process. RF algorithm yielded 98.75% accuracy. However, the study did not undertake processes such as data imputation and data balancing. Wibawa et al. [14] utilized ML algorithms to predict CKD. The Correlation-based technique was used in the FS process. As a result of the experiments, the AdaBoost algorithm achieved the highest classification rate with an accuracy of 98.1%. Farjana et al. [15] utilized different ML algorithms to predict CKD. The XGBoost algorithm outperformed with 98.3% accuracy compared to other classifiers. Ullah and Jamjoom et al. [16] utilized K-NN, SVM, RF, and bagging algorithms to predict CKD. The filter method was selected as the FS method. With an accuracy rate of 99.50%, K-NN algorithms were better than other classifiers. The method used in the study does not incorporate feature selection and data scaling techniques. Arif et al. [17] suggested a robust ML model to predict CKD. The study data was subjected to different pre-processing steps to make it suitable for the classification process. K-NN and NB algorithms were used for the classification phase. The K-NN algorithm achieved a 100% accuracy rate. Venketsan et al. [18] suggested an ensemble learning model based on XGBoost to predict CKD. The study data was subjected to different pre-processing steps to make it suitable for the classification process. The suggested model illustrated 98.00% of accuracy.

3. The Suggested Framework

This study is broken up into multiple sequential stages. In the initial stage, the dataset is undergoing a series of data preprocessing processes. Data preprocessing stages involve filling in missing data, balancing data, normalizing data, and selecting features. After the data preprocessing stage, data splitting begins. Hyperparameter tuning is used to set the hyperparameters of classifiers in the next stage. Individual well-tuned machine learning models were then used to build a stacked ensemble model. Figure 1 demonstrates the workflow of the suggested model.

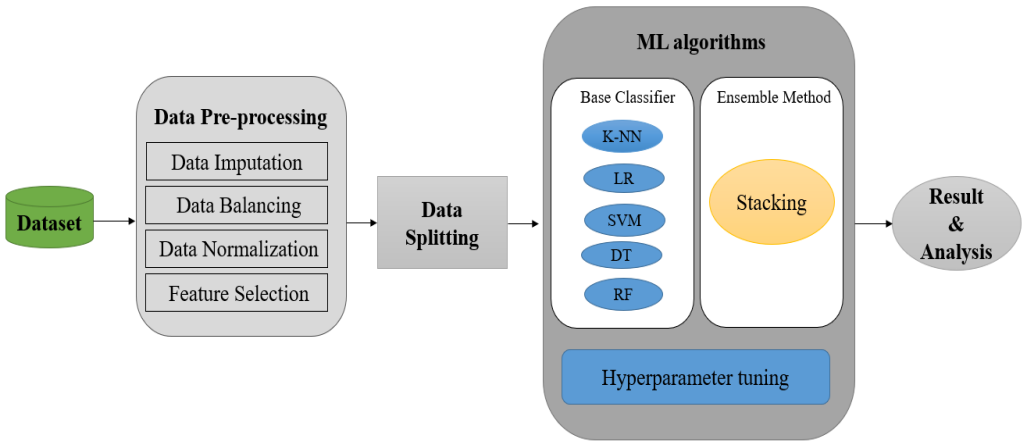

Figure 1: The suggested framework

The suggested model was validated by obtaining the CKD dataset from the UCI Machine Learning Repository [19]. It includes 400 instances with 25 features. Table 1 illustrates the information related to these features. The last feature indicates whether a diagnosis of CKD is present.

Table 1: The dataset description

Number	Features	Data Type	Data Range
1	Age	Numeric	Years
2	Blood pressure	Numeric	mm/Hg
3	Specific gravity	Nominal	[1.005 - 1.025]
4	Albumin	Nominal	[0-5]
5	Sugar	Nominal	[0-5]
6	Red blood cells	Nominal	[Abnormal/Normal]
7	Pus cells	Nominal	[Abnormal/Normal]
8	Pus cells clumps	Nominal	[Present/Not Present]
9	Bacteria	Nominal	[Present/Not Present]
10	Blood glucose random	Numeric	mgs/dl
11	Blood urea	Numeric	mgs/dl
12	Serum creatine	Numeric	mgs/dl
13	Sodium	Numeric	mEq/L
14	Potassium	Numeric	mEq/L
15	Hemoglobin	Numeric	gms
16	Packed cell volume	Numeric	P cv
17	White blood cell count	Numeric	cells/cumm
18	Red blood cell count	Numeric	millions/cmm
19	Hypertension	Nominal	[Yes/No]
20	Diabetes mellitus	Nominal	[Yes/No]
21	Coroner arter disease	Nominal	[Yes/No]
22	Appetite	Nominal	[Good/Poor]
23	Pedal edema	Nominal	[Yes/No]
24	Anemia	Nominal	[Yes/No]
25	Classification	Nominal	[CKD/Not CKD]

3.1. Data preprocessing

Data preprocessing plays a crucial role in achieving high performance in building a model [20]. The raw data of the data set is modified before being pre-processed and converted into a suitable format. This purpose involves categorizing the nominal or categorical variables in the dataset. The features in the dataset that fall under terms of yes/no, good/poor, present/not present, and CKD/Not CKD are

encoded and converted to 0/1 accordingly. The next stage involves the imputation of data. It preserves the vast majority of data and information in a dataset by substituting missing data with a different value. The analysis of the dataset reveals that there are too many missing values. This situation is illustrated in Figure 2. To deal with this problem, a mean-based imputation method is employed. It uses the mean of the observed values for each variable to assign missing values.

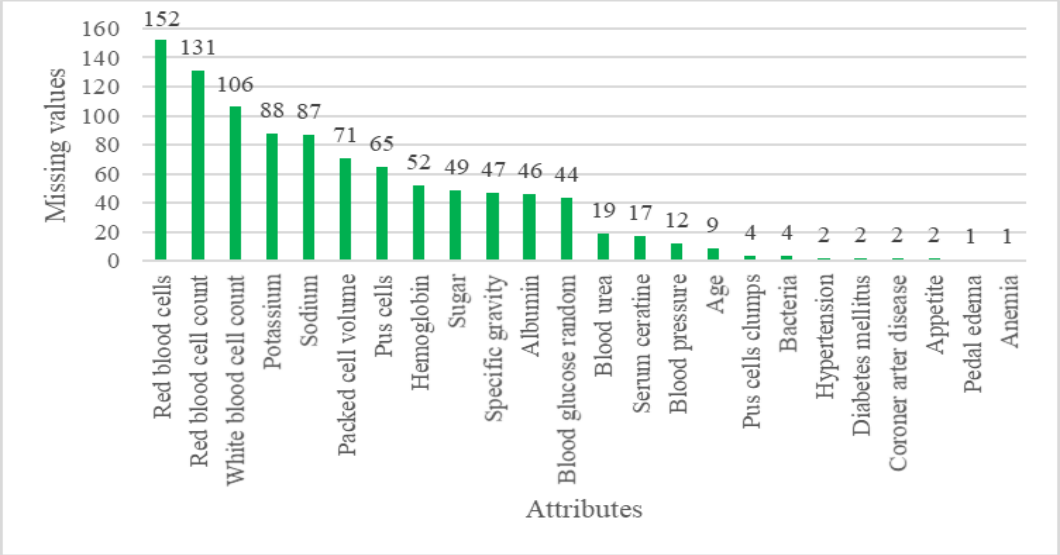

Figure 2: The missing value number of features in the dataset

The data set's 'classification' variable has an unbalanced distribution. For individuals with CKD, the sample size is 250, and for individuals without CKD, it is 150. The Synthetic minority oversampling technique (SMOTE) is used to equate the smaller category to the larger one. The creation of synthetic minority class instances is a way to balance the class distribution of the dataset using this technique. The synthetic samples are produced by connecting lines that connect the nearest neighbors in the feature domain. The basic idea of the algorithm is the creation of a new minority class instance by small steps from one of the minority class instances to one of its k nearest neighbours in the feature space, where k is the parameter of the algorithm. The parameter k in the algorithm refers to the number of nearest neighbours to be taken into account when generating synthetic samples [21]. In this study, the number of k is set to 5. After SMOTE is applied, there is a balance between the distribution of each category. Then, the data set's numeric column values are normalized using the min-max method, which resulted in a medium scaling between 0 and 1 without compromising the value ranges [22]. In the subsequent phase, a FS method is employed to improve the classification performance and reducing computational requirements of ML algorithms can be achieved by selecting relevant and influential features in a dataset. The most discriminatory features in the dataset are identified using recursive feature elimination (RFE). By iteratively removing less important features, this technique optimizes prediction accuracy by creating a subset. The impact of each feature on model performance is assessed by RFE with the help of a ML algorithm and an importance ranking measure [23]. For this study, the feature selection algorithm is based on the SVM-RFE approach. Consequently, five features are selected: blood pressure, blood urea, potassium, white blood cell count, and red blood cell count.

3.2. Data splitting

The importance of data splitting in ML is an essential stage for robust model evaluation and generalization [24]. The process comprises subdividing the dataset into a subset for training and a

subset for testing. The data set is randomly split 80:20 as training and test data. 80% of the data set was used as training and 20% as test data.

3.3. Stacking model

The diagnosis of CKD was done by applying a stacking model after pre-processing. A stacking model consists of a base model (level 0) containing multiple classifiers and a meta-model (level 1) containing the predictions of these base models. The standard stacking procedure may result in overfitting because the "level 0" classifiers are trained on the same training set as the "level 1" classifier's inputs. The stacking model utilizes the concept of cross-validation (CV). The dataset is first partitioned into k folds. Then, in k sequential turns, k-1 folds are employed to fit the base classifiers. In each cycle, the base classifiers are utilized for the rest of the subset not used for model fitting. The 5-fold CV technique is preferred for this process. In the next stage, the resulting predictions are aggregated and input data for the second- level classification [25, 26]. Once the training process is completed, the first-level classifiers are adjusted to the entire dataset, as shown in Figure 3. In the suggested stacking model, LR, RF, K-NN, SVM, and DT algorithms are utilized as the base learner. The stacked approach can be extended to include replacing sub-model predictions with LR and combining them with any learning algorithm. Thus, the LR algorithm is chosen as the meta-learner.

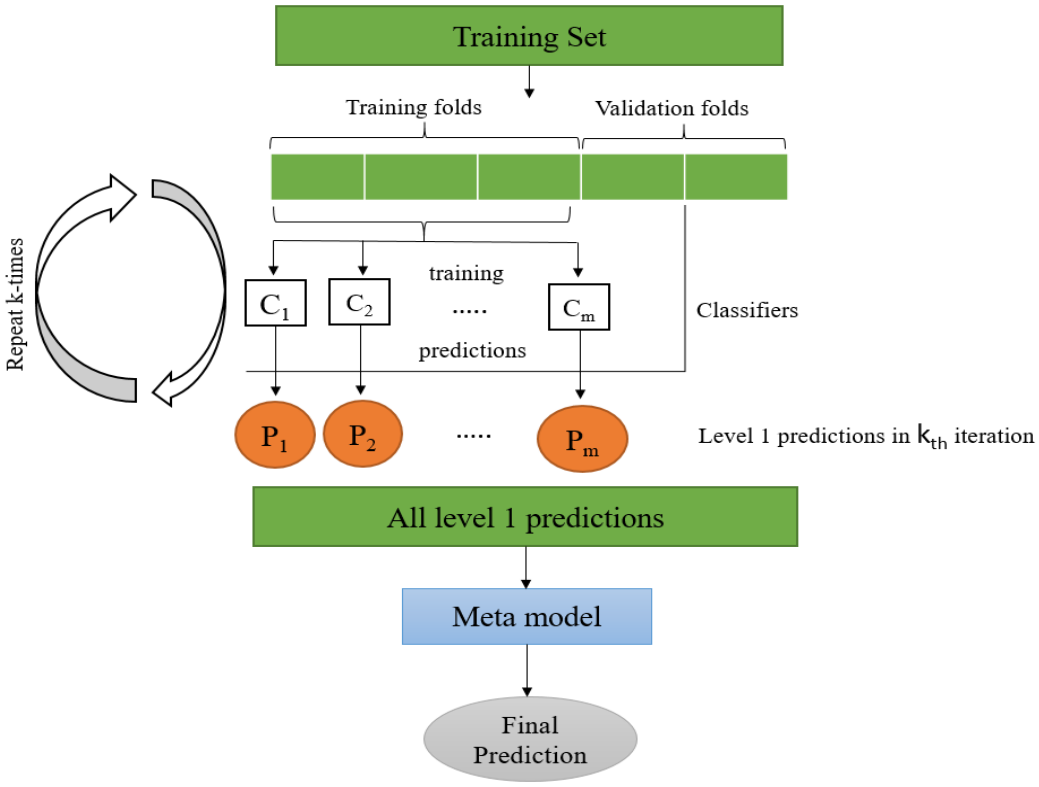

Figure 3: The stacked ensemble model

3.4.Tuning hyperparameters of ML algorithms

The learning process is regulated by multiple hyperparameters in ML algorithms. The performance and stability of ML algorithms can be greatly improved through the optimal tuning of hyperparameters. The Grid search is a technique used to figure out the most effective hyperparameters for algorithms. It breaks up the space of hyperparameters into a distinct grid. The

model's performance is then compared against the hyperparameter combinations with k-fold CV. The evaluation process involves using a 5-fold CV technique. The evaluation of classifier is created depending on the average performance [27]. Table 2 summarizes the hyperparameters of each ML algorithm.

Table 2: Parameters tuning for machine learning.

Model	Hyperparameters	Search Range	The Best Hyperparameter
RF	N_estimators	[10, 50, 100, 200, 500]	100
	Min_samples_split	[2, 3, 5, 7, 10]	5
	Max_depth	[2, 3 ,5, 7, 10]	4
	Min_samples_leaf	[1, 3, 5, 7, 10]	3
DT	Max_feature	[auto, sqrt, log2]	auto
	Ccp_alpha	[0.001, 0.02, 0.03, 0.05, 0.1]	0.03
	Max_ depth	[2, 4, 6, 8, 10]	4
	Criterion	entropy, Gini	Gini
K-NN	N_neighbors	[1-31]	5
	Weights	[uniform, distance]	uniform
	Metrics	[Euclidian, minkowski]	minkowski
	Leaf Size	[10, 20, 30, 40, 50]	30
	P	[1, 2, 3, 4, 5]	2
SVM	C	[1, 50, 100, 200, 500, 1000]	200
	Gamma	[0.001, 0.1, 0.2, 0.3, 0.5, 1]	0.2
	Kernel	[rbf, linear]	linear
LR	Penalty	[l1, l2]	l1
	Solver	[lbfgs, liblinear]	lbfgs
	Max iteration	[100, 500, 1000, 5000, 10000]	1000

4. Experimental Results and Discussion

The findings of the study for predicting CKD are presented in this part. The Jupyter Notebook 3.8.16 in Python was utilized for the experiments, which included packages like Numpy, Pandas, Matplotlib, Seaborn, and Scikit-Learn. The performance of the classifiers was evaluated with a confusion matrix. The mathematical expressions presented in Equations 1-4 can be used to calculate performance metrics using this matrix.

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{FP} + \text{TN} + \text{FP}} \quad (1)$$

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \quad (2)$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}} \quad (3)$$

$$\text{F1} - \text{Score} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (4)$$

A stacked model is proposed in this study to predict CKD. This model first uses five well-tuned individual ML-aware base classifiers, including SVM, K-NN, DT, LR, and RF algorithms (Level 0). Then, the stacked model is used to enhance the performance of these classifiers. In Figure 4, the confusion matrices of both the base and stacked models are depicted.

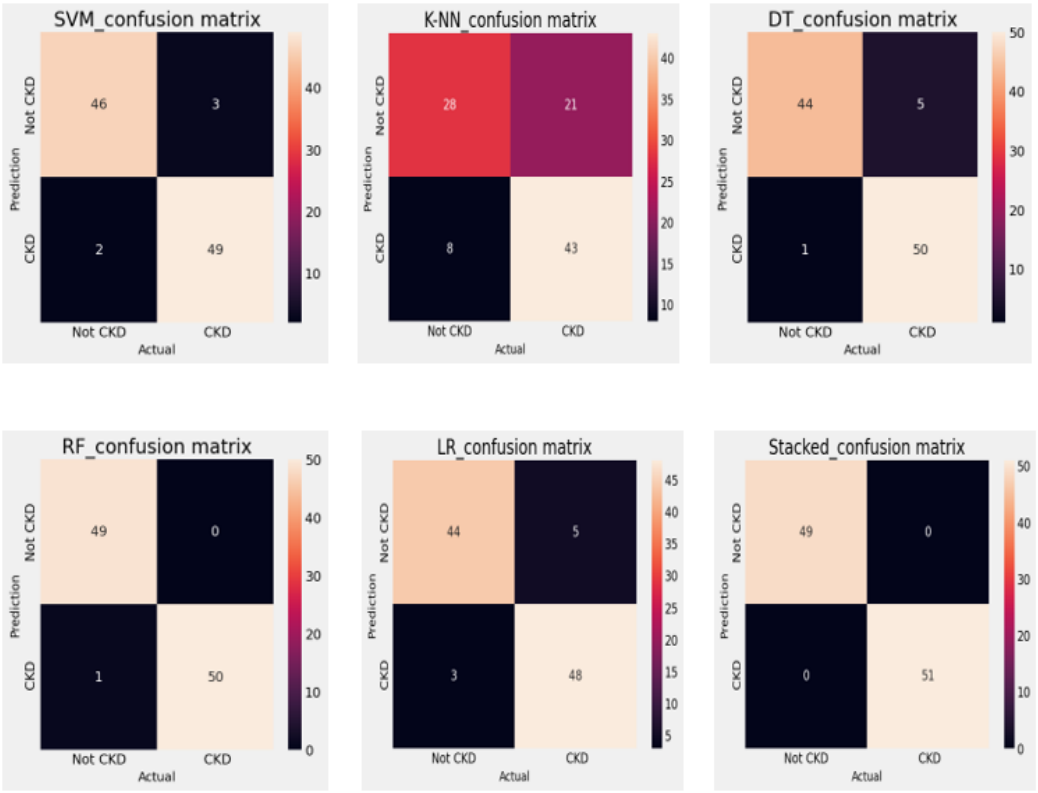

Figure 4: Confusion matrices for ML algorithms

Using these confusion matrices, the performance metrics defined in Equation 1 can be calculated for each classifier. The performance metrics calculated for the classifiers are shown in Table 4 and Figure 5.

Table 4: Comparison of suggested voting-based models with the baseline classifier

Base Classifier (Level 0)				
Models	**Accuracy**	**Precision**	**Recall**	**F1-Score**
SVM	0.95	0.9608	0.9423	0.9515
K-NN	0.71	0.8431	0,6719	0.7478
DT	0.94	0.9804	0.9091	0.9434
RF	0.99	0.9804	1	0.9901
LR	0.92	0.9412	0.9057	0.9231
Ensemble Model (Level 1)				
Model	**Accuracy**	**Precision**	**Recall**	**F1-Score**
Stacked	1	1	1	1

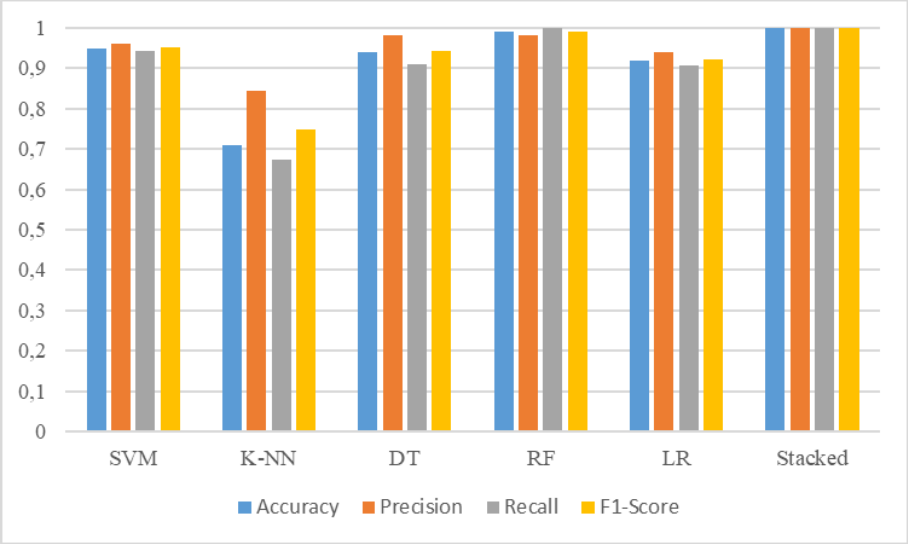

Figure 5: The comparison of classification rates in terms of performance metrics

The RF algorithm is also a type of ensemble learning method incorporating predictions from multiple trained models [28]. In this respect, the RF algorithm is expected to outperform other conventional classifiers. The RF algorithm outperforms all other algorithms with its high classification rates, which included 99% accuracy, 98.04% precision, 100% recall, and 99.01% F1-score. The SVM algorithm with an accuracy of 95.00%, followed by DT and LR with 94% and 92% accuracy. The K-NN algorithm has the lowest performance with 71% accuracy. Although the RF shows a good classification performance, this technique has some limitations. A limitation of this technique is that each model adds the same proportion to the ensemble predictions, regardless of how well the model performs. The Stacked model, an alternative method, can help solve this problem by providing a better classification rate. With 100% accuracy, precision, recall, and F1 score, the proposed stacked model outperformed the baseline classifiers in classification rates. With these high classification rates, the proposed stacked model improves the classification performance of the base classifiers. By using the ROC curve, it is possible to represent the relationship between the true positive rate and the false positive rate. Figure 6 shows the ROC curve of classifiers. The suggested stacked model achieved the highest value of 1.00, which is higher than the RF (0.99), SVM (0.95), DT (0.939), LR (0.92), and K-NN (0.707) algorithms.

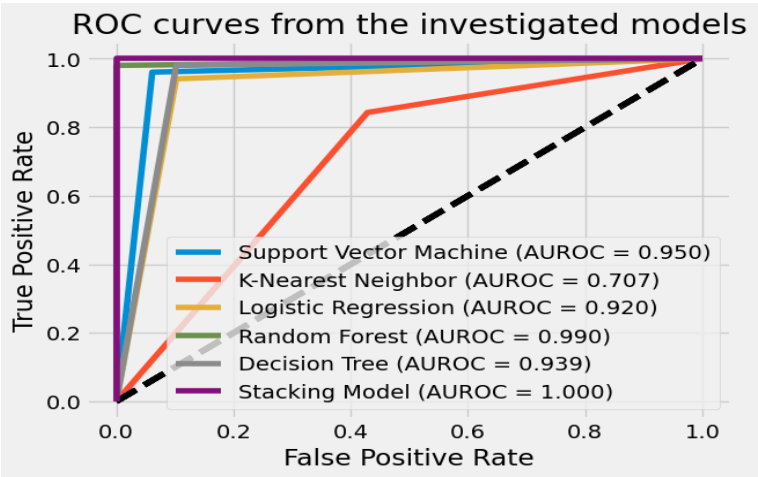

Figure 6: AUC-ROC curve for ML algorithms

Table 5 provides a comparative analysis with previous similar studies for CKD prediction. The results obtained by the suggested model are compared with the studies conducted on the same data set. In the literature, ensemble learning methods such as RF, XGBoost and Bagging, and classical ML algorithms have also been used for CKD prediction. In general, the classification performances of the studies in the literature vary between 95-100%. Most studies in the literature for CKD prediction are not addressed the issues of missing data imputation, handling imbalanced data and hyperparameter optimization. In this study, different preprocessing techniques were applied to make the data set more understandable. In addition, hyperparameter tuning method was used to find the most suitable hyperparameter combinations for ML algorithms. Therefore, the model presented in this study can be considered as a noteworthy. When evaluated from this point of view, it can be said that the stacked model proposed in this study also achieves a high classification rate with an accuracy rate of 100%.

Table 5: Comparison of the suggested model with some existing studies using the CVD dataset

References	Data Imputation	Data Balancing	Hyperparameter Tuning	Model	Accuracy (%)
[8]	-	-	-	Bagging	97.23
[9]	✓	-	-	RFE-RF	99.27
[10]	-	-	-	NB	94.6
[11]	✓	-	-	XGBoost	98.06
[12]	-	✓	-	SVM	98.46
[13]	-	-	-	RF	98.75
[14]	-	-	-	AdaBoost	98.1
[15]	-	-	-	XGBoost	98.3
[16]	-	-	-	K-NN	99.5
[17]	✓	✓	✓	K-NN	100
[18]	✓	-	✓	XGBoost	98
[29]	✓	-	✓	DT	100
[30]	-	-	✓	LR	94.2
Suggested model	✓	✓	✓	Stacked	100

5. Conclusion

In this study, we have designed a stacked ensemble model to effectively predict CKD so that the treatment of CKD patients can be planned before the disease reaches the end stage. The suggested model is tested on a CKD dataset. The dataset goes through a series of preprocessing stages to make it eligible for classification. For the first part of the proposed stacked model, the base classifier, algorithms such as RF, SVM, K-NN, LR and DT algorithms were employed. A hyperparameter tuning approach is employed to set the hyperparameters of the classifiers. Moreover, the presented stacked model has indicated better classification rates when compared to the base classifiers. Although the ensemble model does not give the optimal solution for all problems, it provides a higher classification rate than individual classifiers. We plan to try and test the suggested model on different datasets to verify its robustness. However, the process of classifying diseases faces major challenges due to the limited amount of data. Collaborating with hospitals and other data-generating organizations is necessary to obtain more high-quality medical data for further study and research.

Abbreviations:

CKD	Chronic kidney disease
ML	Machine learning
DT	Decision tree
SVM	Support vector machine
NB	Naive Bayes
ANN	Artificial neural network
RF	Random forest
EL	Ensemble learning
FS	Feature selection
RFE	Recursive feature elimination
SMOTE	Synthetic minority oversampling technique
CV	Cross-validation
ROC	Region of curve

Conflict of Interest Notice
The authors declare that there is no conflict of interest regarding the publication of this paper.

Ethical Approval and Informed Consent
It is declared that during the preparation process of this study, scientific and ethical principles were followed, and all the studies benefited from are stated in the bibliography.

Availability of data and material
Not applicable.

References

[1] AC. Webster, EV Nagler, RL. Morton RL et al. (2017) "Chronic kidney disease". *Lancet Lond Engl* 389(10075):1238–1252, 2017.

[2] CP. Kovesdy, "Epidemiology of chronic kidney disease: an update 2022." *Kidney International Supplements*, 12(1), 7-11, 2022.

[3] J. Qezelbash-Chamak, S. Badamchizadeh, K. Eshghi, Y. Asadi, "A survey of machine learning in kidney disease diagnosis." *Machine Learning with Applications*, 10, 100418, 2022.

[4] F. Sanmarchi, C. Fanconi, D. Golinelli, D. Gori, T. Hernandez-Boussard, A. Capodici, "Predict, diagnose, and treat chronic kidney disease with machine learning: a systematic literature review." *Journal of nephrology*, 1-17, 2023.

[5] O. Sagi & L. Rokach, Ensemble learning: A survey. *Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery*, 8(4), e1249, 2018.

[6] V. Kumar & S. Minz, "Feature selection: a literature review." *SmartCR*, 4(3), 211-229, 2014.

[7] A. Viloria, O. B. P., Lezama, & N. Mercado-Caruzo, "Unbalanced data processing using oversampling: machine learning." *Procedia Computer Science*, 175, 108-113, 2020.

[8] S. Pal, "Chronic Kidney Disease Prediction Using Machine Learning Techniques." *Biomedical Materials & Devices*, 2022.

[9] DA. Debal, D.A., TM. Sitote, "Chronic kidney disease prediction using machine learning techniques", *J Big Data* 9, 109, 2022.

[10] K. Amogh Babu, K. Priyanka, T. Raghavendra Babu T, "Chronic kidney disease prediction based on naive Bayes technique*". International Research Journal of Engineering and Technology (IRJET*) p. 1653–1659, 2019.

[11] MA. Islam, MZH. Majumder, MA Hussein, “Chronic kidney disease prediction based on machine learning algorithms.” *J Pathol Inform*. 12; 14:100189, 2023.
[12] P. Chittora et al., “Prediction of chronic kidney disease - a machine learning perspective,” in *IEEE Access*, vol. 9, pp. 17312-17334, 2021.
[13] Rajeshwari and H. K. Yogish, “Prediction of chronic kidney disease using machine learning technique,” *2022 Fourth International Conference on Cognitive Computing and Information Processing (CCIP)*, Bengaluru, India, 2022, pp. 1-6.
[14] M. S I. Wibawa, M. D. Maysanjaya and I. M. A. W Putra., “Boosted classifier and features selection for enhancing chronic kidney disease diagnose,” *2017 5th International Conference on Cyber and IT Service Management (CITSM)*, Denpasar, Indonesia, 2017, pp. 1-6
[15] A. Farjana, FT. Liza, PP. Pandit, MC. Das, M. Hasan, F. Tabassum, MH. Hossen, “Predicting Chronic Kidney Disease Using Machine Learning Algorithms.” *In Proceedings of the 2023 IEEE 13th Annual Computing and Communication Workshop and Conference,* Las Vegas, NV, USA, 8–11 March 2023; pp. 1267–1271
[16] Z. Ullah, M. Jamjoom, “Early detection and diagnosis of chronic kidney disease based on selected predominant features.” *J. Healthc. Eng*. 2023:3553216, 2023.
[17] Arif, M.S.; Mukheimer, A.; Asif, D. (2023), Enhancing the early detection of chronic kidney disease: a robust machine learning model. *Big Data Cogn. Comput.*, *7*, 144.
[18] VK. Venkatesan, MT. Ramakrishna, I. Izonin, R. Tkachenko, M. Havryliuk, “Efficient data preprocessing with ensemble machine learning technique for the early detection of chronic kidney disease”. *Appl. Sci*., 13(5), 2885, 2023.
[19] L. Rubini, P. Soundarapandian, P. Eswaran, Chronic Kidney Disease. UCI Machine Learning Repository. 2015.
Available online: https://archive.ics.uci.edu/dataset/336/chronic+kidney+disease (accessed on 21.11. 2023).
[20] J. Han, J. Pei J, H. Tong, “Data mining: concepts and techniques.” Morgan kaufmann; 2022.
[21] NV. Chawla, KW. Bowyer, LO. Hall, WP. Kegelmeyer, SMOTE: synthetic minority over-sampling technique.” *Journal of artificial intelligence research*. 16: 321-57, 2002.
[22] D. Singh, B. Singh, “Investigating the impact of data normalization on classification performance.” *Applied Soft Computing*. 97: 105524, 2020.
[23] H. Sanz, C. Valim, E. Vegas, JM. Oller, & F. Reverter, F. “SVM-RFE: selection and visualization of the most relevant features through non-linear kernels.” *BMC bioinformatics*, *19*(1), 1-18, 2018.
[24] VR. Joseph, “Optimal ratio for data splitting.” *Stat. Anal. Data Mining ASA Data Sci. J.*, 15, 531–538, 2022.
[25] A. I. Naimi, LB. Balzer, “Stacked generalization: an introduction to super learning.” *European journal of epidemiology*, 33, 459-464, 2018.
[26] S. Tewari, U.D. Dwivedi, “A comparative study of heterogeneous ensemble methods for the identification of geological lithofacies.” *J Petrol Explor Prod Technol*, 10, 1849–1868, 2020.
[27] D. M., Belete, & M. D. Huchaiah, “Grid search in hyperparameter optimization of machine learning models for prediction of HIV/AIDS test results.” *International Journal of Computers and Applications*, *44*(9), 875-886, 2022.
[28] I. Reis, D. Baron, S. Shahaf, “Probabilistic random forest: A machine learning algorithm for noisy data sets*.” Astron. JW*, 157, 16, 2018.
[29] M. Fattah, N. A. Othman, N. Gower, “Predicting chronic kidney disease using hybrid machine learning based on Apache Spark”, *Comput Intell Neurosci.* 23; 2022:9898831, 2022.
[30] A. Rahman, T. Saba, H. Ali, N. ElHakim, N. Ayesha, “Hybrid machine learning model to predict chronic kidney diseases using handcrafted features for early health rehabilitation using handcrafted features for early health rehabilitation”, *Turkish Journal of Electrical Engineering and Computer Sciences:* Vol. 31: No. 6, Article 4, 2023.