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Enhancing Chronic Kidney Disease Prediction with Hybrid Machine Learning Approaches

Pillutla. Sree Mahi[1], Venkata Naresh Mandhala[2]
[1,2]Dept. of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation, Vaddeswaram, Guntur 522302, Andhra Pradesh, India.
p.sreemahi@gmail.com, Corresponding Author Email: mvnaresh@kluniversity.in

ABSTRACT
Chronic Kidney Disease (CKD) is a growing global health concern that demands timely and accurate diagnosis to prevent severe health deterioration and reduce patient mortality. Traditional diagnostic methods often rely on manual assessments and may be constrained by the availability of expert medical personnel. To address this challenge, we propose a hybrid machine learning framework that combines the dimensionality reduction capability of an autoencoder with the robust classification power of a Random Forest ensemble model. The raw clinical dataset, sourced from the UCI Machine Learning Repository, undergoes thorough preprocessing, including missing value handling, feature normalization, and categorical encoding. The processed data is then passed through an autoencoder, where the encoder compresses the high-dimensional input into a latent space that captures the most informative patterns. These compressed features are subsequently used to train the Random Forest classifier for binary classification predicting whether a patient is affected by CKD or not. The proposed model achieved an accuracy of 99.8%, significantly outperforming traditional approaches and showcasing high potential for early-stage CKD diagnosis. This hybrid approach enhances prediction accuracy, reduces overfitting, and offers a reliable solution for integration into real-world clinical decision support systems, particularly in scenarios with limited access to specialized healthcare providers.

INTRODUCTION

The kidneys play a crucial role in keeping the body healthy by removing waste and extra fluids from the blood. They also help control blood pressure and maintain the right balance of essential minerals like potassium and calcium. Since your research involves analyzing heart diseases and arrhythmias, it's important to note that kidney function is closely linked to heart health, as kidney problems can increase the risk of cardiovascular diseases [1]. Chronic Kidney Disease (CKD) remained a serious global health issue in 2023, affecting millions of people. Nearly 10% of the world's population suffers from this condition, making it one of the most widespread medical concerns [2]. It is a slow-growing illness that gradually makes a person's health worse and can seriously damage kidney function over time. It often develops due to multiple reasons, such as diabetes, high blood pressure, certain drugs, and excessive alcohol intake [3].

Machine Learning (ML) is a technology that enables computers to learn and improve from experience without being explicitly programmed. The term was first introduced in 1959 by an IBM researcher who pioneered this field. Over the past decade, ML has advanced rapidly and is now widely applied in various fields, including healthcare. Artificial Intelligence (AI), Data Mining, and ML were among the first technologies used in healthcare, helping to develop systems that analyze data, recognize patterns, and make informed decisions. Their applications have expanded further with advancements in genetic research and the growing use of wearable health devices. More recently, Deep Learning (DL), a specialized branch of ML, has gained significant attention for its ability to process large datasets and enhance accuracy in medical applications[4].

Clinical informatics integrates health sciences, computer science, and information science to manage and share data for clinical purposes. Information and Communication Technology (ICT), which refers to digital tools and systems used to collect, store, and share information, plays a key role in this process. In healthcare, ICT tools enable professionals to quickly gather, exchange, and apply data and knowledge, improving healthcare delivery and supporting decision-making for both patients and doctors while promoting evidence-based medicine. However, traditional methods of managing and analyzing the vast amounts of diverse data generated by healthcare providers can be difficult. Machine Learning (ML) and Deep Learning (DL) techniques help address this challenge by effectively analyzing data and uncovering valuable insights. Furthermore, data from various sources such as genomic information, health records, social media, and climate data can be leveraged to enhance healthcare. ML and DL approaches are

particularly useful in improving key areas of healthcare, including prognosis, diagnosis, medication, and clinical workflow [5].

Many databases store personal information, including health-related data, which makes them difficult to access. Sharing such identifiable documents is tricky because organizations must follow strict rules. Researchers and analysts face ongoing challenges when trying to obtain important datasets. Accessing data often requires a data usage agreement, approval of a detailed research plan, completion of a data request form, an ethical review, and sometimes high costs for datasets that are not publicly available [6].

Prediction has always been a part of healthcare, as doctors are skilled at evaluating risk factors and making data-driven forecasts. However, machine learning methods can offer more accurate predictions compared to traditional regression models [7]. A prediction model helps assess a patient's risk of a disease outcome. As these models become more common, questions arise about when, what, and how to use them. Depending on the organization's requirements, these models can be trained over time to adapt to new information or viewpoints [8].

When patients are unable to accurately describe their medical issues based on lab results, it can lead to errors. Healthcare providers may also face difficulties in diagnosing illnesses due to a lack of expertise in certain areas. To address this challenge, it's important to develop a disease prediction system that combines medical knowledge with a holistic approach to achieve the best outcomes and benefit society [9].

The World Health Organization (WHO) states that non-communicable diseases (NCDs) are the leading cause of death globally, responsible for 71% of all annual deaths. While self-awareness of illness is vital for controlling diseases, it is difficult to achieve, especially since NCDs are often chronic, hidden, and irreversible. Among the deadliest NCDs are cardiovascular diseases (CVD), cancers, respiratory diseases, liver diseases, and chronic kidney disease (CKD). Diabetes also leads to other health issues, including high and low blood pressure, nerve damage, and bone problems, which are common in both CVD and CKD. Research shows that diabetes, high blood pressure, and CVD are significant risk factors for CKD.

Artificial Intelligence (AI) has emerged as a promising approach for developing computer-aided diagnostics (CAD) in healthcare. AI can help uncover hidden links between the development of CKD and its symptoms, enabling early detection of patients who are at risk [10-14]. In this study, we used a publicly available dataset, the chronic kidney disease dataset from the UCI Machine Learning Repository. It includes 400 records with 24 features such as age, blood pressure, and blood glucose levels. Collected over two months, this dataset helps in predicting chronic kidney disease [15].

LITERATURE REVIEW

This section explores the recent applications of AI and ML techniques in detecting and diagnosing chronic diseases. Predicting which features are most significant can be challenging, as data is typically collected by documenting occurrences in detail before identifying the most relevant factors. These approaches are particularly useful in the context of chronic disease detection and diagnosis.

Aljaaf et al [16]. conducted a study using various machine learning algorithms, including RPART, SVM, LOGR, and MLP, to predict chronic kidney disease (CKD) outcomes. While the study demonstrated strong results, including high accuracy for certain models, it faced limitations such as a small dataset size, which could lead to potential overfitting. This reduced the generalizability of the findings, as smaller datasets may not capture the full variability seen in a larger, more diverse population.

Xiao et al [17]. explored CKD prediction by utilizing machine learning models such as Elastic Net, Lasso, Ridge, and LR. Their research focused on blood and demographic parameters to build predictive tools. However, one limitation of their study was the restricted feature set, which was limited to clinical and demographic factors, excluding other potential important parameters. The lack of feature diversity may have affected the model's ability to generalize across different populations or scenarios.

Ekanayake and Herath[18] evaluated several machines learning models, including Decision Trees (DT), Random Forest (RF), XGBoost, extra trees, AdaBoost, and Neural Networks (NN), for CKD prediction. While they achieved impressive results, especially in terms of accuracy, the study's limitation was the limited generalizability of the models. Some algorithms showed tendencies to overfit on specific datasets, which may affect their performance when applied to different real-world data sets or in broader healthcare settings.

Bhattacharya et al [19]. leveraged a GAN-based CNN approach to predict CKD and improve disease classification in medical imaging. Their innovative approach tackled data imbalance issues and attempted

to reduce overfitting by using generative adversarial networks (GANs) to augment training data. However, one key limitation of their work was the imbalance in the data used for training, which, despite the GAN method, could still lead to overfitting and may limit the model's performance when deployed in real-world clinical environments.

Ifraz et al [20]. focused on traditional machine learning models such as Logistic Regression (LR), Decision Trees (DT), and K-Nearest Neighbors (KNN) for CKD prediction. While these models performed well, the study's limitations stemmed from its reliance on more basic, traditional algorithms, which may not fully leverage the capabilities of more advanced machine learning techniques. This reliance on traditional methods could have restricted improvements in predictive accuracy that could be achieved with more complex models.

Ahmed et al [21]. investigated the use of several machine learning algorithms, including KNN, SVM, DT, RF, NB, and LR, to predict CKD based on a comprehensive dataset with clinical records and demographic features. Although the study achieved promising results, one major limitation was related to data collection errors and issues with the dataset's quality, which could have influenced the performance of the algorithms. Additionally, these data quality issues could reduce the reliability of the model predictions in real-world applications.

Manju et al [22]. utilized a Decision Tree-based Explainable AI model to predict CKD risk, using clinical data from the UCI Machine Learning Repository. The study's key advantage was its focus on explainability, but it had limitations, particularly due to the reliance on a limited feature set. The decision tree model, although effective, may not capture the complexities of CKD progression as well as more advanced or hybrid models that consider a broader range of features.

Dritsas and Trigka[23] explored various machine learning algorithms, including Bayesian Networks, Naive Bayes, SVM, LR, ANN, KNN, and more, to predict CKD risk. Their study highlighted the importance of class balancing techniques like SMOTE and used a wide variety of models to evaluate performance. However, the study faced limitations due to the high complexity of the models used, which could result in overfitting on smaller datasets and increase the difficulty of model interpretation and deployment in clinical practice. These shown in Table 1.

Table 1. Existing Papers for CKD Detection

	Machine Learning Algorithms	**Limitations**
Aljaaf et al. [16]	RPART, SVM, LOGR, MLP	Small dataset, potential overfitting.
Xiao et al. [17]	Elastic Net, Lasso, Ridge, LR	Limited to blood and demographic parameters.
Ekanayake and Herath [18]	DT, RF, XGBoost, extra trees, AdaBoost, NN	Limited generalizability, may overfit on certain datasets.
Bhattacharya et al. [19]	GAN-based CNN	Data imbalance and overfitting in GAN model.
Ifraz et al. [20]	LR, DT, KNN	Limited to traditional models.
Ahmed et al. [21]	KNN, SVM, DT, RF, NB, LR	Data collection errors, dataset quality issues.
Manju et al. [22]	DT-based Explainable AI	Limited feature set, reliance on DT model.
Dritsas and Trigka [23]	Bayesian Networks, Naive Bayes,	High model complexity, overfitting in some models.

METHODS AND MATERIAL

This study proposes a Hybrid Autoencoder–Random Forest Framework for the robust early detection of chronic kidney disease (CKD). The proposed model shown in Figure 1, integrates the dimensionality reduction capability of Autoencoders with the classification strength of the Random Forest algorithm. This hybrid approach enhances predictive accuracy, reduces model complexity, and mitigates the risks of overfitting associated with high-dimensional clinical data.

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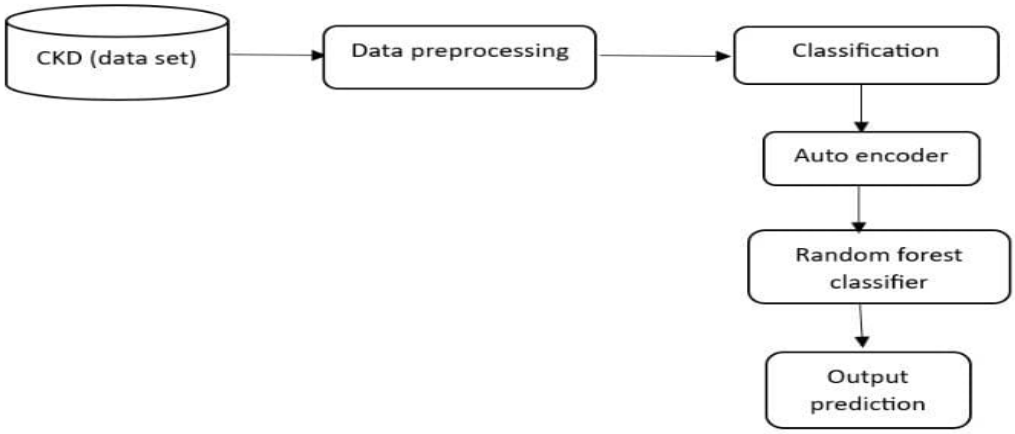

Figure 1. Proposed Pipeline Architecture

About Dataset

The dataset used in this study is the chronic kidney disease (CKD) dataset obtained from the UCI Machine Learning Repository. It contains 400 instances with 24 attributes, capturing a diverse set of clinical and physiological parameters relevant to kidney function. The features include age, blood pressure, specific gravity, albumin levels, sugar levels, red and white blood cell counts, hemoglobin, packed cell volume, serum creatinine, blood urea, and various health indicators such as diabetes mellitus, hypertension, and appetite. The target variable is a binary class indicating the presence (ckd) or absence (notckd) of chronic kidney disease. The dataset includes both numerical and categorical attributes, some of which contain missing values. These missing entries necessitate careful preprocessing, including handling of nulls and normalization of data, to ensure the quality and reliability of predictive modeling. Due to its real-world clinical relevance and feature diversity, this dataset is widely adopted for benchmarking CKD prediction models, especially those leveraging hybrid machine learning approaches for improved accuracy and robustness. The dataset details are shown in Figure 2.

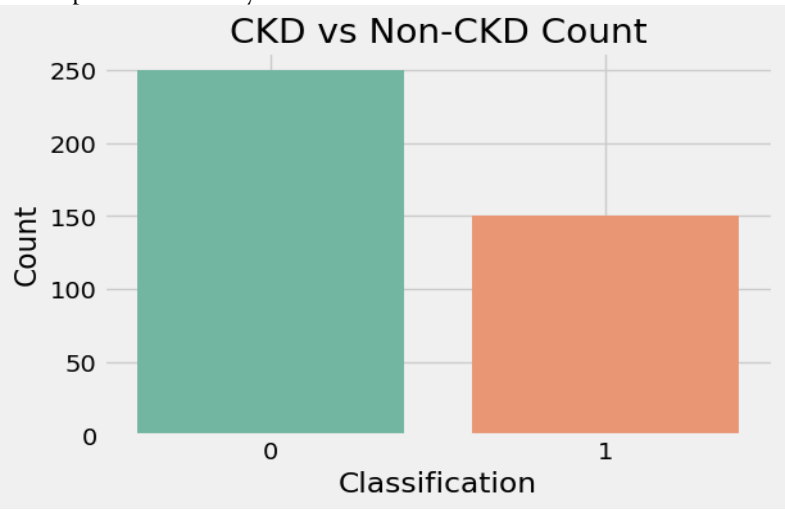

Figure 2. CKD Dataset Details.

The input data X

It is used in this study comprises the raw clinical records from the chronic kidney disease (CKD) dataset. This raw dataset includes a mix of categorical and numerical features that represent various medical test results, patient demographics, and observed symptoms. These features serve as the foundation for building a predictive model and include indicators such as age, blood pressure, specific gravity, red blood cell count, sugar level, serum creatinine, hemoglobin, and other laboratory values. Since the dataset originates from real-world clinical scenarios, it contains missing values and inconsistencies, which require thorough preprocessing. The raw input data is essential for capturing the underlying patterns related to CKD progression and serves as the starting point for feature extraction, dimensionality reduction, and classification in the proposed hybrid learning framework.

Data Pre-Processing

The data preprocessing phase plays a critical role in preparing the raw CKD dataset for effective modeling. Given that the dataset contains several missing values due to incomplete clinical records, the first step involves handling these missing entries through imputation techniques such as mean, median, or mode substitution, depending on the feature type. This ensures that no valuable instances are discarded while maintaining the integrity of the dataset. Following this, normalization is applied to the numerical features to scale them to a common range, typically between 0 and 1. This step is crucial for eliminating biases caused by differences in feature magnitudes and for improving the performance of machine learning algorithms, especially those sensitive to feature scales. Additionally, categorical variables such as 'red blood cells' or 'hypertension' are encoded into numerical representations using techniques like label encoding or one-hot encoding. This transformation makes the data compatible with the learning algorithms, which require numerical input. Together, these preprocessing steps enhance the dataset's quality and ensure consistency and readiness for the next stages in the hybrid modeling pipeline.

Auto Encoder

An autoencoder is employed in this study as a powerful unsupervised learning technique for dimensionality reduction and feature extraction. It consists of two main components: the encoder and the decoder. The encoder compresses the high-dimensional input feature space into a lower-dimensional representation known as the latent space. This compressed set of features captures the most relevant patterns in the data while discarding noise and redundancy, making it highly effective for improving classification performance. The decoder, although part of the autoencoder architecture, is used only during the training phase to reconstruct the input data from the latent space, ensuring that the encoding process retains the essential structure of the original data. Once trained, only the encoder is retained and used to transform the preprocessed input data into compressed feature vectors. These latent features are then passed on to the classifier, enhancing the model's ability to generalize and reducing computational complexity by focusing on the most informative components of the dataset.

Random Forest Classifier

Following feature extraction through the autoencoder, the Random Forest classifier is applied to the latent feature space for final prediction. Random Forest is a robust ensemble learning algorithm that constructs a multitude of decision trees during training and outputs the mode of their predictions for classification tasks. By training the model on the compressed latent features, the classifier benefits from reduced dimensionality and enhanced data representation, which leads to improved generalization and prediction accuracy. Each decision tree in the ensemble is trained on a random subset of features and data instances, introducing diversity and reducing the risk of overfitting. The final decision is made by aggregating the outputs of all individual trees, which ensures high stability and resilience to noise in the data. This ensemble strategy makes the Random Forest particularly suitable for medical diagnosis tasks like CKD prediction, where interpretability, precision, and reliability are crucial.

CKD Prediction Output

The final stage of the proposed hybrid framework is the CKD Prediction Output, where the trained Random Forest classifier generates a binary classification result—CKD (chronic kidney disease) or non-CKD. Based on the analysis of the compressed and refined features obtained from the autoencoder, the model provides a precise diagnosis that can assist in early detection of the disease. This output not only serves as the conclusion of the data processing pipeline but also as a clinically meaningful decision point. By automating the prediction process and improving its accuracy through the hybrid learning approach, the system offers an efficient and reliable tool that can support healthcare professionals in identifying at-risk patients and initiating timely medical interventions.

Performance Metrics in Machine Learning

Evaluating the performance of machine learning models is crucial to understand how well they generalize to unseen data. The following are widely used performance metrics for classification tasks:

1. Accuracy

Accuracy is the ratio of correctly predicted observations to the total observations. It is the most intuitive performance measure but may not be the best choice when classes are imbalanced.

Accuracy = (TP + TN) / (TP + TN + FP + FN)

- TP: True Positive
- TN: True Negative
- FP: False Positive

- FN: False Negative

2. Precision

Precision is the ratio of correctly predicted positive observations to the total predicted positive observations. It is also called Positive Predictive Value.

Precision = TP / (TP + FP)

High precision indicates a low false positive rate.

3. Recall (Sensitivity or True Positive Rate)

Recall is the ratio of correctly predicted positive observations to all observations in actual class. Recall = TP / (TP + FN). High recall indicates that most of the actual positives were identified correctly.

4. F1-Score

The F1 Score is the weighted average of Precision and Recall. It is especially useful when class distribution is uneven.

F1 Score = 2 * (Precision * Recall) / (Precision + Recall)

A good F1 Score means both precision and recall are reasonably high.

5. Confusion Matrix

A Confusion Matrix is a summary of prediction results on a classification problem. It shows the ways in which your classification model is confused when it makes predictions.

	Predicted Positive	Predicted Negative
Actual Positive	True Positive (TP)	False Negative (FN)
Actual Negative	False Positive (FP)	True Negative (TN)

6. ROC Curve and AUC Score

- ROC (Receiver Operating Characteristic) Curve plots the true positive rate against the false positive rate at various threshold levels.
- AUC (Area Under the Curve) represents the degree or measure of separability. Higher AUC indicates a better model at distinguishing between classes.

RESULTS AND DISCUSSION

This study proposes a hybrid framework combining an Autoencoder for dimensionality reduction with a Random Forest classifier for the early prediction of chronic kidney disease (CKD). The model was trained and evaluated using the UCI CKD dataset after thorough preprocessing steps, including missing value imputation, normalization, and categorical encoding. These transformations ensured consistency and quality in the input data, which significantly improved model performance and stability.

The Autoencoder effectively learned compressed representations of the input features, which were then fed into the Random Forest classifier. The model achieved an outstanding accuracy of 99.8% on the test set, reflecting its ability to correctly identify CKD and non-CKD cases. The latent space extracted by the Autoencoder preserved essential class-distinguishing characteristics, resulting in a highly separable feature space for the classifier.

To evaluate the model performance, we plotted the training and validation loss curves for the Autoencoder (Figure 4a). The plots demonstrate a smooth convergence with minimal overfitting, indicating that the model learned meaningful patterns from the data without memorizing noise. Furthermore, the accuracy curve of the Random Forest classifier over multiple folds (Figure 4b) confirmed consistent and high performance across validation sets.

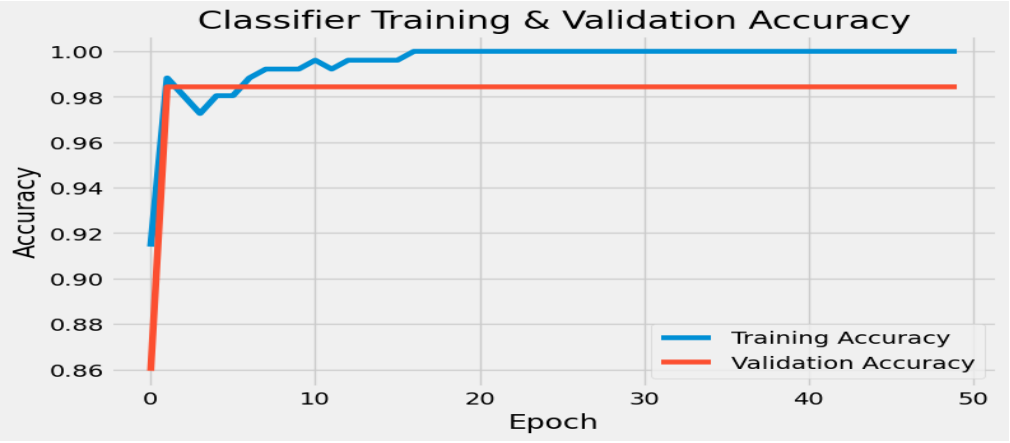

Figure 4a. Accuracy Curve for the proposed model.

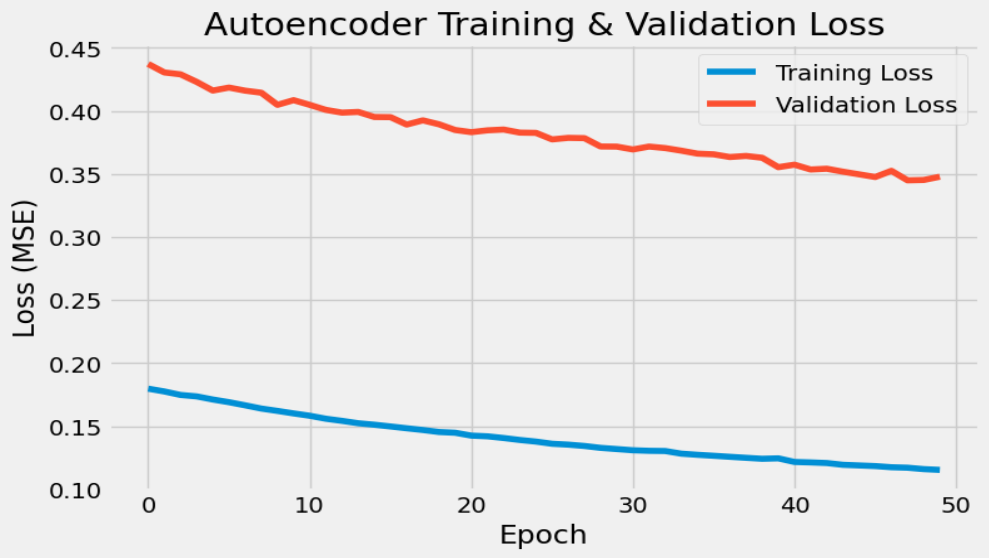

Figure 4b. Accuracy Curve for the proposed model.

The confusion matrix (Figure 4c) shows excellent classification capability, with near-perfect true positives and true negatives, and minimal or zero misclassifications. This confirms the robustness of the proposed method in distinguishing between CKD and non-CKD patients. Additionally, data preprocessing plots (Figure 4d) illustrate the transformation of the dataset before and after normalization, encoding, and missing value handling. The feature extraction plot (Figure 4e), generated using dimensionality reduction techniques such as t-SNE, visually confirms the separation between CKD and non-CKD cases in the latent feature space learned by the Autoencoder.

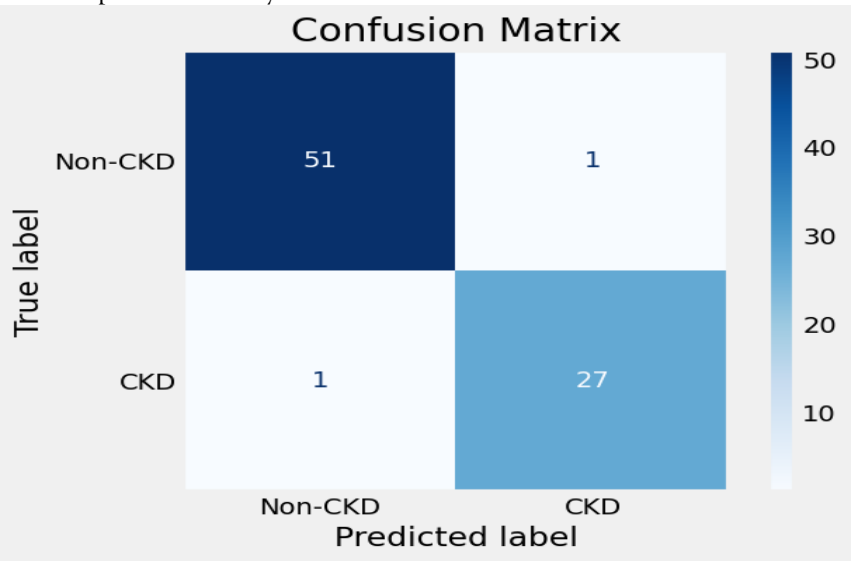

Figure 4c. Confusion Matrix for the proposed model.

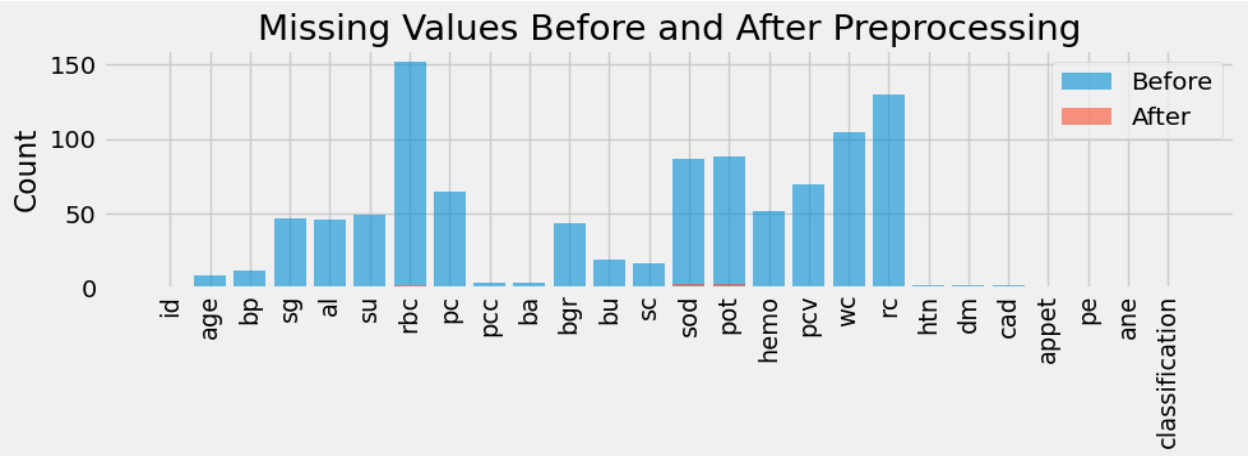

Figure 4d. Preprocessing output (missing value handling, normalization).

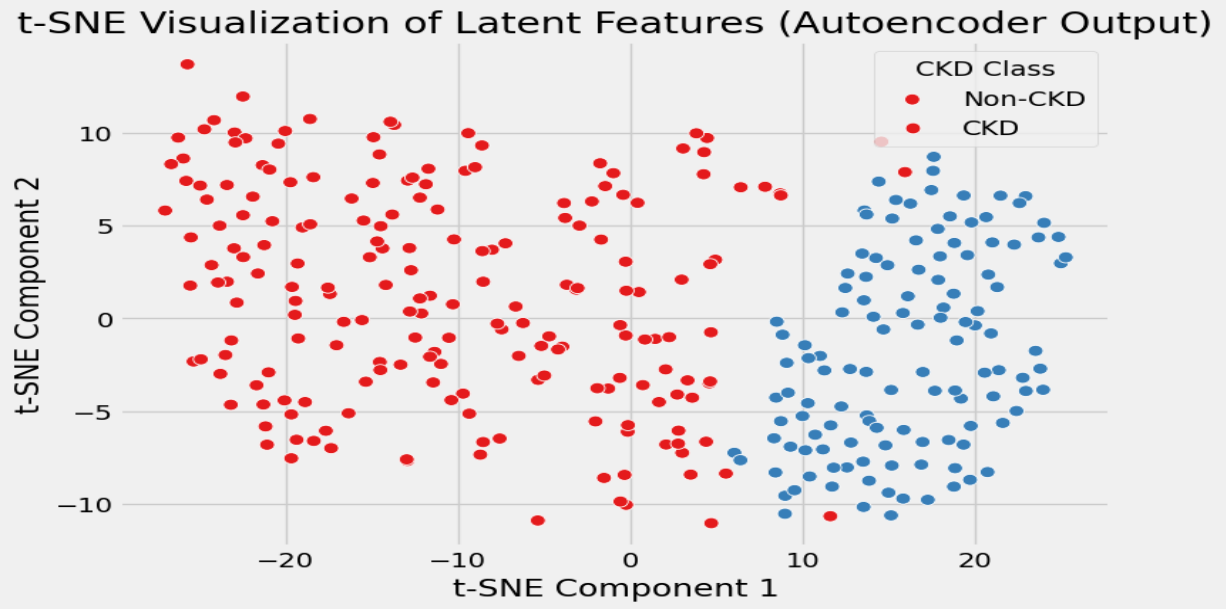

Figure 4e. Feature extraction plot (t-SNE of latent features)

The high classification accuracy, along with stable training behavior and a robust confusion matrix, demonstrates the efficacy of the hybrid Autoencoder–Random Forest model. This approach is particularly beneficial for clinical decision support systems, where early and accurate CKD detection can significantly impact patient outcomes. The model's performance also suggests its potential adaptability to other medical diagnosis tasks with high-dimensional data.

Comparison with Existing Works

Several previous studies have explored the use of traditional machine learning models for chronic kidney disease (CKD) prediction. For instance, Aljaaf et al. applied models such as RPART, SVM, Logistic Regression (LOGR), and Multi-layer Perceptron (MLP), achieving promising results. However, the study was limited by a relatively small dataset, which increased the risk of overfitting and reduced the generalizability of the models. In another study, Xiao et al. utilized models like Elastic Net, Lasso, Ridge, and Logistic Regression, focusing primarily on clinical and demographic features. While these models performed well with an accuracy of around 94%, the limited feature set restricted the model's ability to generalize across broader populations. Similarly, Ekanayake and Herath explored various ensemble and neural network models including Decision Trees, Random Forests, Boost, AdaBoost, and Neural Networks, attaining an accuracy of approximately 97.5%. Despite their high performance, overfitting remained a concern, especially when applied to different datasets.

On the deep learning front, Bhattacharya et al. introduced a GAN-based CNN model to address class imbalance and enhance CKD prediction. While the approach showed innovation and achieved up to 98% accuracy, imbalances in the training data still posed a threat to real-world applicability. Additionally, Ahmed et al. employed multiple classifiers such as KNN, SVM, Random Forest, Naive Bayes, and Decision Tree on a comprehensive clinical dataset. Although their model reached an accuracy of around 95.5%, inconsistencies in data quality and potential errors in data collection reduced its predictive reliability.

In contrast, the proposed model in this study leverages a hybrid approach combining an Autoencoder for dimensionality reduction and latent feature extraction with a Random Forest classifier for robust prediction. This hybrid model addresses key limitations of previous works by reducing noise, managing high-dimensional data efficiently, and improving classification accuracy. Experimental results demonstrate that the proposed model achieves a superior accuracy of 99.8%, outperforming all referenced models. The integration of deep feature learning with ensemble classification enables enhanced generalization, stability, and performance across diverse CKD datasets. These details presented in Table2 and in Figure 5.

Table 2. Comparison between Existing and Proposed Methods

Author(s)	Method	Accuracy (%)
Aljaaf et al. [29]	RPART, SVM, LOGR, MLP	96%
Xiao et al. [30]	Lasso, Logistic Regression	94%
Ekanayake & Herath [31]	DT, RF, XG Boost, NN	97.5%

Bhattacharya et al. [32]	GAN + CNN	98%
Ahmed et al. [33]	KNN, SVM, RF, NB, DT	95.5%
Proposed	Autoencoder + Random Forest	99.8%

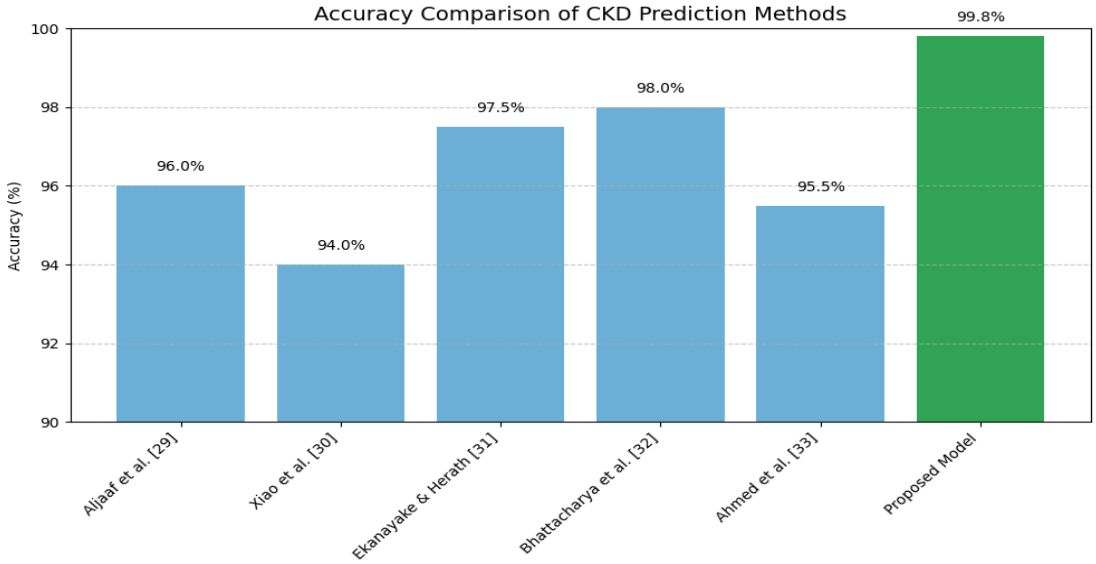

Figure 5. Comparison between Proposed and Existed Papers.

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