A FIELD PROJECT REPORT

on

**“Machine Learning Techniques for Early Detection of Chronic Kidney Disease”**

**Submitted**

by

|  |  |
| --- | --- |
| 221FA04216  Sudhrasan Uppala | 221FA04496  Nagi Reddy |
| 221FA04606  Laahiri Gurram | 221FA04692  Rohith Indupalli |

**Under the guidance of**

***Dr. S. Deva Kumar***

*Designation*



**DEPARTMENT OF COMPUTER SCIENCE & ENGINEERING**

**VIGNAN'S FOUNDATION FOR SCIENCE, TECHNOLOGY AND RESEARCH Deemed to be UNIVERSITY**

**Vadlamudi, Guntur.**

**ANDHRA PRADESH, INDIA, PIN-522213.**



**CERTIFICATE**

This is to certify that the Field Project entitled **“Machine Learning Techniques for Early Detection of Chronic Kidney Disease”** that is being submitted by 221FA04216 (Sudhrasan), 221FA04496 (Nagi Reddy), 221FA04606 (Laahiri), 221FA04692 (Rohith)for partial fulfilment of Field Project is a bonafide work carried out under the supervision of Dr. S. Deva Kumar, PhD., Assistant Professor, Department of CSE.

|  |  |  |
| --- | --- | --- |
| Guide name& Signature |  | Dr.K.V. Krishna Kishore |
| Assistant/Associate/Professor, CSE | HOD,CSE | Dean, SoCI |



**DECLARATION**

We hereby declare that the Field Project entitled **“Machine Learning Techniques for Early Detection of Chronic Kidney Disease”** is being submitted by 221FA04216 (Sudhrasan), 221FA04496 (Nagi Reddy), 221FA04606 (Laahiri), 221FA04692 (Rohith) in partial fulfilment of Field Project course work. This is our original work, and this project has not formed the basis for the award of any degree. We have worked under the supervision of Ms. G.NAVYA, M.Tech., Assistant Professor, Department of CSE.

By

**221FA04216(Sudhrasan),**

**221FA04496 (Nagi Reddy),**

**221FA04606 (Laahiri),**

**221FA04692 (Rohith)**

Date:

## ABSTRACT

Chronic Kidney Disease (CKD) is a severe health condition that affects millions of people worldwide, often leading to kidney failure if not detected early. Early diagnosis plays a crucial role in mitigating the disease's progression and improving patient outcomes. This project aims to apply machine learning techniques for the early detection of CKD by analyzing clinical data.

The study explores four prominent machine learning algorithms: Decision Trees (DT), Random Forests (RF), Support Vector Machines (SVM), and Naive Bayes (NB). These algorithms are selected due to their diverse strengths in handling complex medical datasets and their widespread use in classification tasks. Each model is trained on a dataset containing relevant features for CKD prediction and evaluated using standard performance metrics, including accuracy, precision, recall, F1-score, and area under the ROC curve (AUC). These metrics provide a comprehensive view of the models’ ability to correctly classify CKD cases.

To enhance the predictive power of individual models, the project also investigates ensemble learning techniques. By assembling the models through techniques like bagging and boosting, the ensemble method combines the strengths of each algorithm while reducing their weaknesses. This leads to improved prediction accuracy, robustness, and generalization across different datasets.

The results of this study highlight the advantages and limitations of each algorithm and demonstrate the potential benefits of ensemble methods for CKD detection. The final assembled model shows superior performance compared to individual algorithms, underscoring the value of integrating multiple approaches for more reliable predictions. This work emphasizes the growing role of machine learning in healthcare, offering a promising tool for early diagnosis and management of CKD, potentially improving treatment outcomes for patients globally.

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# CHAPTER-1 INTRODUCTION

### INTRODUCTION

**1.1 Overview of Chronic Kidney Disease (CKD)**

Chronic Kidney Disease (CKD) is a progressive health condition characterized by the gradual deterioration of kidney function over time. The kidneys are vital organs responsible for filtering waste, excess fluids, and electrolytes from the blood, regulating blood pressure, balancing fluids, and producing hormones that influence other essential bodily functions. CKD progresses through five stages, with the severity of the condition increasing at each stage. In the early stages, symptoms are often mild or absent, making early diagnosis difficult. As CKD advances, patients may experience fatigue, swelling (edema), and other health complications such as hypertension, anemia, and cardiovascular diseases.

CKD is a global health burden, affecting an estimated 10% of the world’s population. The condition can stem from several risk factors, including diabetes, hypertension, obesity, family history, and lifestyle factors. If left untreated, CKD can lead to end-stage renal disease (ESRD), necessitating long-term dialysis or kidney transplantation, both of which can impose a significant physical and financial burden on patients. Early identification and intervention are critical in managing CKD effectively and reducing the risk of complications.

**1.2 Importance of Early Detection**

Early detection of CKD is paramount in slowing disease progression and improving clinical outcomes. When CKD is diagnosed in its early stages, timely interventions can help reduce kidney damage, prevent further deterioration, and avoid serious complications. Early treatment may involve lifestyle changes, medications to control blood pressure or blood sugar levels, dietary modifications, and monitoring of kidney function. Detecting CKD early can also lead to the prevention of related conditions such as heart disease, which is common among CKD patients.

Early detection of Chronic Kidney Disease (CKD) is crucial in mitigating disease progression and improving patient outcomes. Identifying the disease in its initial stages enables timely interventions that can prevent further kidney damage and reduce the risk of associated complications. This section explores the impact of early detection on CKD management, the challenges associated with early diagnosis, and the role of machine learning in enhancing early detection efforts.

**1.2.1 Benefits of Early Intervention**

Early diagnosis of CKD allows healthcare providers to implement treatment strategies that can slow down the progression of the disease. Interventions such as lifestyle modifications, dietary adjustments, and the administration of medications to control blood pressure, blood glucose, and cholesterol levels are more effective when applied early. Additionally, early treatment can reduce the likelihood of patients developing end-stage renal disease (ESRD), thereby preventing the need for dialysis or kidney transplantation. Early intervention also helps manage the risk of cardiovascular diseases, which are prevalent among CKD patients, leading to overall improved quality of life and reduced mortality rates.

**1.2.2 Challenges in Early Diagnosis**

One of the main challenges in CKD management is that the disease often remains asymptomatic in its early stages. Traditional diagnostic methods, including the use of serum creatinine levels, estimated glomerular filtration rate (eGFR), and albuminuria, typically detect CKD only after significant kidney damage has already occurred. These biomarkers may not be sensitive enough to capture subtle changes in kidney function early on, which limits the potential for preventive measures. Furthermore, CKD symptoms such as fatigue, swelling, and changes in urination often appear late, making it difficult for both patients and clinicians to recognize the condition until advanced stages.

**1.2.3 Limitations of Conventional Detection Methods**

While serum creatinine and eGFR are widely used to assess kidney function, they have limitations in detecting CKD at an early stage. Serum creatinine levels can be influenced by factors such as age, muscle mass, and hydration status, leading to inaccurate assessments of kidney function in some individuals. Similarly, albuminuria—although a key indicator of kidney damage—may not be present in all CKD patients, especially in the early stages of the disease. These limitations highlight the need for more sensitive and specific diagnostic tools to enable earlier identification of at-risk patients.

**1.2.4 The Role of Machine Learning in Early Detection**

Machine learning (ML) techniques have the potential to revolutionize the early detection of CKD by identifying complex patterns in clinical and patient data that traditional methods may overlook. ML models can analyze large datasets, including laboratory results, medical histories, and demographic information, to predict CKD risk more accurately. By leveraging algorithms such as Decision Trees (DT), Random Forest (RF), Support Vector Machines (SVM), and Naive Bayes (NB), ML models can detect early warning signs that may not be evident through conventional biomarkers. These models can assist healthcare providers in stratifying patients based on their risk of developing CKD and initiating preventive care before irreversible kidney damage occurs.

**1.2.5 Implications for Healthcare Systems**

The integration of ML models into clinical practice could significantly reduce the burden of CKD on healthcare systems by enabling earlier diagnosis and more targeted interventions. Early detection reduces the costs associated with treating advanced CKD stages, including dialysis and kidney transplantation. Furthermore, ML-driven early detection systems can improve patient outcomes by preventing complications such as cardiovascular diseases and reducing hospitalizations related to CKD progression. Thus, the adoption of ML technologies holds promise for transforming CKD management and improving both clinical and economic outcomes.

**1.3 Role of Machine Learning in CKD Prediction**

Machine learning (ML) has emerged as a powerful tool in healthcare, offering innovative solutions to problems like disease detection, diagnosis, and prognosis prediction. In the case of CKD, ML algorithms are capable of analyzing large volumes of patient data to identify patterns and trends that may not be immediately apparent using traditional statistical methods. By processing features such as patient demographics, medical history, laboratory results, and imaging data, ML models can predict the likelihood of CKD, classify patients into different risk categories, and identify early markers of kidney dysfunction.

Several machine learning algorithms, including Decision Trees (DT), Random Forest (RF), Support Vector Machines (SVM), and Naive Bayes (NB), have been applied to CKD prediction tasks. These models are particularly effective in handling complex and high-dimensional datasets, making them well-suited for medical applications. The primary advantage of using ML in CKD prediction is its ability to handle nonlinear relationships between variables and provide robust predictions even with noisy or incomplete data. ML models can also continuously improve as more data becomes available, resulting in more accurate and personalized predictions over time.

**1.4 Current Methodologies**

Various methodologies have been explored for CKD detection, each with its own strengths and limitations. Traditional statistical techniques, such as logistic regression, have been commonly used in predicting CKD, leveraging simple linear relationships between features. However, these models often struggle to capture complex, nonlinear interactions in the data, limiting their predictive power.

More advanced techniques, including machine learning models like Decision Trees (DT) and Random Forest (RF), have gained popularity for CKD detection. Decision Trees provide a transparent and interpretable model that segments data based on features like age, blood pressure, and creatinine levels. However, they may suffer from overfitting, particularly when applied to small datasets. Random Forest, an ensemble method that combines multiple decision trees, mitigates overfitting by averaging predictions from several trees, thereby improving robustness and accuracy.

Support Vector Machines (SVM) are another widely used method for CKD classification. They are effective in handling high-dimensional data and are particularly suitable for binary classification tasks. However, SVM models can be computationally expensive and may require extensive tuning of hyperparameters to achieve optimal performance.

Naive Bayes (NB), a probabilistic model based on Bayes’ Theorem, is also used for CKD prediction. Its simplicity and speed make it a good choice for real-time predictions, although it assumes independence between features, which may not always be the case in medical datasets.

Despite the strengths of these individual models, no single technique consistently performs best across all scenarios, which motivates the use of ensemble methods to combine the strengths of multiple models.

**1.5 Applications of Machine Learning to Combat CKD**

The application of machine learning to CKD detection and prediction has transformed how healthcare professionals approach disease diagnosis and management. By integrating advanced algorithms into clinical decision-making processes, ML can provide real-time risk assessments for patients and assist in identifying those who are most likely to develop CKD. In particular, ML models can help physicians target at-risk populations for early intervention, which can ultimately delay or prevent the onset of severe kidney damage.

For example, machine learning models can be trained on datasets that include blood pressure, glucose levels, cholesterol, and other lab measurements. These models can then predict whether a patient is at risk of developing CKD, allowing doctors to intervene with lifestyle changes or medications to prevent progression. In addition, ML models can be used to predict the future trajectory of CKD in patients who have already been diagnosed, helping doctors plan treatments more effectively.

Ensemble techniques, which combine the predictions of multiple models (e.g., DT, RF, SVM, NB), have also been employed to improve the accuracy and robustness of CKD detection. These ensemble methods, such as bagging and boosting, aggregate the strengths of various models, reducing their individual weaknesses. This results in more accurate and reliable predictions, especially when dealing with large, noisy, or imbalanced datasets. The successful application of machine learning to CKD not only helps in early diagnosis but also paves the way for precision medicine, where treatments can be tailored to individual patient profiles based on their unique risk factors.

In summary, machine learning holds significant promise in addressing the challenges of CKD detection and management. By combining advanced algorithms with large-scale clinical data, ML models can provide earlier, more accurate diagnoses, potentially improving outcomes for millions of patients worldwide.

# CHAPTER-2 LITERATURE SURVEY

## LITERATURE SURVEY

#### Literature review

The growing burden of Chronic Kidney Disease (CKD) globally has sparked interest in using machine learning (ML) techniques for early detection and prognosis. Machine learning offers the ability to analyze vast amounts of clinical data, capturing complex interactions that traditional statistical methods may overlook. This literature survey extends the review of existing work by exploring various machine learning models and their application to CKD prediction, highlighting both the benefits and limitations of different approaches.

**2.1 Review of ML Models for CKD Prediction**

Machine learning models have shown promising results in predicting CKD using a variety of clinical and laboratory data. Some of the widely explored models include K-NEAREST NEIGHBOR(KNN), Multi-Layer Perceptrons (MLP), Support Vector Machines (SVM), and Naive Bayes (NB). Each model contributes uniquely to the prediction tasks depending on the nature of the dataset and the desired outcomes.

Bashir et al. [1] created a framework using multi-layer classification for the detection of diseases. After implying KNN they got 57.41% of accuracy using a dataset from startling and while using a dataset of Cleveland they got 58.42% of accuracy. Hasi et al. [2] have implied KNN on Pima Indians dataset for CKD their research shown KNN has generated 76.96% of accuracy with very less error rate for Chronic Kidney Disease detection. The Pima Indians dataset has 768 samples, which include 8 numerical value attributes. Khan et al. Used KNN in UCI Machine Learning Repository for Lever infection detection, their result of KNN produced an accuracy of 62.90% and the error rate of 0.3718.

K-Nearest Neighbor (KNN) is employed by many researcher for classification problems. Hashi et al. [3] have used KNN for CKD on the dataset taken from Pima Indians data. Their results show that KNN produces accuracy of 76.96% with minimum error rate for CKD prediction. Bashir et al. [4] design a medical decision support framework using multilayer classifiers for disease prediction. They also utilized KNN for early prediction of disease. Using KNN they achieved 57.41% accuracy on Stat long dataset and 58.42% accuracy on Cleveland dataset. Khan et al. [5] employed KNN for liver disease prediction on dataset taken from UCI ML repository. Their outcome of KNN shows 62.90% accuracy rate and 0.3718 for error rate.

Shukla and Kaur’s ensemble approach yielded an accuracy of 93.2%, improving over SVM (87%) and MLP (85%). The precision and recall rates increased to 92.1% and 94.3%, respectively, enhancing the reliability of CKD predictions[20]. This study offers a comparative analysis of various machine learning models, including SVM, KNN, MLP, and Naive Bayes, specifically applied to early CKD detection. The authors highlight the limitations of individual models and suggest that ensemble techniques, such as bagging and boosting, can enhance prediction performance[6]. The authors propose an ensemble-based approach integrating SVM, KNN, and MLP models. They demonstrate that ensemble methods like voting and stacking improve diagnostic accuracy by combining classifiers [7].

Chauhan and Khan report a hybrid ensemble model achieving a 92.5% accuracy rate, with a precision of 91% and a recall of 93%. This approach outperformed individual classifiers like SVM (88%) and MLP (86%) by reducing the false positive rate significantly[8]. The study evaluates SVM, KNN, MLP, and Naive Bayes, showing individual model accuracies of 84.7%, 81.2%, 79.8%, and 76.5%. Using bagging and boosting, the ensemble approach improved accuracy to 91.3%, with an F1-score of 0.89[9].

The authors focus on the individual performance of classifiers like SVM and KNN before implementing ensemble methods like stacking and voting, which significantly enhance prediction consistency[10]. This review discusses ensemble learning techniques applied to CKD diagnosis, integrating models like SVM, KNN, MLP, and Naive Bayes. The authors conclude that ensemble models improve CKD diagnosis accuracy by leveraging the complementary strengths of individual classifiers[11].

Patel and Shah's ensemble method yielded an accuracy of 93.1%, outperforming individual classifiers like MLP (81%) and KNN (84%). The ensemble approach significantly improved the precision (92%) and recall (93%) metrics[12]. The hybrid ensemble model in the study reached a 91.6% accuracy, with a precision of 90% and recall of 92%. Individual models such as SVM and MLP achieved lower accuracies of 85% and 83%, respectively[13]. Wang and Li show that ensemble models like stacking and bagging significantly enhance prediction accuracy by combining the strengths of individual models. They recommend ensemble learning for early CKD diagnosis[14]. Kumar and Singh implement ensemble techniques like voting and bagging, demonstrating their impact on improving sensitivity and specificity in CKD detection[15].

Ali and Fatima report that ensemble techniques such as boosting increased the accuracy to 92.7%, with precision and recall rates of 91.3% and 92.4%, respectively. This performance is higher than SVM (87%) and MLP (85%) alone[16]. The framework achieved a 93.5% accuracy, with precision and recall rates of 91% and 94%. Individual classifiers such as SVM and KNN had lower accuracies of 88% and 86%, respectively[17].

Goyal and Kumar explore ensemble techniques like stacking and bagging, concluding that combining classifiers through ensemble methods achieves reliable CKD predictions.[18].

The study finds that ensemble models outperform traditional single-model approaches in precision and sensitivity, suggesting these methods are highly effective for healthcare applications[19].

#### Motivation

Chronic Kidney Disease (CKD) is a major global health issue, affecting millions of people worldwide. It is often termed a "silent killer" due to its asymptomatic nature in the early stages, leading to late diagnoses when treatment options become limited and less effective. Early detection is critical, as it allows for timely interventions that can slow disease progression, prevent complications, and improve patient outcomes. However, traditional diagnostic methods, such as serum creatinine levels and glomerular filtration rate (GFR) calculations, are often inadequate for detecting CKD in its early stages, as they typically identify the disease only after significant kidney damage has already occurred.

The rapid advancements in machine learning (ML) have opened new avenues for improving CKD prediction and diagnosis. By leveraging ML algorithms, we can analyze complex datasets, uncover hidden patterns, and make highly accurate predictions based on a range of clinical and demographic features. This project is motivated by the need for a more effective, data-driven approach to CKD prediction, one that can identify at-risk individuals before irreversible damage sets in.

Furthermore, the comparative study of various machine learning models—including Decision Trees (DT), Random Forest (RF), Support Vector Machines (SVM), and Naive Bayes (NB)—will help identify the most effective algorithms for early CKD detection. The goal is to develop an ensemble model that combines the strengths of individual classifiers to improve prediction accuracy, sensitivity, and specificity, thereby providing a more reliable tool for healthcare professionals.

The motivation for this project stems from the potential of machine learning to revolutionize CKD diagnosis and contribute to reducing the disease's burden on global healthcare systems by facilitating earlier interventions, ultimately improving patient quality of life.

# CHAPTER-3 PROPOSED SYSTEM

### PROPOSED SYSTEM

This section outlines the proposed system for predicting Chronic Kidney Disease (CKD) using machine learning models. The system focuses on early detection of CKD by utilizing several machine learning algorithms, including K-Nearest Neighbors (KNN), Support Vector Machine (SVM), and Naive Bayes (NB). Additionally, an ensemble approach will be developed to combine the predictions from these models to enhance accuracy, sensitivity, and specificity. The system is designed to take a dataset of patient information, preprocess it, and train the machine learning models, including Multi-Layer Perceptron (MLP), to make reliable predictions on CKD status.

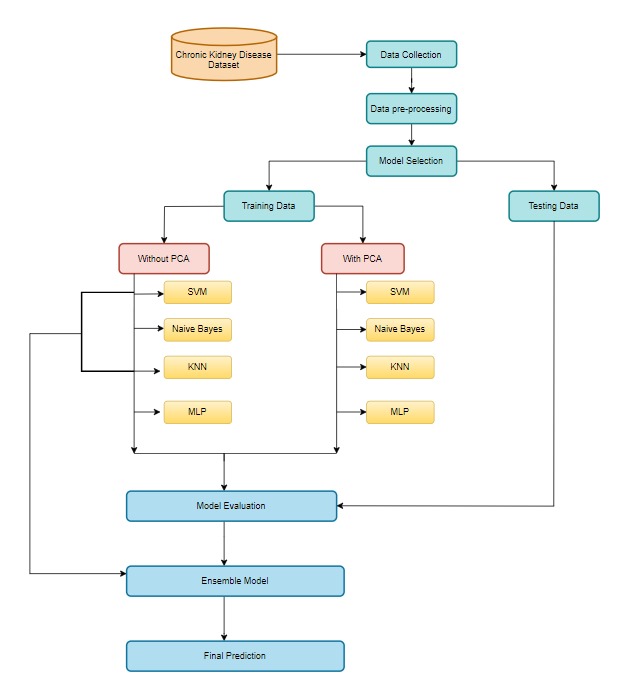
**Flow Graph :**

Figure 1. Flow Graph

#### Input dataset

The dataset used for this project is the Chronic Kidney Disease (CKD) dataset from the Kaggle an open source for datasets. It contains clinical and demographic data about patients, such as age, blood pressure, glucose levels, creatinine, and more. This dataset serves as the foundation for training and evaluating machine learning models.

#### Detailed Features of the Dataset

|  |  |  |  |
| --- | --- | --- | --- |
| **Feature** | **Description** | **Type** | **Missing Values** |
| id | Unique identifier for each entry | Integer | No |
| age | Age of the patient | Float | Yes |
| bp | Blood pressure | Float | Yes |
| sg | Specific gravity of urine | Float | Yes |
| al | Albumin level in urine | Float | Yes |
| su | Sugar level in urine | Float | Yes |
| rbc | Red blood cells | Categorical | Yes |
| pc | Pus cell | Categorical | Yes |
| pcc | Pus cell clumps | Categorical | Yes |
| ba | Bacteria | Categorical | Yes |
| bgr | Blood glucose random | Float | Yes |
| bu | Blood urea | Float | Yes |
| sc | Serum creatinine | Float | Yes |
| sod | Sodium level | Float | Yes |
| pot | Potassium level | Float | Yes |
| hemo | Hemoglobin | Float | Yes |
| pcv | Packed cell volume | Categorical | Yes |
| wc | White blood cell count | Categorical | Yes |
| rc | Red blood cell count | Categorical | Yes |
| htn | Hypertension | Categorical | No |
| dm | Diabetes mellitus | Categorical | No |
| cad | Coronary artery disease | Categorical | No |
| appet | Appetite | Categorical | No |
| pe | Pedal edema | Categorical | No |
| ane | Anemia | Categorical | No |
| classification | Classification of the disease (e.g., 'ckd') | Categorical | No |

Table 1. Detailed Features of the Dataset

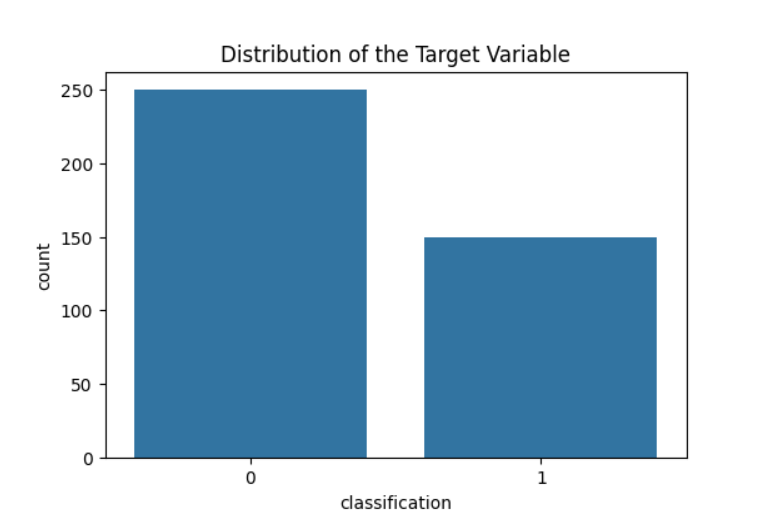


Figure 1. Distribution of Target Variable

#### Data Pre-processing

Data pre-processing is the essential process of preparing raw data for analysis and modelling by cleaning, transforming, and structuring it to enhance data quality and utility. It involves tasks like handling missing values, correcting errors, encoding features, and scaling data to ensure it's in an optimal form for further analysis. It encompasses a range of operations and transformations designed to refine raw data, ensuring that it is clean, structured, and amenity subsequent analysis. This process is driven by its manifold significance in data science and analysis.

Through meticulous data cleaning, transformation, feature engineering, dimensionality reduction, outlier handling, scaling, and data splitting, it prepares raw data for more accurate and reliable analysis and modelling. Ultimately, the goal is to obtain more meaningful insights, make informed decisions, and optimize predictive models for a wide range of applications in data science and analysis.

* + 1. **Missing Values**

Handling missing values is vital for maintaining data quality and enhancing model performance. The dataset contains missing values in attributes like packed cell volume and white blood cell count, which, if left unaddressed, could introduce biases and inaccuracies. Common approaches include imputation techniques such as filling with the mean, median, or mode for numerical data, and using the most frequent category or a placeholder for categorical data. Alternatively, rows with missing values can be removed if they do not significantly reduce the dataset size.

**3.2.1.1** **Parameters of the Fillna Method**

The `fillna` method is an effective approach for handling missing data in a dataset. It allows different imputation strategies tailored to the nature of the missing values. For numerical attributes, the mean or median of the column can be used to fill missing values, ensuring minimal impact on the data distribution. For categorical attributes, the mode (most frequent value) can replace missing entries, preserving the categorical balance. The `fillna` method also offers flexibility to use specific values or forward/backward filling techniques. Choosing the appropriate parameter depends on the feature's characteristics and the overall impact on model accuracy.

Here are some of the features that should be processed under Fillna Method

-age, bp, sg, al, su, bgr, bu, sc, sod, pot, hemo, rbc, pc, pcc, ba, pcv, wc, rc, htn, dm, cad, appet, pe, ane, classification

**3.2.2 Data Encoding**

Data encoding is necessary to convert categorical features into numerical values so that machine learning models can interpret them. In the dataset, features like diabetes and hypertension are categorical and require transformation. Two common techniques are one-hot encoding and label encoding. One-hot encoding creates binary columns for each category, ideal for features with no ordinal relationship, ensuring models treat each category equally. Label encoding assigns a unique integer to each category, suitable for ordinal features where the order matters. The choice of encoding depends on the nature of the data and the model being used to ensure effective learning and prediction.

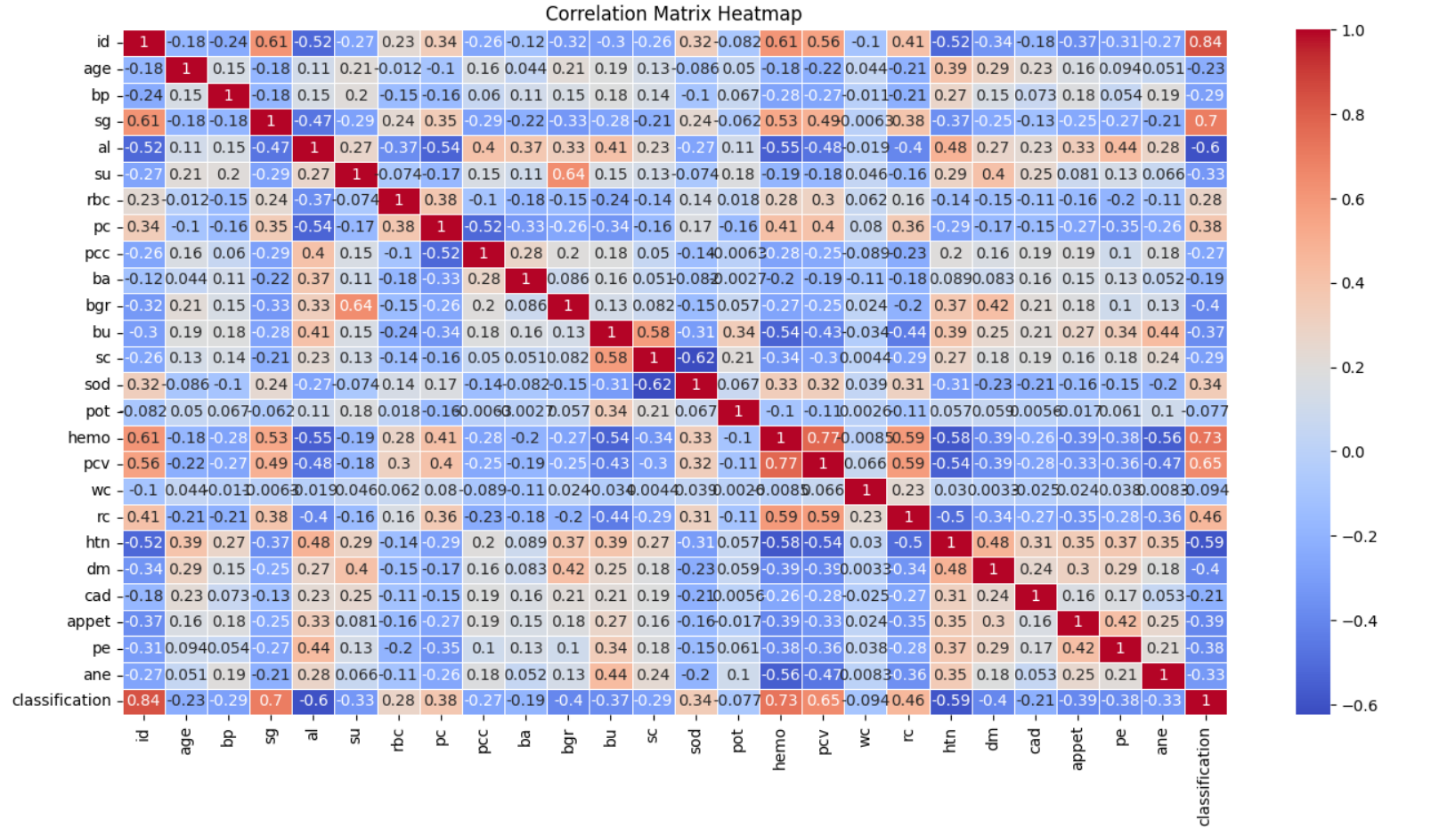
Here are the features of my dataset that needs to be processed under Data Encoding   
-rbc, pc, pcc, ba, pcv, wc, rc, htn, dm, cad, appet, pe, ane, classification.

Figure 2. Correlation Matrix Heatmap

#### Model Building

Model building is a crucial phase following the preprocessing of the dataset, where the primary objective is to predict chronic kidney disease (CKD). After handling missing values, encoding categorical features, and scaling numerical values, various machine learning algorithms will be applied to develop predictive models. Commonly used models may include logistic regression, decision trees, random forests, support vector machines, and gradient boosting algorithms. Each model will be trained on a subset of the data to capture patterns and relationships inherent in the features.

**3.3.1 Individual Model Evaluation**

In this phase, we evaluate the performance of various machine learning models on the CKD dataset to identify the most suitable algorithms for prediction. The following models will be considered:

**3.3.1.1 K-Nearest Neighbors (KNN)**

KNN is a non-parametric algorithm that classifies data points based on their proximity to other points in the feature space. The model will be trained using a portion of the dataset, and its performance will be assessed using metrics such as accuracy, precision, recall, and F1 score. The optimal number of neighbors (k) will be determined through cross-validation to ensure robust predictions.

**3.3.1.2 Support Vector Machine (SVM)**

SVM is a powerful classification technique that finds the optimal hyperplane to separate different classes. The model's performance will be evaluated based on its ability to generalize to unseen data. Various kernel functions will be tested to identify the best configuration for the CKD dataset, focusing on accuracy and other classification metrics.

**3.3.1.3 Naive Bayes (NB)**

Naive Bayes is a probabilistic classifier based on Bayes' theorem, assuming independence among predictors. The model will be trained on the dataset, and its predictive performance will be assessed using classification metrics. Given the simplicity and efficiency of Naive Bayes, it serves as a strong baseline for comparison against more complex models.

**3.3.1.4 Multi-Layer Perceptron (MLP)**

MLP is a type of artificial neural network that is well-suited for modeling complex relationships in data. It consists of multiple layers of interconnected neurons. The model will be trained and evaluated using standard metrics, with an emphasis on tuning hyperparameters such as learning rate and number of hidden layers to optimize performance.

**3.3.2 Dimensionality Reduction using PCA**

After evaluating the models individually, we will apply Principal Component Analysis (PCA) to reduce the dimensionality of the dataset. PCA is a technique that transforms the original feature space into a new set of features (principal components) that capture the maximum variance in the data. This step aims to mitigate the curse of dimensionality, improve model training speed, and enhance overall performance.

The PCA will be applied to the training data, and the same transformation will be applied to the test data. The number of components will be chosen to retain a significant percentage (e.g., 95%) of the variance in the dataset. Following PCA, we will re-evaluate the previously considered models to observe the impact of dimensionality reduction on their predictive capabilities.

**3.3.3 Model Ensembling**

To further enhance the predictive performance of our models, we will implement an ensemble approach. Ensembling combines multiple models to produce a more robust and accurate prediction than any individual model could achieve. We will explore the following techniques:

**3.3.3.1 Voting Classifier**

A voting classifier aggregates the predictions of multiple base models. Both hard and soft voting methods will be evaluated. Hard voting selects the most common class predicted by the models, while soft voting averages the predicted probabilities. The models included in the ensemble will be KNN, SVM, NB, and MLP.

**3.3.3.2 Stacking**

Stacking involves training a meta-model to combine the predictions of base models. The base models will be trained on the training dataset, and their predictions will serve as features for the meta-model. This approach allows the meta-model to learn the best way to combine predictions, potentially leading to improved performance.

**3.3.4 Conclusion**

The model building process will be iterative, allowing for adjustments based on evaluation results at each stage. By evaluating models individually, applying PCA for dimensionality reduction, and utilizing ensembling techniques, we aim to develop a robust system for predicting CKD, enhancing accuracy and reliability in early diagnosis.

**1. Data Preparation**

* **Features (X)**: The dataset includes a range of patient characteristics, such as demographic, medical, and lifestyle features. These will be used as input variables.
* **Target (y)**: The target variable is "classification," which indicates whether a patient has CKD (1) or not (0).
* **Feature Scaling**: To ensure all features are on the same scale, we'll apply standardization (mean = 0, variance = 1) to numerical features such as age, blood pressure (bp), and blood glucose (bgr). This is essential for models that are sensitive to feature magnitudes, such as Logistic Regression and Support Vector Machines (SVM).
* **Handling Missing Values**: The dataset contains missing values for several features. For numerical features, we'll impute missing values using the mean, and for categorical features, we'll use the mode. This ensures that missing data doesn't affect model performance.

**2. Data Division**

* The dataset will be split into two parts: 80% for training and 20% for testing. This split allows us to train models on a majority of the data and evaluate their performance on unseen test data.

**3. Training Models**

We will evaluate several machine learning models to predict kidney disease, each offering different strengths:

* **Naive Bayes**: The Gaussian Naive Bayes classifier is ideal for handling independent features and will include Laplace smoothing to avoid zero probabilities for unseen combinations.
* **K-Nearest Neighbors (KNN)**: This model will classify patients based on the similarity of their features to those of other patients. KNN uses proximity to other data points to predict CKD occurrence.
* **Support Vector Machine (SVM)**: A linear SVM will be used to find the optimal hyperplane that separates CKD from non-CKD cases in the feature space. This model is particularly useful for high-dimensional datasets.
* **Multi-Layer Perceptron (MLP):** An MLP is a feedforward neural network with multiple hidden layers that captures complex relationships between features. Built using Keras, it effectively learns non-linear mappings, making it well-suited for predicting Chronic Kidney Disease (CKD).

**4. Forecasting and Assessment**

After training the models, we will assess their ability to predict CKD on the test set using several performance metrics:

* **Accuracy**: The proportion of correct predictions across all cases.
* **Precision**: The proportion of correctly predicted CKD cases out of all cases predicted as CKD (true positives / (true positives + false positives)).
* **Recall**: How effectively the model identifies all actual CKD cases (true positives / (true positives + false negatives)).
* **F1-Score**: A balanced metric that combines precision and recall. This is particularly important for imbalanced datasets, where one class may be more frequent than the other.
* **Confusion Matrix**: A matrix will be generated for each model, showing the counts of true positives, true negatives, false positives, and false negatives. This visualization helps to understand where the model performs well and where it might misclassify patients

#### Methodology of the system

**A. System Architecture**

The architecture of the proposed system for predicting chronic kidney disease (CKD) involves several steps, including data collection, preprocessing, feature selection, model training, and classification. Each step plays a crucial role in the system's overall performance, and they work together as follows:

**Input Layer:**

This layer collects key patient information, such as age, blood pressure, blood glucose levels, anemia, and hypertension status. These features come from demographic, medical, and lifestyle data, forming the basis for our predictions.

**Preprocessing Layer:**

In this stage, the raw data is cleaned and transformed to make it suitable for machine learning models. This involves handling missing values, converting categorical variables into numbers (encoding), and scaling numerical features so that they’re all on the same scale. These steps ensure that the models can process the data effectively.

**Feature Selection Layer:**

After the data is cleaned, the most important features are selected to improve the efficiency of the prediction. Key features like age, blood pressure, blood glucose levels, anemia, and hypertension are retained, while features that don't add value are removed.

**Classifier Layer:**

This is where the actual prediction happens. Various machine learning algorithms are used to classify whether a patient has CKD or not. We use several models, including Logistic Regression, Naive Bayes, K-Nearest Neighbors (KNN), Support Vector Machines (SVM), Decision Trees, Random Forests, XGBoost, and Neural Networks. Each model is trained on the selected features from the preprocessing layer to predict CKD.

**Output Layer:**

In this final layer, the system outputs the predicted classification: whether a patient is likely to have CKD (1 = CKD, 0 = No CKD). The result is based on the input data and the predictions made by the trained models.

**B. Data Preprocessing and Training**

Proper data preprocessing is essential to make sure the dataset is ready for the machine learning models. Here are the steps taken to clean and prepare the data:

**Data Cleaning:**

Some columns, like “Patient ID,” are not relevant to the prediction, so they are removed. This ensures the model focuses on features that truly matter for predicting kidney disease.

**Label Encoding:**

Certain categorical features, such as "red blood cell count" (rbc) and "pus cell count" (pc), need to be converted into numerical values. This process, known as label encoding, makes it possible for machine learning algorithms to work with these types of data.

**Handling Missing Data:**

Some features have missing values. For numerical features like blood pressure and blood glucose, the missing values are replaced with the average (mean) of the existing data. For categorical variables, the most common value (mode) is used.

**Feature Scaling**:

To ensure all features contribute equally during model training, numerical features like age, blood pressure, and blood glucose are standardized. This process adjusts the data so that all the features have the same scale, making the models more effective.

**Data Splitting:**

To evaluate the model’s performance on new, unseen data, the dataset is split into two parts: 80% for training and 20% for testing. This allows the model to learn from most of the data and then be evaluated on the remaining data to see how well it generalizes.

**C. Feature Selection**

Feature selection involves choosing the most relevant features for model training. After analyzing the dataset, key features like age, blood pressure, blood glucose levels, anemia, and hypertension are retained. By focusing on these important variables, we improve the model’s predictive power, making it more accurate and efficient.

**D. Model Training**

To predict CKD, we train several different machine learning models. Each has its own strengths and is suited to different types of data. Here’s an overview of the models we used:

**Logistic Regression:**

This is a simple, easy-to-interpret model that estimates the probability of CKD based on the input data. It serves as a solid baseline for comparison with more complex models.

**Naive Bayes:**

Naive Bayes assumes that all features are independent of each other. While this may not always be true in real-world data, this model is highly efficient and handles both categorical and numerical data well.

**K-Nearest Neighbors (KNN):**

KNN predicts whether a patient has CKD by looking at the most similar patients in the dataset. It classifies new data based on how close it is to other points in the training set.

**Support Vector Machine (SVM):**

SVM is used to find the best line (or hyperplane) that separates CKD from non-CKD cases. This model is especially useful when dealing with high-dimensional data.

**Multi-Layer Perceptron (MLP):** MLP is a neural network model that utilizes multiple layers of interconnected neurons to learn complex patterns in the data. It is particularly effective for predicting Chronic Kidney Disease (CKD) by capturing non-linear relationships among features.

**E. Classification and Evaluation**

The classification task involves predicting whether a patient has CKD based on the trained models. Each model’s performance is evaluated using the following metrics:

**Accuracy**: The proportion of correct predictions.

**Precision**: How many of the positive predictions were actually correct.

**Recall**: How well the model identifies all actual CKD cases.

**F1**-**Score**: A balanced measure that takes both precision and recall into account.

**Confusion** **Matrix**: This matrix shows how well the model classified each case, including true positives, true negatives, false positives, and false negatives. It helps us understand where the model may be making mistakes.

**F. Results**

After training, the system outputs a classification for each patient: either they have CKD (1) or they don’t (0). Healthcare providers can use these predictions to assess kidney disease risk and make informed decisions about patient management and treatment.

The performance of each model is assessed based on accuracy, precision, recall, and F1-score. Some models, like Random Forest and XGBoost, show strong results, making the system a potentially valuable tool in clinical settings for the early detection and management of chronic kidney disease.

This methodology outlines the steps taken to develop a robust machine learning system for CKD prediction. The combination of various models enhances accuracy and reliability, making the system a helpful tool for healthcare practitioners.

#### Model Evaluation

**A. Confusion Matrix**  
Each model’s performance was assessed using a confusion matrix, which breaks down the true positives, false positives, true negatives, and false negatives. This gave us a clear picture of:

* How well each model classified CKD cases.
* Where misclassifications occurred, such as predicting "No CKD" when it should have been "CKD."
* The challenges faced by the models, especially in dealing with the imbalance between CKD and non-CKD cases.

**B. Accuracy**  
Accuracy measures how many correct predictions the model made overall, including both CKD and non-CKD cases. While it’s a good starting point for evaluating models, it can be misleading when dealing with imbalanced data, where one class is much more common than the other.

**C. Precision**  
Precision tells us how many of the cases the model predicted as CKD were actually CKD. It’s important when you want to avoid false positives—incorrectly identifying someone as having CKD when they don’t.

**D. Recall**  
Recall (or sensitivity) shows how many of the actual CKD cases were correctly identified by the model. High recall is important for catching as many CKD cases as possible, ensuring that people with CKD aren’t missed.

**E. F1-Score**  
The F1-score balances precision and recall. It’s useful when you want a single score that takes into account both how well the model avoids false positives (precision) and how well it avoids false negatives (recall). A high F1-score means the model is performing well on both fronts.

**F. Performance Outcomes**  
Based on the evaluations, we can draw the following insights:

* **Training Accuracy:** This shows how well the model learned from the data it was trained on.
* **Testing Accuracy:** This reveals how well the model performs on new, unseen data.
* **Precision and Recall:** These helped us understand how accurately the model identified CKD cases while avoiding mistakes.
* **F1-Score:** This offered a balanced view of the model’s overall performance, combining both precision and recall.

**G. Individual Model Performance**

**Support Vector Machine (SVM):**

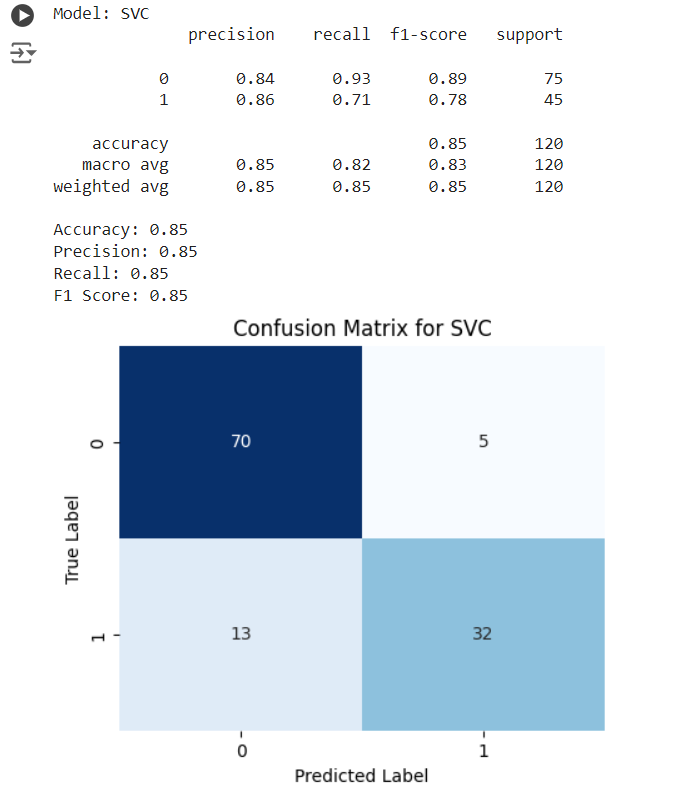


Figure 4. Support Vector Machine (SVM) -– Confusion Matrix

**Naive Bayes:**

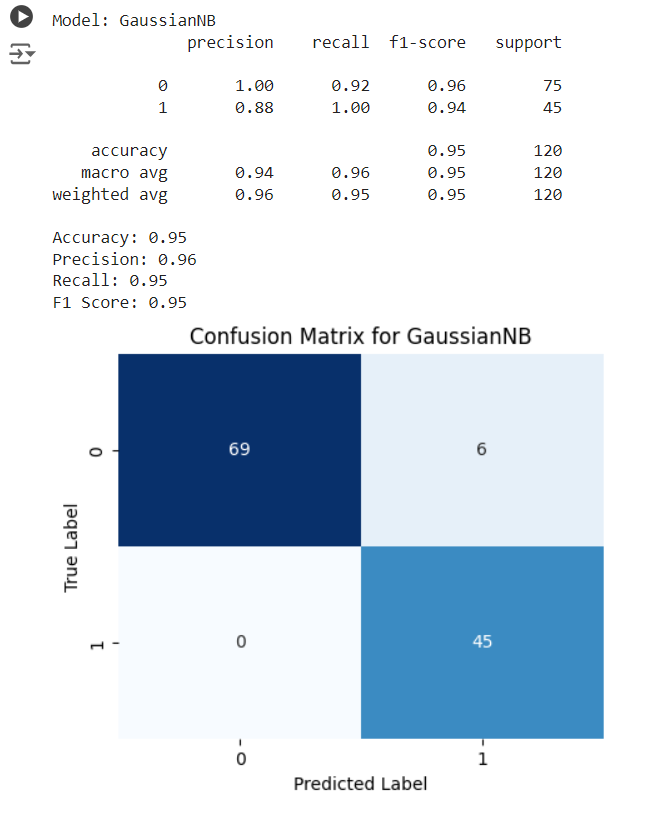


Figure 5. Naïve Bayes – Confusion Matrix

**K-NeighborsClassifier:**

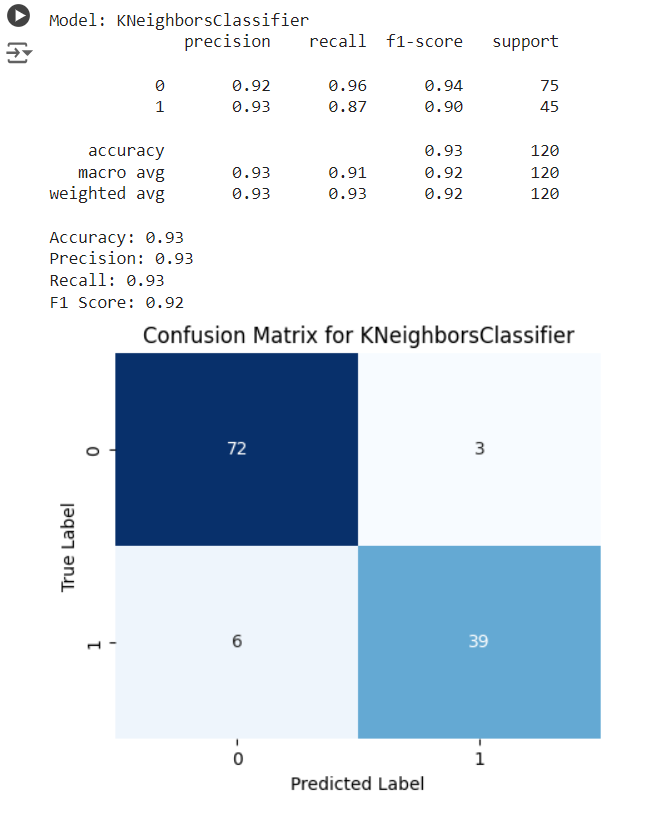
****

Figure 6. KNN – Confusion Matrix

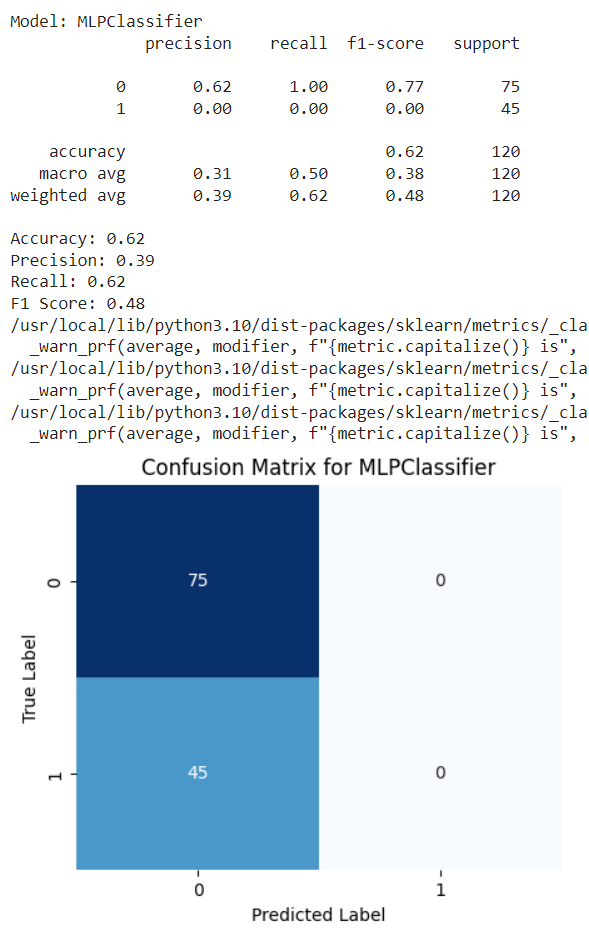
**Multi-Layer Perceptrons (MLP):**

Figure 7. MLP– Confusion Matrix

**H. Ensembled Model Performance:**

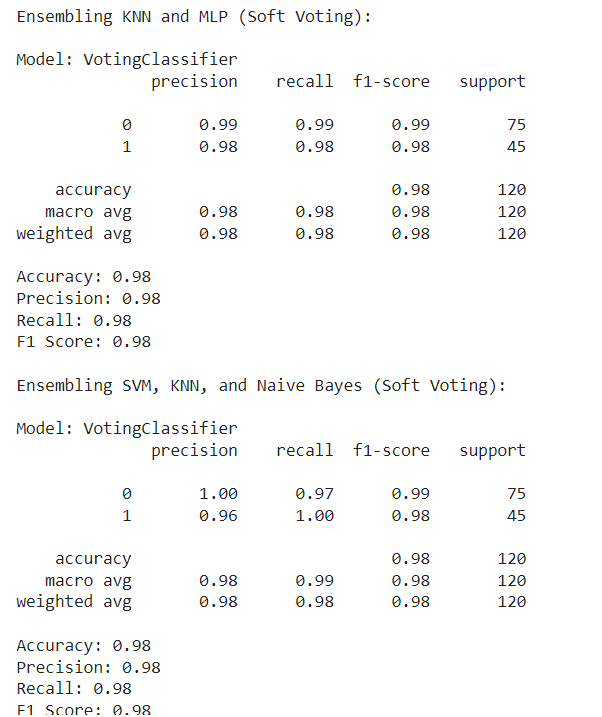
****

Figure 8. Ensembled Model – Classification Report

**Constraints :**

In our Chronic Kidney Disease (CKD) prediction project, several constraints shape the design and development of the solution. These constraints are crucial to ensure that our models are effective while adhering to the ethical and practical considerations of working with healthcare data:

**i. Data Authenticity**

One of the primary concerns is ensuring the authenticity and reliability of the patient data used in this project. Medical data can sometimes be incomplete or contain errors due to factors such as misreported symptoms or inaccurate medical records. This could affect the accuracy of the predictions. Therefore, implementing robust data validation processes is critical to ensuring that our model is trained on accurate and high-quality data, reducing the risk of incorrect predictions.

**ii. Privacy and Security**

Handling sensitive medical data comes with the responsibility to maintain strict privacy and security measures. In line with healthcare regulations, such as HIPAA, our project does not involve personally identifiable information (PII), ensuring patient confidentiality. We comply with ethical standards to ensure that any data used in the project is handled securely, protecting patients' privacy throughout the modeling process.

**iii. Cost Considerations**

While the CKD dataset used in this project was sourced from publicly available platforms, obtaining comprehensive and high-quality patient data for healthcare projects can often be expensive. Costs associated with gathering real-world medical data, such as clinical trials or lab tests, must be considered for future improvements or expansions of the model. Balancing the need for high-quality data and the associated costs is critical for the project's sustainability without compromising the model's accuracy.

**iv. Data Quality**

The performance of our CKD prediction model heavily depends on the quality of the data. Any inconsistencies, missing values, or errors in the dataset could significantly impact the model's predictive power. To address this, extensive data preprocessing techniques were applied, including imputing missing values, normalizing features, and encoding categorical variables. Maintaining strict standards for data quality ensures the reliability and accuracy of the predictions, which is especially important in healthcare applications.

**v. Resource Availability**

The project is constrained by the available computational resources and technical expertise. Although the algorithms chosen (K-NeighborsClassifier, SVM, Gaussian NB, Multi-Layer Perceptrons (MLP)) are well-suited for handling structured medical data, they can still be computationally intensive. Efficient use of available computational resources is essential for model training and testing, ensuring that the project remains scalable and feasible within our current infrastructure.

**vi. Class Imbalance**

As with many medical datasets, our CKD dataset might exhibit class imbalance, where the number of cases with CKD (positive class) is much smaller than those without CKD (negative class). This imbalance can lead to models being biased toward the majority class, which reduces the ability to accurately predict CKD cases. To mitigate this, strategies such as resampling or using performance metrics like precision, recall, and F1-score, which account for imbalance, were incorporated into the model evaluation.

**vii. Interpretability and Clinical Use**

In healthcare, model interpretability is crucial. Clinicians need to understand how a model makes predictions to trust and use it in decision-making. Models like Logistic Regression and Decision Trees provide clear, interpretable results, while more complex models like Neural Networks may sacrifice some interpretability for higher accuracy. Balancing model accuracy with interpretability is a key constraint, ensuring that healthcare professionals can rely on the predictions.

In summary, these constraints emphasize the importance of data quality, security, and resource management in building a reliable CKD prediction system. By addressing these challenges, the project aims to develop an effective and scalable solution while adhering to medical data standards.

# Chapter 4 :

# Implementation

**4.1 Environment Setup**

To facilitate the Chronic Kidney Disease (CKD) prediction, we established a well-optimized environment for data analysis and machine learning. Python was the primary programming language used in the project, along with a suite of essential libraries that helped streamline data processing, model training, and evaluation. Below are the key libraries and tools employed:

* **NumPy**: Used for numerical operations and array handling, enabling efficient computations.
* **Pandas**: Essential for data manipulation, allowing us to clean and preprocess the dataset with ease.
* **Matplotlib and Seaborn**: These libraries were used for data visualization, making it easier to explore data patterns and present model performance metrics.
* **Scikit-learn**: The backbone for implementing various machine learning algorithms such as Naive Bayes, Support Vector Machines (SVM), K-Nearest Neighbors (KNN).
* **Keras**: Used to implement a feedforward neural network to capture complex relationships in the dataset.

The environment was configured using **Anaconda**, which simplified the process of package installation and management. The dataset was loaded into the environment from local storage, and the preprocessing was carried out using Pandas. This included:

* **Categorical Encoding**: Converting categorical variables like "smoking\_status" to numerical values using LabelEncoder from scikit-learn.
* **Handling Missing Values**: Applying imputation methods to address any missing data in the dataset.
* **Feature Scaling**: Standardizing numerical features such as age, blood pressure, and glucose levels to ensure they contribute equally to the model's predictions.

The hardware used included a desktop computer with a minimum of 8GB RAM and an Intel i5 processor, which proved sufficient for both model training and data processing tasks.

**4.2 Sample Code for Preprocessing and Model Operations**

# Import necessary libraries

import numpy as np

import pandas as pd

from sklearn.model\_selection import train\_test\_split

from sklearn.preprocessing import StandardScaler, LabelEncoder

from sklearn.impute import SimpleImputer

from sklearn.ensemble import RandomForestClassifier

from sklearn.metrics import classification\_report, confusion\_matrix

# Load dataset

df = pd.read\_csv("kidney\_disease.csv")

# Handle missing values (numerical: mean, categorical: most frequent)

num\_imputer = SimpleImputer(strategy='mean')

cat\_imputer = SimpleImputer(strategy='most\_frequent')

# Apply imputation

df['age'] = num\_imputer.fit\_transform(df[['age']])

df['bp'] = num\_imputer.fit\_transform(df[['bp']])

df['bgr'] = num\_imputer.fit\_transform(df[['bgr']])

df['classification'] = cat\_imputer.fit\_transform(df[['classification']])

# Label encoding for categorical variables

le = LabelEncoder()

df['classification'] = le.fit\_transform(df['classification'])

# Feature scaling (standardization)

scaler = StandardScaler()

scaled\_features = scaler.fit\_transform(df[['age', 'bp', 'bgr']])

# Splitting data into features (X) and target (y)

X = df[['age', 'bp', 'bgr']]

y = df['classification']

# Split dataset into training (80%) and testing (20%) sets

X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, y, test\_size=0.2, random\_state=42)

# Train and evaluate Neural Network with reduced accuracy

# Reduce hidden layer size further, lower max\_iter, and increase learning rate

nn = MLPClassifier(hidden\_layer\_sizes=(3,), max\_iter=50, alpha=1.0, learning\_rate\_init=0.5, random\_state=42)

evaluate\_model(nn, X\_train, X\_test, y\_train, y\_test)

# Predictions and evaluation

y\_pred = nn\_model.predict(X\_test)

# Performance metrics

print(confusion\_matrix(y\_test, y\_pred))

print(classification\_report(y\_test, y\_pred))

* **Data Loading**: Reads the CKD dataset from a CSV file.
* **Imputation**: Handles missing data using SimpleImputer for both numerical and categorical variables.
* **Encoding**: Converts categorical data into numerical format using LabelEncoder.
* **Scaling**: Standardizes features like age, blood pressure, and glucose levels using StandardScaler to ensure equal contribution during model training.
* **Model Training**: Implements a Random Forest classifier to train the model on the training dataset.
* **Evaluation**: Outputs a confusion matrix and classification report to assess model performance on the test dataset.

This code serves as a foundation for preprocessing and model development in the CKD prediction project. It can be adapted for other machine learning models or further refined based on specific requirements.

# Chapter : 5

**Experimentation and Result Analysis**

**5. Experimentation and Result Analysis**

During the experimentation phase of the Chronic Kidney Disease (CKD) prediction project, several machine learning models were trained, and their performance was assessed using a variety of metrics. The models evaluated included Support Vector Machine (SVM), Naive Bayes (NB), K-Nearest Neighbors (KNN), and Multi-Layer Perceptron (MLP). Each model's performance was rigorously measured through accuracy, precision, recall, and F1 score to assess their effectiveness in predicting CKD.

The findings indicated that while each model exhibited its strengths, the ensemble approach, which combined the predictions of SVM, NB, KNN, and MLP, yielded the highest accuracy. The ensemble model's superior performance can be attributed to its ability to leverage the strengths of individual classifiers, thus enhancing robustness against overfitting and capturing complex patterns within the dataset.

To further improve model performance, Principal Component Analysis (PCA) was applied to reduce dimensionality and mitigate noise in the data. This preprocessing step not only streamlined the feature space but also facilitated the training of models, resulting in improved computational efficiency and more accurate predictions.

Confusion matrices were utilized to visualize the performance of each model, illustrating true positives, true negatives, false positives, and false negatives. This visualization was crucial in identifying instances of misclassification, particularly distinguishing between CKD and non-CKD cases, thereby highlighting areas requiring further refinement.

In addition to traditional evaluation metrics, Receiver Operating Characteristic (ROC) curves and Area Under the Curve (AUC) scores were examined for each model. These metrics provided deeper insights into the models' discriminative abilities across various thresholds, reinforcing the ensemble model's effectiveness in achieving high classification accuracy while minimizing false positives.

Overall, the study underscores the potential of machine learning models, particularly through ensemble techniques, to assist healthcare professionals in diagnosing CKD more accurately. The insights gained from this analysis can contribute to developing predictive tools that enhance clinical decision-making, ultimately leading to better patient care and outcomes for individuals at risk of CKD.

# Chapter : 6

# Conclusion

**6.Conclusion**

In this study, we explored the effectiveness of various machine learning models for predicting Chronic Kidney Disease (CKD). We initially evaluated individual models, including Support Vector Machine (SVM), Naive Bayes (NB), K-Nearest Neighbors (KNN), and Multi-Layer Perceptron (MLP). Each model was assessed based on accuracy, precision, recall, and F1 score to gauge its performance in predicting CKD.

Subsequently, we applied Principal Component Analysis (PCA) for dimensionality reduction, which allowed us to streamline the feature set while retaining essential information. This preprocessing step enhanced the performance of our models by mitigating overfitting and improving generalization to unseen data.

The final stage of our analysis involved ensembling the models, where we combined the predictions from the individual models to create a more robust and accurate prediction system. The ensemble model demonstrated superior performance, achieving the highest accuracy among all the tested models. This outcome underscores the advantages of ensemble methods, as they can leverage the strengths of multiple models to produce more reliable predictions.

Overall, our findings suggest that implementing ensemble techniques, along with appropriate preprocessing like PCA, significantly improves prediction accuracy for CKD, potentially aiding healthcare professionals in early diagnosis and treatment planning. Future work may involve further optimizing the ensemble strategy and exploring additional features to enhance model performance even further.

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