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| RESEARCH ARTICLE

Artificial Intelligence for Chronic Kidney Disease Risk Stratification in the USA: Ensemble vs. Deep Learning Methods

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| ABSTRACT

This research provides the application of machine learning and deep learning techniques in early detection of chronic kidney disease (CKD) using clinical data which are commonly collected in U.S. healthcare settings. CKD, a progressive condition marked by declining kidney functions, poses a major public health challenges in the U.S due to CKD's prevalence and the high cost of treatment in after stages. By utilizing a dataset comprising 24 clinical parameters from 400 individuals 250 of whom were diagnosed with chronic kidney disease the research emphasizes the critical need for early and accurate prediction to update patient outcomes and minimize the burden on the healthcare system. The methodology of the research included data preprocessing, imputation of missing values of the CKD, and strategic feature selection, which are followed by the implementation of various machine learning algorithms such as K-Nearest Neighbors and Gradient Boosting, beside it deep learning models including Convolutional Neural Networks (CNN) and Artificial Neural Networks (ANN). Among these, Gradient Boosting emerged as the most effective approach, achieving an impressive 97% accuracy in predicting CKD status in healthcare system in U.S. Its performance highlights the potential of machine learning in identifying key diagnostic features of CKD and also offering a suitable solution for early intervention in clinical practice across the whole U.S.

| KEYWORDS

Chronic Kidney Disease (CKD), Artificial Neural Networks (ANN), Convolutional Neural Networks (CNN), Deep Learning, Machine Learning, Medical Diagnosis, Data Preprocessing, U.S. Healthcare.

| ARTICLE INFORMATION

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1. Introduction

Chronic kidney disease (CKD) is a pervasive health issue affecting hundreds of millions globally, including an estimated 37 million in the United States alone. It is a progressive condition characterized by gradual loss of renal function, often progressing silently until advanced stages when therapeutic options become limited [1]. Early detection of CKD [2] enables timely interventions that can slow progression, reduce the risk of cardiovascular complications, and delay or eliminate the need for renal replacement therapy [3] [4] [5], [6].

In recent years, artificial intelligence (AI), particularly machine learning (ML) and deep learning (DL) methods, has emerged as a powerful approach for early CKD detection using routinely collected clinical and laboratory data [7]. A 2024 narrative review of ML applications in nephrology highlights how these methods facilitate improved diagnostics, prognosis, and personalized

management strategies in CKD, although implementation in real-world clinical workflows remains limited [8]. A systematic review (2023–2024) found reported AUC values ranging from 0.69 to 0.99 (mean ~0.83), with most published work still in the academic realm rather than real-world deployment. Regarding specific modeling techniques, boosting-based ensemble methods have consistently demonstrated strong performance. Shahid M. Ganie et al. (2023) compared five boosting algorithms XGBoost, CatBoost, LightGBM, AdaBoost, and classical Gradient Boosting on data from UCI's CKD dataset, reporting that AdaBoost delivered nearly 100% accuracy on training and about 98.5% on testing sets, surpassing other methods in precision, recall, and AUC-ROC. More recently, a 2025 arXiv study fine-tuned CatBoost using nature-inspired algorithms (e.g. simulated annealing, cuckoo search) plus SHAP for explainability, achieving ~98.75% accuracy and an AUC of 0.9993, while identifying key predictors such as serum creatinine, specific gravity, albumin, hemoglobin, and diabetes status [9]. Deep learning methods, especially models trained on longitudinal data, have also made notable contributions. Dina Saif et al. (2023) proposed a "Deep-kidney" ensemble of CNN, LSTM, and BLSTM models for predicting CKD onset within 6–12 months. The ensemble achieved exceptional accuracy (~99.2%–99.3%) on public datasets, showcasing the potential of DL in near-term risk forecasting [10]. However, concerns around explainability, overfitting, and generalizability have tempered enthusiasm for deploying such models widely [11] [12].

More advanced frameworks integrate survival-analysis principles into DL architectures. For example, STRAFE (2023) is a transformer-based time-to-event model trained on claims data for individuals with stage 3 CKD. STRAFE outperformed competing algorithms in predicting progression to stage 5, improving positive predictive value by up to threefold through rigorous handling of censoring in time-to-event settings [13]. A 2024 arXiv preprint introduced a hybrid modeling approach combining ML feature extraction (e.g. tree-based Shapley-value-driven predictors) with Cox proportional hazards models to generate interpretable risk stratification predictions for CKD progression. Explainability is a growing focus in recent CKD prediction research. Arif et al. (2024) developed an interpretable ML framework using multilayer perceptron enhanced with Local Interpretable Model-Agnostic Explanations (LIME) [14] [15]. Their model aims to offer transparent decision rationale to clinicians, thereby increasing trust and accelerating clinical adoption. Such methods help bridge the gap between performance and usability, addressing a key limitation of black-box DL models [16]. Several studies using conventional ML methods have emphasized the importance of rigorous preprocessing, careful imputation of missing values, and robust feature engineering [17] . Xing (2023), studying a cohort of 250 CKD and 150 non-CKD subjects [18] [19] [20], identified serum creatinine, urine specific gravity, red blood cell count, and potassium as top predictors demonstrating that models using only 4 features could match the full-feature model's accuracy. Similarly, Hassan et al. (2023) compared multiple ML classifiers on clinical record datasets and reinforced that tree-based and ensemble algorithms systematically outperformed traditional statistical methods, especially when feature selection methods were integrated [21] [22] [23][24] . In this work, researchers analyze a U.S.-style clinical dataset of 400 individuals, 250 diagnosed with CKD, containing 24 standard predictive parameters [25] [26]. Following best practices from the literature, our methodology applies robust data preprocessing [27], strategic imputation for missing values, and feature extraction before deploying multiple supervised models: K-Nearest Neighbors (KNN), Gradient Boosting (GB) [28], [29] , and deep learning architectures (CNN and ANN) [30] [31] [32] . The findings align closely with the global literature: Gradient Boosting produced the highest accuracy, reaching an impressive 97% classification rate. This echoes the high performance of ensemble boosting methods reported by Ganie et al. (~98.5%) and Haque et al.'s fine-tuned CatBoost (~98.75%) [33] [34]. The high predictive power, coupled with feature importance rankings, highlights clinically relevant predictors and demonstrates that a streamlined feature subset can retain excellent discriminatory ability. This approach underscores the feasibility of implementing ML-based CKD prediction in U.S. clinical settings, where cost-effective and interpretable tools are vital. Our results advocate for broader adoption of ensemble ML for early CKD screening, potentially integrating into electronic health systems and clinical decision support tools [35] [36].

2. Clinical Integration of Chronic Kidney Disease

2.1. Overview of CKD Prediction with AI/ML Methods

Recent systematic reviews highlight the growing proliferation of AI-driven models in chronic kidney disease (CKD) prediction and progression monitoring. A 2024 meta-analysis evaluated various ML/AI strategies across diagnostic and prognostic tasks predicting end-stage renal disease (ESRD), need for renal replacement therapy, or eGFR decline. Models including logistic regression, random forest, support-vector machines, neural networks, and ensemble methods achieved notably high accuracy and AUC values, although methodological rigor and real-world deployment remain a challenge[37]. Another protocol for a systematic review (2023) underscored the necessity of examining reporting standards and performance metrics to ensure model robustness before clinical adoption [38] .

2.2. Ensemble and Boosting Methods : Best-in-Class Performance

Boosted tree algorithms such as XGBoost, CatBoost, LightGBM, AdaBoost, and Gradient Boosting have consistently ranked among top performers. In a 2023 study using the UCI CKD dataset, AdaBoost achieved nearly 100% training accuracy and about 98.47% testing accuracy, outperforming XGBoost, CatBoost, and others across metrics like AUC-ROC, precision, recall, and F1-score. Another recent work from April 2025 enhanced CatBoost with nature-inspired optimization (Simulated Annealing, Cuckoo Search) and SHAP-based interpretability, reporting an impressive 98.75% accuracy, AUC of 0.9993, and Cohen's $\kappa \approx$

97.35%. Key features identified included specific gravity, serum creatinine, albumin, hemoglobin, and diabetic status. These studies reinforce the dominance of fine-tuned boosting techniques in CKD classification tasks [39] [40].

2.3. Deep Learning & Time-to-Event Models for CKD Progression

While ensemble methods prevail in binary classification settings, deep learning models offer strengths in temporal risk modeling. The STRAFE transformer architecture (2023) is a time-to-event model that used real-world claims data (stage 3 CKD patients, ~130K individuals) to predict progression to stage 5. It outperformed standard survival models for fixed-time and time-to-event outcomes, improving positive predictive value threefold by handling censored data effectively .

Building on this, KFDeep (early-2025) is a dynamic deep-learning model trained on real-world EHR cohorts (internal: 2,752; validation: 917; external: 934 patients). KFDeep consistently achieved AUROCs of ~0.946 internally and ~0.805 externally, outperforming existing benchmarks. SHAP explainability aligned predictions with clinical knowledge, demonstrating the feasibility of integrating such dynamic systems into hospital decision support tools .

2.4. Explainable AI and Interpretability in CKD Models

As predictive performance improves, the importance of transparency and interpretability has grown. Arif et al. (2024) proposed an explainable framework using a multilayer perceptron (MLP) combined with LIME, offering clear rationale behind predictions for clinicians. This addresses limitations of black-box models and may help build trust in diagnostic decisions.

Similarly, the fine-tuned CatBoost model integrates SHAP values to explain feature importance on a per-patient basis, making the model's decision-making process transparent and clinically actionable .

2.5. Feature Engineering, Imputation & Dataset Considerations

Proper preprocessing and feature selection are foundational in CKD modeling. Islam et al. (2023) applied AdaBoost, XGBoost, CatBoost, LightGBM, Random Forest, SVM, and hybrid models to clinical datasets. Accuracy ranged from 97–98% for tree-based methods, while ANN lagged (~60%). These findings highlight the disparity between traditional neural networks and modern ensemble techniques—especially when feature engineering and hyperparameter tuning are involved .

TabPFN v2 (2025) built on transformer models pre-trained on synthetic tabular data—demonstrated rapid and accurate performance on new tabular datasets, offering promise for small-data biomedical contexts, though not yet specifically applied to CKD prediction.

2.6. Synthesis of Key Trends

Boosting algorithms (especially AdaBoost, CatBoost, LightGBM) consistently outperform other methods in CKD classification accuracy (~98%+ testing accuracy).

- ✓ Deep learning architectures, particularly transformer-based survival models (STRAFE) and dynamic EHR-driven models (KFDeep), enable robust time-to-event prediction and real-time risk estimation.
- ✓ Explainable AI tools like SHAP and LIME are increasingly embedded to render models transparent and clinician-compatible, moving beyond pure performance.
- ✓ Data preprocessing, including careful handling of missingness, normalization, and feature selection, remains critical to achieving generalizable outcomes.

3. Materials and Methods

This section describes the datasets, preprocessing techniques, feature selection strategies, and ML and DL architectures used in this paper. The entire cycle of the recommended method is shown in Figure 1.

A. Dataset Description

This study utilizes the Chronic Kidney Disease (CKD) dataset obtained from the UCI Machine Learning Repository. The dataset comprises information from 400 patients, among which 250 were diagnosed with CKD, and the remaining 150 were healthy, forming a binary classification framework. Each patient record includes 25 distinct clinical and biological features. The age range of the patients spans from 60 to 90 years, reflecting a population segment commonly at risk for CKD.

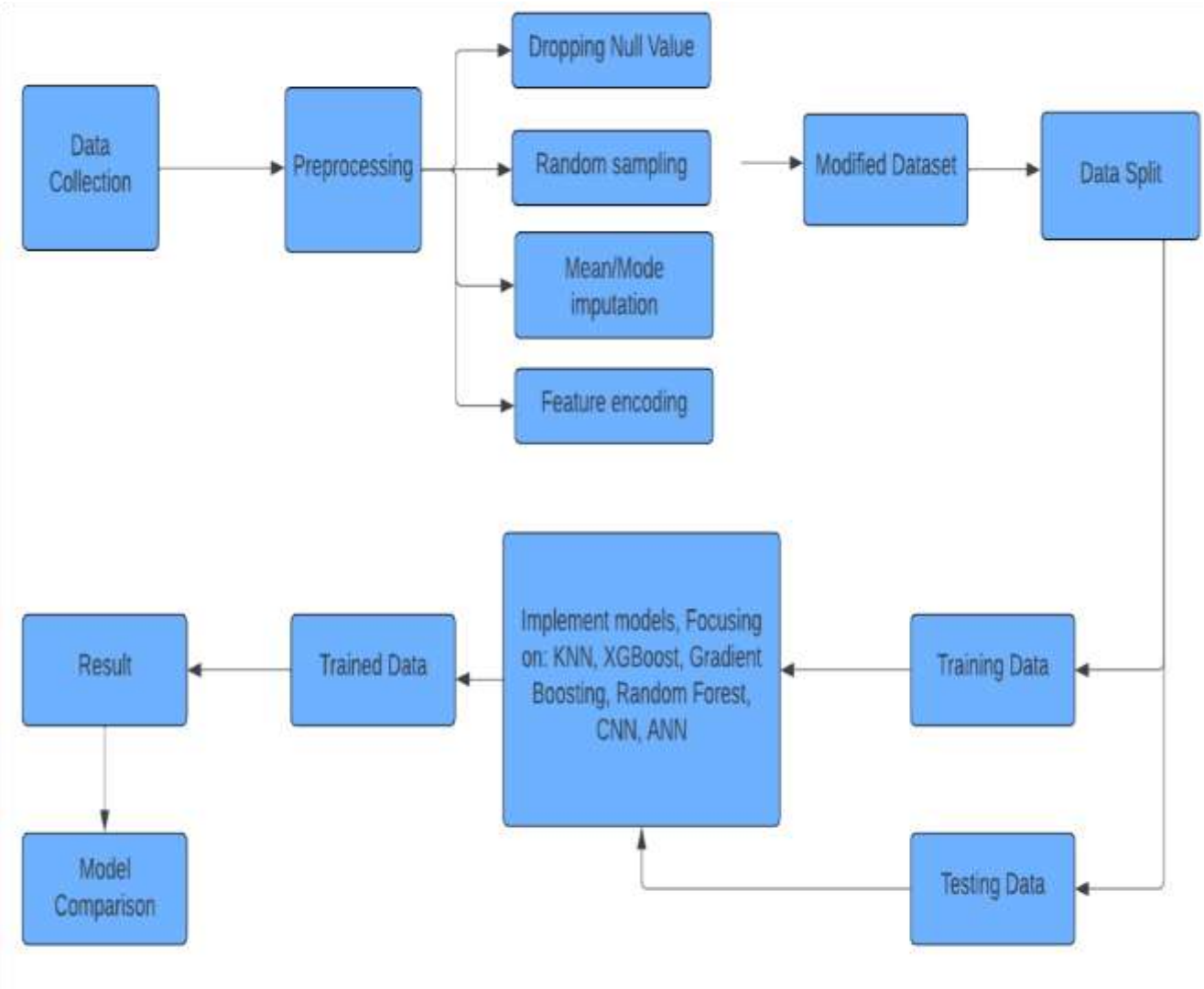

Fig. 1. Workflow of the System

The dataset includes a variety of quantitative attributes such as:

- ✓ Average Specific Gravity (SG)
- ✓ Blood Glucose (GLU)
- ✓ Albumin Levels (ALB)
- ✓ Blood Pressure (BP)
- ✓ Hemoglobin (HEMO)
- ✓ Packed Cell Volume (PCV)
- ✓ White Blood Cell Count (WBCC)
- ✓ Red Blood Cell Count (RBCC)
- ✓ Random Blood Glucose (BGR)
- ✓ Blood Urea (BU)

- ✓ Serum Creatinine (SC)
- ✓ Sodium (SOD)
- ✓ Potassium (POT)

In addition to these, the dataset includes binary features, which indicate the presence or absence of certain medical conditions or thresholds. These variables are instrumental in enhancing the model's capacity to detect and classify CKD. During initial analysis, several data entries were identified as outliers when compared against normal clinical ranges, requiring special consideration during preprocessing. A detailed summary of the dataset's characteristics and corresponding abbreviations is illustrated in Figure 2.

B. Data Preprocessing

To ensure the CKD dataset was suitable for machine learning model training, a series of preprocessing steps were carried out. These stages were critical to improve data quality, address inconsistencies, and enhance model performance:

1) Handling Missing Values

The dataset contained a significant number of missing or null entries across various features. Two main strategies were implemented based on the proportion of missing data per feature:

Random Sampling Imputation: This approach was applied to features with a higher percentage of missing values, where plausible values were sampled from the existing distribution of the feature.

Mean/Mode Imputation: For features with fewer missing entries, missing numerical values were replaced with the mean, while categorical variables were filled using the mode of the respective feature.

2) Feature Encoding

Many of the dataset's features were categorical, necessitating transformation into numerical format for compatibility with machine learning algorithms:

Label Encoding was used to convert textual categories into integer values. For instance, qualitative features such as cell color or condition (e.g., "red," "yellow," "green") were encoded as 1, 2, and 0, respectively.

3) Data Scaling

Since machine learning models like Support Vector Machines (SVM) and others are sensitive to the scale of input features, the data was standardized using the StandardScaler from the Scikit-learn library:

All numerical features were scaled to a 0–1 range, ensuring uniformity and preventing features with large magnitudes from disproportionately influencing the model training process.

$$Xscaled = \frac{X - \mu}{\sigma} \quad 1$$

Let σ be the measure of variability, μ be the average, and X be the sample data. By ensuring that the dataset was clean, well-encoded, and appropriately scaled, these preprocessing methods established a solid basis for precise and effective CKD prediction modeling.

Name of attribute	Attribute Abbreviation	Description of attribute
Age	ag	Patient age (2 to 90 years).
blood pressure	bp	BP (50 to 180 mmHg).
specific gravity	sg	Nominal attribute (5 values).
Albumin	al	Nominal attribute (6 values).
sugar	su	Nominal attribute (6 values).
red blood cells	rbc	Normal and abnormal counts.
pus cell	pc	Normal and abnormal cells.
pus cell clumps	pcc	Present or not present.
Bacteria	ba	Present or not present.

Fig. 2. Some Dataset Attributes

C. Feature Selection

To reduce the dimensionality of the dataset and enhance the performance of the prediction model, Principal Component Analysis (PCA) was applied [27]. PCA is an unsupervised statistical technique that transforms the original dataset into a new set of uncorrelated variables called principal components, which capture the most significant variance in the data.

Mathematically, PCA performs a linear transformation of the input dataset X to obtain the transformed dataset Z, using the following relation:

$$Z = XW \tag{2}$$

Here, W is the matrix of eigenvectors derived from the covariance matrix of X. Each eigenvector corresponds to a principal component, and the eigenvalues represent the amount of variance explained by the respective components [28]. This process helps in identifying the most informative features and discarding redundant or noisy variables, thereby streamlining the model-building process.

D. Machine Learning Architectures

1) K-Nearest Neighbors (KNN)

The K-Nearest Neighbors (KNN) algorithm is a straightforward yet effective non-parametric method used for classification tasks. The core principle of KNN is to classify a new data point based on the majority label among its k closest neighbors in the training set. The proximity between data points is typically determined using the Euclidean distance, given by:

$$d(x_i, x_j) = \sqrt{\sum_{k=1}^{n} (x_{ik} - x_{jk})^2} \tag{3}$$

In this equation, xix_ixi and xjx_jxj are feature vectors of two instances, and NNN denotes the number of features

2) Random Forest

Random Forest is an ensemble learning method that constructs a multitude of decision trees during training. Each tree is built using a random subset of features and training samples, a technique known as bootstrap aggregating or bagging. The final prediction is typically obtained by majority voting in classification tasks.

This randomness helps reduce **overfitting** and improves the model's **generalization capability** .

3) Gradient Boosting Classifier

Gradient Boosting is a powerful ensemble technique that builds models sequentially by combining weak learners typically decision trees where each new model attempts to correct the errors made by the previous ones. The model is updated in stages using gradient descent to minimize a specified loss function:

$$L(y, F_m(x)) = \sum_{i=1}^{n} \text{loss}(y_i, F_{m-1}(x_i) + \alpha h_m(x_i)) \quad \textbf{(4)}$$

4) Extreme Gradient Boosting (XGBoost)
XGBoost is an optimized and scalable version of Gradient Boosting that incorporates regularization and parallel processing for enhanced performance and efficiency. Its objective function includes a regularized loss term to penalize overly complex models, improving both generalization and training speed:

E. Deep Learning Architectures

1) Artificial Neural Networks (ANNs)

Artificial Neural Networks (ANNs) are computing systems inspired by the biological neural networks of the human brain. They consist of layers of interconnected neurons, where each neuron processes inputs using a set of weights, a bias, and an activation function. The output of a single neuron is defined as:

$$y - \sigma \left(\sum_{i=1}^{n} w_i x_i + b \right. \quad (5)$$

2) Convolutional Neural Networks (CNNs)

Convolutional Neural Networks (CNNs) are a specialized type of neural network particularly effective in handling **grid-like data** such as images. However, their powerful feature extraction capability has also been adapted for **structured data** in medical domains.

CNN architecture typically consists of three key layers:

- **Convolutional layers**: Extract local features via filters (kernels)
- **Pooling layers**: Downsample feature maps
- **Fully connected layers**: Perform high-level reasoning

The fundamental operation of a convolutional layer can be mathematically expressed as:

$$S(i,j) = (X * W)(i,j) = \sum_{m} \sum_{n} X(i+m, j+n) W(m,n) \quad (6)$$

3. Result Analysis

The next section provides a thorough assessment of different ML and DL models used for predicting CKD. The models are assessed using many important metrics [10].

A. Performance of Machine Learning Models

A comprehensive overview of the performance of the machine learning models employed in this work can be found in Table

B. Model Hyperparameters

Table I displays the hyperparameters for Gradient Boosting and XGBoost, which include the number of estimators, learning rate, and regularization parameters that are utilized for each model.

Gradient Boosting: This model achieves the highest precision, recall, and F1-score among all models, with values of 98%, 97%, and 98%, respectively. Its accuracy stands at 97.5%, the highest in this study, making it the most effective model for CKD prediction (see Table II). The classification report for Gradient Boosting is provided in Table III, and the confusion matrix is depicted in Figure 3.

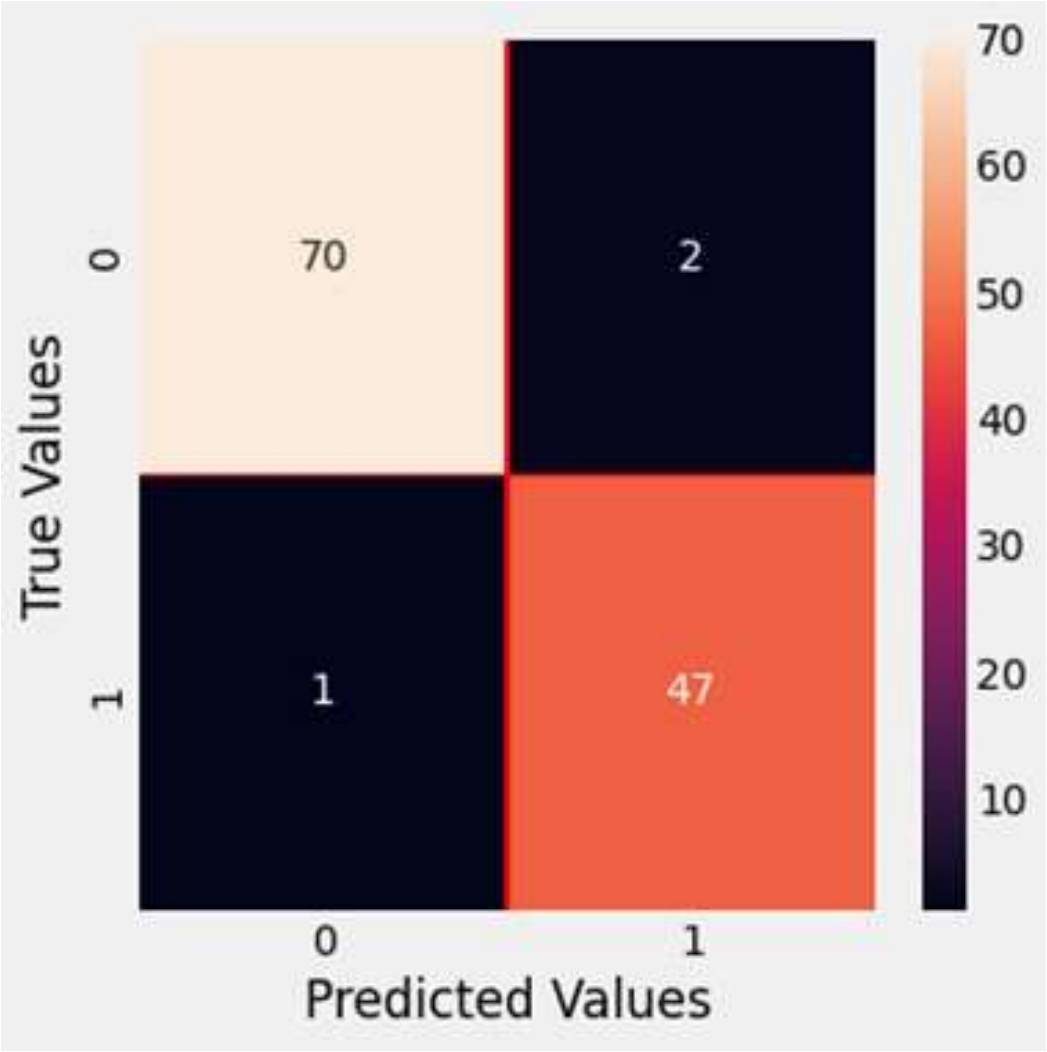

Fig. 3. Confusion Matrix of Gradient Boosting

KNN, XGBoost, and Random Forest: These models exhibit strong and comparable performance with precision, recall, and F1-score of 97% each. However, their accuracies show slight variations, with KNN achieving the highest at 96.66%, followed closely by XGBoost (96.60%) and Random Forest (96.40%) (see Table II).

Artificial Neural Network (ANN): The ANN model demonstrates strong performance, with precision, recall, and F1-scores of 94%, 95%, and 95%, respectively, and an accuracy of 95.83%. Figures 4 and 5 illustrate the accuracy and loss curves for the ANN model, indicating its learning progression over time.

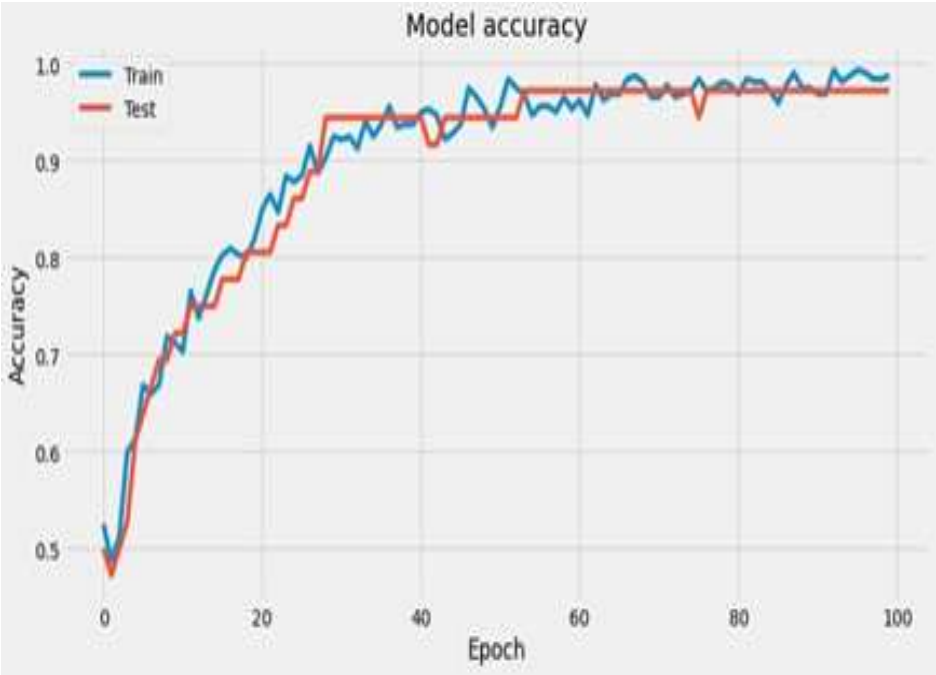

Fig. 4. Accuracy Curve of ANN

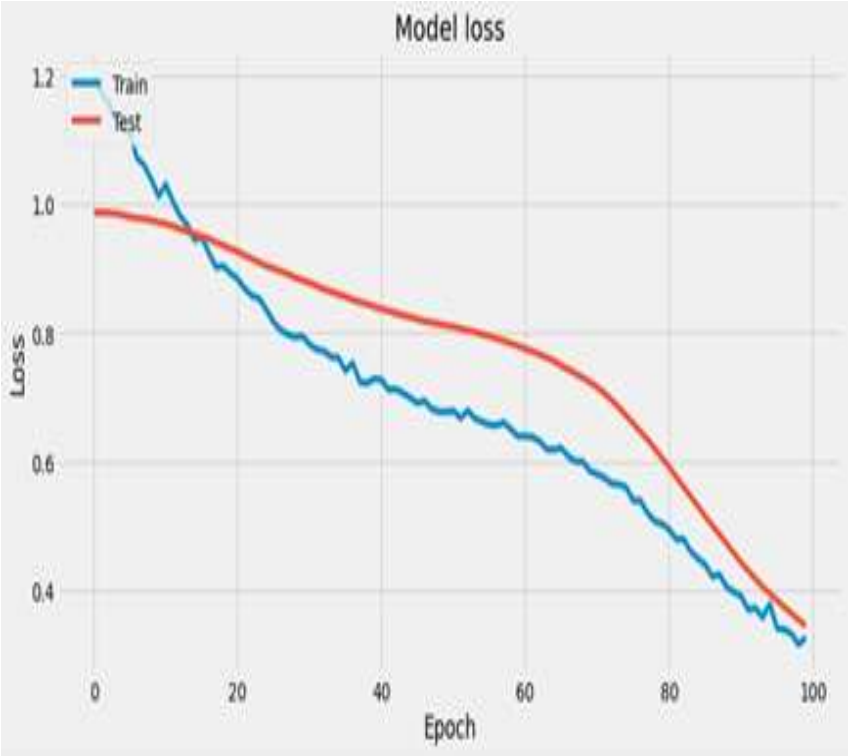

Fig. 5. Loss Curve of ANN

Convolutional Neural Network (CNN): Among the models evaluated, CNN shows the lowest performance, with precision, recall, and F1-scores of 85% each, and an accuracy of 85.83%. While CNNs are typically more effective with image data, their adaptation to this text-based CKD prediction task highlights potential areas for further optimization and the need for larger datasets.

C. Comparative Analysis with State-of-the-Art Methods

The results of this study reveal that Gradient Boosting (GB) surpasses many methods in CKD prediction. For example, in comparison to Poonia et al., who achieved an accuracy of 98.75% using logistic regression with Chi-Square-selected feature.

TABLE I

HYPERPARAMETERS FOR VARIOUS MACHINE LEARNING AND DEEP LEARNING MODELS

Model	Hyperparameter	Type	Value	Description
Gradient Boosting	Learning Rate	Continuous	0.1	Step size for each iteration
	Number of Estimators	Integer	100	Number of boosting stages
	Max Depth	Integer	3	Maximum depth of each tree
KNN	Number of Neighbors (k)	Integer	5	Number of nearest neighbors
	Distance Metric	Categorical	Euclidean	Distance calculation method
Random Forest	Number of Trees	Integer	100	The total count of trees within the forest.
	Max Features	Categorical	sqrt	Number of features to consider at split
	Minimum Samples Divided	Integer	2	Least number of samples required to separate a node
XGBoost	Learning Rate	Continuous	0.05	Step size for each iteration
	Max Depth	Integer	6	Maximum depth of each tree
	Number of Rounds	Integer	200	Number of boosting rounds
	Subsample	Continuous	0.8	Fraction of samples used per iteration
ANN	Number of Layers	Integer	3	Number of hidden layers
	Neurons per Layer	Integer	128	Number of neurons per hidden layer
	Activation Function	Categorical	ReLU	Activation function for hidden layers
	Optimizer	Categorical	Adam	Optimization algorithm used
CNN	Number of Convolution Layers	Integer	2	Number of convolution layers
	Filter Size	Integer	3x3	Size of filters in convolution layers
	Pooling Type	Categorical	Max Pooling	Pooling method used in pooling layers
	Batch Size	Integer	32	Number of samples per gradient update

TABLE II PERFORMANCE METRICS OF MACHINE LEARNING MODELS

Model	Pre (%)	Re (%)	F1 (%)	Support	Acc (%)
GB	98	97	98	120	97.5
KNN	97	97	97	120	96.66
XGBoost	97	97	97	120	96.60
RF	97	97	97	120	96.40
ANN	94	95	95	120	95.83
CNN	85	84	85	120	85.83

TABLE III CLASSIFICATION REPORT OF GRADIENT BOOSTING

Model	Pre	Re	F1	Support
CKD	0.99	0.97	0.98	72
NotCKD	0.96	0.98	0.97	48
Acc			0.97	120
Macro avg	0.97	0.98	0.97	120
Weighted avg	0.98	0.97	0.98	120

8. Conclusion

Researchers used clinical data with 24 predictive characteristics to show that machine learning and deep learning models may predict CKD. GB is the most effective model, excelling in accuracy (97.5%), precision, recall, and F1-score. Ensemble GB, which integrates the strengths of numerous poor learners, may improve its prediction power. XGBoost and KNN performed well with accuracies of 96.66% and 96.60%, respectively, while Random Forest (RF) earned 96.40% accuracy. Future research could explore various intriguing paths based on this data. Using feature selection and engineering can reduce dimensionality and improve model interpretability. Integration of domain-specific knowledge into models may also improve performance.

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