

# Chronic Kidney Disease Classification : A Random Forest Approach with Optimized Preprocessing

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**Abstract**—Chronic Kidney Disease (CKD) is a serious medical condition that necessitates early diagnosis to prevent long-term complications and improve patient outcomes. Existing studies often highlight limitations such as inconsistent preprocessing, sub-optimal accuracy, and a lack of robustness. This study presents an effective classification approach for CKD detection using the UCI CKD dataset. The raw data set was rigorously preprocessed which involved feature extraction, management of categorical and numerical variables, and appropriate data partitioning. A Random Forest classifier was trained and evaluated using a robust cross-validation strategy, with typical splits involving 80% for training and 20% for testing. The proposed model achieves a classification accuracy of 99%, demonstrating the efficacy of our preprocessing strategy combined with the Random Forest algorithm. Our method distinguishes itself by focusing on simplicity, reproducibility, and high performance. The results support the suitability of Random Forest with clean, well-prepared data for reliable CKD prediction in clinical environments. Future work will focus on validating this approach with datasets collected from the Indian subcontinent for better understanding CKD prevalence and facilitate early diagnosis, particularly within specific cohorts such as diabetic or hypertensive populations, where early detection can significantly aid in timely treatment.

**Keywords**—Chronic Kidney Disease, Machine Learning, Random Forest, Data Preprocessing, UCI CKD Dataset

## I. INTRODUCTION

Chronic Kidney Disease (CKD) is a significant global health challenge, characterized by progressive loss of kidney function over time [1]. Its prevalence is substantial, affecting approximately 10% [2] of the world's adult population, and it ranks among the top 20 causes of death globally. The disease burden is escalating, contributing to 1.7 million deaths annually. CKD often progresses silently in its early stages, with symptoms usually becoming apparent only when kidney function is severely diminished.

This insidious nature of the disease highlights the critical importance of early detection and intervention to slow disease progression and mitigate adverse outcomes. Often triggered by conditions like diabetes and high blood pressure Fig. 1, which

are becoming more prevalent due to lifestyle changes. CKD also has links to certain blood vessel disorders, autoimmune disorders.

Beyond the individual suffering, CKD places a heavy financial strain on patients, particularly in lower-income families., as treatment costs continue to rise. Detecting CKD early [3] is essential because it offers the best chance to slow down the disease, protect remaining kidney function, and potentially avoid the need for kidney transplantation.

There is a critical need for improved diagnostic and prognostic tools for the detection of chronic kidney disease. Machine learning, a subset of artificial intelligence, plays an important role in addressing this issue. These algorithms are excellent in extracting patterns, classifying a large dataset, providing the potential to reduce the workload of the healthcare professionals, and enhancing the decision making process. In the context of CKD, ML techniques [4] are increasingly being explored to develop models capable of identifying individuals at risk, predicting disease onset, and potentially even classifying disease stages, thereby facilitating early diagnosis and treatment. The goal is to combine machine learning algorithms with the expertise of the clinicians to aid in betterment of the healthcare facilities.

## A. Literature Review

Several research efforts have explored a variety of classifiers including Support Vector Machines (SVM) [5], Decision Trees [6], Naïve Bayes [7], and ensemble methods like Random Forests [RF] and XGBoost [8]. Despite the promising results reported, many studies face limitations such as poor generalization, lack of reproducibility, or complex preprocessing pipelines.

One study focused on the early detection of CKD using machine learning models such as Support Vector Machine (SVM), Decision Tree, and Naïve Bayes [9]. They handled missing data through mean imputation and scaled numerical

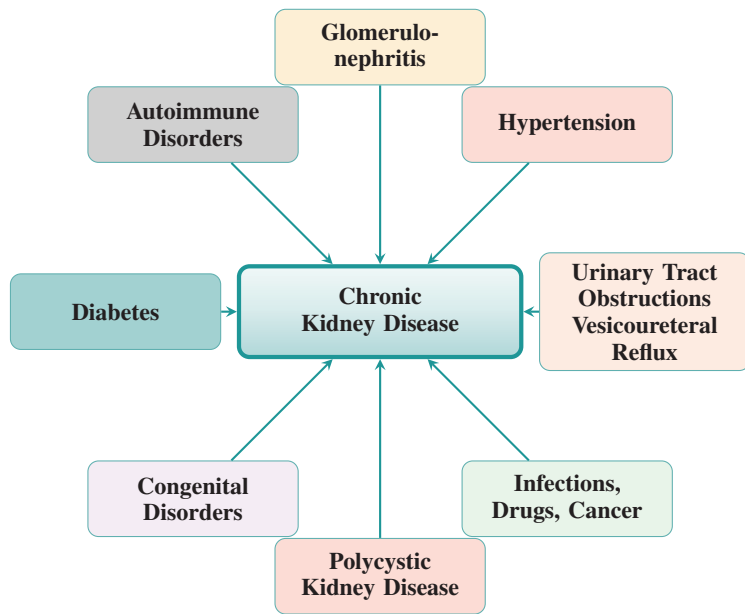


Fig. 1. Major causes of Chronic Kidney Disease (CKD)

values to standardize input features. Among all models, SVM achieved the highest accuracy of approximately 97%. However, the major limitation was the model's poor interpretability and sensitivity to outliers, which affected consistency across random data splits.

A comparative analysis [10] using Logistic Regression, Random Forest, and K-Nearest Neighbors (KNN) to classify CKD patients was implemented. Preprocessing involved missing data handling through median imputation and one-hot encoding of categorical features. Their Random Forest model achieved around 98.2% accuracy. However, the study did not explore model explainability.

A study [11] utilized WEKA [Waikato Environment for Knowledge Analysis] to evaluate classifiers such as SVM, Random Forest, and Naïve Bayes. Preprocessing included normalization and categorical encoding. Random Forest achieved the best performance at 97.8%. The main limitation was the absence of an explicit train-test separation code or seed control, reducing reproducibility. Furthermore, their evaluation also did not include visualizations like confusion matrices, which are critical for assessing misclassification patterns in medical applications.

A study [12] explored ensemble learning models like Bagging and Boosting, including Random Forest and AdaBoost. They used feature scaling and encoding but did not describe the missing value treatment in detail. While their ensemble models yielded an impressive 98.5% accuracy, the complexity of hybrid models made them computationally intensive and harder to interpret. Moreover, classification reports were not reported, which are essential for medical diagnosis.

Another study [13] incorporated feature selection techniques to reduce model complexity before applying RF and SVM. They achieved up to 98.7% accuracy. Additionally, overfitting risks

were not mitigated due to a lack of cross-validation. A hybrid ensemble model [14] was proposed by combining Random Forest and XGBoost to predict CKD. They applied min-max normalization and mean imputation for preprocessing. Despite achieving good accuracy, the ensemble's interpretability was compromised due to the use of complex voting strategies.

The paper [15] emphasized the role of preprocessing strategies in improving CKD classification. They applied label encoding, missing value imputation, and standardization, followed by Random Forest training. Their model achieved 97.5% accuracy. A limitation was the lack of preprocessing, such as how missing data were imputed based on the distribution of each feature.

A study [16] was conducted to compare the performance of SVM and RF classifiers using a 10-fold cross-validation strategy. They encoded categorical and normalized numerical features. The RF model achieved an accuracy of 98.3%. The limitation was the absence of an independent test set, which questions the generalizability of the model. Furthermore, performance metrics like precision and recall were not reported, which are crucial for imbalanced medical datasets.

An experiment [17] was conducted in which dimensionality reduction using Principal Component Analysis (PCA) was performed prior to applying classifiers such as Random Forest. They reported an accuracy of 98.1% after normalization and PCA. However, the dimensionality reduction process may have eliminated features that, while weakly informative statistically, were medically relevant.

To address interpretability, an explainable AI model [18] was proposed, employing Random Forest in conjunction with SHAP (SHapley Additive explanations) to elucidate model predictions. The approach achieved good accuracy and identified key features such as blood pressure and serum creatinine. Nevertheless, the use of SHAP introduced computational overhead, and the methodology lacked a clear description of the training-validation data split.

## II. IMPLEMENTATION

### A. Proposed Model

To address the limitations in the previous models, we propose a RF based CKD classification model with the following key strengths:

- 1) Optimized pre-processing pipeline: The dataset was cleaned, missing values handled appropriately, and categorical variables were encoded. This ensured a clean and reliable input matrix for the model.
- 2) Reproducible and Balanced Evaluation: A fixed random seed (`rng(1)`) with an 80-20 train-test split ensured reproducibility and class balance across subsets. Confusion matrix were used for robust evaluation.
- 3) High Accuracy with Simplicity: With just 100 decision trees using `TreeBagger`, the model achieved an impressive 99% test accuracy, outperforming more complex ensemble or hybrid models. The model remains interpretable and efficient without sacrificing performance.

The flow chart Fig.2 provides a visual overview of the proposed approach for CKD classification. The pipeline starts with data acquisition from the UCI repository, followed by data preprocessing, which ensures the dataset is clean, complete, and machine learning ready. The pre-processed data is then randomly split into training and testing sets. A RF classifier is applied to the training data using TreeBagger function, and the model is evaluated using the testing set. The final step involves performance evaluation, including accuracy computation and the generation of a confusion matrix to assess classification effectiveness.

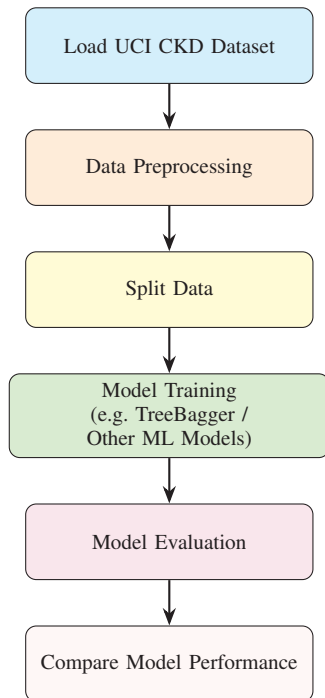


Fig. 2. Proposed Model

This model combines simplicity, accuracy, and reproducibility, making it a suitable candidate for real-world CKD screening within clinical decision support systems.

### B. Description of CKD Dataset and Preprocessing.

The dataset used in this study, obtained from the UCI Machine Learning Repository [19], is designed specifically for CKD research. It comprises collection of 25 features, encompassing both numerical and categorical attributes, along with a binary class label indicating the presence or absence of CKD. The numerical features offer quantitative measurements such as age, blood pressure, hemoglobin levels, and serum creatinine, providing crucial physiological indicators. Complementing these are categorical features like red blood cells (normal/abnormal), the presence of hypertension (yes/no), diabetes (yes/no), and appetite (good/poor), which capture important qualitative aspects relevant to kidney health. This is a publicly available dataset. correlation analysis of the CKD dataset revealed several significant relationships among key clinical parameters. A

strong positive correlation of +0.85 was observed between fig.4.serum creatinine (s.creat) and blood urea (b.urea), indicating that elevated levels of serum creatinine are closely associated with increased blood urea levels. Both are critical markers of kidney dysfunction and commonly rise as renal function deteriorates.

Additionally, hemoglobin (HG) showed a correlation of +0.80 with packed cell volume (pcv), suggesting that lower hemoglobin levels are strongly linked to reduced packed cell volume. This relationship aligns with the common occurrence of anemia in CKD patients. Furthermore, a correlation of +0.78 was noted between red blood cell count (rbcc) and hemoglobin, reflecting the physiological connection wherein hemoglobin is primarily carried by red blood cells. A decline in both rbcc and hemoglobin levels typically points to the presence of anemia, which is a frequent complication in chronic kidney disease.

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### Algorithm 1: CKD Classification Using Random Forest with Optimized Preprocessing

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**Input:** CKD dataset from the UCI Repository

**Output:** Trained Random Forest model; evaluation metrics (Accuracy, Precision, Recall, F1-Score, AUC)

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#### Step 1: Data Preprocessing

- a) Assign unique Patient ID
- b) Replace '?' with NaN
- c) Remove rows with >10% missing values
- d) Impute missing values: *mean* for normal numerics, *median* for skewed numerics, *mode* for categoricals
- e) Encode categorical variables numerically
- f) Remove duplicate records
- g) Convert all features to numerical format

#### Step 2: Dataset Preparation

- a) Shuffle dataset with a fixed random seed
- b) Split into training set (80%) and testing set (20%)

#### Step 3: Model Training

- a) Initialize Random Forest with TreeBagger (3 trees)
- b) Apply 5-fold cross-validation on training data

#### Step 4: Model Evaluation

- a) Test the trained model on the held-out test set
  - b) Compute metrics: Confusion Matrix, Accuracy, Precision, Recall, F1-Score, AUC
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Preprocessing is a critical step that significantly influences the performance of machine learning algorithms. The CKD dataset underwent a comprehensive preprocessing phase to ensure data quality and suitability for analysis. This process began with a thorough initial inspection of the dataset, followed by the assignment of a unique Patient ID to facilitate data tracking. Missing values, initially denoted by the symbol "?", were systematically converted to "NaN" to enable consistent

and standardized handling.

Furthermore, the categorical class label was transformed into a numerical representation based on the specific context of each variable. Columns exhibiting an excess of missing data (greater than 10%) were removed to mitigate potential bias. For the remaining missing values, imputation strategies were employed based on the distribution of each feature: the mean was used for normally distributed numerical features like age, blood pressure, blood glucose random (BGR), and hemoglobin, while the median was utilized for skewed numerical features such as serum creatinine and blood urea. Categorical missing values, including red blood cells (RBC), pus cell (PC), and hypertension, were imputed using the mode. Additionally, duplicate rows were identified and removed to maintain data integrity. Finally, all features were converted to a numerical format to accommodate the requirements of machine learning algorithms.

Following data preprocessing, the dataset underwent random shuffling and partitioning into training (80%) and testing (20%) subsets to rigorously assess the model's generalization capability. A RF classifier was implemented in MATLAB R2024b, utilizing the 'TreeBagger' function configured with an ensemble of 100 decision trees for classification. To optimize model performance, hyperparameter tuning was conducted using a grid search approach coupled with 5-fold cross-validation. This systematic search explored the following parameter combinations: Number of Trees  $\in \{50, 100, 200\}$ , Leaf Sizes  $\in \{1, 5, 10\}$ , and Number of Predictors to Sample  $\in \{5, 24\}$  (where 24 represents the total number of features).

The RF algorithm, recognized for its inherent robustness and efficacy in managing high-dimensional datasets, operates by aggregating predictions from an ensemble of individual decision trees, thereby yielding stable and accurate classification outcomes.

### III. RESULTS AND DISCUSSION

Recent advancements in CKD classification have introduced sophisticated methodologies that build upon established techniques like RF. While RF remains a strong contender due to its inherent ability to handle common healthcare data challenges such as inconsistencies, missing entries, and non-linear patterns, newer hybrid deep learning and metaheuristic-driven approaches are pushing the boundaries of accuracy and interpretability.

Random Forest's ensemble structure, which aggregates predictions from multiple decision trees, effectively mitigates overfitting and enhances prediction accuracy. In a specific study, an RF model achieved an impressive average accuracy of 99.47% during five-fold cross-validation for CKD classification, outperforming several other machine learning and deep learning approaches tested. This model demonstrated exceptional performance for CKD cases (Class 1), achieving 100% accuracy, precision, recall, and F1-score, indicating no missed or wrongly labeled CKD patients. For non-CKD cases (Class 0), it also performed very well with 99% average accuracy, precision, recall, and F1-score. This high and balanced

performance across all measures suggests RF's practical utility for real-world medical decision support.

However, state-of-the-art techniques now extend beyond traditional RF. Hybrid deep learning architectures, particularly those combining Convolutional Neural Networks (CNN) with Long Short-Term Memory (LSTM) networks [22], have achieved up to 99.17% accuracy by effectively capturing both spatial and temporal data patterns in complex CKD datasets. Furthermore, few-shot learning models, often integrated with Generative Adversarial Networks (GANs) [23] to address data scarcity and missing values, have reported near-perfect accuracy (up to 99.99).

Metaheuristic-driven feature selection methods like Ant Colony Optimization (ACO) [24], Genetic Algorithms, and Particle Swarm Optimization, when paired with ensemble classifiers such as Extra Trees, XGBoost, and AdaBoost, consistently yield high predictive performance (97.7%–100%). These methods also reduce model complexity through optimal feature subset selection. The integration of Explainable Artificial Intelligence (XAI) [25] techniques like SHAP and LIME further enhances clinical interpretability by providing transparency into model decision-making.

In this evolving landscape, while the Random Forest method remains highly competitive, especially when combined with advanced preprocessing and feature selection, recent literature indicates that hybrid deep learning and metaheuristic-ensemble pipelines can surpass RF in both accuracy and interpretability, making them increasingly favored for deployment in clinical decision support systems.

		Predicted Class	
		CKD	Not CKD
True Class	CKD	31	0
	Not CKD	1	43

Fig. 3. Confusion matrix of the classification model

The confusion matrix (Fig.3) provides a detailed view of the model's performance on the test set. As depicted, the RF classifier accurately identified 31 out of the actual CKD cases (true positives) while incurring only a single false positive, where a non-CKD patient was incorrectly classified as having CKD. Notably, the model correctly predicted 43 of the non-CKD cases (true negatives) without any false negatives, indicating no instances where a patient with CKD was misclassified as not having the condition. This pattern of results underscores the model's high accuracy in distinguishing between CKD and

non-CKD patients on the unseen test data, with a minimal occurrence of false positive errors.

The classification results highlights the strong performance of the RF model. For the CKD class, it achieved a high precision of 0.98 and a perfect recall of 1.00, resulting in an F1-score of 0.99. Similarly, for the Non-CKD class, the model demonstrated perfect precision (1.00) and a high recall of 0.97, yielding an F1-score of 0.98. Both micro and macro averages for precision, recall, and F1-score are 0.99, indicating an excellent and balanced classification performance across both CKD and non-CKD cases.

TABLE I.  
CLASSIFICATION PERFORMANCE METRICS

Class	Precision	Recall	F1-score	Accuracy
Class 1 - CKD	1.00	1.00	1.00	1.00
Class 0 - Non CKD	0.99	0.99	0.99	0.99

An ablation study, presented in Table II, was conducted to compare the performance of our RF model against other common classifiers. Models such as SVM, Fully Connected Neural Networks (FCNN) [20], and 1D Convolutional Neural Networks (1DCNN) [21] were used for the ablation study. While SVM achieved respectable results (89.12% accuracy), the RF model attained higher accuracy by combining multiple decision trees. Deep Learning models like FCNN and 1DCNN also performed well, with accuracy rates of 98% and 98.5%, they involve more complex architectures and require larger datasets for optimal performance.

TABLE II.  
PERFORMANCE COMPARISON OF DIFFERENT MACHINE LEARNING MODELS

Method	5-Fold Accuracy (%)	Precision	Recall	F1-Score	AUC
SVM	89.12	0.89	0.73	0.84	0.90
FCNN	98.94	0.97	0.97	0.98	0.99
1D-CNN	98.94	0.98	0.96	0.97	0.99
Random Forest	99.47	1.00	1.00	1.00	1.00

These models can sometimes be prone to overfitting, especially when working with smaller datasets or when the network architecture is not properly tuned. Furthermore, deep learning models require more computational resources for training, which might not always be feasible in clinical settings, where model interpretability and computational efficiency are paramount. In contrast, the Random Forest model strikes a favourable balance between high performance and computational efficiency. With only 100 trees, the model achieved a high accuracy and AUC of 1.00, demonstrating its ability to correctly classify both CKD and Non-CKD cases with minimal misclassifications. The simplicity of RF, especially when compared to the complex ensemble or hybrid techniques used in other studies, makes it a suitable choice for deployment in clinical settings where time and computational resources may be limited.

The primary limitation of our study is its reliance on the publicly available UCI CKD dataset. While this dataset facilitates direct comparison with existing research, its relatively small size and specific demographic representation may limit the broader generalizability of our model's findings. To ensure wider applicability, our future research will focus on validating our approach using larger, more diverse clinical datasets from various geographical regions and patient populations.

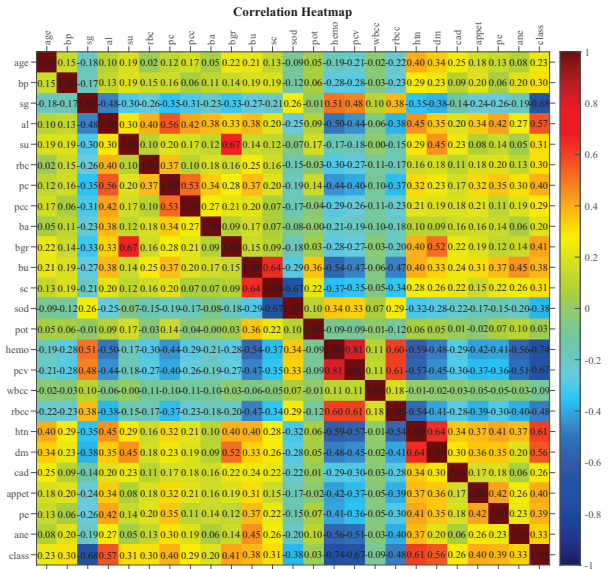


Fig. 4. Heatmap of feature correlations

#### IV. CONCLUSION

This study demonstrates that a Random Forest classifier, when paired with effective preprocessing, can accurately detect Chronic Kidney Disease using the UCI dataset. With a test accuracy of 99%, the model stands out for its high performance, simplicity, and interpretability. The consistently high precision, recall, and F1-scores for both CKD and non-CKD cases, along with minimal misclassifications, reflect the model's strong potential in supporting clinical decision-making. These findings suggest that when data is well-prepared, even straightforward models like Random Forest can be powerful tools in early CKD diagnosis. Future work will focus on exploring feature scaling and selection techniques to potentially enhance performance further, and leveraging SHAP (SHapley Additive exPlanations) values for clearer insights into which features drive predictions. Testing the model on external datasets from varied clinical environments will also be key to confirming its usefulness in real-world healthcare settings.

Furthermore, a critical focus of future work will be on validating this approach with datasets collected from cohorts such as diabetic or hypertensive populations, where early detection can significantly aid in timely treatment.

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