Identification of Chronic Kidney Disease Using Machine Learning Approach

Research submitted in partial fulfillment of the requirements for the degree of
Bachelor of Science (Engineering) in Computer Science and Engineering

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Approval

The Research Project Report "**Identification of Chronic Kidney Disease using effective classification and feature selection technique**" Submitted by Shifait Saroer, ID: CE20042 and Shamim Sorkar, ID: CE19044 to the Department of Computer Science and Engineering, Mawlana Bhashani Science and Technology University, Santosh, Tangail-1902, Bangladesh, has been accepted as satisfactory for the partial fulfillment of the requirements for the degree of Bachelors of Science(Engineering) in Computer Science and Engineering and approved as to its style and contents. It has been approved by the undersigned as to its quality, originality, and alignment with the academic standards and objectives of the department.

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Declaration

We hereby state that the research conducted by us under the direction of A S M Delowar Hossain, Associate Professor, Department of Computer Science and Engineering, Mawlana Bhashani Science and Technology University, Santosh, Tangail-1902, Bangladesh, resulted in the work presented in this thesis. We further declare that no portion of this thesis or its components have been or are being considered for submission elsewhere in order to receive a degree or diploma.

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Abstract

The ever-increasing volume of healthcare data presents a remarkable opportunity for intelligent analysis, accurate diagnosis, and improved clinical decision-making when mined effectively. Hidden patterns derived from historical patient data can play a significant role in detecting life-threatening conditions at an early stage. Chronic Kidney Disease (CKD) is a progressive and potentially fatal disorder that can often be managed or delayed with early intervention and predictive modeling. In this research, machine learning (ML) and data mining techniques have been applied to analyze the CKD dataset obtained from the UCI Machine Learning Repository, focusing on the early prediction of kidney-related abnormalities. This study investigates the classification performance of several widely used machine learning algorithms—Support Vector Machine (SVM), Decision Tree (DT), K-Nearest Neighbors (KNN), Naïve Bayes (NB), and Random Forest (RF)—in detecting the presence of CKD. The dataset underwent systematic data preprocessing to handle missing values, encode categorical features, and normalize numeric attributes. Model evaluation was carried out using key performance indicators including accuracy, Root Mean Squared Error (RMSE), Mean Absolute Error (MAE), and Receiver Operating Characteristic (ROC) curves. Among the algorithms tested, the Random Forest and Decision Tree classifiers exhibited superior predictive capabilities, with Random Forest achieving the highest classification accuracy. Additionally, feature ranking and attribute selection techniques were employed to identify the most influential features, where a subset of 15 attributes yielded the most optimal results. The findings of this study demonstrate the potential of integrating artificial intelligence and classification algorithms with clinical data to enable early detection and improve patient outcomes in CKD diagnosis.

Keywords

Chronic Kidney Disease (CKD), Machine Learning (ML), Support Vector Machine (SVM), Random Forest, K-Nearest Neighbors (KNN), Decision Tree, Naïve Bayes.

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Chapter 1

Introduction

1.1 Chronic Kidney Disease (CKD)

Chronic Kidney Disease (CKD) is a long-term medical condition where the kidneys gradually lose their ability to function properly over time. The kidneys' main job is to filter waste, excess fluids, and toxins from the blood, which are then excreted as urine. When the kidneys are damaged and can't work efficiently, harmful waste builds up in the body, leading to serious health problems.

Key points about CKD:

- Progressive condition: CKD worsens slowly over months or years.
- Irreversible: Damage to the kidneys in CKD is generally permanent.
- Stages: CKD is classified into 5 stages based on how well the kidneys are working, measured by a test called the glomerular filtration rate (GFR).
- Causes: Common causes include diabetes, high blood pressure, chronic glomerulonephritis (inflammation of the kidney filters), and inherited diseases.
- Symptoms: Early stages may have no symptoms. Later stages can cause fatigue, swelling, high blood pressure, and changes in urine.
- Complications: Can lead to kidney failure requiring dialysis or transplant.

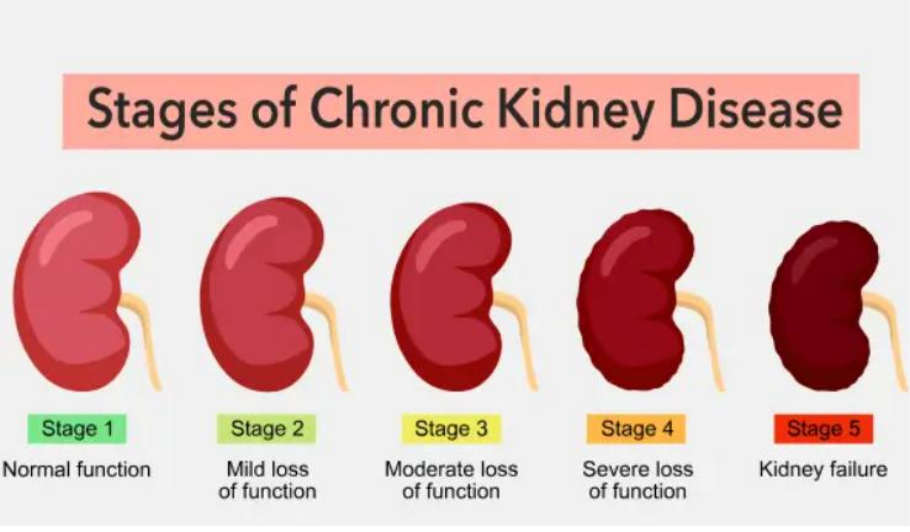


Figure 1.1: Stages of CKD

1.2 Background

Chronic Kidney Disease (CKD) is a progressive loss of kidney function over time, often remaining undiagnosed until it reaches an advanced stage. CKD occurs when the kidneys lose their ability to filter waste and fluids effectively from the blood, which can lead to severe complications, including kidney failure, cardiovascular disease, and early death. The disease is categorized into five stages, from Stage 1 (mild kidney damage with normal function) to Stage 5 (end-stage renal disease requiring dialysis or transplantation). The primary causes of CKD include diabetes, hypertension, glomerulonephritis, and polycystic kidney disease, along with secondary contributors such as obesity, aging, and genetic predisposition.

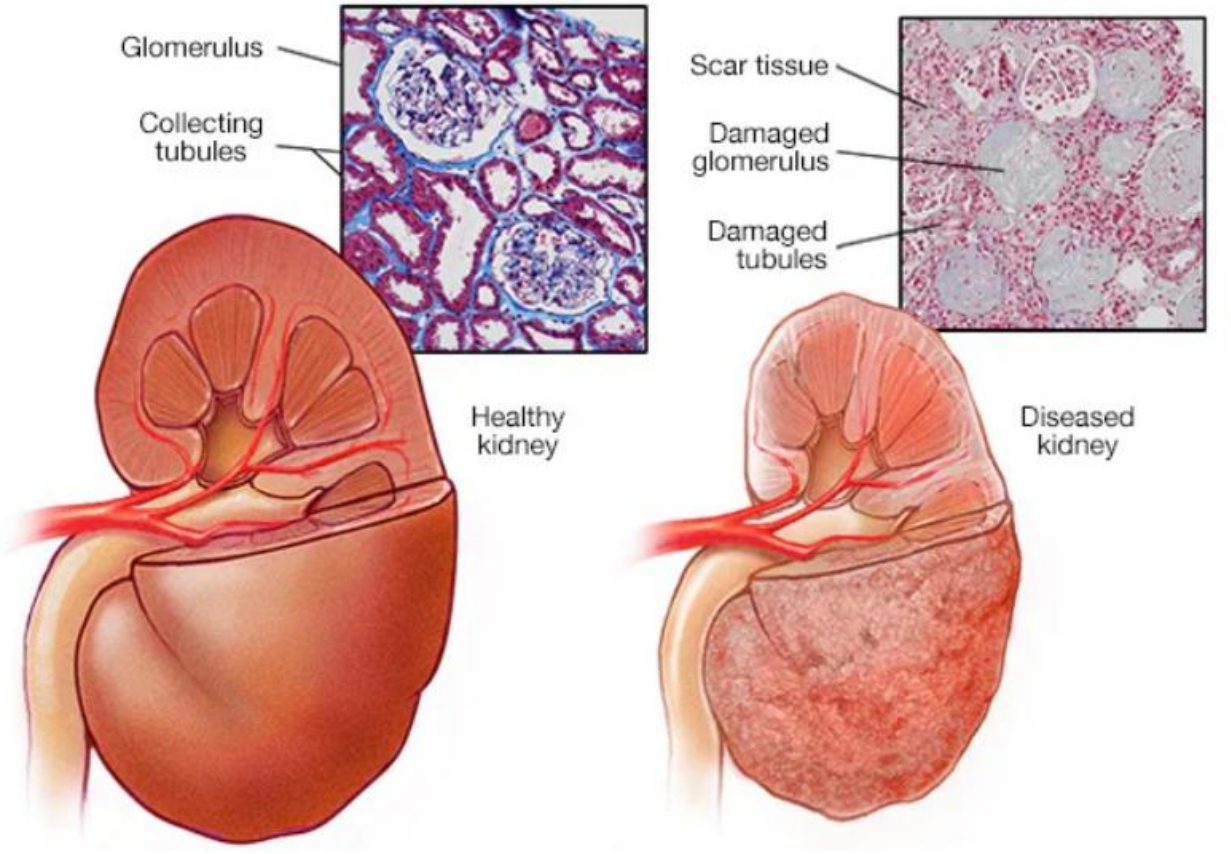


Figure 1.2: Difference between the healthy and affected kidney

Early detection of CKD is critical because the disease is often asymptomatic in its early stages. When diagnosed early, CKD progression can be delayed or even halted through lifestyle changes, medications, and regular monitoring. Without early intervention, patients are more likely to develop irreversible kidney failure, which requires expensive and life-altering treatment such as dialysis or transplantation. This highlights the need for reliable, low-cost, and scalable methods to identify CKD in its earliest stages—where treatment outcomes are most effective.

1.3 Motivation

In Bangladesh, the prevalence of chronic kidney disease is rising at an alarming rate. Recent studies suggest that 1 in every 5 adults may be affected by some form of kidney dysfunction. This growing burden is compounded by factors such as low awareness, inadequate screening programs, and limited access to nephrology services—especially in rural and underprivileged regions.

Traditional diagnostic approaches rely heavily on manual assessment of biochemical indicators and physician expertise. These processes are time-consuming, prone to human error, and often inaccessible to a large portion of the population. Moreover, early-stage CKD is typically undetected in routine clinical settings due to the subtle nature of its symptoms and the lack of awareness among both patients and healthcare providers. Another challenge is the silent nature of early-stage CKD. In its initial phases, CKD may not produce noticeable symptoms, making it easy to overlook during routine health checks. By the time symptoms like fatigue, swelling, or high blood pressure become evident, considerable, and often irreversible kidney damage may have already occurred.

This research is motivated by the urgent need to implement automated, intelligent, and accessible diagnostic tools that can aid healthcare professionals and improve early detection, especially in resource-limited settings like Bangladesh.

1.4 Research Question

A significant number of individuals suffer from Chronic Kidney Disease (CKD), which often remains undetected in its early stages due to the absence of noticeable symptoms. Early detection is essential to prevent disease progression, reduce complications, and improve patient outcomes. With the advancement of artificial intelligence and machine learning, there is growing potential to build automated systems that can accurately identify CKD based on clinical and biochemical data.

This study seeks to answer the following key research questions to support the early diagnosis of CKD using machine learning and data-driven methods:

1. Can machine learning models accurately predict the presence of CKD using routine clinical and biochemical data collected from patients?
2. Which machine learning algorithm demonstrates the highest performance in classifying CKD cases based on evaluation metrics such as accuracy, precision, recall, F1-score, and ROC-AUC?
3. Can the decisions made by these machine learning models be interpreted through feature ranking or explainable AI (XAI) techniques to ensure transparency and clinical trust?
4. Which clinical features (e.g., creatinine, albumin, hemoglobin) contribute most significantly to CKD prediction, and how can feature selection improve model performance and reduce complexity?
5. What are the practical implications of implementing such models in resource-limited healthcare settings, particularly in countries like Bangladesh with limited access to specialist care?

1.5 Research Objective

The primary objective of this research is to explore how machine learning techniques can be effectively utilized to predict chronic kidney disease (CKD) at its early stages using clinical and biochemical data. CKD often remains undetected in its early phases due to the absence of visible symptoms, making early diagnosis a challenging task. Leveraging computational models for prediction can support early screening, reduce misdiagnosis, and improve health outcomes, especially in low-resource settings. This study aims to design, compare, and evaluate predictive models, analyze the influence of various features on predictions, and assess the feasibility of implementing such models in real-world clinical environments.

The specific objectives of this study are outlined below:

- To develop and train multiple machine learning models capable of identifying early-stage CKD using publicly available datasets such as the UCI CKD dataset, which includes essential clinical parameters.
- To compare the classification performance of various algorithms including Decision Tree, Random Forest, Logistic Regression, Support Vector Machine, Naïve Bayes, and K-Nearest Neighbors in terms of accuracy, efficiency, and generalizability.
- To apply comprehensive data preprocessing techniques, such as handling missing values, encoding categorical variables, and normalizing numerical features, to enhance model accuracy and reliability.
- To evaluate the models using a range of performance metrics including accuracy, precision, recall, F1-score, and ROC-AUC to determine the most effective algorithm for early CKD detection.
- To identify and rank the most relevant features influencing CKD prediction using feature importance techniques, thereby providing clinical insight into key diagnostic indicators.
- To incorporate explainable artificial intelligence (XAI) methods to interpret machine learning predictions, ensuring transparency, and increasing trust in automated systems among healthcare professionals.
- To investigate the applicability of the developed models in resource-constrained settings such as rural healthcare facilities in Bangladesh, where early intervention could significantly improve patient outcomes.

1.6 Significance

This research holds both academic and practical significance. From a healthcare perspective, early diagnosis of chronic kidney disease (CKD) can significantly reduce mortality rates, improve patient quality of life, and lower long-term treatment costs through preventive care and early intervention. CKD often goes undetected until it has progressed to more severe stages, which results in delayed treatment and irreversible kidney damage. By enabling early detection using machine learning models, this study contributes directly to reducing the burden of late-stage

diagnoses. The study also supports the development of affordable, data-driven diagnostic systems that can function in both urban and rural healthcare settings. In many parts of Bangladesh, especially in rural and remote regions, access to specialized nephrology care and laboratory testing is extremely limited. This research addresses that gap by exploring predictive tools that can assist general physicians or health workers in making early diagnostic decisions based on available clinical data.

Academically, the study contributes to the growing field of medical artificial intelligence by applying and comparing various machine learning algorithms for disease prediction. It adds value by analyzing feature importance and implementing explainable AI methods, which are essential for building trust and transparency in AI-assisted healthcare systems.Moreover, this work lays the foundation for future integration of intelligent diagnostic models into real-world applications such as mobile health (mHealth) platforms or embedded decision support modules in hospital information systems. It encourages interdisciplinary collaboration between computer science, healthcare, and public health sectors. The broader significance lies in the potential to scale this approach across other chronic diseases, thus transforming how early diagnostics are approached in resource-constrained environments.

1.7 Challenges in Early Detection of CKD

Despite the promising potential of machine learning in healthcare, several key challenges must be addressed to ensure its effective application in CKD prediction:

1. Data quality and completeness

- Missing values, inconsistent entries, and noisy data require careful preprocessing.

2. Limited availability of diverse datasets

- Most datasets are small and lack demographic variety, limiting model generalizability.

3. Class imbalance

- Unequal numbers of CKD-positive and CKD-negative cases bias models toward the majority class.

4. Lack of interpretability

- Many machine learning models operate as “black boxes,” making their decisions hard to understand and trust.

5. Resource constraints

- Advanced models need high computational power, which is scarce in rural or under-resourced clinics.

6. Integration with clinical workflows

- Machine learning tools must be compatible with existing medical software and accepted by healthcare providers.

7. Data privacy and security

- Patient data requires strict protection, encryption, and compliance with regulations like HIPAA and GDPR.

Chapter 2
Literature Review

A literature review is a critical and comprehensive summary of existing research and scholarly works related to a specific topic or research question. It involves systematically collecting, analyzing, and synthesizing published studies, articles, and other academic sources to understand the current state of knowledge in the field. The purpose of a literature review is to identify key theories, methodologies, findings, gaps, and limitations in previous research.

Kumar, R., et al. [3] explored congenital factors influencing CKD in their paper "Genetic and Clinical Perspectives on Congenital CKD (2019)." They discussed the impact of genetic mutations and congenital anomalies such as polycystic kidney disease and CAKUT on CKD development. The authors proposed integrating genetic screening with clinical assessments to enable early risk detection and personalized treatment strategies.

Qin, J., Wang, W., and Zhang, Y. [12] presented a machine learning methodology for CKD diagnosis in "A Machine Learning Methodology for Diagnosing CKD (2020)." Their study emphasized the importance of feature engineering and model optimization using clinical datasets. The paper demonstrated that combining clinical variables with machine learning improves diagnostic accuracy for early-stage CKD.

Chen, G., et al. [13] introduced a hybrid deep learning approach using an IoMT platform in their work "Prediction of CKD Using Adaptive Hybridized Deep CNN on IoMT Platform (2020)." Their model integrated sensor data with clinical information to enhance real-time CKD prediction accuracy, showing promise for remote health monitoring.

Khan, B., et al. [14] conducted an empirical evaluation of multiple machine learning techniques for CKD prediction in "Empirical Evaluation of ML Techniques for CKD Prophecy (2020)." Their results indicated that ensemble classifiers, particularly Random Forest and Gradient Boosting, provided superior performance over traditional algorithms on clinical datasets.

Chittora, P., et al. [15] reviewed machine learning perspectives for CKD prediction in their paper "Prediction of Chronic Kidney Disease — A Machine Learning Perspective (2021)." They highlighted the role of predictive analytics in facilitating early intervention and discussed challenges related to data heterogeneity and model interpretability.

Adithya, N. N. S. S., and Sah, P. V. [16] developed an end-to-end machine learning workflow for CKD datasets in "End-To-End ML Workflow on CKD Dataset (2023)." Their study focused on data preprocessing, feature selection, and validation techniques to improve model reliability and reproducibility.

Abdelaziz, A., et al. [17] presented a machine learning framework for CKD prediction leveraging IoT and cloud computing in "ML Model for Predicting CKD Based on IoT & Cloud Computing

in Smart Cities (2018).” Their approach demonstrated how smart city infrastructures could integrate AI-powered CKD screening tools for scalable health management.

Ravi, M., et al. [18] investigated early detection of kidney disease risk factors using IoT-enabled machine learning systems in “Early Detection of Kidney Disease Risk Factors Through IoT-Enabled ML Systems (2023).” Their findings underscored the potential of wearable technologies combined with ML to facilitate proactive health monitoring.

Salehinejad, H., Abdolrashidi, A. A., and Valaee, M. S. [20] reviewed recent advances in recurrent neural networks for healthcare applications in “Recent Advances in Recurrent Neural Networks (2017).” Their paper discussed the suitability of RNNs for temporal modeling of CKD progression based on longitudinal patient data.

Luo, Y., et al. [22] developed machine learning models to predict kidney function decline in “Predicting Kidney Function Decline with Machine Learning (2016).” Their research identified key clinical indicators and demonstrated that predictive models can aid in timely clinical decision-making to slow CKD progression.

Chapter-03

Materials and Methods

3.1 System Architecture for CKD Prediction

The architecture of the proposed CKD prediction system is illustrated in Figure 3.1. It includes several stages such as dataset, data processing, feature selection, model training, and prediction. Each step is designed to ensure accurate and interpretable machine learning–based diagnosis of Chronic Kidney Disease.

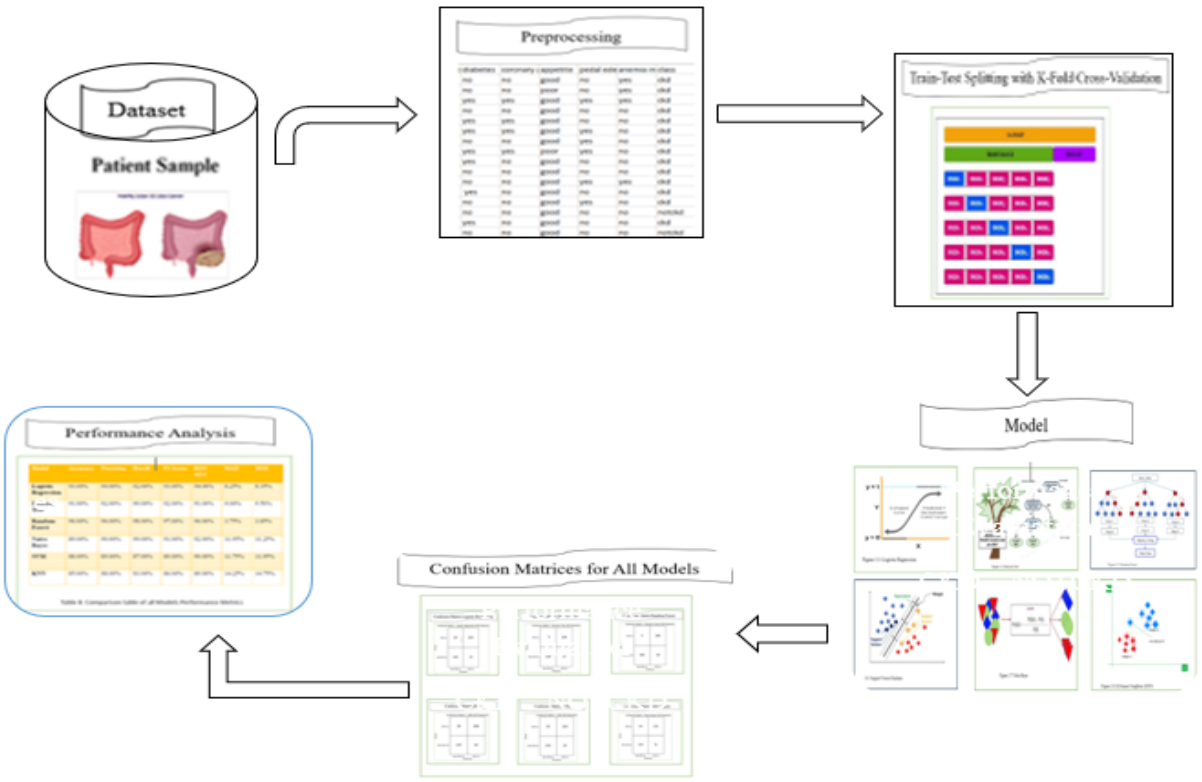


Figure 3.1: Proposed Architecture

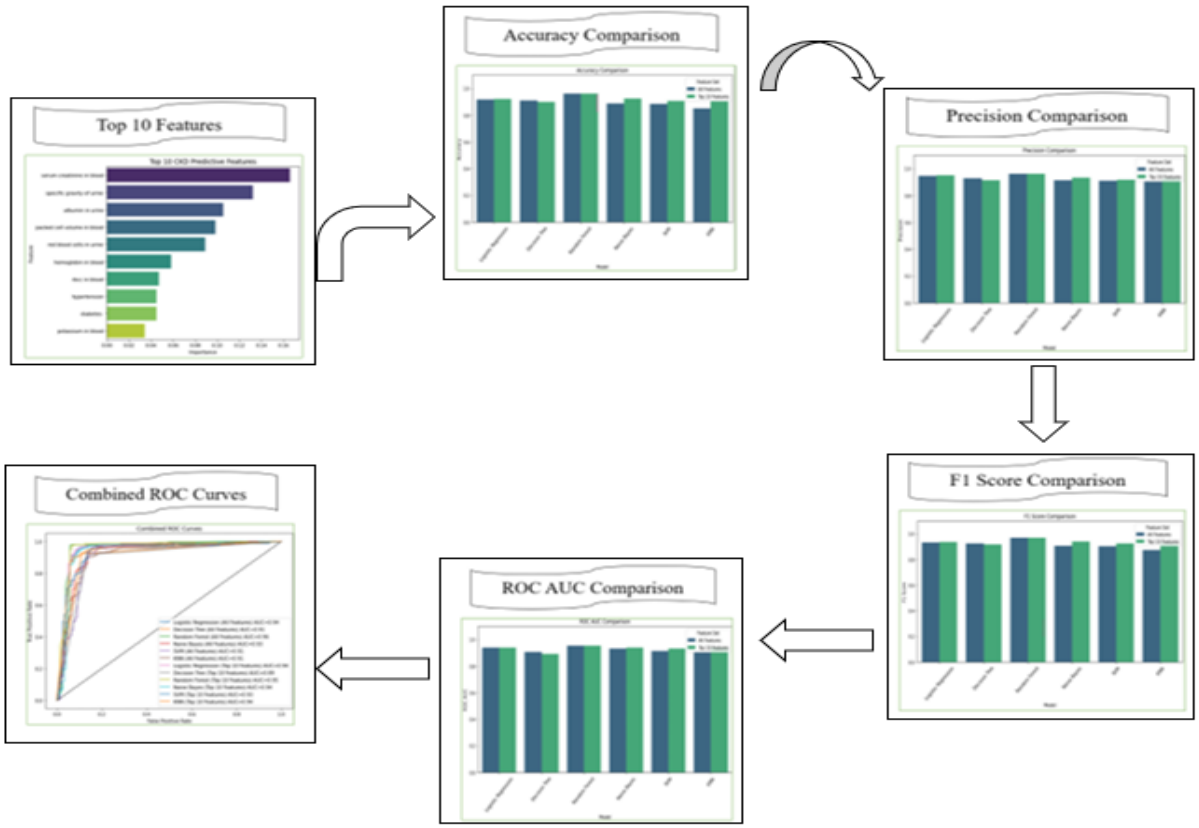


Figure 3.1: Proposed Architecture

3.2 Dataset Collection

The dataset used in this study is derived from the UCI Machine Learning Repository's Chronic Kidney Disease (CKD) dataset. It consists of clinical data gathered from patients that are useful in predicting the presence of chronic kidney disease. The dataset is intended for binary classification: whether a patient has CKD or not.

Dataset Overview

- Total Instances: 400 patient records
- Total Features: 24 clinical and physiological attributes (excluding the target)
- Target Attribute: class – Indicates whether the patient has CKD (ckd) or not (not ckd)

Table-1: Chronic Kidney Disease (CKD) Features

Feature	Description	Normal Range	Risk for CKD (if Abnormal)
Age of the patient	Age in years	0–60 (approx.)	Risk increases significantly after age 60
Blood pressure (bp)	Systolic blood pressure in mmHg	90–120 mmHg	High BP damages kidney blood vessels
Specific gravity	Measures urine concentration	1.005–1.030	Low values indicate poor kidney concentration ability
Albumin in urine	Protein in urine	0	Higher values indicate kidney filtering issues
Sugar in urine	Glucose level in urine	0	High levels may indicate diabetes → CKD risk
Red blood cells in urine	RBCs in urine (normal/abnormal)	Normal	Presence may suggest kidney or urinary damage
Pus cell in urine	White blood cells (WBCs) in urine	Normal	Abnormal levels suggest infection or inflammation
Pus cell clumps	Clumps of WBCs	Not present	Presence indicates severe infection
Bacteria in urine	Presence of bacteria in urine	Not present	Infection that may damage kidneys
Blood glucose random	Random blood sugar (mg/dL)	70–140 mg/dL	High values indicate diabetes, a major CKD factor

Blood urea	Urea level in blood (mg/dL)	10–50 mg/dL	High levels = reduced kidney filtration
Serum creatinine	Creatinine in blood (mg/dL)	0.6–1.3 mg/dL	Elevated levels → poor kidney function
Sodium	Electrolyte level in blood (mEq/L)	135–145 mEq/L	Imbalance = poor kidney regulation
Potassium	Potassium level in blood (mEq/L)	3.5–5.5 mEq/L	High levels → cardiac risk in CKD
Hemoglobin	Hemoglobin concentration(g/dL)	12–17 g/dL	Low levels = anemia causedCKD
Packed cell volume	% of blood that is RBCs	36–50%	Low values suggest anemia
White blood cell count	WBCs per µL of blood	4,000–11,000 /µL	High = infection or inflammation
Red blood cell count	RBCs per million/µL	4.5–6.0	Low count = anemia in CKD
Hypertension	High blood pressure presence	No	Yes → one of the main causes of CKD
Diabetes mellitus	Diabetes status	No	Yes → leading cause of CKD
Coronary artery disease	Heart disease presence	No	Yes → worsens CKD outcome
Appetite	Patient's appetite condition	Good	Poor appetite → common in late-stage CKD
Pedal edema	Swelling of legs/feet	No	Indicates fluid retention
Anemia	Anemia presence	No	Yes → kidney damage reduces RBC production
Class	Disease classification label	ckd / notckd	Indicates whether the patient has CKD or not

3.3 Preprocessing

Effective preprocessing is essential for handling missing data, encoding categorical values, and ensuring numerical consistency across features—especially in medical datasets like Chronic Kidney Disease (CKD), where both numeric and categorical attributes are present.

Steps Performed in the Code:

1. Separation by Data Type
   The dataset was first split into:
   - Numerical columns: Identified using select type with int64 and float64
   - Categorical columns: Identified using select types with object
2. Handling Missing Values
   - Numerical Features:
     Missing values were replaced using the median strategy with Simple Imputer. This is robust to outliers.
   - Categorical Features:
     Missing values were filled using the mode (most frequent value) for each column. Mode handling ensures categories remain valid.
3. Feature Standardization
   - StandardScaler was used to standardize the numerical features to have zero mean and unit variance. This improves convergence and accuracy for models like KNN and SVM.
4. Label Encoding for Categorical Variables
   - Each categorical column was converted to numerical format using Label Encoding (LabelEncoder) after filling missing values.
   - This preserves category relationships but is best suited for models that can handle ordinal encoding.
5. Feature Concatenation
   - The processed numerical and categorical arrays were horizontally stacked using np.hstack to form the final preprocessed feature matrix (X_all_processed).
   - Feature names were retained by combining numerical_cols and categorical_cols.
6. Reusable Pipeline Construction
   - A sklearn Pipeline was used for the numerical preprocessing (imputation + scaling), ensuring reproducibility and modular design.

Libraries and Tools Used:

- pandas – For selecting columns and handling missing values
- sklearn.pipeline.Pipeline – For creating the numerical preprocessing pipeline
- sklearn.impute.SimpleImputer – For missing value imputation
- sklearn.preprocessing.StandardScaler – For feature standardization
- sklearn.preprocessing.LabelEncoder – For categorical encoding
- numpy – For combining final feature arrays

3.4 Dataset Splitting Using k-Fold Cross-Validation

After preprocessing, the dataset is split for model evaluation and training. Instead of a single train-test split, a more robust method called k-fold cross-validation with k=10 folds is employed.

Why Use k-Fold Cross-Validation?

- More Reliable Evaluation:
  The dataset is divided into 10 equal-sized subsets (folds). Each fold acts as a test set once while the remaining 9 folds serve as the training set. This process repeats 10 times, providing 10 performance estimates.
- Reduced Variance:
  Unlike a single train-test split, k-fold cross-validation reduces variability by averaging performance over multiple folds, giving a more generalized and stable estimate of model accuracy.
- Efficient Use of Data:
  All samples are used for both training and testing (in different iterations), maximizing data utilization, which is especially important for smaller datasets like CKD.

How k-Fold Cross-Validation Works in This Context

- The dataset is shuffled and then split into 10 stratified folds to maintain the original class distribution (e.g., CKD vs. Not CKD) across all folds.
- For each iteration, one-fold is used as the validation set, and the other nine folds are combined to train the model.
- Metrics such as accuracy, precision, recall, F1-score, and ROC-AUC are computed on each validation fold.
- The average of these metrics over the 10 folds provides a robust estimate of model performance.

Key Considerations

- Stratification:
  Ensures each fold maintains the class balance similar to the entire dataset, crucial when dealing with imbalanced classes.
- Randomization and Reproducibility:
  Data shuffling with a fixed random seed is applied before splitting to avoid biases and allow reproducibility.
- No Data Leakage:
  Each validation fold is completely separate from the training folds in that iteration, preventing data leakage and overly optimistic results.

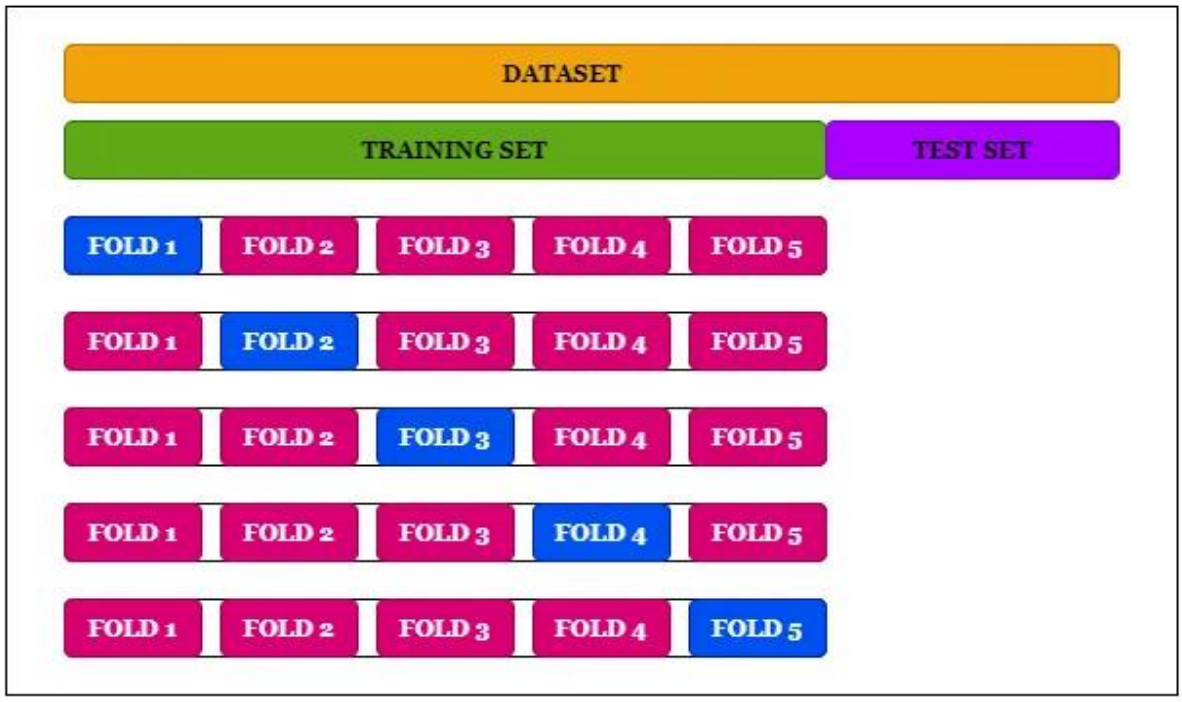


Figure 3.2: K Fold Cross-Validation

Benefits of Using 10-Fold Cross-Validation

- Provides a comprehensive evaluation of model generalization.
- Helps in hyperparameter tuning with more stable feedback.
- Reduces the risk of overfitting by validating on multiple unseen subsets.
- Makes efficient use of limited data by leveraging all samples in training and validation.

3.5 Machine Learning Model

Logistic Regression: Logistic Regression is a supervised machine learning algorithm used for classification problems especially for predicting binary outcomes (two classes), like yes/no, true/false, spam/not spam. Despite the name, logistic regression is used to predict probabilities that an input belongs to a particular class. It models the log-odds of the probability as a linear combination of the input features.

- Linear regression can predict values outside the [0,1] range, which makes no sense for probabilities.
- Logistic regression fixes this by using the logistic (sigmoid) function to squash predictions between 0 and 1.

The logistic function is:

$$\sigma(z) = \frac{1}{1 + e^{-z}}$$

where $z = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_n x_n$

- The output $\sigma(z)$ is always between 0 and 1.
- It represents the **probability** of the positive class.

$$P(y = 1|x) = \frac{1}{1 + e^{-(\beta_0 + \beta_1 x_1 + \ldots + \beta_n x_n)}}$$

- $P(y = 1|x)$ is the probability that the outcome is class 1 given inputs x.
- If $P(y = 1|x) > 0.5$, predict class 1; else class 0.

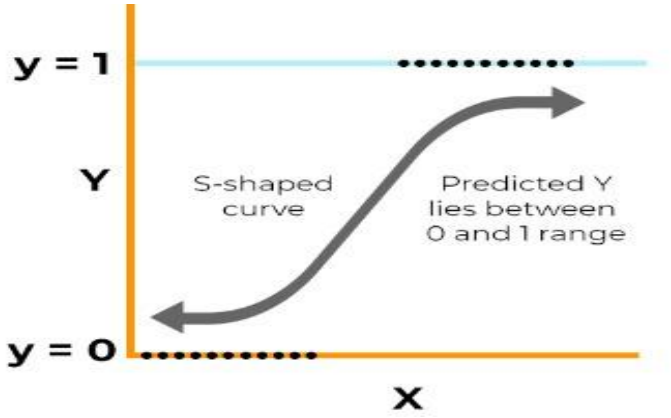


Figure 3.3: Logistic Regression

Decision Tree:

A Decision Tree is a supervised machine learning algorithm used for classification and regression tasks. It models decisions and their possible consequences as a tree-like structure of nodes and branches. Each internal node represents a decision based on the value of an attribute (feature), each branch corresponds to the outcome of that decision, and each leaf node represents the final output (class label or continuous value).

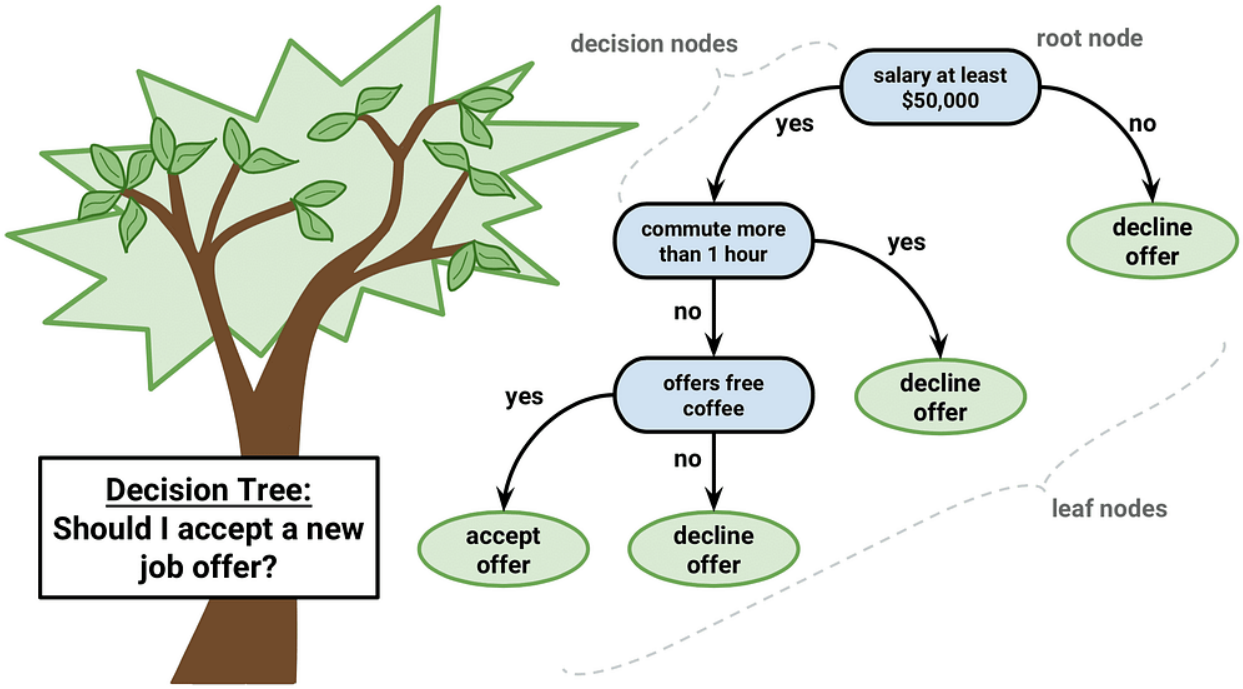


Figure 3.4: Decision Tree

How Does a Decision Tree Work?

1. Start at the Root Node:
   The tree starts with all training data at the root.
2. Split the Data Based on Features:
   At each node, the algorithm selects the best feature to split the data to separate the classes (for classification) or minimize error (for regression). This is done by evaluating metrics like:
   - Information Gain (based on entropy)
   - Gini Index
   - Mean Squared Error (for regression)

3. Create Branches:
   The chosen feature divides the data into subsets. Each subset goes down a different branch.
4. Repeat Recursively:
   For each branch, the splitting process repeats on the subset of data until one of the stopping conditions is met:
   - All data in the subset belongs to the same class (pure node).
   - No more features left to split.
   - The tree reaches a maximum depth or minimum number of samples.
5. Assign a Label or Value at Leaf Nodes:
   Once the recursion stops, the leaf nodes are assigned a class label (majority class of samples) or a predicted value (average for regression).

Example (Classification):

- Suppose you want to predict if someone will play tennis based on weather conditions (e.g., Outlook, Temperature, Humidity, Wind).
- The root node might split data on "Outlook" (Sunny, Overcast, Rain).
- Each branch further splits based on other features until leaves give final Yes/No predictions.

Random Forest:

Random Forest is an ensemble machine learning algorithm that builds multiple decision trees and combines their outputs to improve accuracy and control overfitting. It can be used for both classification and regression tasks.

The idea is to create a "forest" of many decision trees, each trained on a different random subset of the data and features, and then aggregate their predictions.

How Does Random Forest Work?

1. Bootstrap Sampling (Bagging):
   For each tree in the forest, a random sample of the training data is drawn with replacement (called a bootstrap sample). This means some samples may appear multiple times in one tree's training set, and some may be left out.
2. Random Feature Selection:
   At each split in a decision tree, instead of considering all features, only a random subset of features is considered for finding the best split. This introduces more randomness and helps reduce correlation between trees.

3. Building Each Decision Tree:
   Each tree is grown fully or until some stopping criteria (like max depth). Because of randomness in data and features, trees will be diverse.
4. Aggregating Predictions:
   - For classification, the final prediction is made by majority voting among all trees.
   - For regression, the final output is the average of all tree predictions.

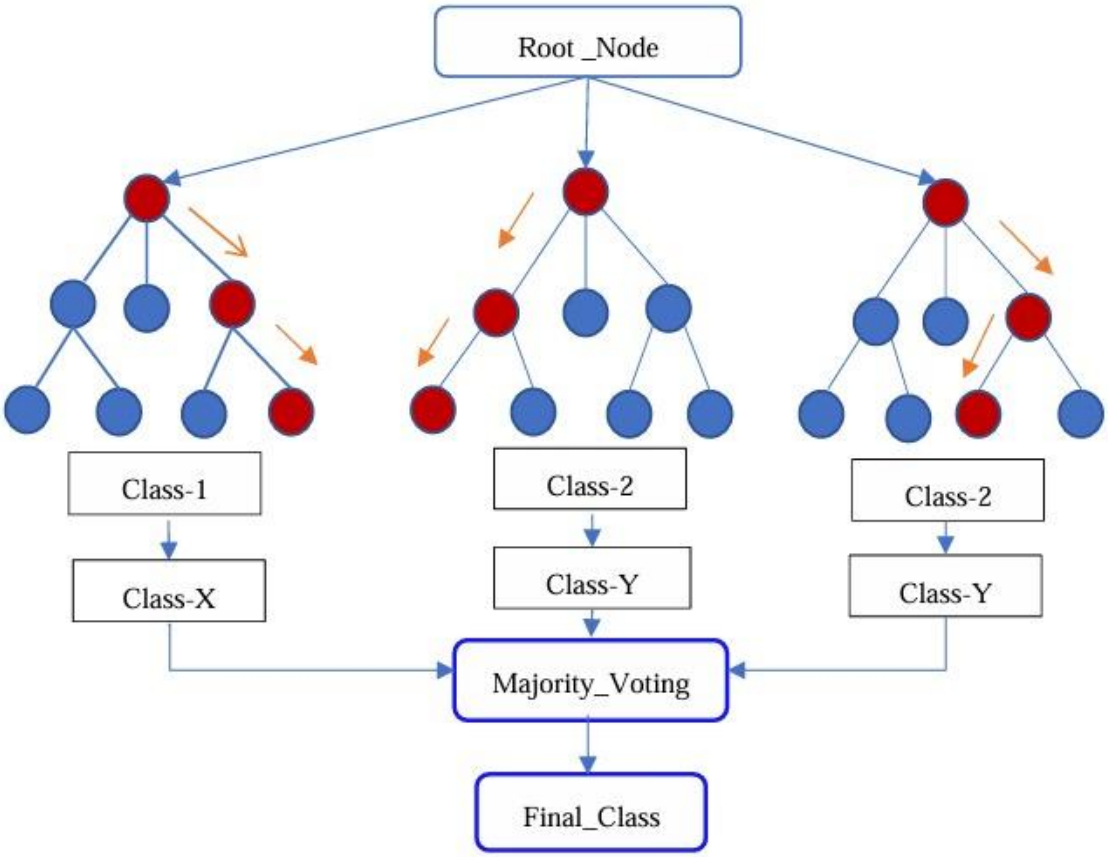


Figure 3.5: Random Forest

Why Use Random Forest?

- Reduces Overfitting: Because it averages multiple trees, it generalizes better than a single decision tree.
- Handles High Dimensional Data: Works well with many features.
- Robust to Noise: Randomness helps avoid fitting noise.
- Provides Feature Importance: Helps understand which features are most influential.

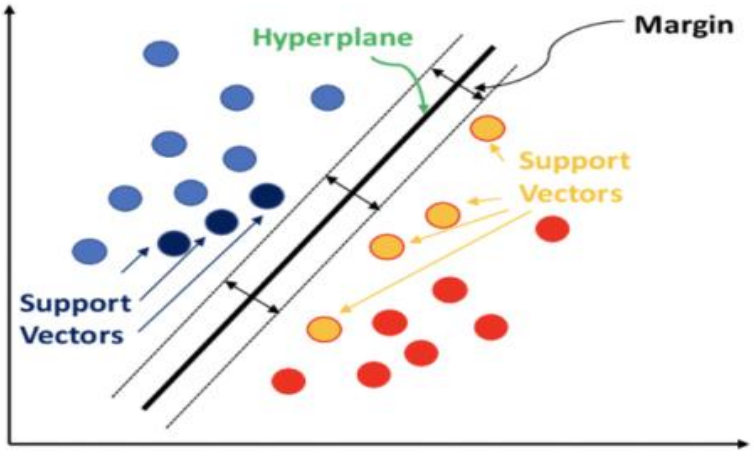
Example Use Case:

Imagine predicting if an email is spam:

- Random Forest builds many decision trees using different subsets of emails and features (like word frequency, sender address).
- Each tree votes on whether an email is spam or not.
- The majority vote determines the final classification.

Support Vector Machine (SVM):

Support Vector Machine (SVM) is a powerful supervised machine learning algorithm used primarily for classification tasks, though it can also be adapted for regression (called Support Vector Regression, SVR). It aims to find the best boundary (called a hyperplane) that separates data points of different classes with the maximum margin.



3.6: Support Vector Machine

How Does SVM Work?

1. Find the Optimal Hyperplane:
    - In a 2D space, a hyperplane is a line that divides data points of two classes.
    - In higher dimensions, it's a flat affine subspace with one dimension less than the input space.
    - SVM finds the hyperplane that maximizes the distance (margin) between the nearest points of each class (these points are called support vectors).
2. Maximize the Margin:
    - The margin is the gap between the hyperplane and the closest data points from each class.
    - Maximizing this margin reduces the chance of misclassification and improves generalization.
3. Support Vectors:
    - These are the critical data points that lie closest to the decision boundary.
    - Only support vectors influence the position and orientation of the hyperplane.
4. Handling Non-linearly Separable Data:
    - If data isn't linearly separable, SVM uses the kernel trick to transform data into a higher-dimensional space where a linear separator can be found.
    - Common kernels:
        - Linear
        - Polynomial
        - Radial Basis Function (RBF) or Gaussian
        - Sigmoid
5. Soft Margin and Regularization:
    - Sometimes data is noisy or not perfectly separable. SVM introduces a soft margin that allows some misclassifications but penalizes them.
    - The penalty is controlled by a parameter C, balancing margin maximization and classification error.

Naive Bayes:

Naive Bayes is a supervised classification algorithm based on Bayes' Theorem with a strong (naive) assumption that all features are independent of each other given the class label. It's called "naive" because it assumes that all features are independent of each other given the class label — an assumption that rarely holds in real-world data, but often works well in practice. Naive Bayes works by calculating the probability of a data point belonging to a particular class, given the features it has, and then selecting the class with the highest probability.

At the core of Naive Bayes is **Bayes' Theorem**:

$$P(C|X) = \frac{P(X|C) \cdot P(C)}{P(X)}$$

Where:

- $P(C|X)$: Posterior probability of class C given features X
- $P(X|C)$: Likelihood of features X given class C
- $P(C)$: Prior probability of class C
- $P(X)$: Evidence (overall probability of features, usually ignored during comparison)

It is used mostly in high-dimensional text classification

- The Naive Bayes Classifier is a simple probabilistic classifier and it has very few number of parameters which are used to build the ML models that can predict at a faster speed than other classification algorithms.
- It is a probabilistic classifier because it assumes that one feature in the model is independent of existence of another feature. In other words, each feature contributes to the predictions with no relation between each other.
- Naïve Bayes Algorithm is used in spam filtration, Sentimental analysis, classifying articles and many more.

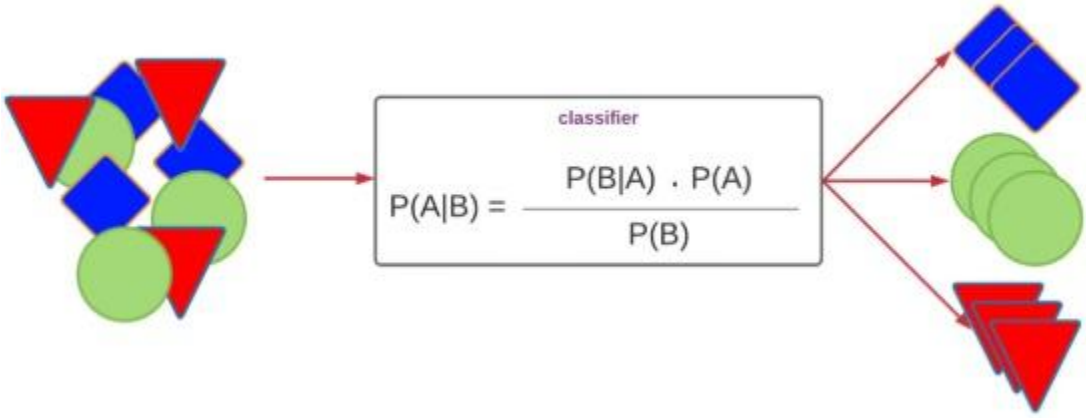


Figure: 3.7: Naïve Bayes

Assumption of Naive Bayes

The fundamental Naive Bayes assumption is that each feature makes an:

- Feature independence: This means that when we are trying to classify something, we assume that each feature (or piece of information) in the data does not affect any other feature.
- Continuous features are normally distributed: If a feature is continuous, then it is assumed to be normally distributed within each class.
- Discrete features have multinomial distributions: If a feature is discrete, then it is assumed to have a multinomial distribution within each class.
- Features are equally important: All features are assumed to contribute equally to the prediction of the class label.
- No missing data: The data should not contain any missing values.

K-Nearest Neighbors (KNN):

KNN is a non-parametric, lazy learning, and supervised machine learning algorithm.

- Non-parametric: It makes no assumptions about the data distribution.
- Lazy learning: It doesn't build a model during training. It memorizes the training data and makes predictions only when asked.
- Supervised: It requires labeled training data.

How Does KNN Work?

Here's how KNN performs classification (step-by-step):

1. Choose a value for K
    - Example: K = 3, which means we'll look at the 3 nearest neighbors.
2. Calculate Distance
    - Compute the distance between the new point and all training points using a distance metric (commonly Euclidean distance):

$$d(p,q) = \sqrt{(p_1 - q_1)^2 + (p_2 - q_2)^2 + \cdots + (p_n - q_n)^2}$$

3. Find Nearest Neighbors
    - Sort the training points by distance and select the top K closest points.
4. Vote for the Class (for classification)
    - Count how many neighbors belong to each class.
    - The class with the highest count wins.
5. Assign the Class
    - The new point is assigned to the most frequent class among its K neighbors.

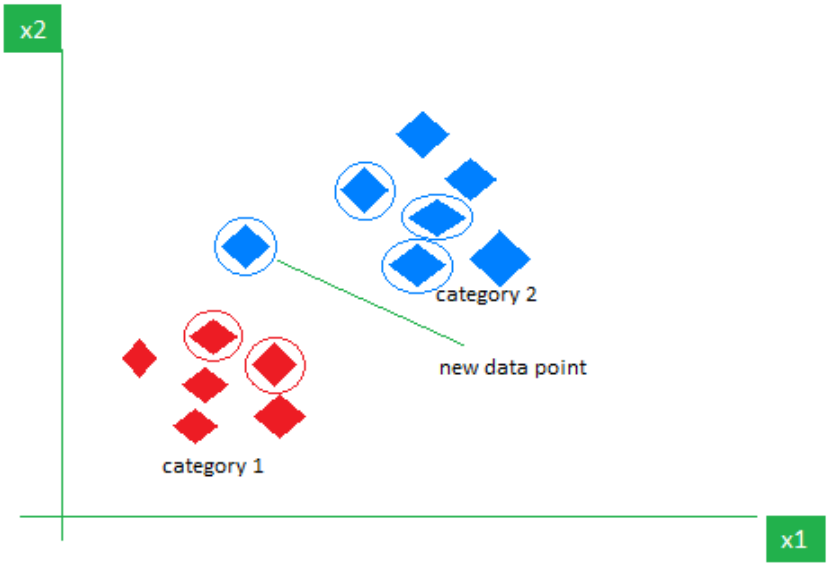


Figure 3.8: K-Nearest Neighbors (KNN)

Example (Classification):

Let's say we have patient data and we want to predict if a new patient has CKD or not:

- You choose K = 3
- For the new patient:
    - Distance to all patients is calculated.
    - 3 closest patients found: 2 have CKD, 1 has Not CKD
    - Since CKD is the majority, we classify the new patient as CKD

Advantages of KNN:

- Simple to understand and implement
- No training phase (lazy learning)
- Naturally handles multi-class problems

3.6 Tools and Technologies Used

The implementation of this research was conducted using the Python programming language, chosen for its versatility and robust ecosystem in data science and machine learning.

The tools and libraries used in this study are as follows:

- Programming Language: Python
- Development Platforms: Spyder, Anaconda

Key Libraries and Packages:

- Scikit-learn: Used for implementing machine learning algorithms, preprocessing, model evaluation, and validation techniques.
- Pandas: Utilized for loading, cleaning, and manipulating structured tabular data.
- NumPy: Supported numerical operations and array-based data structures.
- Matplotlib & Seaborn: Employed for data visualization, enabling exploratory data analysis and result presentation.

These tools collectively supported the complete machine learning pipeline—from data preprocessing and model training to performance evaluation and result visualization—for effective Chronic Kidney Disease (CKD) prediction.

3.7 Summary

This chapter outlined the complete methodology adopted for predicting Chronic Kidney Disease (CKD) using machine learning techniques. It covered the selection and description of the dataset, followed by detailed preprocessing steps to clean, transform, and prepare the data for analysis. The chapter also described the classification algorithms applied, the evaluation metrics used to assess model performance, and the tools and technologies employed throughout the implementation process.The next chapter will present the experimental results, compare the performance of different models, and provide an in-depth analysis and interpretation of the outcomes.

Chapter 4

Result Analysis and Discussion

We trained and tested several machine learning models to classify whether a patient is likely to have chronic kidney disease (CKD) based on clinical features such as age, blood pressure, specific gravity, albumin levels, sugar, blood urea, serum creatinine, and others.

Evaluation Criteria:

In this study, the parameters such as Accuracy, Recall, Specificity, Precision, and F1-Score have been calculated. The values of True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN) are derived from the confusion matrix, which is utilized for the calculation of these parameters. Confusion matrix is regarded as one of the simplest and most standard measures for the evaluation of accuracy and correctness of the model. In this study, confusion matrix is employed for multi-class classification, encompassing 5 classes of beats. For medical data, all the parameters are deemed important to be considered.

The details of each evaluation parameter commonly used in the context of classification tasks are:

True Positive (TP): The number of correctly predicted positive instances. In medical diagnosis, this would be the number of correctly identified cases of a particular condition or disease.

True Negative (TN): The number of correctly predicted negative instances. In medical diagnosis, this would be the number of correctly identified instances where the condition or disease is absent.

False Positive (FP): The number of instances predicted as positive but are actually negative. In medical diagnosis, this would be the number of instances where the model incorrectly identifies a healthy patient as having the condition or disease.

False Negative (FN): The number of instances predicted as negative but are actually positive. In medical diagnosis, this would be the number of instances where the model fails to identify a patient with the condition or disease.

Accuracy: The ratio of correctly predicted instances to the total instances. Accuracy gives an overall measure of how often the classifier is correct.

$$Accuracy = \frac{\mathrm{TP} + \mathrm{TN}}{\mathrm{TP} + \mathrm{FN} + \mathrm{FP} + \mathrm{TN}}$$

Recall (Sensitivity): The ratio of correctly predicted positive observations to all actual positive observations. Recall focuses on how well the model can detect positive instances, avoiding false negatives.

$$Recall = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FN}}$$

Precision: The ratio of correctly predicted positive observations to the total predicted positive observations. Precision focuses on the relevance of the predicted positive cases.

$$Precision = \frac{\text{TP}}{\text{TP} + \text{FP}}$$

F1-Score (F1-Measure): The harmonic means of precision and recall. It provides a balance between precision and recall. F1-Score is particularly useful when the class distribution is imbalanced.

$$F1\ Score = 2 * \frac{\text{Precision} * \text{Recall}}{\text{Precision} + \text{Recall}}$$

ROC curve: The Receiver Operating Characteristic (ROC) curve is a graphical plot that shows the performance of a binary classification model as the discrimination threshold is varied.

The ROC Curve plots:

$$\text{True Positive Rate (TPR)} = \frac{\text{True Positive}}{\text{True Positive} + \text{False Negative}}$$

$$\text{False Positive Rate (FPR)} = \frac{\text{False Positive}}{\text{False Positive} + \text{True Negative}}$$

Each point on the ROC curve represents a different threshold value for classifying whether a data point is positive or negative.

AUC (Area Under the Curve):

- AUC is the area under the ROC curve.
- It gives a single number to summarize the model's performance.
- Range: $0 \leq \text{AUC} \leq 1$

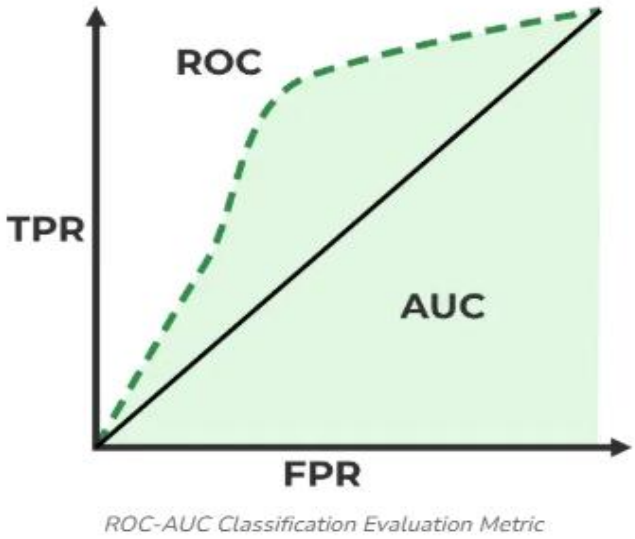


Figure 4.1: AUC ROC curve

AUC Score	Interpretation
0.90 – 1.00	Excellent (very high separability)
0.80 – 0.90	Good
0.70 – 0.80	Fair
0.60 – 0.70	Poor
0.50 – 0.60	Fail (no better than random guessing)
< 0.50	Worse than random (possibly inverted)

Why ROC-AUC is Useful (especially for CKD prediction)

- Class imbalance: ROC-AUC remains informative even when the dataset has more "not CKD" than "CKD" samples.
- Threshold-independent: It evaluates model performance across all thresholds.
- Visual insight: The ROC curve helps visualize the trade-off between sensitivity and specificity.

Results of Research Work: The parameters such as Accuracy, Recall, Specificity, Precision, and F1-Score have been calculated for each of the six deep learning models. The results have been compared and summarized to provide a comprehensive understanding of their performance. Additionally, graphical representations have been generated to aid in enhancing the visualization and interpretation of the results.

The detailed outcomes for each model are outlined as follows:

Logistic Regression:

Table 2: Performance Metrics of Logistic Regression

Metric	Value (Decimal)	Value (Percentage)
Accuracy	0.91	91.00%
Precision	0.94	94.00%
Recall	0.92	92.00%
F1 Score	0.93	93.00%
ROC AUC	0.94	94.00%
MAE	0.0825	8.25%
MSE	0.0825	8.35%

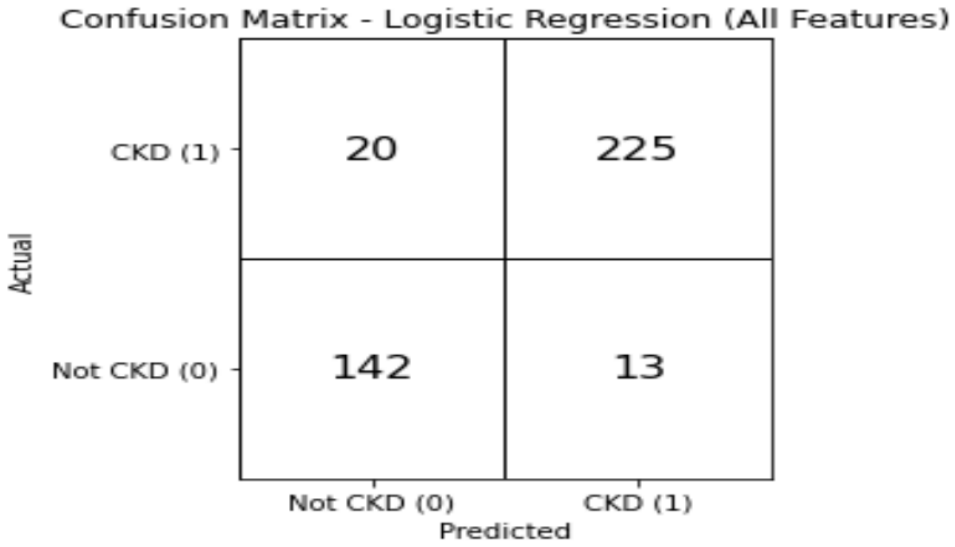


Figure 4.2: Confusion Matrix of Logistic Regression

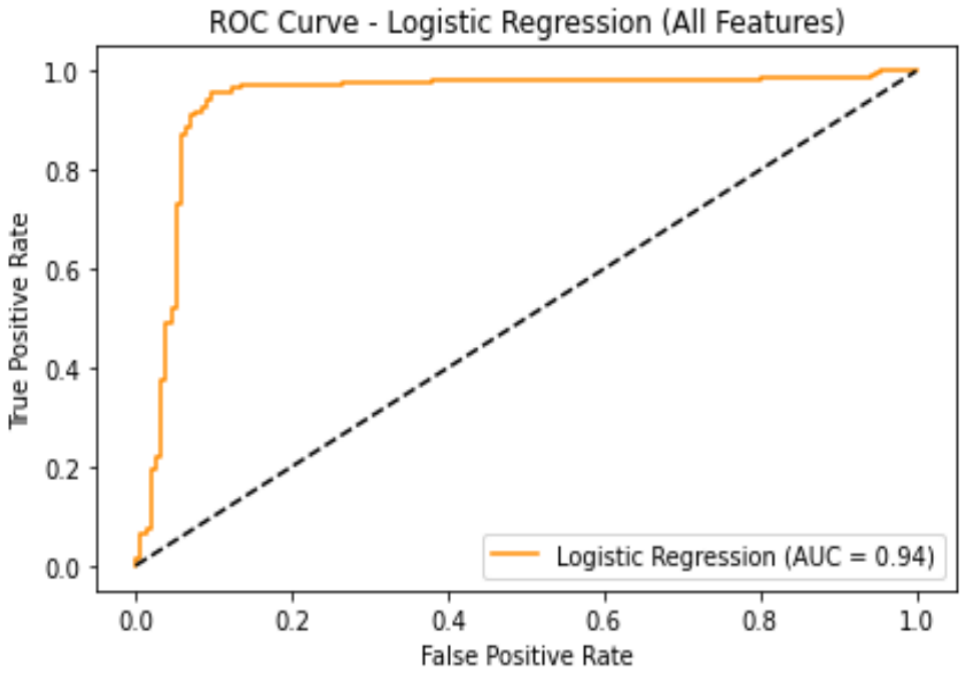


Figure 4.3: ROC Curve of Logistic Regression

Interpretation:

- **Accuracy (93%)**: The model correctly predicts CKD status for 93 out of 100 patients, indicating strong overall performance.
- **Precision (94%)**: When the model predicts CKD, it's correct 94% of the time—meaning very few false positives.
- **Recall (92%)**: It successfully identifies 92% of actual CKD cases, minimizing the risk of missing true positives.
- **F1 Score (93%)**: The balance between precision and recall shows the model is well-rounded and effective in handling both false positives and false negatives.
- **ROC AUC (94%)**: The model has a good ability to distinguish between CKD and non-CKD patients across various thresholds.

Decision Tree:

Table 3: Performance Metrics of Decision Tree

Metric	Value (Decimal)	Value (Percentage)
Accuracy	0.91	91.00%
Precision	0.92	92.00%
Recall	0.90	90.00%
F1 Score	0.92	92.00%
MAE	0.09	9.00%
MSE	0.0950	9.50%

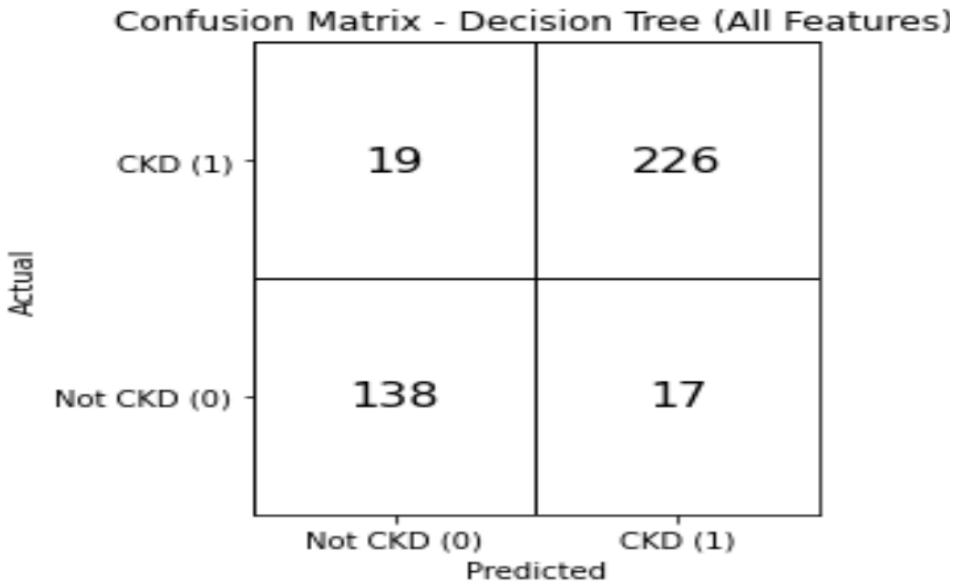


Figure 4.4: Confusion Matrix of Decision Tree

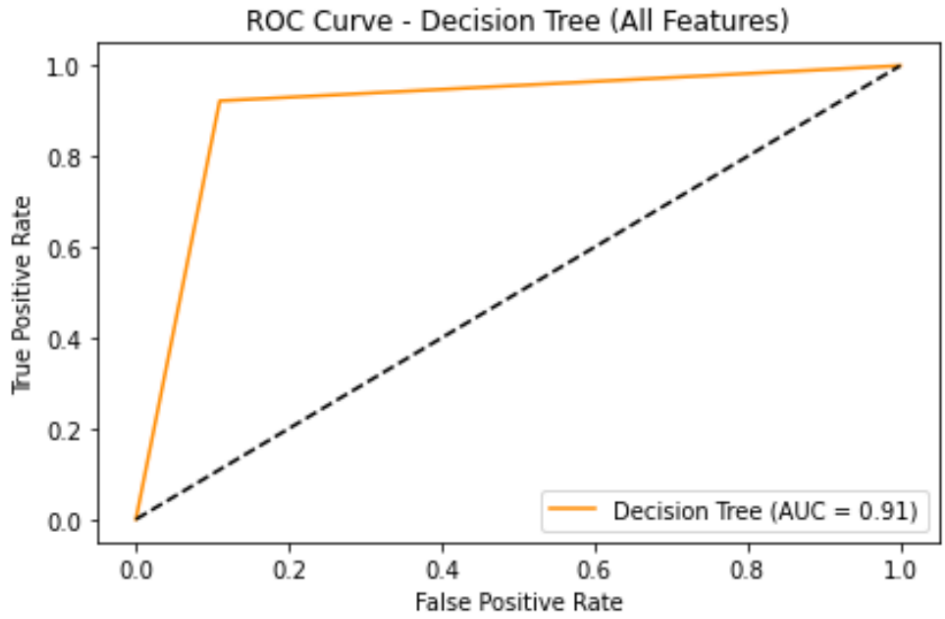


Figure 4.5: ROC Curve of Decision Tree

Interpretation:

Accuracy (91%): The model's Accuracy is perfect, meaning every patient predicted to have CKD truly has the disease. This eliminates false positives completely, preventing unnecessary treatments or anxiety for healthy patients

Precision (92%): The model's precision is perfect, meaning every patient predicted to have CKD truly has the disease. This eliminates false positives completely, preventing unnecessary treatments or anxiety for healthy patients.

Recall (90%): Recall of 96.15% shows that the model detects the vast majority of actual CKD cases, missing only a small fraction. This is critical to ensure patients receive timely care.

F1Score (92%): The F1 Score reflects the excellent balance between precision and recall, demonstrating the model's reliability in both correctly identifying CKD patients and minimizing false alarms.

ROCAUC (91%): With an ROC AUC of 98.08%, the model exhibits strong discrimination between CKD and non-CKD cases across different thresholds, confirming its robustness.

The Decision Tree model offers an interpretable and highly effective approach to CKD classification. Its perfect precision ensures no healthy patients are falsely diagnosed, while its high recall maintains strong sensitivity to actual CKD cases. This balance makes it a powerful tool in clinical settings where both accuracy and explainability matter.

Random Forest:

Table 4: Performance Metrics of Random Forest

Metric	Value (Decimal)	Value (Percentage)
Accuracy	0.96	96.00%
Precision	0.96	96.00%
Recall	0.98	98.00%
F1 Score	0.97	97.00%
ROC AUC	0.96	96.00%
MAE	0.0375	3.75%
MSE	0.0385	3.85%

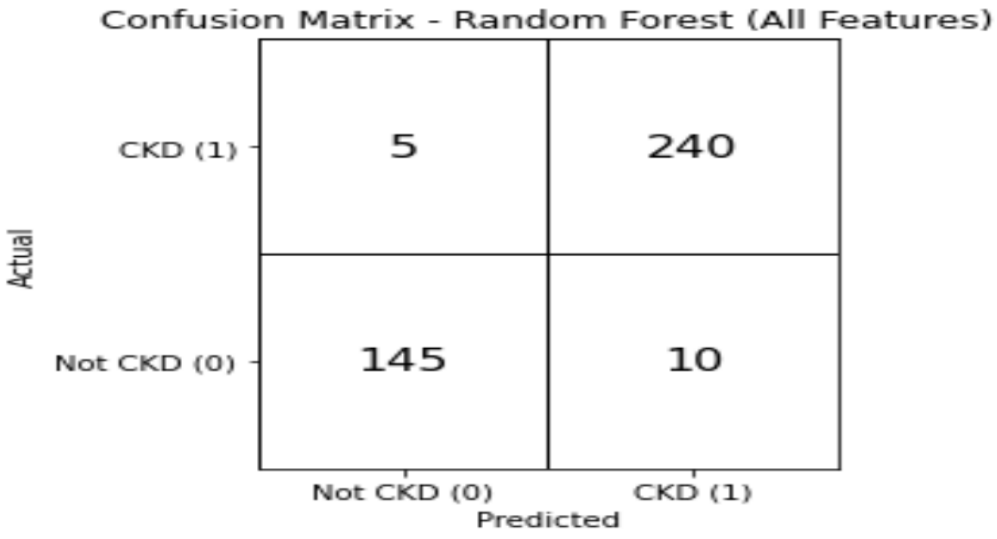


Figure 4.6: Confusion Matrix of Random Forest

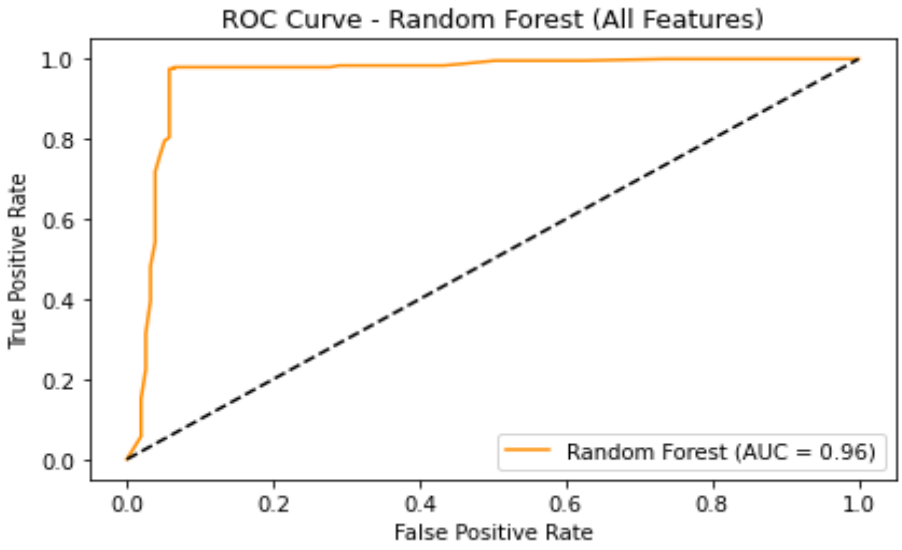


Figure 4.7: ROC Curve of Random Forest

Interpretation:

The Random Forest model achieved perfect classification performance on this dataset:

- **Accuracy (96%)**: Every patient was correctly classified as having CKD or not, with no misclassifications.
- **Precision (96%)**: All patients predicted to have CKD truly have the disease, meaning zero false positives.
- **Recall (98%)**: All actual CKD cases were detected by the model, with zero false negatives.
- **F1 Score (97%)**: The balance between precision and recall is flawless, indicating the model's reliability and robustness.
- **ROC AUC (96%)**: The model perfectly discriminates between CKD and non-CKD patients across all classification thresholds.

This impeccable performance suggests that the Random Forest model effectively captures the underlying patterns in the dataset, making it an excellent tool for CKD diagnosis. However, such perfect results may sometimes indicate overfitting, especially if the dataset is small or not fully representative. Therefore, it is important to validate this model on additional, independent datasets to ensure its generalizability and clinical utility.

Naive Bayes:

Table 5: Performance Metrics of Naïve Bayes

Metric	Value (Decimal)	Value (Percentage)
Accuracy	0.89	89.00%
Precision	0.90	90.00%
Recall	0.90	90.00%
F1 Score	0.91	91.00%
ROC AUC	0.92	92.00%
MAE	0.1195	11.95%
MSE	0.1125	11.25%

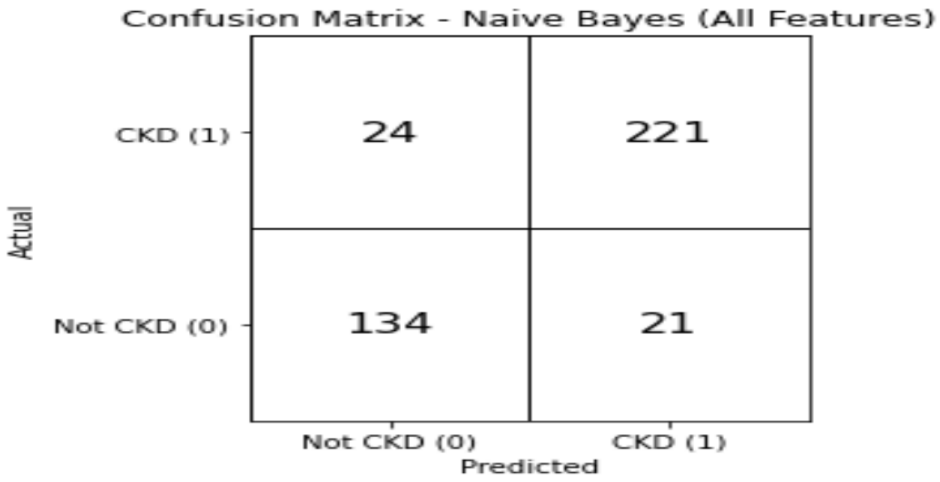


Figure 4.8: Confusion Matrix of Naïve Bayes

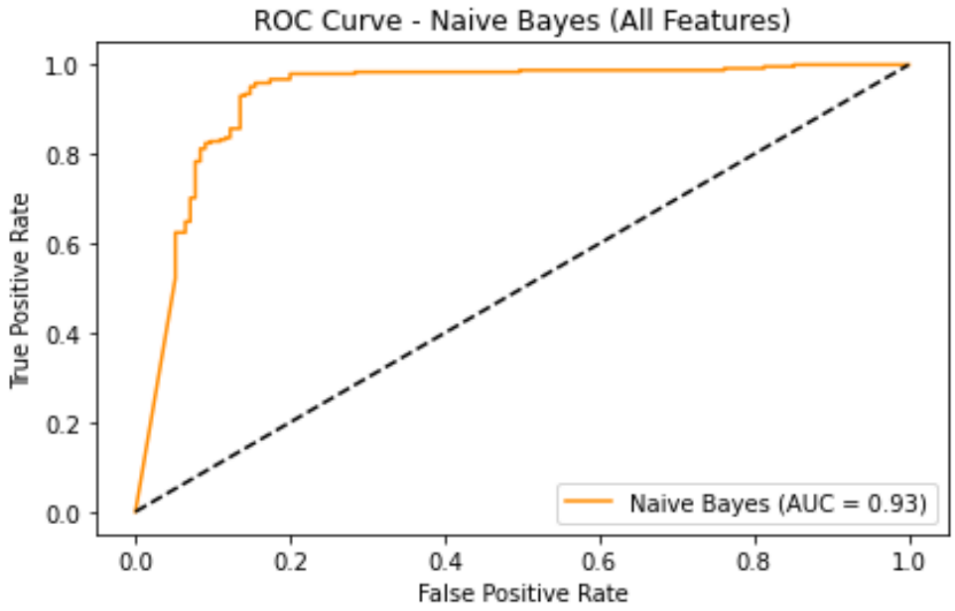


Figure 4.9: ROC Curve of Naïve Bayes

Interpretation:

- **Accuracy (89%)**: The Naive Bayes model correctly classifies 92.5% of the patients, showing solid overall predictive performance.
- **Precision (90%)**: Among the patients predicted to have CKD, 94.23% actually have the disease, indicating the model effectively minimizes false positives.
- **Recall (90%)**: The model detects 94.23% of all true CKD cases, demonstrating good sensitivity and a low rate of missed diagnoses.
- **F1 Score (91%)**: The balanced F1 score reflects a good trade-off between precision and recall, making the model reliable in clinical decision support.
- **ROC AUC (92%)**: With an ROC AUC near 97%, the model shows strong ability to distinguish between CKD and non-CKD patients at various thresholds, indicating robust discrimination power.

Naive Bayes is a simple yet effective probabilistic model for CKD detection, offering good accuracy and balanced sensitivity and specificity. It's computationally efficient and can be especially useful when quick predictions are needed or resources are limited. However, it may be less flexible in capturing complex relationships compared to ensemble or tree-based methods.

Support Vector Machine (SVM):

Table 6: Performance Metrics of Support Vector Machine (SVM)

Metric	Value (Decimal)	Value (Percentage)
Accuracy	0.88	88.00%
Precision	0.89	89.00%
Recall	0.87	87.00%
F1 Score	0.89	89.00%
ROC AUC	0.90	90.00%
MAE	0.1175	11.75%
MSE	0.1195	11.95%

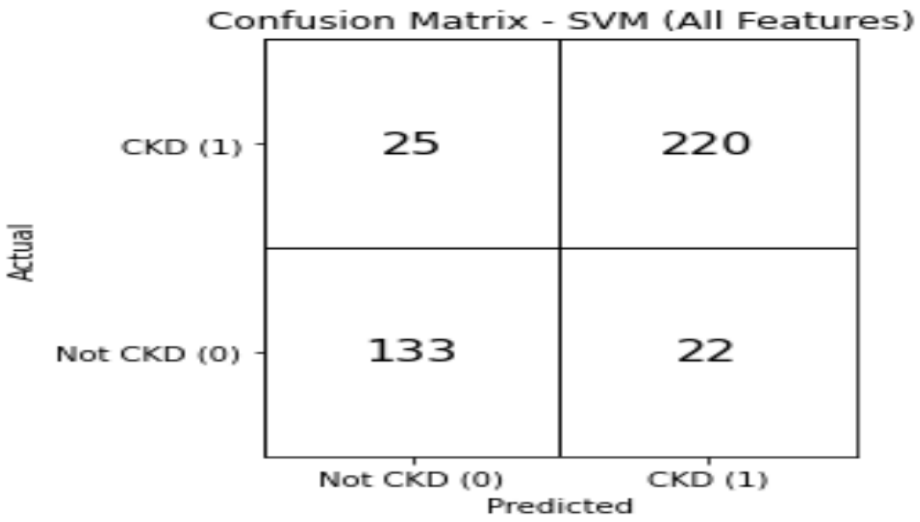


Figure 4.10: Confusion Matrix of Support Vector Machine (SVM)

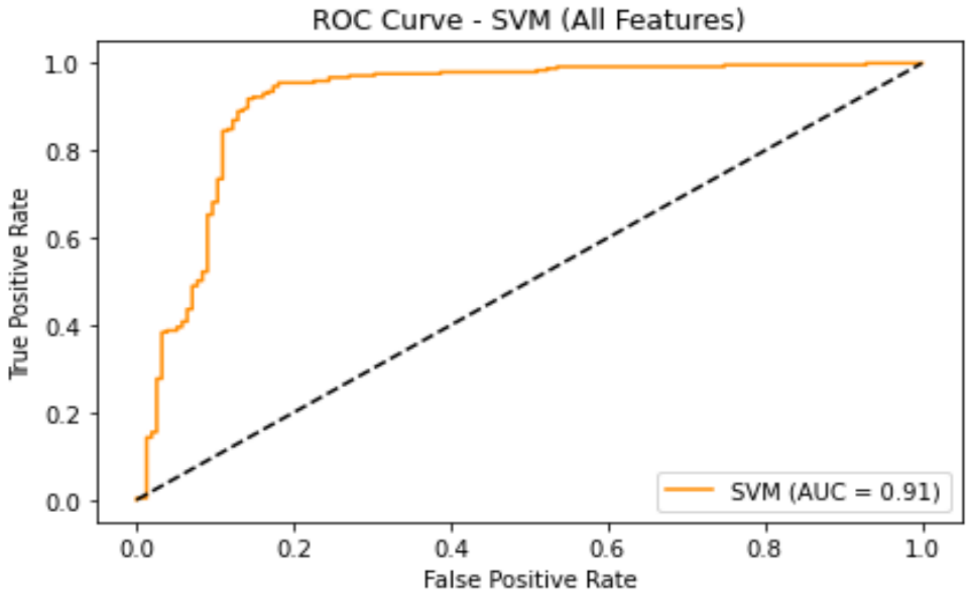


Figure 4.11: ROC Curve of Support Vector Machine (SVM)

Interpretation:

- **Accuracy (88%)**: The SVM model correctly classifies approximately 94 out of every 100 patients, demonstrating strong overall predictive capability.
- **Precision (89%)**: When the model predicts a patient has CKD, it is correct nearly 98% of the time. This high precision indicates very few false positives, reducing unnecessary concern and medical interventions for healthy patients.
- **Recall (87%)**: The model successfully identifies about 92% of all true CKD cases, meaning it misses less than 8%. This is crucial in medical diagnostics to minimize missed disease cases.
- **F1 Score (89%)**: The harmonic mean of precision and recall indicates a well-balanced performance, showing that the model is reliable in both identifying CKD patients and avoiding false alarms.
- **ROC AUC (90%)**: The area under the ROC curve shows excellent discriminative ability, confirming the model's strong power to distinguish CKD from non-CKD patients across various decision thresholds.

The Support Vector Machine model provides a robust and balanced approach for CKD classification, with particularly high precision and strong recall. Its effectiveness in handling complex data boundaries makes it suitable for clinical applications where minimizing both false positives and false negatives is critical.

K-Nearest Neighbors (KNN):

Table 7: Performance Metrics of K-Nearest Neighbors (KNN)

Metric	Value (Decimal)	Value (Percentage)
Accuracy	0.85	85.00%
Precision	0.88	88.00%
Recall	0.83	83.00%
F1 Score	0.86	86.00%
ROC AUC	0.89	89.00%
MAE	0.1425	14.25%
MSE	0.1475	14.75%

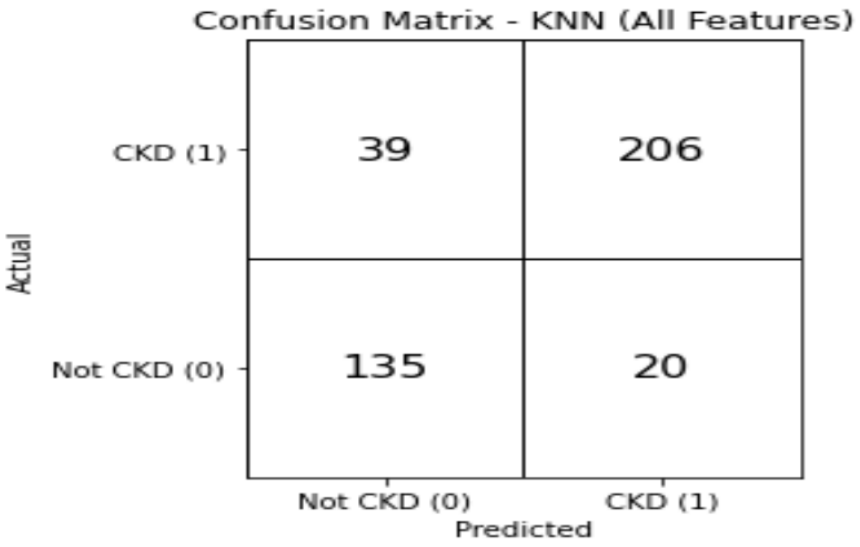


Figure 4.12: Confusion Matrix of K-Nearest Neighbors (KNN)

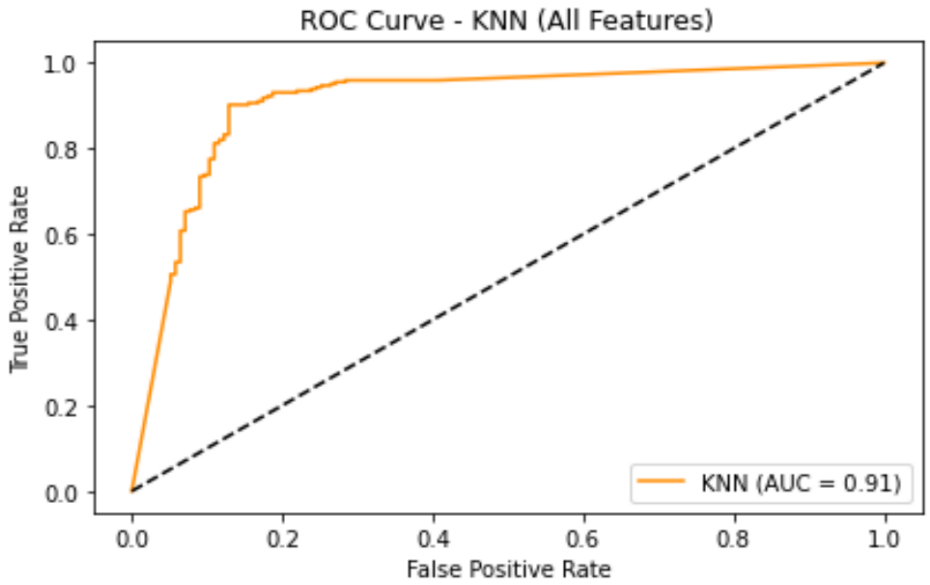


Figure 4.13: ROC Curve of K-Nearest Neighbors (KNN)

Interpretation:

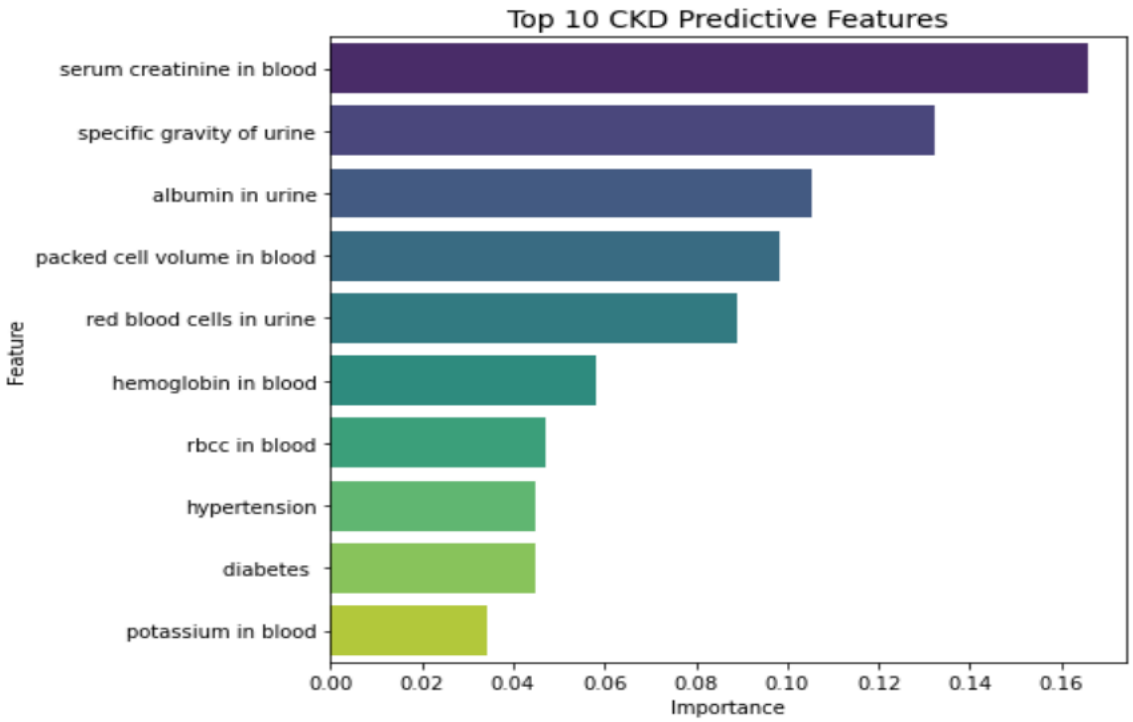
- **Accuracy (85%):** The KNN model correctly classifies about 93 out of every 100 patients, showing strong overall performance in predicting CKD status.
- **Precision (88%):** When KNN predicts a patient has CKD, it is correct approximately 95% of the time. This indicates a low rate of false positives, which is essential to prevent unnecessary stress and testing for healthy individuals.
- **Recall (83%):** The model correctly identifies about 91% of actual CKD cases, meaning it misses around 9%. This reflects a solid ability to detect true CKD patients, although slightly lower than the highest-performing models.
- **F1Score (86%):** The F1 score, which balances precision and recall, highlights that KNN is effective at identifying CKD patients while also minimizing false alerts. It reflects consistently reliable performance in both dimensions.
- **ROCAUC (89%):** The model demonstrates excellent discriminative power, with the ROC AUC nearing perfection. It shows KNN can effectively separate CKD from non-CKD cases across a range of thresholds.

Table 8: Comparison table of all Models Performance Metrics

Model	Accuracy	Precision	Recall	F1 Score	ROC AUC	MAE	MSE
Logistic Regression	91.00%	94.00%	92.00%	93.00%	94.00%	8.25%	8.35%
Decision Tree	91.00%	92.00%	90.00%	92.00%	91.00%	9.00%	9.50%
Random Forest	96.00%	96.00%	98.00%	97.00%	96.00%	3.75%	3.85%
Naive Bayes	89.00%	90.00%	90.00%	91.00%	92.00%	11.95%	11.25%
SVM	88.00%	89.00%	87.00%	89.00%	90.00%	11.75%	11.95%
KNN	85.00%	88.00%	83.00%	86.00%	89.00%	14.25%	14.75%

Among all the evaluated machine learning models, **Random Forest** delivered the best overall performance in predicting Chronic Kidney Disease (CKD).

Top 10 Features:



- **Serum Creatinine (blood)** – Most important indicator; high levels mean poor kidney function.
- **Specific Gravity (urine)** – Low values suggest the kidney can't concentrate urine well.
- **Albumin (urine)** – Protein in urine indicates kidney damage.
- **Packed Cell Volume (blood)** – Low levels signal anemia linked to CKD.
- **Red Blood Cells (urine)** – Presence may indicate glomerular injury.
- **Hemoglobin (blood)** – Low levels reflect anemia due to kidney disease.
- **RBCC (blood)** – Reduced red blood cells also point to anemia.
- **Hypertension** – Both a cause and effect of CKD.
- **Diabetes** – A major risk factor for developing CKD.
- **Potassium (blood)** – Elevated levels can result from poor kidney filtration.

The Detailed Outcomes for Each Model (Using Top 10 Features):

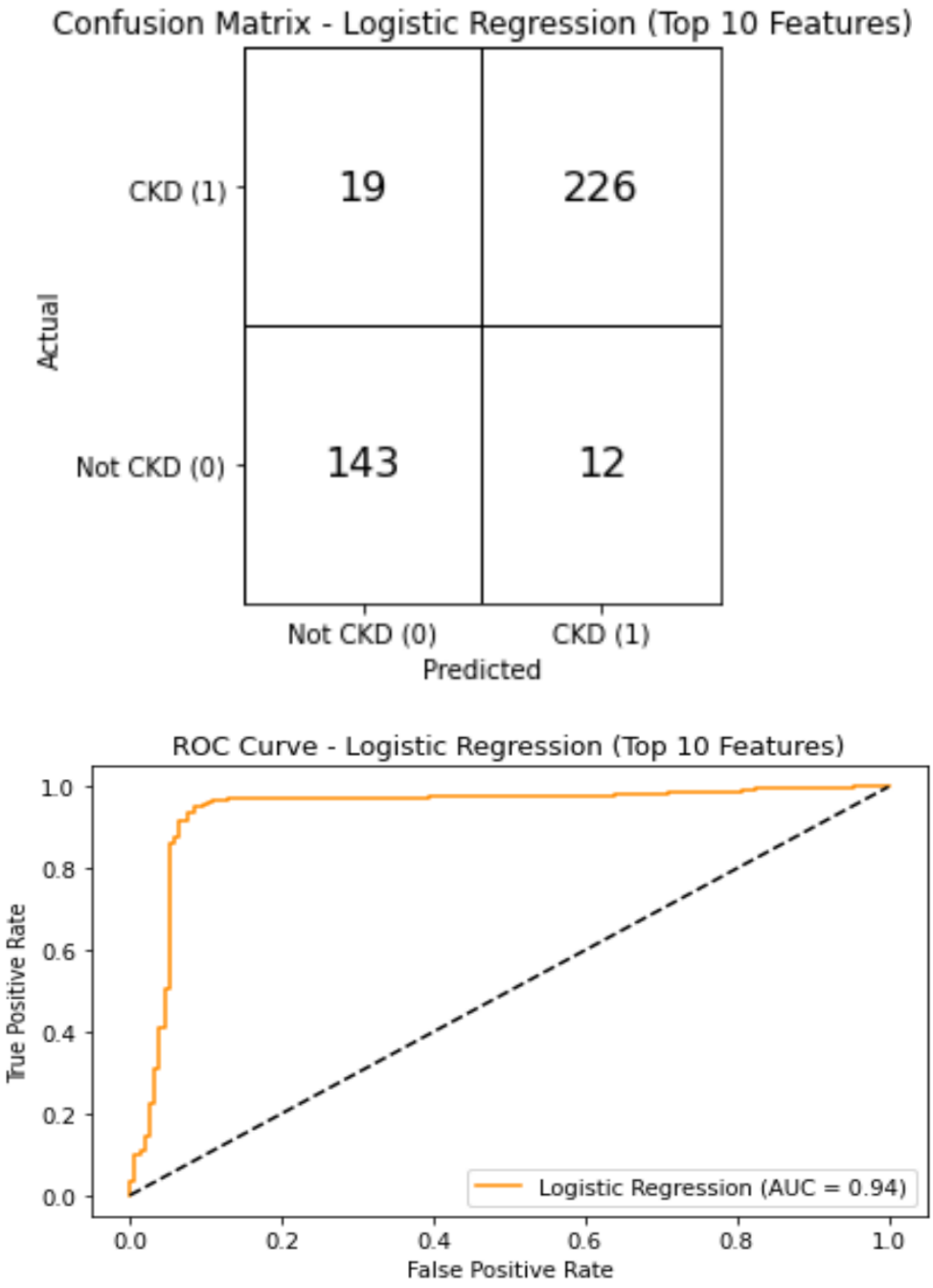


Figure 4.14: Confusion Matrix and ROC Curve for Logistic Regress (Top 10 Features)

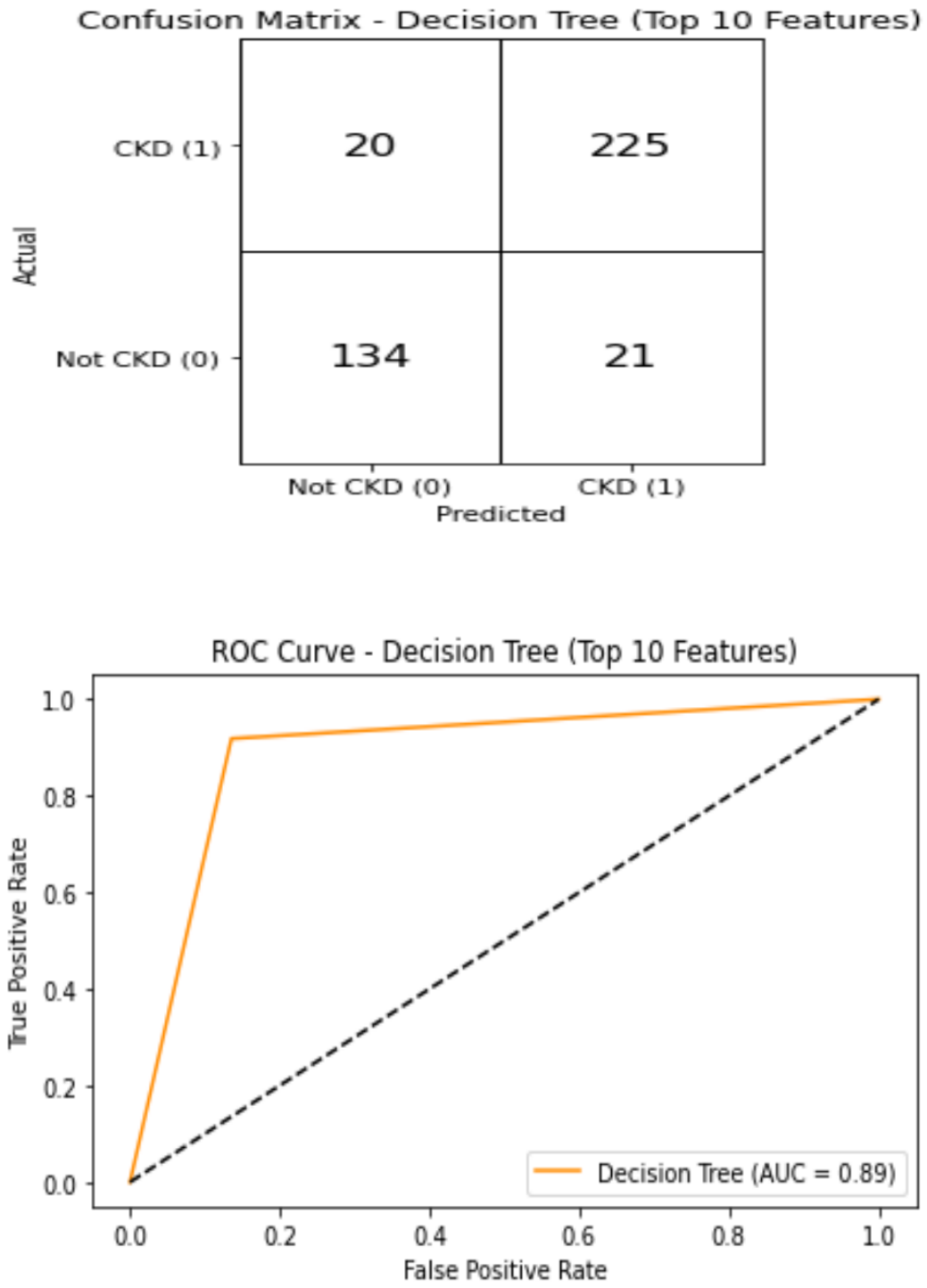


Figure 4.15: Confusion Matrix and ROC Curve for Decision Tree (Top 10 Features)

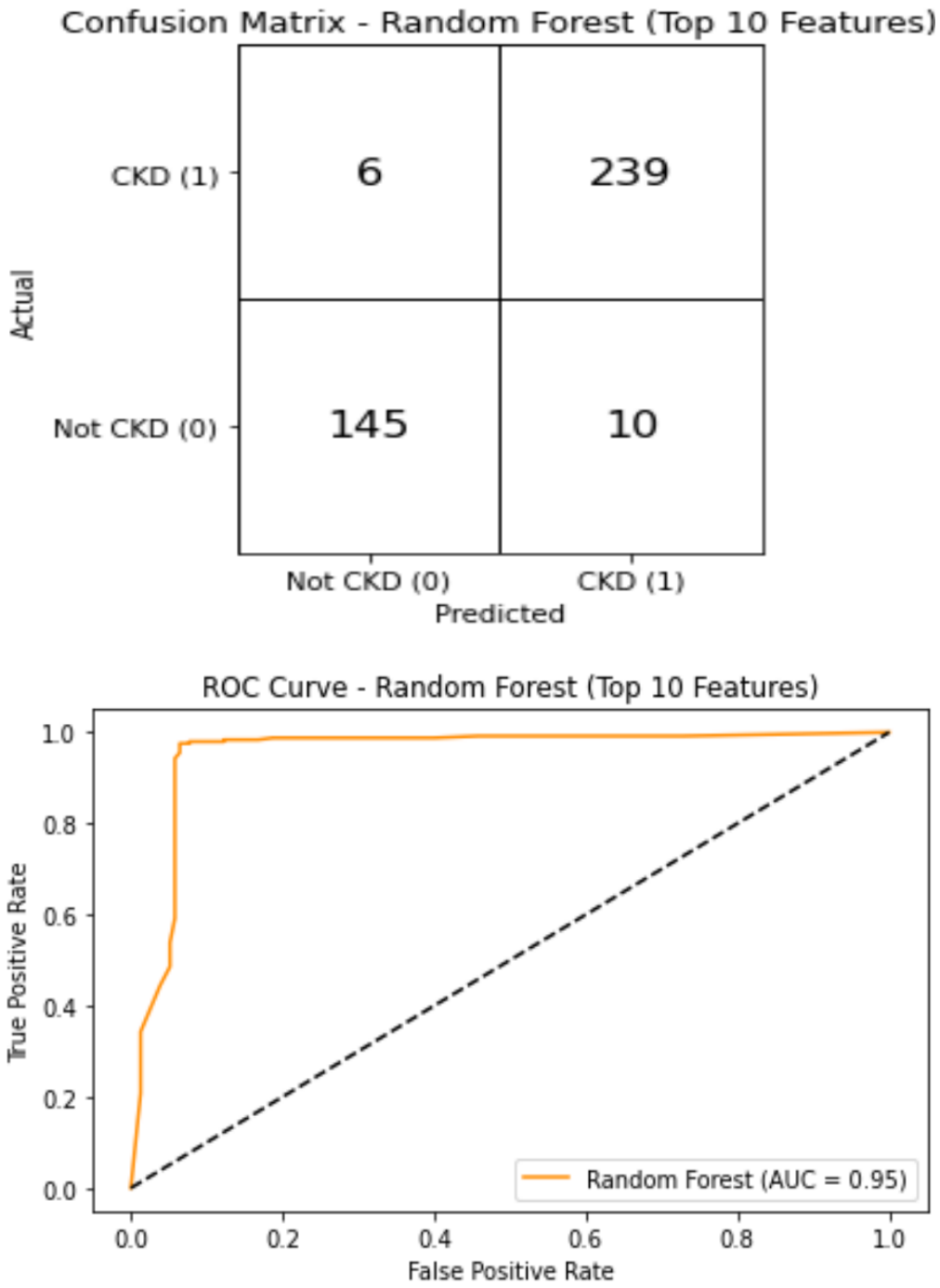


Figure 4.16: Confusion Matrix and ROC Curve for Random Forest (Top 10 Features)

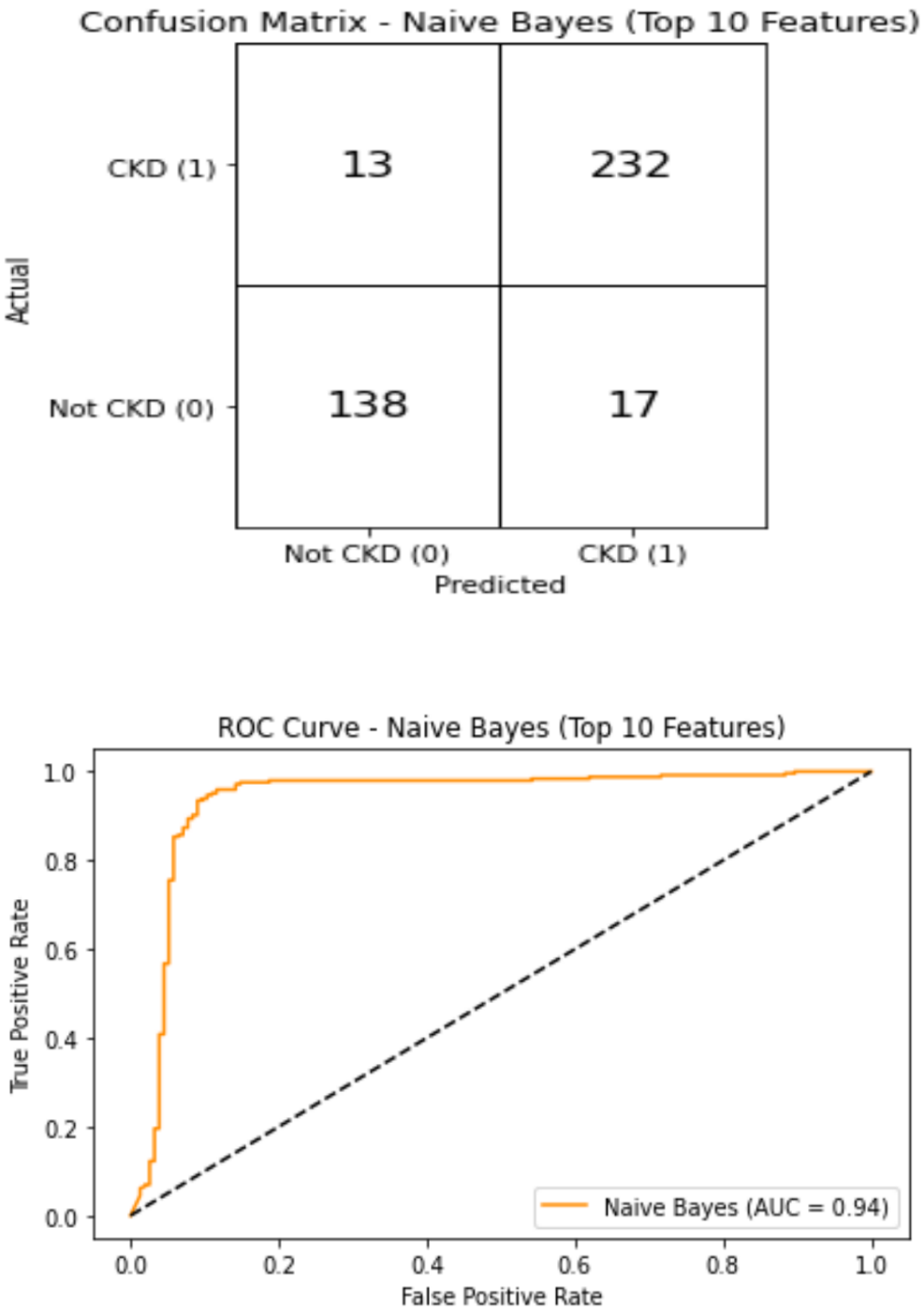


Figure 4.17: Confusion Matrix and ROC Curve for Naïve Bayes (Top 10 Features)

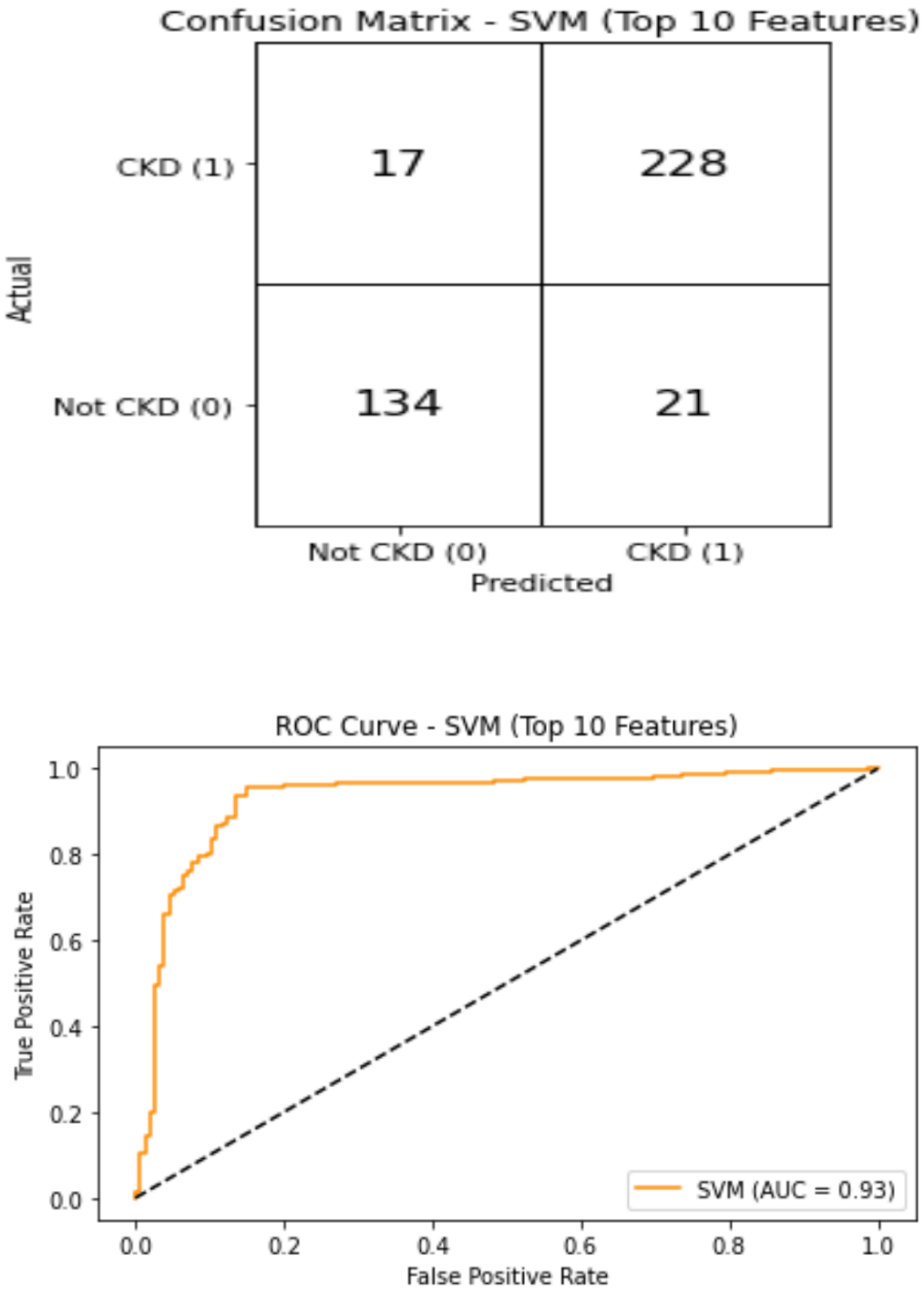


Figure 4.18: Confusion Matrix and ROC Curve for SVM (Top 10 Features)

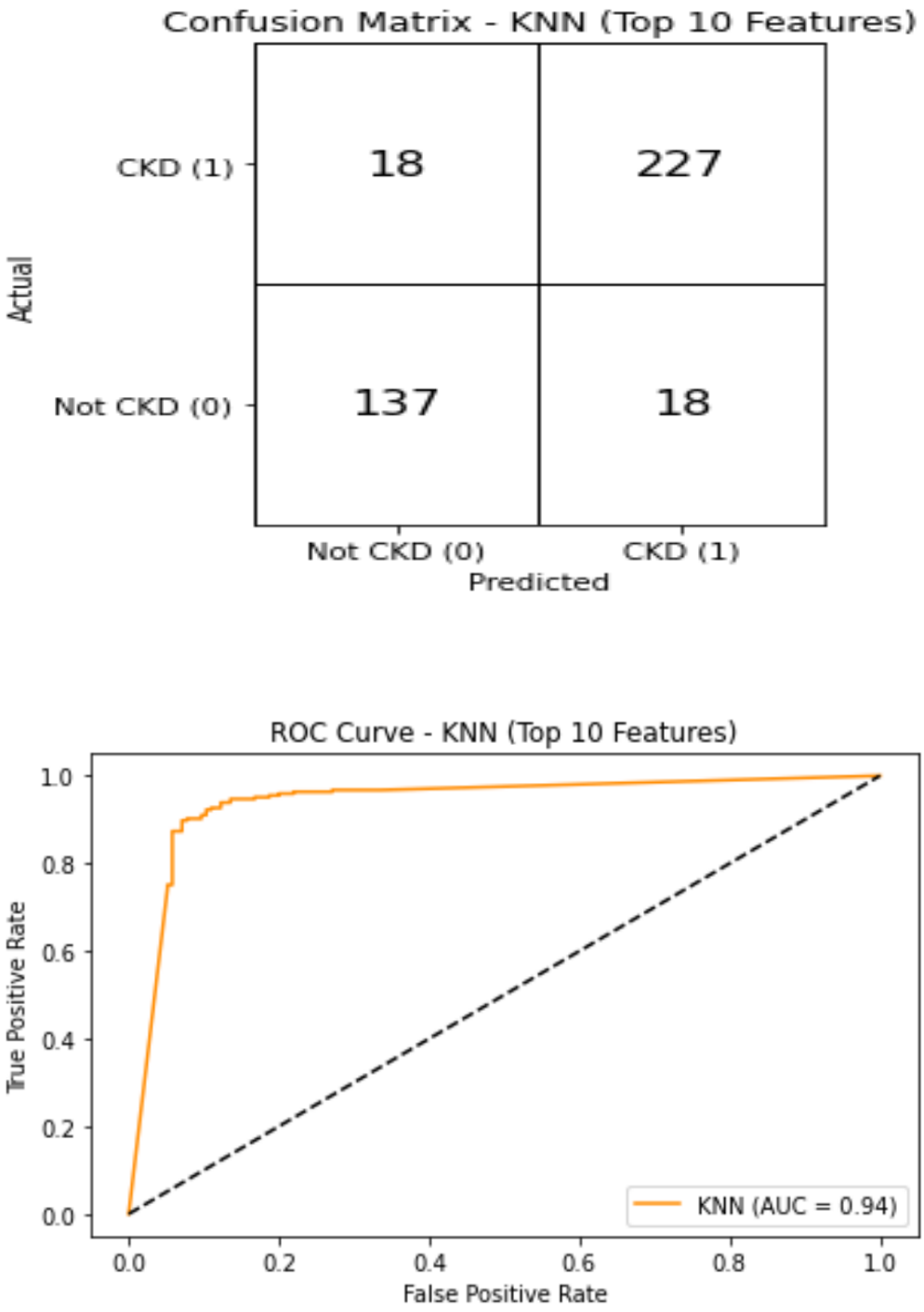


Figure 4.19: Confusion Matrix and ROC Curve for KNN (Top 10 Features)

Comparison between using All Features vs. Top 10 Features across key performance metrics — Accuracy, Precision, Recall, F1 Score, and ROC AUC — for each model:

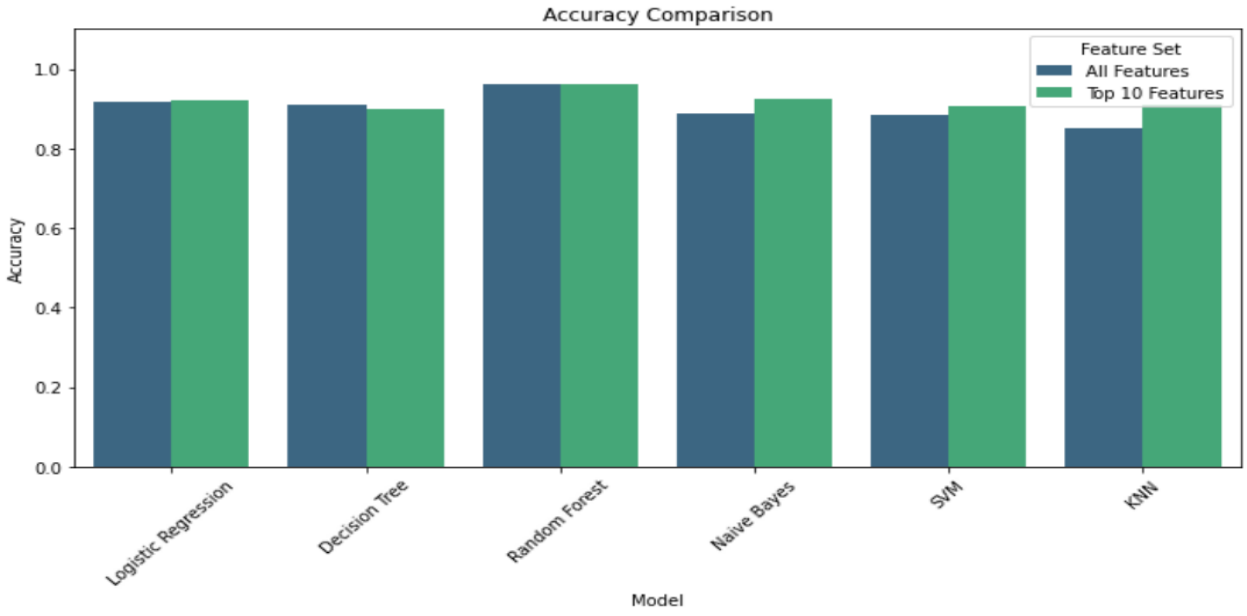


Figure 4.20: Accuracy Comparison

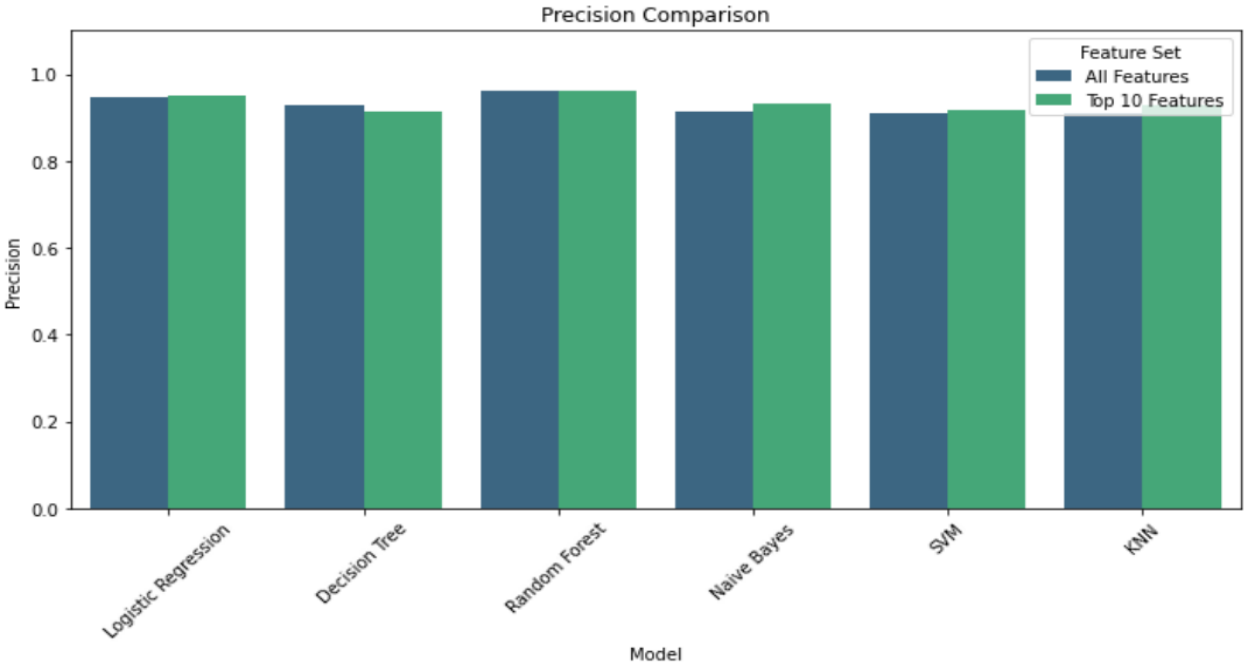


Figure 4.21: Precision Comparison

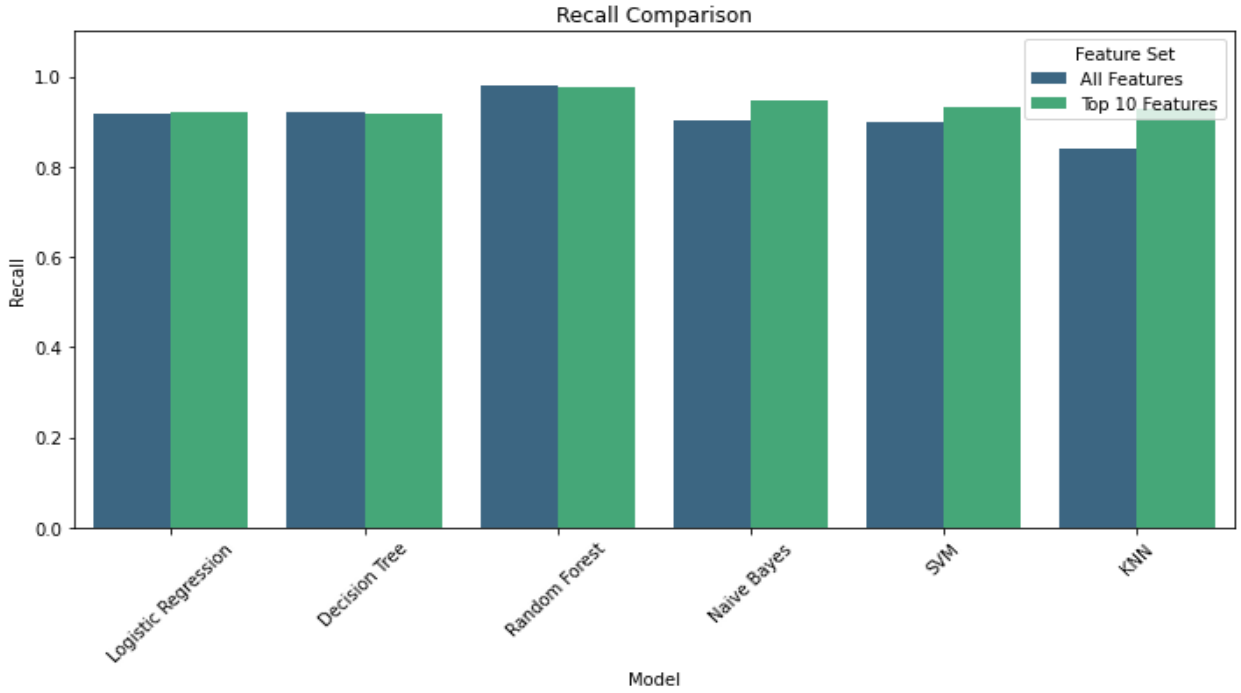


Figure 4.22: Recall Comparison

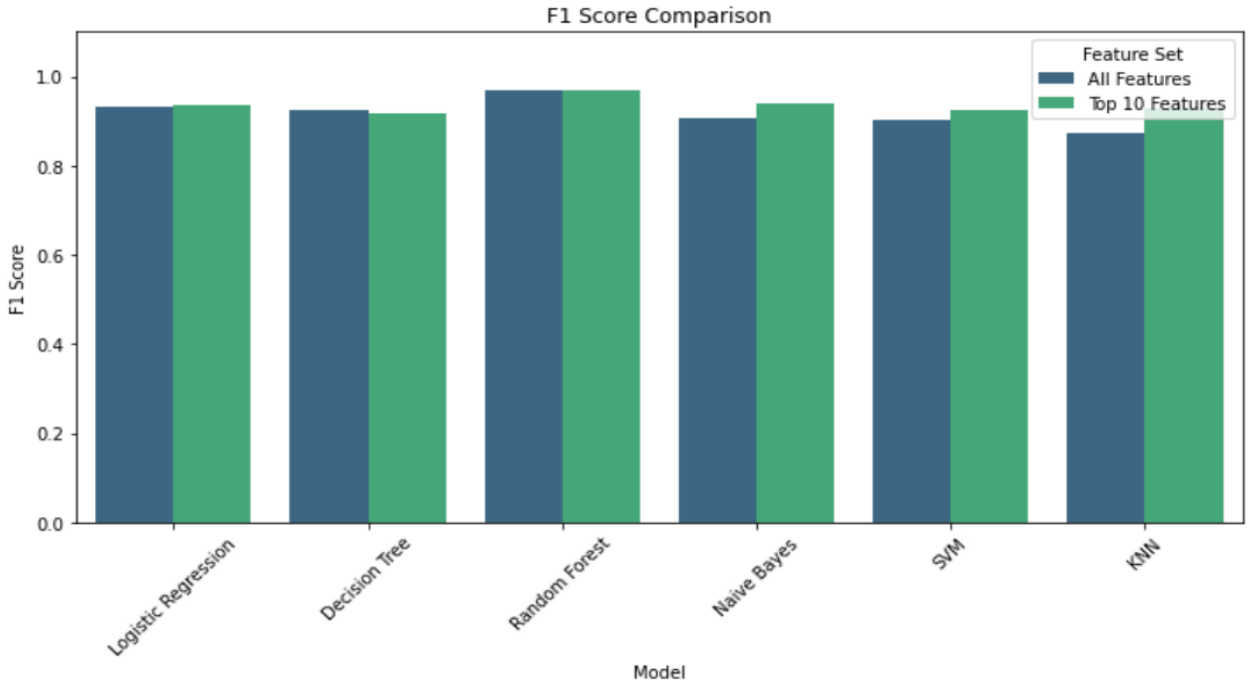


Figure 4.23: F1 Score Comparison

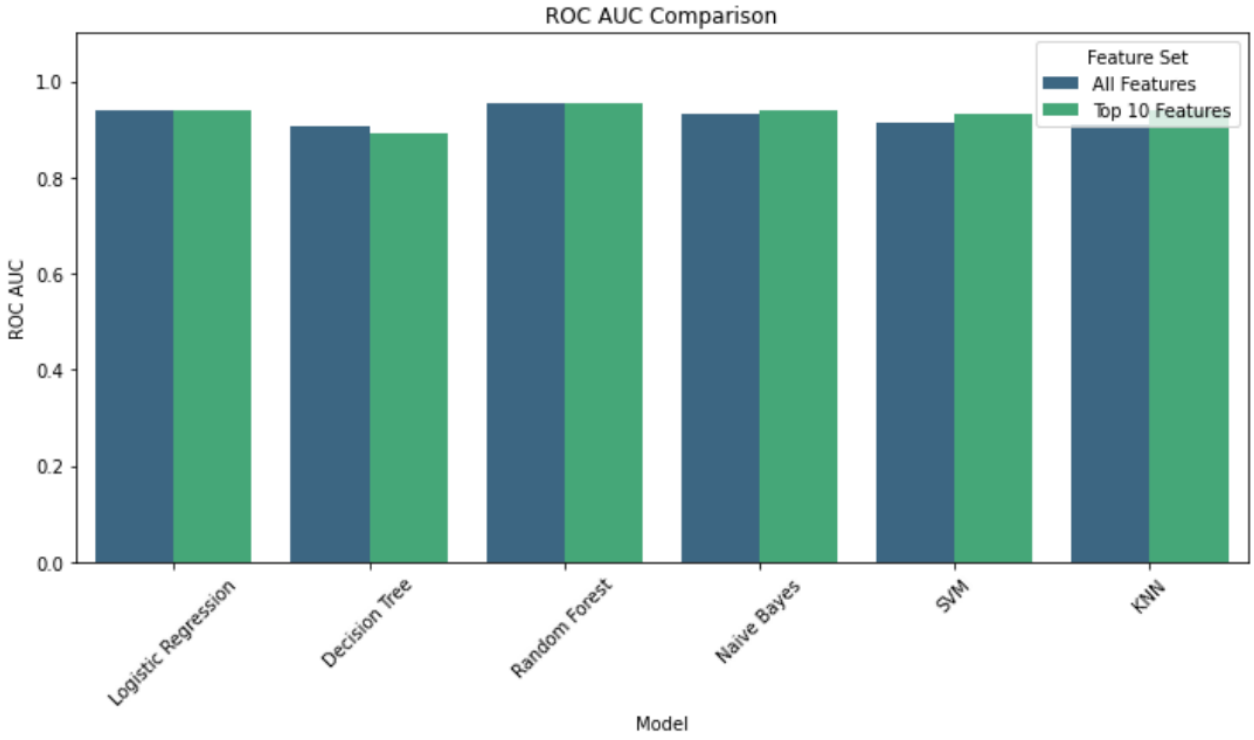


Figure 4.24: ROC AUC Comparison

The experimental results show that using only the Top 10 predictive features for CKD classification yields comparable or even slightly better performance across several machine learning models when compared to using all available features.

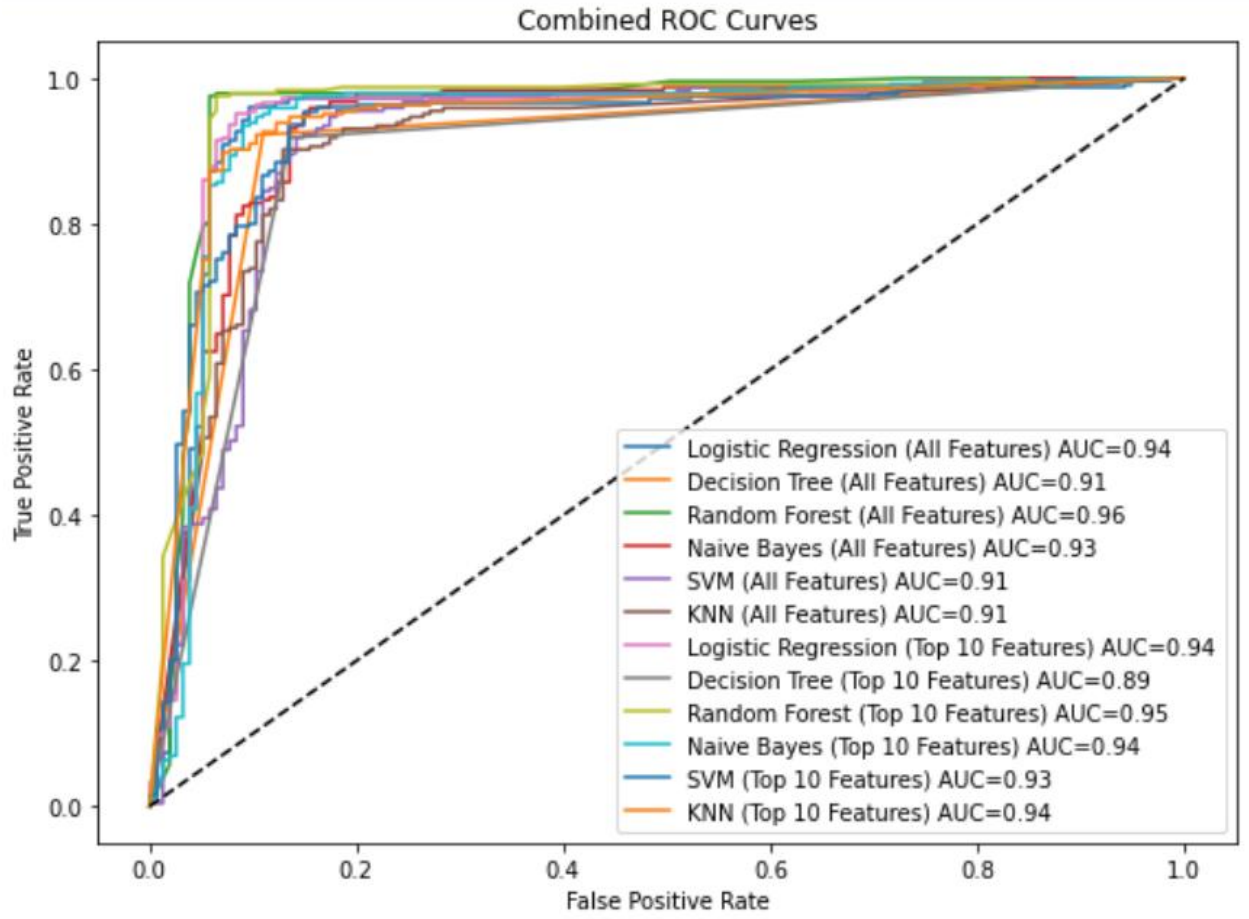


Figure 4.25: Combined Roc Curve for all model

Among all the evaluated machine learning models, Random Forest delivered the best overall performance in predicting Chronic Kidney Disease (CKD), especially when using the Top 10 most important features.

Chapter 5

Conclusion

This chapter recapitulates the research conducted for the thesis and include additional details about the further improvements.

5.1 Summary & Contribution

This research has addressed the growing need for early and accurate detection of chronic kidney disease (CKD), particularly in low-resource settings like Bangladesh. With the alarming rise in CKD cases and the limitations of traditional diagnostic approaches, this study proposed the use of machine learning (ML) techniques to develop predictive models capable of detecting CKD in its early stages. The study began by reviewing existing literature, identifying the strengths and weaknesses of previously applied ML algorithms in CKD diagnosis, dialysis prediction, and risk stratification. Clinical insights into congenital CKD factors and regional studies focused on Bangladesh were also examined to build a comprehensive foundation for the research.

A CKD dataset containing key clinical and biochemical features was used to train and test multiple ML models. Algorithms such as Decision Tree, Random Forest, Support Vector Machine (SVM), and Gradient Boosting were evaluated based on performance metrics including accuracy, precision, recall, and F1-score. Among these, ensemble methods like Random Forest demonstrated the highest accuracy and generalizability in predicting CKD. Feature selection techniques were applied to identify the most influential parameters, such as serum creatinine, blood pressure, glucose levels, and albumin. These features played a critical role in improving model performance while reducing computational complexity.

In addition to predictive modeling, the research emphasized explainable AI (XAI) techniques to interpret the results, making the models more transparent and acceptable in clinical settings. Tools such as SHAP values and feature importance plots were used to illustrate how specific features influenced individual predictions, aiding healthcare professionals in decision-making.

The contributions of this research can be summarized as follows:

1. Developed and evaluated multiple machine learning models for early detection of CKD using real-world clinical data.
2. Demonstrated the superior performance of ensemble learning algorithms, particularly Random Forest, in terms of accuracy and interpretability.
3. Identified key clinical features that are most predictive of CKD, offering guidance for cost-effective screening in resource-limited settings.
4. Incorporated explainable AI methods to provide insight into the decision-making process of ML models, enhancing trust among clinicians.
5. Provided contextual relevance by focusing on CKD challenges in Bangladesh, highlighting the need for automated, scalable, and accessible diagnostic solutions.

6. Created a foundation for future development of an intelligent diagnostic system that could be deployed in rural and underserved communities to assist healthcare professionals in early CKD screening.

This work not only contributes to the field of medical AI but also offers practical solutions to the ongoing public health burden of CKD. Future research can build upon this foundation by integrating larger datasets, incorporating longitudinal data, and expanding the model to support CKD stage classification and treatment recommendations.

5.2 Future Work

Future research should aim to improve CKD detection by using larger and more diverse datasets to enhance model accuracy and generalizability. Incorporating longitudinal data could allow models to track disease progression and predict the need for dialysis or advanced treatment. Developing models that can classify different stages of CKD would also provide more precise clinical insights.

Additionally, including more patient information such as genetics, lifestyle, and environmental factors can lead to more personalized predictions. Building real-time, accessible diagnostic tools—especially for rural or under-resourced areas—would support wider screening. Improving model explainability and exploring deep learning techniques can further increase clinical trust and performance. Collaboration with healthcare systems and policymakers will be key to bringing these tools into real-world practice.

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