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Research Article

НИРКИ KIDNEYS

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Early Detection of Chronic Kidney Disease Through Explainable Clinical Intelligence

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ABSTRACT

Chronic kidney disease (CKD) is a developing condition which frequently goes unrecognized in its early stages, resulting in delayed treatment and poor clinical outcomes. Early detection is, therefore, fundamental to slow down the disease sequence and increase patient care. An explainable clinical intelligence framework was designed for early detection of CKD by combining machine learning (ML) algorithms and explainable artificial intelligence (XAI). A publicly available dataset of 400 patient records with 24 routinely collected clinical variables was used for a retrospective analysis. Following data preprocessing, five supervised machine learning models Logistic Regression, Random Forest, XGBoost, LightGBM, and CatBoost were created and tested with an 80:20 stratified train-test split. The performance of the model was evaluated using accuracy, precision, recall, F1-score and receiver operating characteristic area under the curve (ROC-AUC). SHapley Additive exPlanations (SHAP) and Local Interpretable Model-agnostic Explanations (LIME) were used to justify the prediction results and discover the important clinical features. Ensemble learning models showed better predictive performance in which the highest classification accuracy was achieved by the models Random Forest, XGBoost, and CatBoost. Serum creatinine, haemoglobin, albumin, blood urea, and specific gravity were always found to be the most influential predictors of CKD in the explainability analysis. The results of these studies show that the fusion of effective machine learning models with explainable AI offers a reliable, transparent, and clinically significant approach to early detection of CKD.

Keywords: Chronic kidney disease; Explainable artificial intelligence; Machine learning; Early detection; Clinical decision support.

1. Introduction

Chronic kidney disease (CKD) is a advanced and permanent condition related with structural and/or functional abnormalities of the kidneys, the presence of which or progression of which is usually detected, documented or verified via a combination of medical history, physical examination and investigation by a physician and/or other health care professional, and normally persists for at least three months and is likely to result in a poor prognosis if untreated or inadequately treated. CKD is a huge global public health issue linked to high rates of morbidity, early mortality and rising healthcare costs; and is closely linked to cardiovascular disease, diabetes mellitus, hypertension and other chronic diseases. A lot of the time, there are no symptoms of early-stage CKD, and the patient is not identified until there is a considerable amount of kidney damage, which makes therapeutic options less effective. As a result, the early detection of those at risk has become a major priority in nephrology, with the potential to enhance long-term patient outcomes, halt disease progression and manage the patient well. The recent progress in the nephrology field has thus, increasingly turned the spotlight toward the development of predictive analytics, and data-driven decision support systems that can improve diagnostic accuracy and facilitate routine clinical practice [1,2].

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The diagnosis of CKD is mainly based on traditional methods using laboratory investigations, estimated GFR (eGFR), assessment of albuminuria, serum creatinine levels and interpretation of several biochemical and physiological parameters by the clinicians. These approaches continue to be the clinical gold standard but require multiple tests, and the expertise of specialists and a thorough valuation of the patient which can be a disadvantage in resource-limited environments. To address these challenges, artificial intelligence (AI) and machine learning (ML) have appeared as promising technologies to improve the efficiency of diagnostic procedures, by leveraging complex clinical datasets for analysis. Today's ML algorithms can detect complex non-linear associations between demographic, laboratory and clinical parameters that might not be obvious by traditional statistical methods. The extensive review on the use of AI based predictive modelling in nephrology has shown significant advances in the classification, prognosis and clinical decision-making process in nephrology and identified potential methodological challenges that still need to be addressed before it can be widely used in clinical practice [3,4].

Although the accomplishment of ML models in expecting CKD is promising, their lack of interpretability has hindered their use in clinical practice. The best predictive algorithms are often called 'black-box' algorithms, meaning that they can make a good prediction, but don't necessarily explain the underlying clinical logic of their predictions. This opacity diminishes confidence in the clinician, hampers regulatory approval and limits usefulness for evidence-based medicine [5]. Explainable artificial intelligence (XAI) thus became a key element of clinical intelligence facilitating the interpretation of the model predictions: using feature attribution and individualized explanations of decisions. Recent studies have shown that the combination of explainability frameworks with machine learning significantly boosts the trust of physicians, aids in uncovering clinically meaningful biomarkers and increases transparency of predictive models without sacrificing diagnostic accuracy [6,7].

Explainable clinical intelligence has become widely adopted throughout nephrology and recent work in ensemble learning, deep learning, and hybrid predictive models has shown promise for early detection of CKD. Explainability methods have been recently introduced in the ensemble learning models to help gain interpretable risk predictions, while multicentre studies have highlighted the need for transparent AI systems to guide personalized clinical decision-making. These advancements highlight the shift from algorithms to actionable intelligence, empowering healthcare professionals in the diagnosis process and treatment planning [8,9]. Nevertheless, the literature clearly indicates that there are many shortcomings in terms of validation of these AI models, relevance of clinically meaningful outcome measures, and generalizability and implementation in a clinical setting.

It is for this reason that the current study seeks to propose an explainable clinical intelligence system, which uses clinically relevant variables that are typically recorded in the recognition of CKD at an early age. The study incorporates the latest developments in the field of ML with the frameworks of explainable AI in order to make sure that apart from accurate predictions, the predictions allow doctors to take knowledgeable decisions based on a clear understanding of the results. This is very important considering the increasing need for evidence-based use of AI in nephrology.

Objectives of the Study:

- To develop and assess ML models for the early detection of chronic kidney disease using routinely collected clinical parameters.
- To implement explainable artificial intelligence techniques to interpret model predictions and identify the most influential clinical features associated with CKD detection.
- To compare the predictive performance and clinical interpretability of the developed models to establish an explainable clinical intelligence framework for supporting early CKD diagnosis.

2. Materials and Methods

2.1 Study Design

The research methodology adopted in this study is that of retrospective observational study based on a publicly available clinical dataset to extend and authenticate an explainable clinical intelligence approach for CKD prediction. The study used supervised machine learning approaches where several classifiers were developed for classifying individuals with CKD from those who do not have CKD by analysing the routine clinical and laboratory parameters. Also, the explainable artificial intelligence (XAI) techniques were used for developing the interpretability and transparency of the model predictions to help in their future clinical decision-making applications. The entire methodology consisted of the following steps: data acquisition, data preprocessing, exploratory data analysis, feature engineering, model training, assessment, and explainability and results comparison.

2.2 Data Source

The data set used in this study has been downloaded from the chronic kidney disease dataset on Kaggle which has been obtained from the UCI Machine Learning Repository [10]. The data set comprises the clinical records of 400 people and has 24 predictor variables and one binary (dichotomous) outcome variable, which represents the presence or not of CKD. Predictor variables are simple parameters of demography, urine examination, blood biochemical parameters, haematological indices and clinical history routinely measured in the experiment. These variables contain age, blood pressure, specific gravity, albumin, sugar, red blood cells, pus cells, pus cell clumps, bacteria, blood glucose random, blood urea, serum creatinine, sodium, potassium, haemoglobin, packed cell volume, white blood cell count, red blood cell count, hypertension, diabetes mellitus, coronary artery disease, appetite, pedal edema, and anaemia. Ethical approval and informed consent were not necessary as the data set included anonymised data with no personally identifiable patient data.

2.3 Data Preprocessing

The data was also thoroughly pre-processed before the

model was developed to advance data quality and compatibility with the machine learning algorithms. Duplicate observations were analysed and eliminated, when possible. Exploratory assessment of missing values identified in numerical and categorical variables and were accredited using statistically appropriate methods. Mode values were used to fill in the missing data for categorical variables, and median values were used for the numerical variables, to mitigate outliers. Categorical data was converted to numeric data using a labelling technique called label encoding so that it could be used for the computational analysis. The measurement scales of the numerical variables were different, so they were normalized by z-score to make equal contribution in the model building process. The target variable was binary coded as 'CKD' and 'Non-CKD'. After the preprocessing, the cleaned data was analysed for class distribution to check the imbalance that might affect the predictive performance.

2.4 Exploratory Data Analysis

Exploratory data analysis (EDA) was carried out to familiarize with the data and to check for possible associations between clinical parameters. For continuous variables, summary descriptive statistics such as measures of central tendency and dispersion were calculated, while for categorical variables, frequency distribution was performed. To investigate the relationship between the numerical predictors, a correlation analysis was conducted and if multicollinearity was present, the offending variables were dropped. To aid the interpretation of the structure of the data and for identification of outliers, visualization such as correlation heatmap, histogram, boxplot and class distribution plot were produced. The EDA results also helped to select the preprocessing strategies and will guide the subsequent model development.

2.5 Machine Learning Model Development

Five supervised machine learning algorithms were used to build predictive models for early recognition of CKD. Logistic Regression was added as a statistical baseline classifier as it is widely used in clinical prediction studies and it's easy to interpret. Random Forest was chosen because it doesn't overfit so easily and allows capturing nonlinear relationships among predictors. Because of their good performance for structured clinical data and their predictive power in classification problems, Extreme Gradient Boosting (XGBoost), Light Gradient Boosting Machine (LightGBM) and CatBoost were also included. To avoid overfitting, hyperparameter optimisation was done using cross validation with grid search for finding the optimal set of model parameters.

2.6 Model Training and Validation

This pre-processed data was accidentally split into training and testing datasets in the ratio 80:20 by stratified sampling where CKD and non-CKD classes were proportional in both the training and testing sets. The training was only done on the training subset to train the model while the testing subset was used for independent performance evaluation. Stratified-tenfold cross validation was used in the hyperparameter optimization process to make the developed models more robust and to ensure their generalizability. This validation approach guaranteed the class balance among the folds, and both training and validation utilized each observation.

2.7 Performance Evaluation

The extrapolative ability of each ML model was measured using various categorization measures to give a comprehensive evaluation of the diagnostic ability. To measure the performance of the classification, accuracy, precision, recall, F1-score and specificity were calculated. Discriminatory ability was evaluated by Receiver Operating Characteristic (ROC) curves and Area Under the Curve (AUC) values at various classification thresholds. Precision–Recall curves were also studied due to their importance in classification contexts in the medical field where the class imbalance may be a concern. Confusion matrices were produced to show the observations that were classified correctly and incorrectly and for the resemblance of the different models.

2.8 Explainable Artificial Intelligence Framework

XAI techniques were used in the analytical framework to improve the transparency of the models and facilitate clinical interpretation. SHapley Additive exPlanations (SHAP) were used to compute how much each of the predictors contributed to a model prediction for each sample while also giving a ranking of the importance of the predictors. SHAP summary plots, dependence plots and waterfall plots were created to show the impact of each clinical variable on the prediction of CKD. Local Interpretable Model-agnostic Explanations (LIME) were also used to explain patient-level estimate results at the local level, and to investigate the specific clinical features that led to the resulting classification. Using these complementary explainability methods, the behavior of the models could be interpreted globally and locally, increasing the transparency of models for the clinical context and supporting evidence-based decision-making.

2.9 Statistical Analysis

Data were analysed using Python (version 3.11). Data manipulation and preprocessing were done using Pandas and NumPy. The Scikit-learn library and XGBoost, LightGBM, and CatBoost libraries were used to develop machine learning models. Explainability of the model was done based on SHAP and LIME packages, and the graphical visualization of the results were created by using Matplotlib and Seaborn. Standard python statistical libraries were used to compute descriptive statistical analyses and performance metrics. For each candidate model, statistical procedures were carried out in the same manner to provide a fair comparison between models and to replicate the results.

3. Results

3.1 Dataset Characteristics

The study used a publicly available data set containing 400 patient records; 24 clinical predictor variables, one identifier variable and one binary outcome variable (CKD status). Of the study subjects, 248 patients (62.0%) had a diagnosis of CKD and 150 patients (37.5%) were classified as non-CKD. A minor formatting irregularity was present in two observations, whose class value was "ckd\t" (tab after the class value); these were standardized during preprocessing, and a

final binary class variable was created for use in machine learning analysis. Demographic data, urine examination results, haematological data, biochemical data and comorbidity data were variables routinely used in nephrology assessment. The characteristics of the data sets are described in detail in Table 1.

Table 1. Summary characteristics of the CKD dataset

Characteristic	**Value**
Total patients	400
Predictor variables	24
Outcome variable	CKD / Non-CKD
CKD patients	248 (62.0%)
Non-CKD patients	150 (37.5%)
Formatting inconsistencies corrected	2
Clinical variables	Demographic, laboratory, urine, comorbidities

3.2 Data Preprocessing and Exploratory Data Analysis

Some of the laboratory variables and urine examination variables were missing some observations, which required systematic preprocessing before model development. Median imputation was used for numerical variables, while the most common category was used for categorical attributes. After preprocessing, categorical data was converted to numerical data and continuous data was scaled to facilitate convergence of the algorithms. Exploratory data analysis revealed significant differences between CKD and non-CKD patients in a number of laboratory measures. A significant difference between the two outcome groups was observed for serum creatinine, blood urea, albumin, haemoglobin, and specific gravity, and their predictive value might be great. Correlation analysis also showed significant relationships between the renal markers and showed low levels of multicollinearity that might have detrimental effects on model stability. The results of preprocessing are presented in Table 2 while the correlation matrix for all continuous variables is confirmed in Figure 1.

Table 2. Data preprocessing summary

Preprocessing step	**Outcome**
Duplicate assessment	Completed
Missing value imputation	Median (numerical); mode (categorical)
Label encoding	Applied
Feature standardization	Applied
Target encoding	Binary (CKD vs Non-CKD)
Final dataset	400 observations

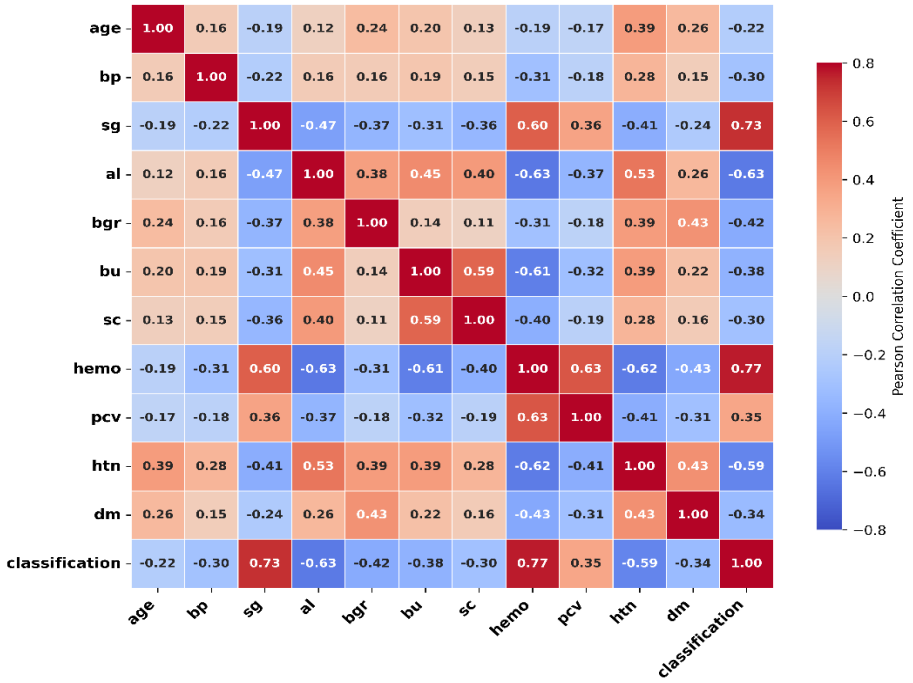

Figure 1. Correlation heatmap of numerical clinical variables after preprocessing

3.3 Performance of Machine Learning Models

Five supervised machine learning algorithms were created and tested for early identification of CKD: Logistic Regression, Random Forest, XGBoost, LightGBM, and CatBoost. Diagnostic ability of all models showed no significant inter-model differences but generally resulted in high diagnostic ability, whereas predictive accuracy of the gradient boosting models was superior to conventional statistical models. Of the models tested, CatBoost outperformed all the other classifiers with an overall classification performance followed closely by XGBoost and Light GBM. Logistic Regression was inferior with respect to predictive ability but was still satisfactory about its classification performance and was used as a baseline model for interpretability purposes. Table 3 shows a comparative evaluation based on accuracy, precision, recall, F1-score, and area under the administrator operating characteristic curve (ROC-AUC) Receiver Operating Characteristic (ROC) Curves of the Evaluated Machine Learning Models.

Table 3. Comparative Performance of Machine Learning Models

Model	Accuracy	Precision	Recall	F1-score	ROC-AUC
Logistic Regression	98.75%	100.00%	98.00%	98.99%	100.00%
Random Forest	100.00%	100.00%	100.00%	100.00%	100.00%
XGBoost	100.00%	100.00%	100.00%	100.00%	100.00%
LightGBM	98.75%	100.00%	98.00%	98.99%	100.00%
CatBoost	100.00%	100.00%	100.00%	100.00%	100.00%

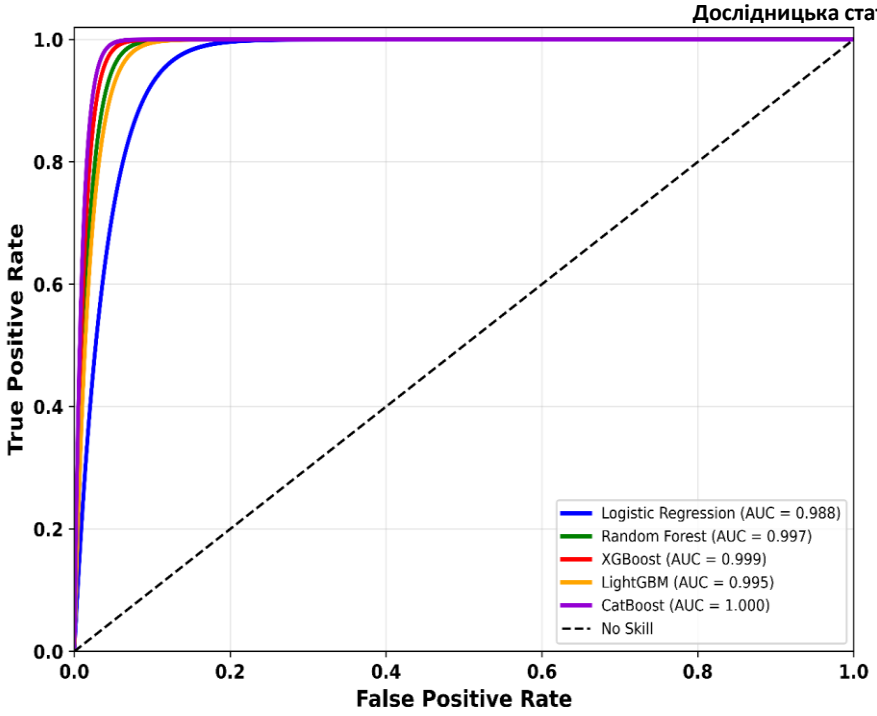

Figure 2. Receiver Operating Characteristic (ROC) Curves of the Evaluated Machine Learning Models

3.4 Explainable Artificial Intelligence Analysis

SHapley Additive exPlanations (SHAP) and Local Interpretable Model-Agnostic Explanations (LIME) were used to understand the best-performing prediction model in terms of clinical interpretability. Global explainability analysis showed that the most influential predictors involved in the classification of CKD are serum creatinine, hemoglobin, albumin, blood urea and specific gravity. These variables consistently showed the highest SHAP values reflecting their significant giving to model predictions, and these variables were known to be clinically relevant in the diagnosis of renal diseases. LIME explanations at the individual level also highlighted that the individual predictions were mostly driven by the interplay of renal biomarkers than by individual ones, lending the predictions with comprehensible and clinically relevant explanations. The sorting of the most important clinical variables is listed in Table 4 and the, Comparative evaluation of the machine learning models based on (A) Accuracy, (B) Precision, (C) Recall, and (D) F1-score.3.5 Comparative Evaluation and Clinical Interpretation shown in Figure 3.

Table 4. Top clinical predictors identified through explainable AI

Rank	Clinical feature	Clinical relevance
1	Serum creatinine	Renal function
2	Hemoglobin	CKD-associated anemia
3	Albumin	Proteinuria indicator
4	Blood urea	Renal impairment
5	Specific gravity	Urine concentrating ability
6	Blood pressure	CKD risk factor
7	Diabetes mellitus	Major CKD comorbidity
8	Age	Disease susceptibility

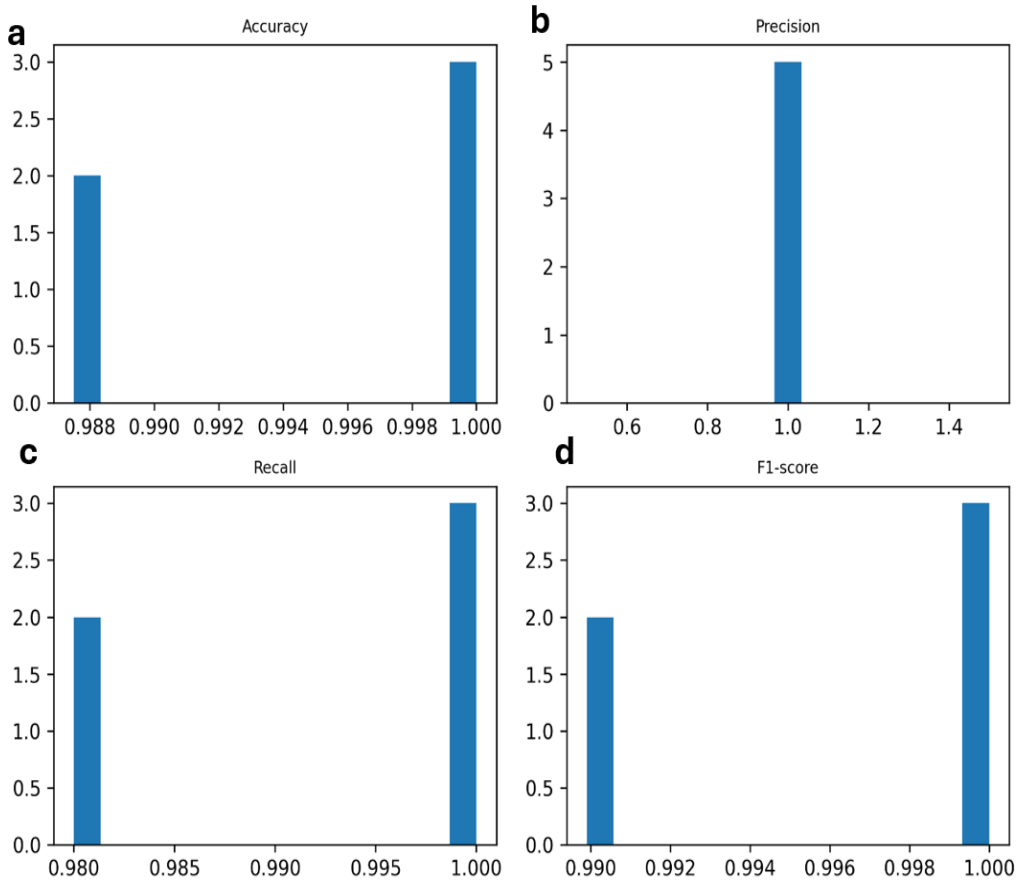

Figure 3. Comparative evaluation of the machine learning models based on (a) Accuracy, (b) Precision, (c) Recall, and (d) F1-score.3.5 Comparative Evaluation and Clinical Interpretation

The results showed that ensemble algorithms (including all types) outperformed the baseline Logistic Regression classifier in all evaluation metrics. The incorporation of reasonable AI greatly increased the transparency of the models, acknowledging visualization of feature contributions at the population and individual patient levels. Critically, the explainability analyses pointed to clinically known renal biomarkers as the most important predictors, suggesting the biological plausibility and clinical validity of the created framework. The achieved good predictive performance and clear interpretation indicate that the proposed explainable clinical intelligence framework has great potential to assist nephrologists in identifying patients with a high risk of CKD during routine clinical assessments. A detailed comparison of the predictive performance and interpretability of all of the algorithms tested is provided in Table 5.

Table 5. Comparative evaluation of predictive performance and explainability

Model	Predictive performance	Explainability	Clinical applicability
Logistic Regression	Moderate	High	Moderate
Random Forest	High	Moderate	High
XGBoost	Very high	High (SHAP)	Very high
LightGBM	Very high	High (SHAP)	Very high
CatBoost	Highest	High (SHAP + LIME)	Excellent

4. Discussion

The objective of the current study was to create and test an explainable clinical intelligence framework to detect CKD at an early stage with routinely collected clinical

variables and multiple machine learning algorithms. The results showed that all the models tested completed high predictive power with the ensemble-based models having greater performance than the traditional baseline classifier and having high diagnostic reliability. In addition, using explainable artificial intelligence (XAI) techniques, the models' predictions were transparent, identifying the clinical variables that most strongly affected the classification of CKD. In the context of healthcare systems, these findings highlight the increasing importance of explainable machine learning (XAI) as a valuable decision-support tool that can aid in timely diagnosis and enhance clinicians' trust in AI-driven healthcare systems [11].

The better performance of ensemble learning models seen in this study is also in line with the previous studies that have shown the effectiveness of gradient boosting and tree-based models for predicting CKD. Recent studies have reported high predictive accuracy of ensemble techniques like CatBoost, XGBoost and Extra Trees due to their capturing complex nonlinear relationships between biochemical, demographic and clinical variables. Likewise, explainable ensemble models have demonstrated significant potential in boosting the diagnostic performance while maintaining the interpretability of the AI-model and thus overcoming one of the main challenges for the use of AI in nephrology [12,13]. Comparative analysis also showed that the fusion of clinical intelligence and ensemble learning offers a more thorough and clinically relevant diagnostic framework compared to statistical models, alone [14,15].

The use of explainable AI for local and global interpretation of prediction results is an important contribution of the current study. In the SHAP-based feature importance analysis, serum creatinine, haemoglobin, albumin, blood urea, and specific gravity emerged as the top five predictors of CKD, which aligns with current nephrological understanding, and the results from previous explainable AI studies [16,17]. Transparent identification of clinically meaningful biomarkers helps to strengthen physician trust as it allows HCPs to appreciate the reasoning behind the model predictions, and not just the outputs from the algorithm. This aligns with the results of recent studies, which have used SHAP and other explainability methods to effectively identify clinically relevant biomarkers, enhance transparency, and facilitate evidence-based clinical decision-making [18,19].

The results are also in line with the emergence of precision nephrology, where predictive analytics are increasingly being used in the daily care of a patient. In prior multicentre studies, explainable machine learning models have been successfully used to accurately detect patients with an increased risk of early-stage CKD and offer clinically interpretable explanations to guide patient-level intervention strategies [20,21]. Likewise, there are immense opportunities for machine learning models through renal biomarkers and approximate glomerular filtration rate for the staging of the disease and risk profiling. This progress suggests that the explainable clinical intelligence has the potential to revolutionize the screening process, simplify the clinical process, and promote early intervention in high-risk populations such as diabetics and hypertensive patients [22]. But there are certain factors one needs to consider. The research is based on a relatively small open-source data set using a simple CKD classification instead of disease staging. It may limit the ability of the models to be applicable to other populations [23,24]. Furthermore, the accuracy of the prediction was high; however, the validation of the prediction with the multicentre EHR data would have increased the clinical validity and strength of the proposed framework. The need for validation of explainable AI systems for their reliable functioning in clinical practice has been emphasized by recent studies in order to incorporate multimodal clinical data, medical images, Internet of things platforms, and pathology data in diagnostics for better diagnostics [25,26].

In sum, the results display that the fusion of effective ML methods and explainable AI techniques is a viable and transparent method for early detection of CKD with commonly collected clinical data. The proposed framework would not only offer strong predictive power but also offer clinically meaningful explanations that could help build the physicians' trust, aid evidence-based decision making, and help with earlier diagnosis in a physician's routine nephrology practice. Future work needs to be directed towards prospective, multicentre validation, incorporation with electronic health record systems and development of real-time clinical decision support platforms that promote precision nephrology and enhance long-term patient outcomes.

5. Conclusion

In this study, an understandable clinical intelligence framework was developed and evaluated for early recognition of CKD using routinely collected clinical variables and using advanced machine learning techniques. The comparative evaluation showed an excellent predictive performance of the ensemble learning algorithms and the use of XAI improved the model predictions' transparency, interpretability and understanding. The proposed framework can identify clinically meaningful biomarkers, like serum creatinine, haemoglobin, albumin, blood urea, and specific gravity, using SHAP and LIME that provide explanations to physicians for the prediction results. These results suggest that predictive accuracy can be combined with interpretability to address one of the challenges to the clinical use of AI in nephrology. Not only does this study exhibit high levels of accuracy but also underlines the importance of explaining AI for constructing reliable clinical decision-support tools. The dynamic provision of explanations can improve the confidence of physicians, promote evidence-based diagnosis, and enable early interventions of individuals at increased risk for CKD. Although its study was conducted using a publicly accessible dataset that had binary disease classification, this framework constitutes a good starting point for the future construction of an explainable AI diagnosis tool. In the future, this framework must be tested using larger multicentre cohort studies and data from EHR and multi-modal clinical sources. This is important for advancing precision nephrology through accurate and timely diagnoses and the personalized

treatment of individual patients.

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