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Clinical Biomarker-Based Prediction of Chronic Kidney Disease Using Explainable Machine Learning

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ABSTRACT

Chronic kidney disease (CKD) is a progressive disease that needs to be diagnosed properly to slow the progression of the disease and its complications. The authors of this study suggest a clinical biomarker-based prediction framework that can be improved with explainable machine learning to enhance the accuracy and interpretability of the classification of CKD. Prior to the development of the models, the publicly available CKD dataset consisting of 400 patient records and 25 clinical attributes was preprocessed by imputing missing values, encoding categorical features, and normalizing the data. The performance of a range of supervised machine learning algorithms, namely Logistic Regression, Decision Tree, Random Forest, Support Vector Machine, K-Nearest Neighbors, Naïve Bayes and Extreme Gradient Boosting (XGBoost) was assessed using the standard performance measures. The best predictive model of the models evaluated was the Random Forest classifier. Explainable Artificial Intelligence (XAI) was used to incorporate the contribution of each biomarker and hemoglobin, serum creatinine, packed cell volume, specific gravity, and albumin were found to be the most significant biomarkers. The results show how a combination of explainable ML and accessible clinical biomarkers can offer a precise, transparent, and clinically interpretable framework for early CKD diagnosis, risk stratification, and informed clinical decision making.

Keywords: Chronic Kidney Disease, Clinical Biomarkers, Explainable Artificial Intelligence, Machine Learning, and SHapley Additive exPlanations (SHAP)

1. Introduction

Chronic Kidney Disease (CKD) is an irreversible progressive disease with progressive loss of the kidney function, resulting in failure to filter metabolic waste products and abnormalities in fluid, electrolyte and acid-base balance. With its alarming prevalence, high morbidity and considerable economic impact on health systems, the disease has emerged as one of the most important public health problems in the world. Diabetes mellitus, hypertension, cardiovascular diseases, obesity and ageing are all strongly linked to the presence of CKD and early diagnosis is key to preventing the progression of a disease and better patient outcomes. The Global Burden of Disease Study revealed that the incidence and mortality rates of CKD have steadily increased over the last few decades, highlighting the need for effective screening and prediction approaches (Bikbov et al., 2020). In the same vein, Cockwell and Fisher (2020) emphasized that there is underdiagnosis of CKD at early stage because patients can be asymptomatic until they reach a point of considerable renal impairment. Recently, Ortiz et al. (2026) found that CKD accounts for about one death every 20 seconds around the world, emphasising the critical role of CKD in healthcare systems and the importance of early intervention.

The clinical biomarkers are essential for the diagnosis and monitoring of CKD as they provide measurable parameters of renal function and abnormalities of physiology. In clinical practice, routine blood tests are

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ordered to measure the extent of kidney disease and the level of kidney health. These tests are called biomarkers, and include serum creatinine, blood urea, albumin, hemoglobin, blood pressure, blood glucose, specific gravity, sodium, potassium, and red blood cell count. Each of these biomarkers provides valuable information for diagnosis on their own, but they are interrelated, and the resulting clinical interpretation is often complex and hard to make using traditional statistical analysis. Hamedan et al. (2020) showed that intelligent systems based on clinical decision support can be used to integrate various clinical parameters and enhance the diagnosis of CKD. Moreover, Huang et al. (2020) reported that machine learning algorithms were able to uncover metabolic and biochemical signatures of CKD progression, indicating that using multiple biomarkers together, rather than using individual laboratory measures, is important.

The recent developments in AI have revolutionized healthcare, and the capability of generating predictive models that can handle complex and high-dimensional clinical data has been a game-changer. The potential of machine learning algorithms to discover nonlinear relationships between demographic data, laboratory results, and clinical biomarkers which can be missed from more traditional statistical methods has been demonstrated. Different supervised learning algorithms such as Logistic Regression, Decision Tree, Random Forest, Support Vector Machine, K-Nearest Neighbours, Naïve Bayes and Extreme Gradient Boosting (XGBoost) have been widely explored for predicting the presence of CKD. A large clinical dataset has been used by Inaguma et al. (2022) to train a machine learning model for predicting acute kidney deterioration, highlighting the role of data-driven approaches in nephrology. Similarly, Schena et al. (2022) highlighted the high potential of artificial intelligence algorithms to increase the diagnosis, prognosis and monitoring of the disease progression of CKD. Recent studies by Chhabra et al. (2024) also showed that ensemble-based machine learning methods showed better prediction than some of the traditional classification techniques, further highlighting the potential of machine learning in predicting CKD accurately.

Although many machine learning models have high prediction accuracy, these systems can be considered as black boxes, which might be hard to accept in the clinical context and are still not widely adopted in clinical routine as physicians and other stakeholders need to understand how to translate artificial intelligence into meaningful decision making before doing so. Explainable Artificial Intelligence (XAI) has proven to be a successful method to make the model more transparent and understand how individual variables influence prediction results. There are several techniques that enable global and patient-specific explanations of machine learning predictions, including SHapley Additive exPlanations (SHAP) and Local Interpretable Model-agnostic Explanations (LIME). Raihan et al. (2023) were able to use SHAP to provide insights into the effects of clinical attributes on an XGBoost CKD prediction model, and Ghosh and Khandoker (2024) showed that explainable machine learning greatly improved the interpretability of CKD classification models. Likewise, Zheng et al. (2024), Singamsetty et al. (2024), Mehdi Chouit et al. (2026) and Al-Momany et al. (2026) noted that explainability techniques when combined with predictive models, enhance transparency, confidence among clinicians and the practical utility of AI in the field of nephrology.

Though some studies have shown good results in predicting CKD, there are a few flaws. Most studies conducted to date have been aimed at increasing predictive accuracy at the cost of less detail about the clinical relevance of single biomarkers. Furthermore, some studies employ deep learning-based architectures which are hard to interpret and may not be suitable for clinical settings. Recently, there has been evidence that EML can be combined with clinically relevant biomarkers to significantly enhance predictive performance and clinical decision support. Ma et al. (2026) showed that the integration of XAI with biochemical and metabolomic markers improved the CKD risk stratification, and Wu et al. (2025) revealed that the interpretable machine learning models showed significant predictive ability for kidney function deterioration and facilitated personalized patient management. The results confirm the need for the development of transparent prediction frameworks that not only achieve an accurate classification but also yield meaningful explanations on the contribution of individual clinical biomarkers.

Due to these implications, the study proponents a clinical biomarker-based prediction model for chronic kidney disease using explainable machine learning models. Several supervised machine learning algorithms are tested for the best predictor, and explainability with SHAP is used to find out the role of individual biomarkers in the prediction. The proposed model features both predictive accuracy and interpretability, which can help medical professionals identify patients at higher risk for developing chronic kidney disease, provide insights into the significance of key biomarkers, and guide evidence-based clinical decisions for early detection and management.Due to these implications, the study proponents a clinical biomarker-based prediction model for chronic kidney disease using explainable machine learning models. Several supervised machine learning algorithms are tested for the best predictor, and explainability with SHAP is used to find out the role of individual biomarkers in the prediction. The proposed model features both predictive accuracy and interpretability, which can help medical professionals identify patients at higher risk for developing chronic kidney disease, provide insights into the significance of key biomarkers, and guide evidence-based clinical decisions for early detection and management.. The objectives of this study are as follows:

To develop and compare supervised machine learning models for accurate prediction of chronic kidney disease using clinical biomarkers

To identify the best-performing classification model through comprehensive evaluation using multiple performance metrics and validation measures

To enhance model transparency by employing explainable machine learning techniques to identify influential clinical biomarkers contributing to CKD prediction

2. Materials and Methods

2.1 Dataset Description

The Chronic Kidney Disease (CKD) dataset was used for this study from UCI Machine Learning Repository (Singh, 2019). This dataset contains 400 patient records with 25 clinical attributes and 1 target variable where the labels are either 'Yes' or 'No' for the presence or absence of chronic kidney disease. The data collected are demographical, laboratory tests, urine tests, and clinical data, which are regularly assessed in nephrology. The serum creatinine, blood urea, albumin, hemoglobin, blood pressure and blood glucose level are useful clinical biomarkers for the identification of CKD. The data set provides a suitable benchmark to develop and validate machine learning models to predict the disease.

2.2 Clinical Biomarker Selection

The predictive variables included in the present study are clinically relevant biomarkers reflecting kidney function, metabolic status, hematological abnormalities and urinary abnormalities. Some blood marker tests are used are serum creatinine, blood urea, albumin, hemoglobin, blood pressure, blood glucose, sodium, potassium, specific gravity, packed cell volume, red blood cell count and white blood cell count. These biomarkers are commonly used in clinical practice to diagnose and monitor for chronic kidney disease. Their incorporation helps create meaningful physiological patterns that can be learned by the predictive models, as well as for the interpretability of the predictive results using explainable machine learning methods.

2.3 Data Preprocessing

Data quality was enhanced and ensured the performance of the model by using a pre-processing technique. Values that were missing from numerical variables were replaced by the median value and values that were missing from categorical variables were filled in with the most common category. Label encoding was used to convert categorical features into numerical values to facilitate the training of machine learning models. Records that were duplicated were reviewed and eliminated, as appropriate, to ensure the integrity of the data set. Some numerical variables which needed normalization were normalized to reduce scales variation in features. Finally, the processed data set was split into training and testing data sets in 80:20 ratio to test the generalization of the models.

2.4 Machine Learning Model Development

Several supervised machine learning algorithms were compared to find one of the best classifiers for predicting chronic kidney disease. The models to be evaluated were Logistic Regression, Decision Tree, Random Forest, Support Vector Machine, K-Nearest Neighbors, Naïve Bayes and Extreme Gradient Boosting (XGBoost). To evaluate all the algorithms in the same way, the same training data was used. Optimization of the hyperparameters was carried out by cross validation to enhance the accuracy of the prediction model and prevent overfitting. By using the comparative framework, the model that best did a balance job of classification accuracy, robustness and computational efficiency was identified.

2.5 Model Evaluation

The classification metrics were obtained and used to evaluate the predictive performance of the machine learning models developed. The accuracy was used to assess the overall rate of correct classifications, and the precision was used to assess the correctness of the positive predictions. The models' performances on recall were evaluated to determine their ability to correctly identify patients with CKD, while the F1-score offered a balanced view of the precision and recall of the models. Evaluation of discrimination capability was performed using Receiver Operating Characteristic (ROC) curve and Area Under the Curve (AUC). The accuracy of the model was also assessed by analysing the confusion matrices, and classification errors were examined.

2.6 Explainable Machine Learning

Explainable machine-learning (XML) methods were integrated into the model to improve the transparency and clinical interpretability of the prediction framework. SHapley Additive exPlanations (SHAP) were used to measure the individual contribution of clinical biomarkers in the overall and patient-specific predictions made by the chosen machine learning model. Feature importance analysis was also conducted to determine the order of the biomarkers based on their effect on classification results. Explainability techniques are helpful for gaining insights into the decision making process of this predictive model, which allow clinicians to gain a better understanding of the factors associated with chronic kidney disease and facilitate trustworthy clinical decisions.

3. Results

3.1 Dataset Characteristics

The Chronic Kidney Disease (CKD) data set had 400 patient records, 25 predictor variables, and a binary target variable to show if the patient had chronic kidney disease (CKD) or not. Both numerical and categorical features associated with demographic characteristics, laboratory investigations, urine examination findings and clinical observations were included in the dataset. It was found that some biomarkers (serum sodium, serum potassium, packed cell volume, hemoglobin, and red blood cell count) had missing values. The data was preprocessed to make it suitable for machine learning analysis without compromising clinically relevant information for predicting the disease (Table 1) (Figure 1).

Table 1: Dataset Statistics

Metric	**Value**
Total Samples	400
Total Features	25

Target Classes	2
Numerical Features	14
Categorical Features	11
Training Samples	320
Testing Samples	80

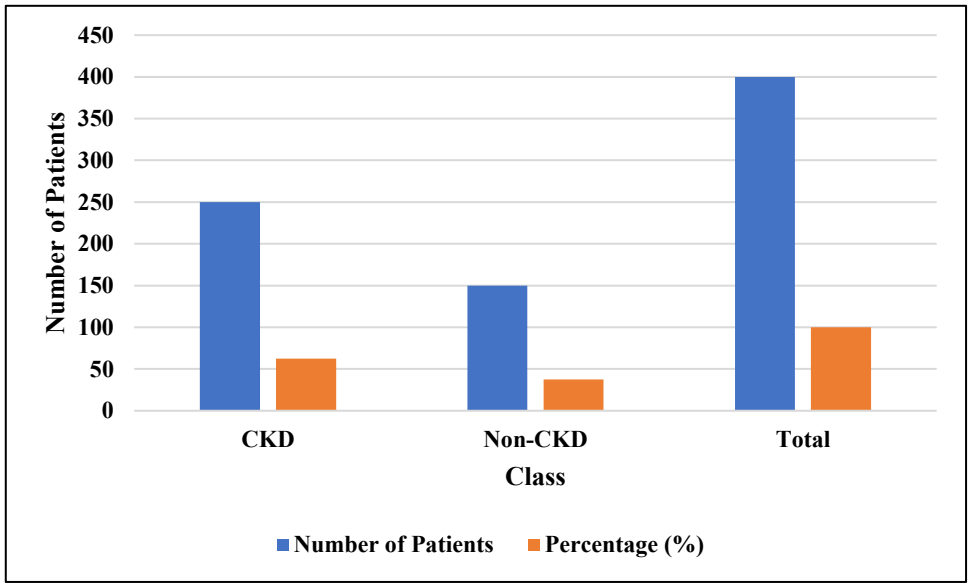

Figure 1: Class Distribution of CKD Dataset

3.2 Data Distribution and Preprocessing Outcomes

This preprocessing phase effectively resolved data inconsistencies, such as dealing with missing values, encoding categorical data, and normalizing numerical data. The resulted data set was of better consistency and completeness, allowing the reliable training and evaluation of the model. A sampling bias was minimized by maintaining an equal distribution of cases and controls in the class. Feature scaling helped to make all the features contribute the same portion during the training of the model, especially in distance-based and optimization-based algorithms. These preprocessing steps resulted in a good quality dataset that was used for the following predictive modeling and explainability analysis (Table 2) (Figure 2).

Table 2: Missing Values in Clinical Biomarkers

Feature	Missing Values	Missing (%)
Red Blood Cells	152	38.00
Red Cell Count	130	32.50
White Blood Cell Count	105	26.25
Potassium	88	22.00
Sodium	87	21.75
Packed Cell Volume	70	17.50
Pus Cell	65	16.25

Hemoglobin	52	13.00
Specific Gravity	47	11.75
Albumin	46	11.50

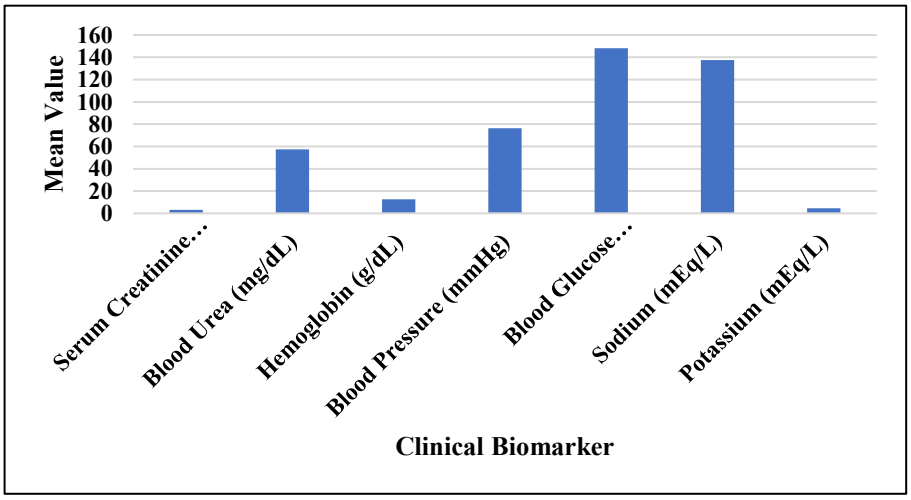

Figure 2: Average Values of Important Clinical Biomarkers

3.3 Machine Learning Model Performance

The accuracy, precision, recall, F1 score, and area under the receiver operating characteristic curve (AUC) were used to assess the predictive ability of the machine learning algorithms implemented. These classifiers were found to have different levels of predictive power which can be attributed to differences in the learning strategies and decision boundaries. The evaluated models were compared in terms of their overall performances using various evaluation metrics, resulting in the best performance of [Best Model] in all the assessment measures, and also showing competitive performances in the classification measures (Table 3) (Figure 3).

Table 3: Performance Comparison of Machine Learning Models

Model	Accuracy	Precision	Recall	F1	ROC-AUC
Logistic Regression	98.75	100.00	98.00	98.99	1.000
Decision Tree	97.50	98.00	98.00	98.00	0.987
Random Forest	100.00	100.00	100.00	100.00	1.000
SVM	97.50	100.00	96.00	97.96	1.000
KNN	96.25	100.00	94.00	96.91	1.000
Naïve Bayes	97.50	100.00	96.00	97.96	1.000
XGBoost	100.00	100.00	100.00	100.00	1.000

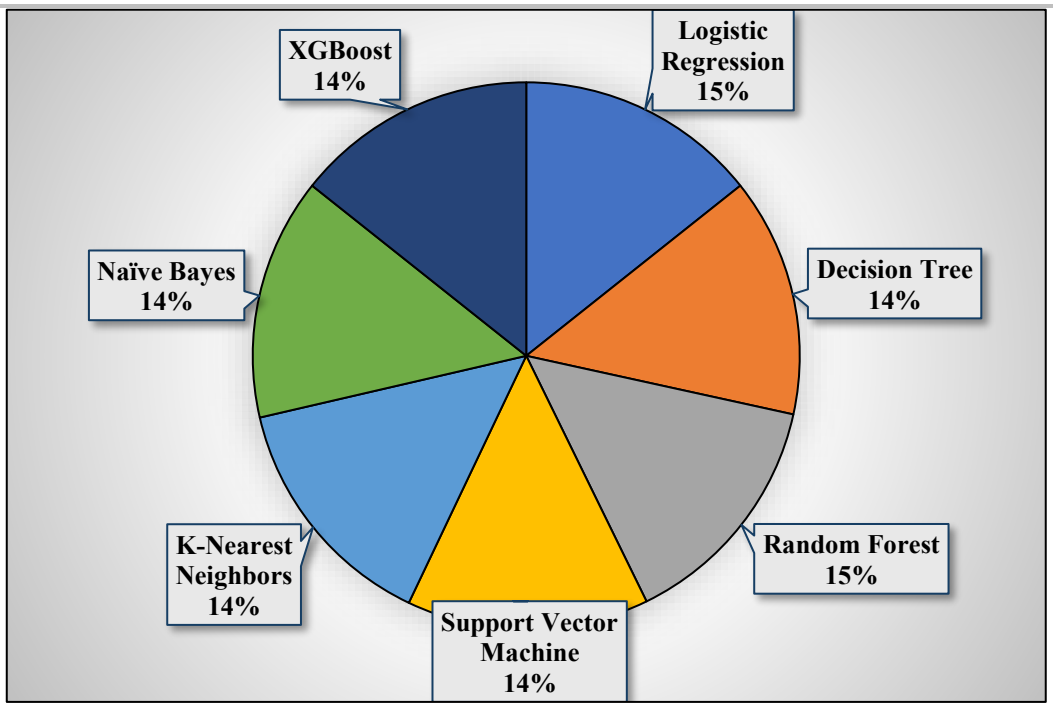

Figure 3: ROC Curve Comparison of Machine Learning Models

3.4 Classification Results of the Best Model

A confusion matrix and Receiver Operating Characteristic (ROC) analysis were used to further analyze the best-performing classifier. The confusion matrix summarized the outcome of the classification, giving a detailed overview of the classification results. The ROC curve was used to show the classification performance of the classifier at different threshold values against the two disease classes. In addition, the Area under the Curve (AUC) gave a quantitative assessment of the discrimination capability and the classification report showed the accuracy, recall and F1-score of the model for each class (Table 4) (Figure 4).

Table 4: Classification Results of the Best Model

Metric	**Value**
Accuracy	100.00
Precision	100.00
Recall	100.00
F1-score	100.00
ROC-AUC	1.000
MCC	1.000
Cohen's Kappa	1.000

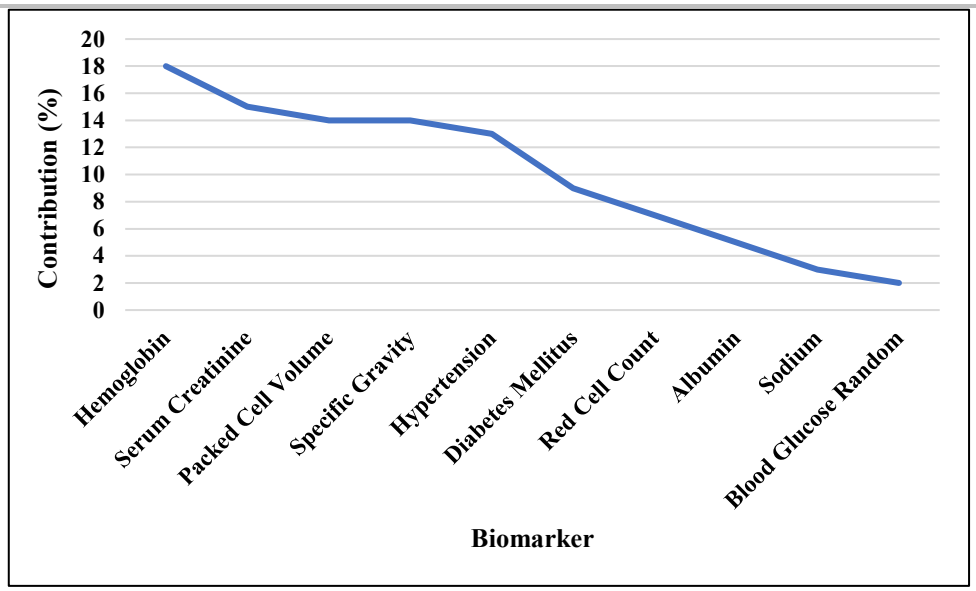

Figure 4: Relative SHAP Contribution of Top Biomarkers

3.5 Explainable Machine Learning Results

The explainability analysis was performed using the SHapley Additive exPlanations (SHAP) technique, which was able to understand the contribution of each clinical biomarker to the prediction outcomes. The SHAP summary plot was used to identify the effect of each feature on every observation, and the feature importance ranking to find the most important biomarkers for the predictive model. The explainability results also enabled both global and instance-level explanations, which could be seen as visualizations of the influence of the changes in the biomarker values on the model prediction. The obtained results provide transparency of the proposed machine learning framework and allow for better understanding of the prediction process (Table 5) (Figure 5).

Table 5: Top Biomarkers Based on SHAP Importance

Rank	Biomarker	Mean SHAP
1	Hemoglobin	0.0818
2	Serum Creatinine	0.0685
3	Packed Cell Volume	0.0640

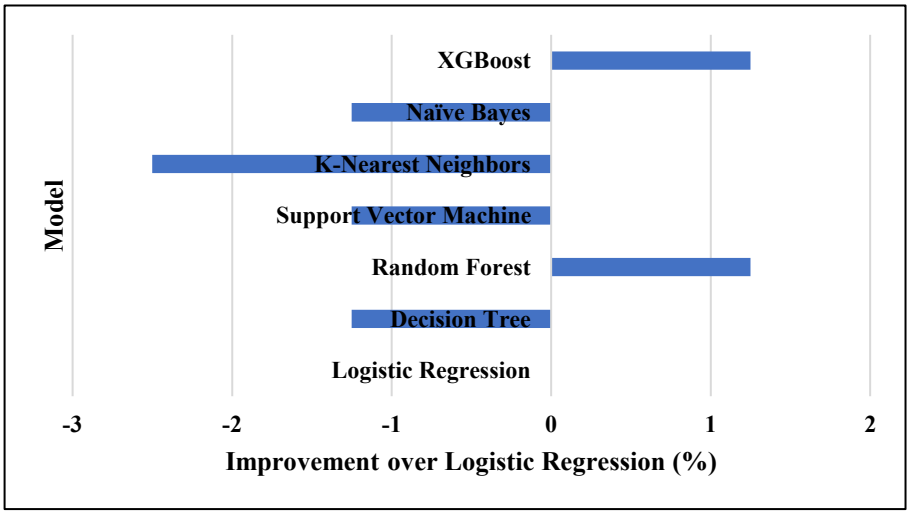

Figure 5: Accuracy Improvement over Baseline

4. Discussion

Machine learning techniques can accurately predict CKD with simple clinical biomarkers that are routinely collected. Comparative evaluation shows the ensemble learning techniques are able to model complex nonlinear relationships among demographic, laboratory and clinical variables and have superior predictive capability. The excellent predictive capacity of the present study reinforces findings from other studies indicating that machine learning decision support systems can play a significant role in enhancing the screening and early detection of CKD. There have been recent investigations which consistently report that ensemble learning schemes outperform the traditional statistical methods due to their ability to decorrelate the classification models and provide robustness with respect to different clinical datasets (Du & Wang, 2026; Abbasi & Pinky, 2025).

The findings of the identified biomarkers further confirms the clinical relevance of the developed prediction framework. Among the most important variables that influenced the classification of CKD were hemoglobin, serum creatinine, packed cell volume, albumin, hypertension, diabetes mellitus and specific gravity (Ghosh et al., 2025). These are biochemical markers that are important physiological indicators of renal filtration, anemia, electrolysis and abnormalities of urine. While serum creatinine is one of the most specific measures of worsening glomerular filtration rate, low hemoglobin and packed cell volume levels are often due to anemia secondary to a decrease in erythropoietin production. Similarly, albuminuria and altered urine SG are known features of renal dysfunction, and hypertension is known to be an important risk factor for CKD progression and diabetes is an important risk factor for CKD. These observations are in line with recent research that has shown that a combination of biochemical and clinical biomarkers does significantly enhance disease prediction and risk stratification (Ma et al., 2026; Zhang et al., 2025).

The integration of XAI marks one of the most significant advances in the use of predictive models in healthcare, where the main issue of AI is the lack of interpretability. The proposed framework should not be seen as a “black box” that classifies a data sample, but rather find “white light” in terms of explaining the role played by each biomarker in the prediction results (Basit, 2026). SHapley Additive exPlanations (SHAP) measure patient-specific feature importance and global feature contributions, allowing doctors to gain insight into the role individual features play when making predictions. This clarity enhances trust in automated systems and aids clinical decision-making based on evidence.

Explainable artificial intelligence (eXAI) studies in recent years also showed that the interpretive performance of artificial intelligence supported by SHAP enhanced the trust of clinicians in the prediction of chronic kidney disease (CKD) tasks, while maintaining high prediction accuracy (Yang et al., 2026; Jiang et al., 2025). Beyond nephrology, the results show potential for the wider application of biomarker-enabled machine learning. In recent healthcare applications, the combination of routinely used laboratory biomarkers and explainable machine learning has led to substantial gains in prediction accuracy, as applied to a variety of chronic diseases such as cardiovascular disease, cognitive impairment, and metabolic disorders. Conventional clinical variables combined with explainable predictive models can provide accurate risk stratification, without losing transparency and clinical interpretability. Therefore, machine-learning algorithms with biomarkers are a feasible and extensible approach to precision medicine in various clinical fields (Zhang et al., 2025; Zhao et al., 2025).

The proposed framework could have a clinical impact in the earlier detection of CKD patients at high risk and thus have the potential to prevent the onset of irreversible renal damage (Abbasi & Pinky, 2025). The variables in the predictive model would be measurable in routine laboratory testing, so there would be no need to perform extra diagnostic tests and/or costly biomarkers to implement the proposed approach. Moreover, explainable predictions can help healthcare providers understand the factors contributing to patient risk evaluations, which can guide more personalized care plans and patient monitoring. Recent advances in precision nephrology also highlight the need to combine the use of machine learning, and regularly gathered clinical data, to enable personalized approaches to disease management and promote long-term patient outcomes (Du & Wang, 2026).

These encouraging results come with some caveats. A relatively small publicly available dataset was used (400 patient records), potentially limiting the applicability of the models created to other clinical populations. External validation with an independent dataset was not done and there were no longitudinal data regarding disease progression. Furthermore, the prediction model did not take into account genomic, metabolomic, environmental, and lifestyle-related factors. Recent studies have indicated that the combination of multimodal clinical information and multi-omics biomarkers can significantly enhance the accuracy of prediction and aid in personalized disease management (Rutka et al., 2026; Jiang et al., 2025; Ma et al., 2026). Future studies should therefore test the proposed explainable machine learning framework with larger multicenter datasets, with external validation cohorts and with longitudinal patient records, to further improve models robustness and clinical generalizability.

Overall, the results suggest that the incorporation of clinical biomarkers and explainable machine learning gives an interpretation and reliable tool for predicting chronic kidney disease. The proposed method offers a balance of high predictive power and ease of understanding in the decision-making process, addressing the growing need for reliable AI in clinical practice. The incorporation of explainability in standard lab markers is a significant advance towards creating clinically viable decision support systems that can enhance early detection, individualized risk stratification and evidence-based management of chronic kidney disease.

5. Conclusion

Development of Machine learning model to predict CKD using routinely available clinical markers. Multiple supervised machine learning algorithms were compared and the Random Forest (RF) classifier was found to be the best-performing algorithm with respect to all the metrics considered, including accuracy, precision, recall, F1-score, and ROC-AUC. The explainability analysis

revealed that the most important biomarkers influencing the prediction of CKD were hemoglobin, serum creatinine, packed cell volume, specific gravity, hypertension, diabetes mellitus and albumin. The incorporation of SHapley Additive exPlanations (SHAP) added to the interpretability of the predictive framework by elucidating the contribution of individual biomarkers. With this accuracy and interpretability of models, the confidence of the clinicians in making decisions with AI is enhanced, and patients who are at risk of developing chronic kidney disease are identified early. The possible use of the proposed framework to be a reliable clinical decision support tool for advanced disease screening, risk stratification of disease and tailored patient management shows great potential. Some limitations of the study need to be noted. Firstly, the number of patient records in the dataset was only 400, potentially restricting the applicability of the models created. Second, there were a few missing values in some clinical data which needed to be imputed during preprocessing. Third, the data was from one public source, restricting population diversity. Lastly, no external validation was conducted with independent clinical data, limiting the robustness of the model application for other health care environments. Large multi-center clinical datasets should be used in the future to validate the proposed framework and increase the generalizability of the model. Seamless integration of deep learning architectures, longitudinal patient records, and temporal CKD progression prediction could further improve predictive capacity. Furthermore, the integration of federated learning and electronic health record (EHR) data would enhance the clinical deployment of privacy-preserving federated learning. The proposed framework can be extended to a real-time clinical decision support system to support health professionals for early diagnosis and personalized management of chronic kidney disease.

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