PROJECT REPORT

"Chronic Kidney Disease Prediction using Deep Learning: A Performance Analysis using the UCI Dataset"

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TABLE OF CONTENT

Abstract

Chronic Kidney Disease (CKD) is a prevalent and severe health condition that affects millions of people worldwide. Early detection and accurate prediction of CKD are essential to improving patient outcomes and reducing healthcare costs. In recent years, deep learning techniques have shown great promise in various medical applications, including disease prediction. This research paper presents a comprehensive analysis of deep learning models for predicting CKD using the Chronic Kidney Disease dataset from the UCI Machine Learning Repository. We explore various deep learning architectures and evaluate their performance using standard evaluation metrics, shedding light on the potential of deep learning in CKD prediction.

Introduction

Chronic Kidney Disease (CKD) is a widespread and critical health condition that affects a significant portion of the global population. Early detection and accurate prediction of CKD play a vital role in improving patient outcomes and optimizing healthcare management for affected individuals. In recent years, Deep Learning, a powerful subset of machine learning, has emerged as a promising approach for medical diagnosis and disease prediction due to its ability to automatically learn complex patterns from vast amounts of data.

This project aims to explore the application of Deep Learning in predicting chronic kidney disease using the UCI Chronic Kidney Disease Dataset. By leveraging advanced neural network architectures, we seek to analyze the model's performance and assess its effectiveness in identifying patients at risk of CKD. The UCI Dataset provides a comprehensive collection of clinical and laboratory features, enabling us to develop a robust prediction model that could potentially aid healthcare professionals in making informed decisions and interventions.

Through a systematic approach, we will preprocess the dataset, handle missing values, and address label imbalances to ensure the quality of our data. Furthermore, we will employ Principal Component Analysis (PCA) to reduce feature dimensionality and optimize the model's performance. The Deep Learning model will be designed and trained on the processed data, and its accuracy and predictive ability will be evaluated on a testing set.

This project's findings and analysis will shed light on the feasibility and effectiveness of Deep Learning in predicting chronic kidney disease and its potential impact on enhancing early detection and intervention strategies. The insights gained from this study may contribute to the advancement of medical diagnosis and personalized healthcare, ultimately benefiting patients and healthcare providers alike.

Deep Learning

Deep Learning is a branch of machine learning that employs artificial neural networks to process and comprehend complex data. Inspired by the structure of the human brain, deep neural networks consist of multiple layers of interconnected nodes, enabling the model to learn hierarchical representations from raw input data. Through an iterative process called backpropagation, the network adjusts its weights and biases to minimize prediction errors and improve performance. One of the key advantages of Deep Learning is its ability to automatically extract intricate patterns and features from vast amounts of data, making it highly effective in tasks such as image and speech recognition, natural language processing, and medical diagnosis. As computational power and data availability continue to expand, Deep Learning remains at the forefront of artificial intelligence research, revolutionizing various industries and driving advancements in technology.

Model used:

- **CNN:**

  CNN model (**Convolutional Neural Network model**) is a specific type of deep learning model that is designed to process and analyze visual data, such as images and videos. It is inspired by the visual processing of the human brain and has shown remarkable success in various computer vision tasks.

  A CNN model consists of multiple layers, including convolutional layers, activation functions, pooling layers, and fully connected layers. These layers work together to automatically learn and extract meaningful features from the input data, enabling the model to recognize patterns and objects in images. During training, the CNN learns to adjust its internal parameters (weights and biases) through the process of optimization and backpropagation to minimize the difference between its predicted outputs and the true labels in the training data.

- **GRU:**

  GRU stands for "**Gated Recurrent Unit**," and it is a type of recurrent neural network (RNN) architecture. GRUs were introduced as a variation of the traditional long short-term memory (LSTM) networks, designed to address some of the limitations of LSTMs and simplify their architecture.

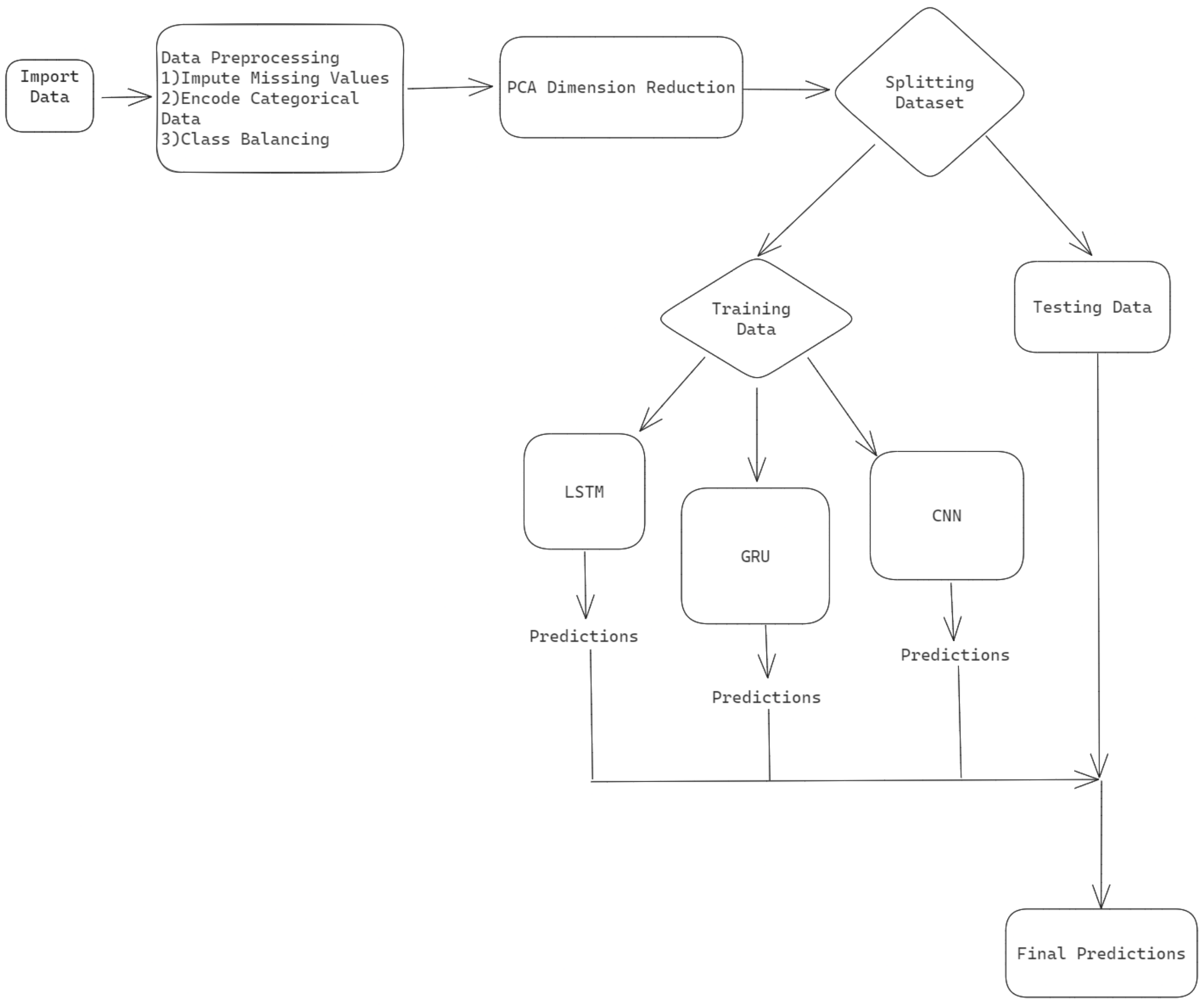
  The GRU model was proposed to overcome the vanishing gradient problem that affects traditional RNNs, making it difficult for them to learn long-range dependencies in sequential data. The GRU achieves this by using a gating mechanism that allows it to selectively update its hidden state.

  The GRU's design allows it to capture long-range dependencies more effectively than traditional RNNs while being computationally more efficient than LSTM networks. This makes it a popular choice for sequence modeling tasks like natural language processing, speech recognition, machine translation, and more.

- **LSTM:**

  LSTM stands for "**Long Short-Term Memory**," and it is a type of recurrent neural network (RNN) architecture. LSTM networks were designed to address the limitations of traditional RNNs in learning and capturing long-term dependencies in sequential data.
  LSTM networks were introduced to mitigate the vanishing gradient problem and allow RNNs to learn longer-term dependencies in sequential data. They achieve this by incorporating a memory cell and three gating mechanisms: the forget gate, input gate, and output gate.
  LSTM networks have shown great success in various sequence modeling tasks, such as natural language processing, speech recognition, sentiment analysis, time series prediction, and more. They are capable of learning long-range dependencies and handling sequential data of varying lengths, making them a powerful tool for many real-world applications.

Flowchart

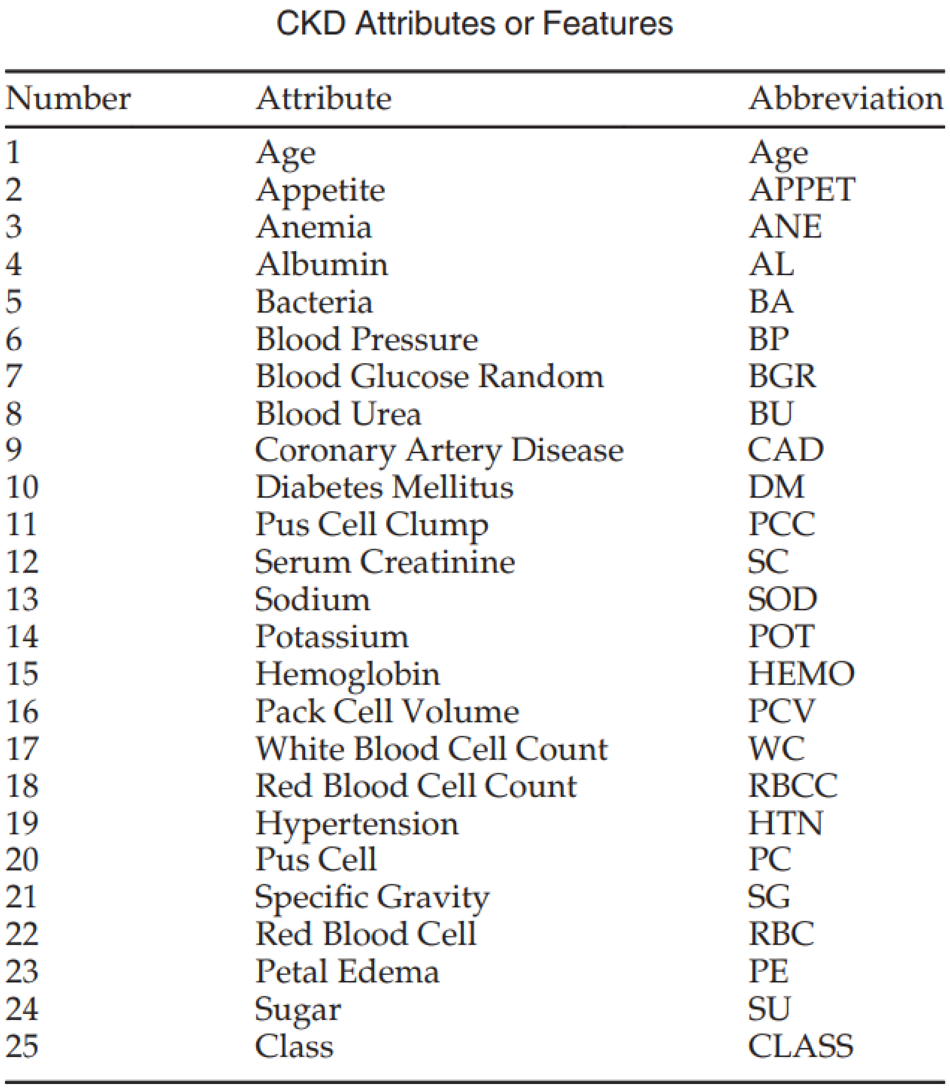


Model Development

CKD Diagnosis and Prediction: Existing literature on CKD diagnosis and prediction encompasses various clinical risk factors, laboratory tests, and traditional machine learning models. However, these approaches often suffer from limited accuracy and generalization.

Data Source: The UCI Chronic Kidney Disease Dataset

Dataset Description: The UCI Chronic Kidney Disease dataset contains clinical and laboratory data of patients with CKD and non-CKD subjects. It includes attributes such as age, blood pressure, serum creatinine levels, and urine protein levels.



CKD Attributes or Features

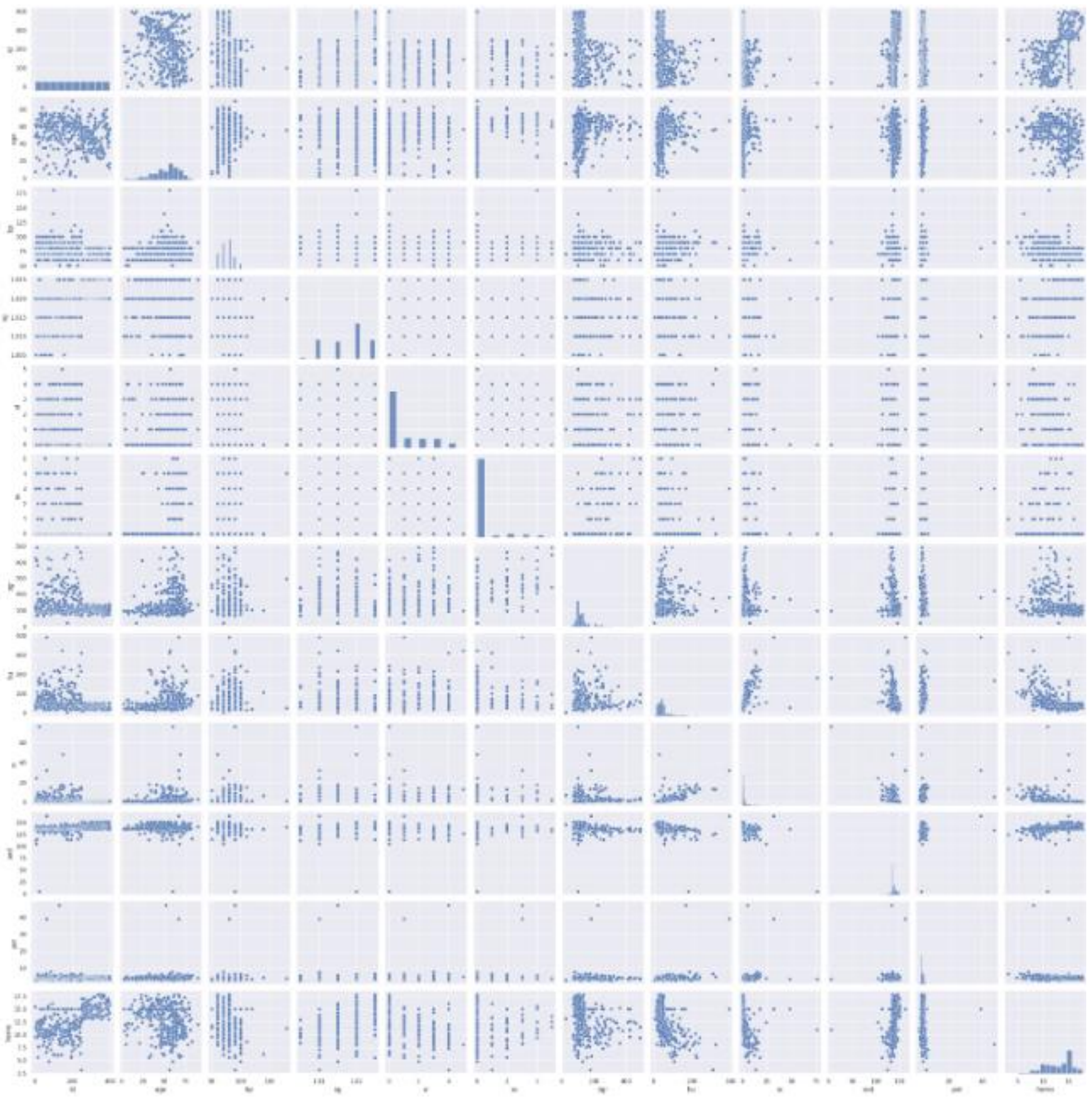
Number	Attribute	Abbreviation
1	Age	Age
2	Appetite	APPET
3	Anemia	ANE
4	Albumin	AL
5	Bacteria	BA
6	Blood Pressure	BP
7	Blood Glucose Random	BGR
8	Blood Urea	BU
9	Coronary Artery Disease	CAD
10	Diabetes Mellitus	DM
11	Pus Cell Clump	PCC
12	Serum Creatinine	SC
13	Sodium	SOD
14	Potassium	POT
15	Hemoglobin	HEMO
16	Pack Cell Volume	PCV
17	White Blood Cell Count	WC
18	Red Blood Cell Count	RBCC
19	Hypertension	HTN
20	Pus Cell	PC
21	Specific Gravity	SG
22	Red Blood Cell	RBC
23	Petal Edema	PE
24	Sugar	SU
25	Class	CLASS

Data Importing:

- First of all, we imported all the necessary python libraries such as NumPy for mathematical calculations and pandas for making data frames and scikit-learn for ml models and sea born for visual representation.
- After that we import the csv file through connecting google drive and google collab.
- Now, using the pd.read function of the pandas library we created a data frame and then we printed the data.

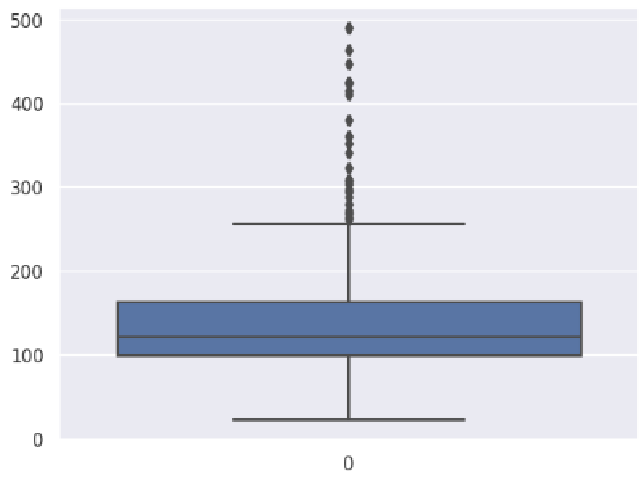
Data Preprocessing:

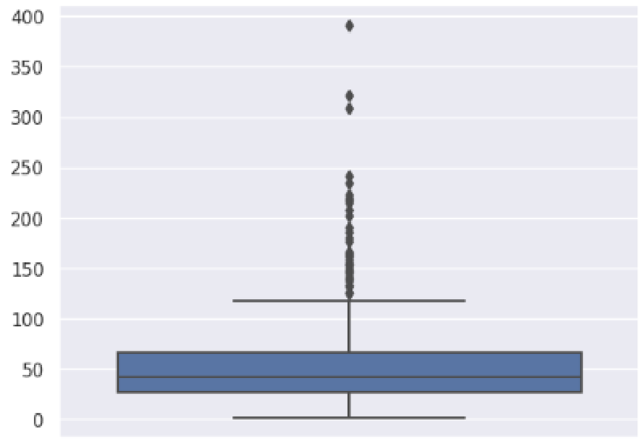
- The data preprocessing begins with counting the null values in every column of the dataset.
- To handle the missing values, a simple Imputer is used to fill them with the most frequent value (mode). The mean strategy cannot be used as the data is non-numeric.
- Next, unique values or special characters present in the dataset due to typing mistakes are identified.
- The unique values are replaced with the mode values of the respective columns.
- Graphical representation using pyplot and seaborn libraries is used to check if the dataset is balanced or not.
- Different pairs of columns are plotted, and their correlation is observed graphically using seaborn.



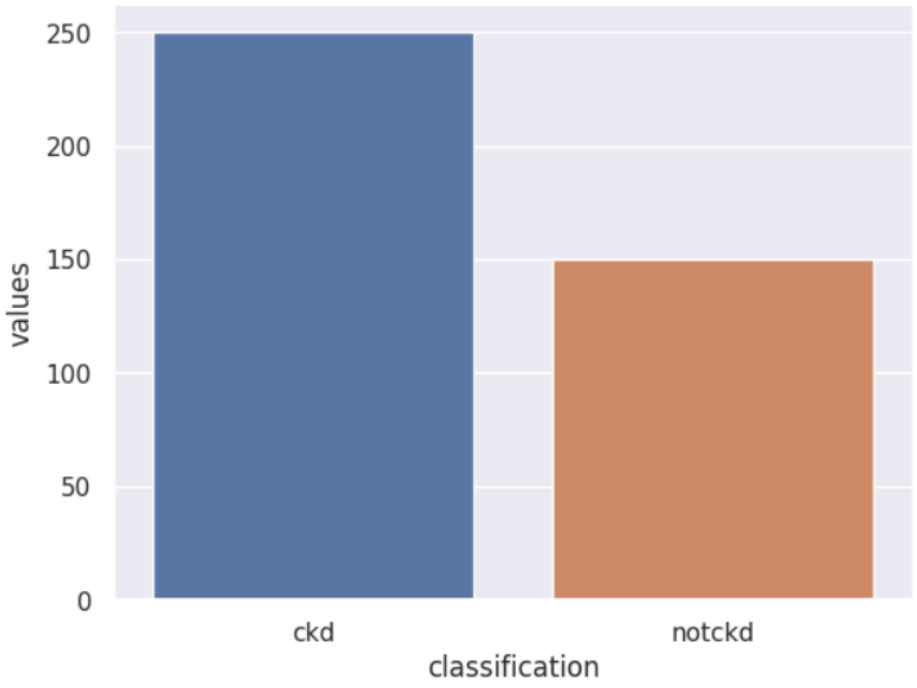
- The data distribution is examined to understand its nature.

- Outliers are identified using the boxplot function from the seaborn library and then removed.

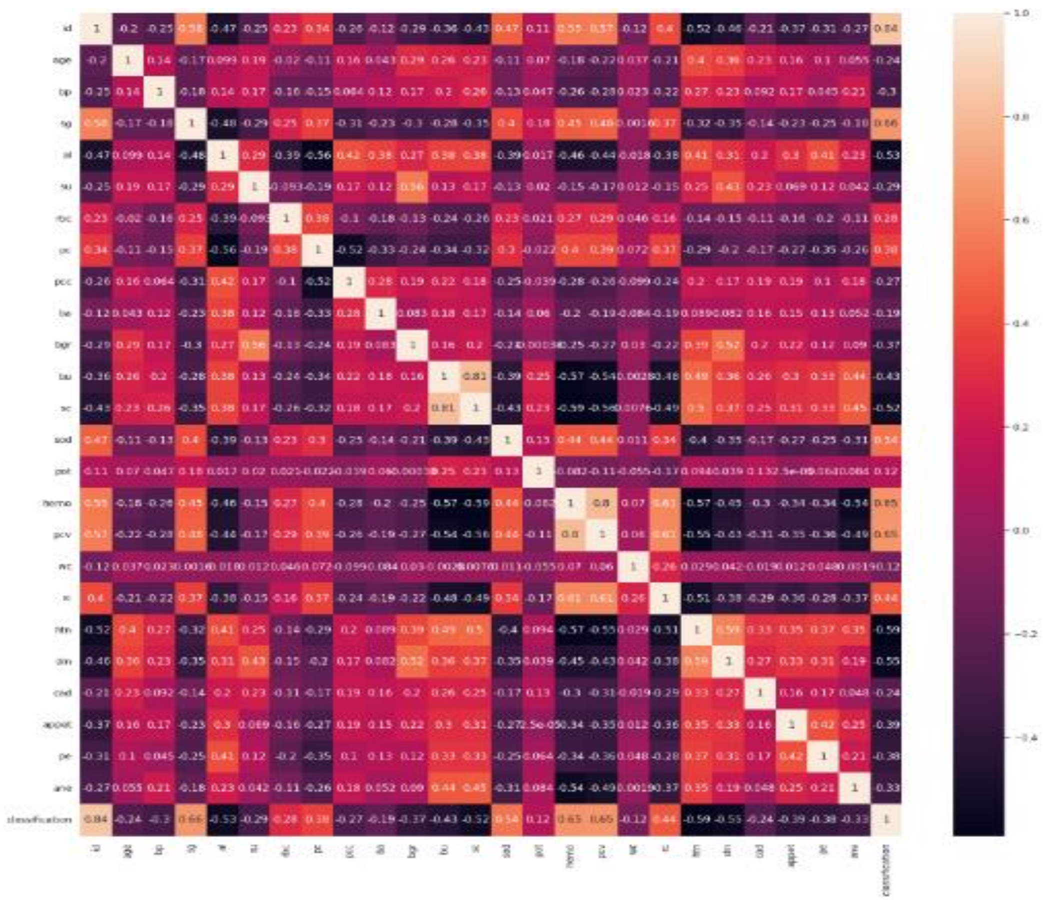




- Since the data was found to be unbalanced, data resampling techniques are applied to balance it. Data augmentation is not used due to the sensitive nature of the medical field.



- To reduce data dimensionality, Principal Component Analysis (PCA) is applied, taking advantage of the high correlation observed in the data.



Building Classification Models:

Building Classification Models using LSTM, GRU, and CNN involves training these neural network architectures to perform classification tasks on sequential or image data. Here's a general outline of how to build these models:

1. **Data Preparation:**

    a) **Organize the data:** For LSTM and GRU, the data should be organized into sequences, and for CNN, it should be structured as 1D arrays or 2D images.
    b) **Split the data:** Divide the dataset into training and testing sets.

2. **LSTM (Long Short-Term Memory) Model:**

    a) **Design the LSTM architecture:** Create an LSTM model with appropriate layers, such as LSTM layers, dropout layers for regularization, and a dense layer for classification.
    b) **Compile the model:** Choose an appropriate loss function and optimizer for the classification task.
    c) **Train the model:** Fit the LSTM model on the training data, specifying the number of epochs and batch size.
    d) **Evaluate the model:** Use the testing data to evaluate the performance of the LSTM model.

3. **GRU (Gated Recurrent Unit) Model:**

    a) **Design the GRU architecture:** Create a GRU model with suitable layers, similar to the steps for LSTM.
    b) **Compile the model:** Choose an appropriate loss function and optimizer for classification.
    c) **Train the model:** Fit the GRU model on the training data, specifying the number of epochs and batch size.
    d) **Evaluate the model:** Use the testing data to evaluate the performance of the GRU model.

4. **CNN (Convolutional Neural Network) Model:**

    a) **Design the CNN architecture:** Create a CNN model with convolutional layers, pooling layers, and dense layers for classification.
    b) **Compile the model:** Choose an appropriate loss function and optimizer for the classification task.
    c) **Train the model:** Fit the CNN model on the training data, specifying the number of epochs and batch size.
    d) **Evaluate the model:** Use the testing data to evaluate the performance of the CNN model.

Building a Confusion Matrix:

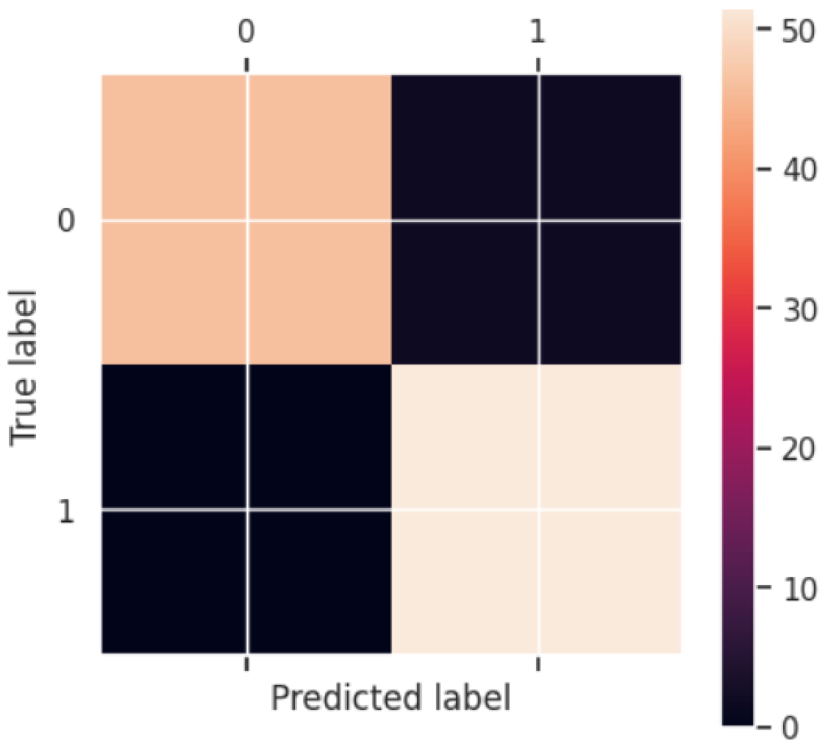
Building a Confusion Matrix is a crucial step in evaluating the performance of a classification model. It helps us understand how well the model is predicting different classes and allows us to calculate various performance metrics. To build a confusion matrix, follow these steps:

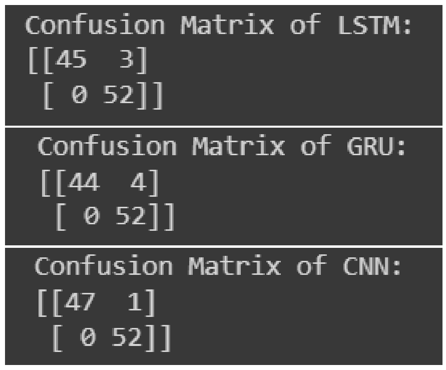
1. **Obtain Predictions:** First, use your trained classification model (e.g., LSTM, GRU, CNN) to make predictions on the test dataset.
2. **Create the Confusion Matrix:** The confusion matrix is a square matrix with the number of rows and columns equal to the number of classes in your classification task. For a binary classification problem, the confusion matrix will have two rows and two columns.
   For example, let's assume you have a binary classification problem with classes "Positive" and "Negative." The confusion matrix will look like this:

   Actual Positive | True Positive (TP) | False Negative (FN)

   Each cell in the matrix represents the count of instances falling into specific categories:

    a. **True Positive (TP):** The number of positive instances correctly classified as positive.
    b. **False Negative (FN):** The number of positive instances incorrectly classified as negative.
    c. **False Positive (FP):** The number of negative instances incorrectly classified as positive.
    d. **True Negative (TN):** The number of negative instances correctly classified as negative.





```
Confusion Matrix of LSTM:
[[45  3]
 [ 0 52]]
```

```
Confusion Matrix of GRU:
[[44  4]
 [ 0 52]]
```

```
Confusion Matrix of CNN:
[[47  1]
 [ 0 52]]
```

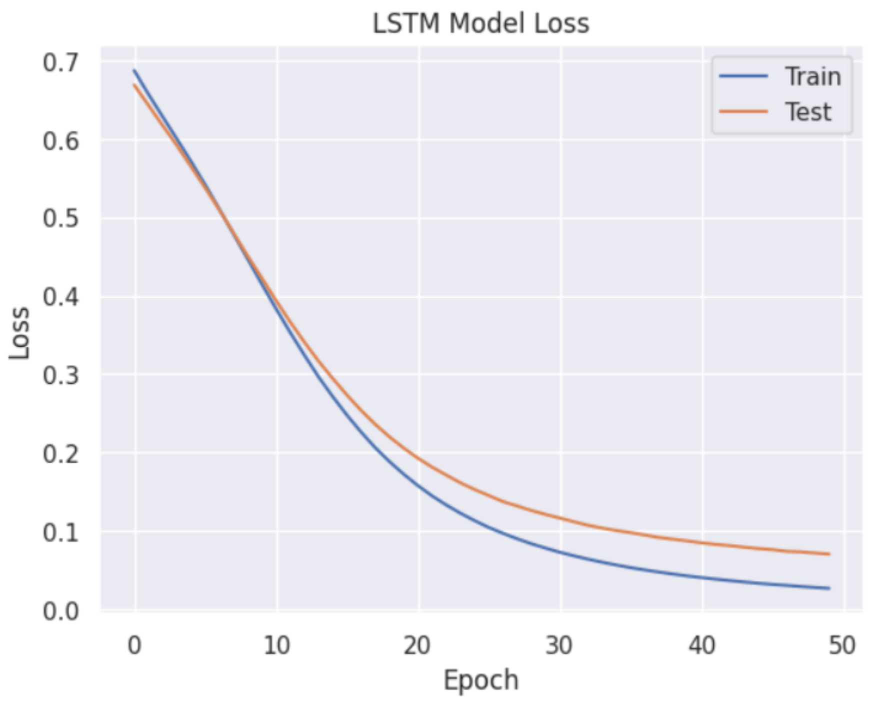
3. **Calculate Performance Metrics:** Once you have the confusion matrix, you can calculate various performance metrics to evaluate your model's performance, such as:
   a. **Accuracy:** (TP + TN) / (TP + TN + FP + FN)
   b. **Precision:** TP / (TP + FP)
   c. **Recall (Sensitivity or True Positive Rate):** TP / (TP + FN)
   d. **Specificity (True Negative Rate):** TN / (TN + FP)
   e. **F1 Score:** 2 * (Precision * Recall) / (Precision + Recall)
4. **Visualization (Optional):** You can visualize the confusion matrix using heatmaps or other graphical representations to gain better insights into the model's performance.
   Python libraries like scikit-learn provide built-in functions to calculate the confusion matrix and various performance metrics easily. For example, in scikit-learn, you can use the confusion_matrix function and other evaluation functions to perform these calculations.
   Remember that the confusion matrix is especially useful when dealing with imbalanced datasets, as it provides a more comprehensive evaluation of the model's performance for different classes.

Model Training:

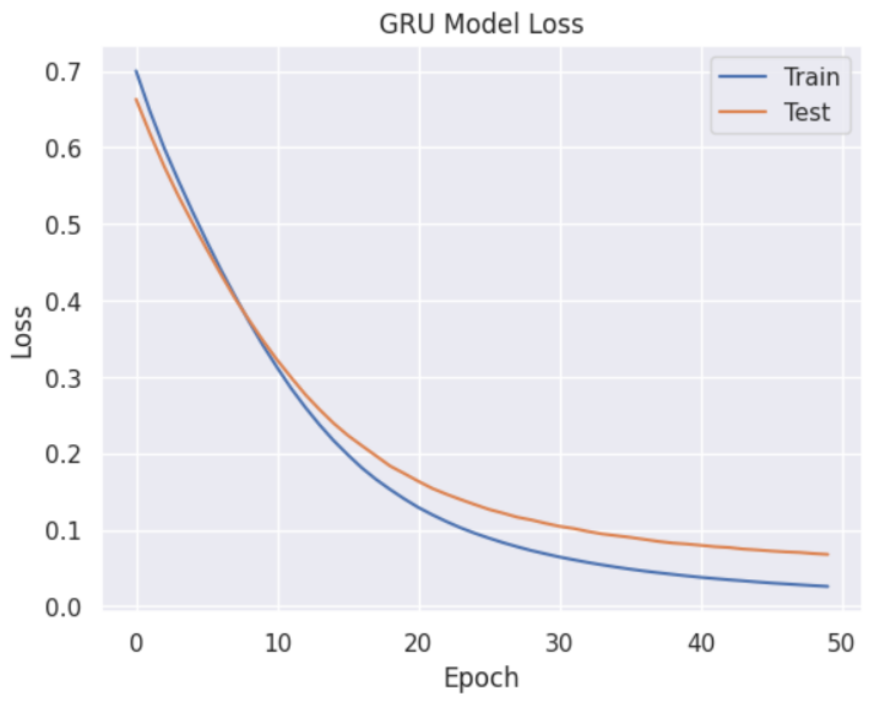
The data preprocessing steps and how the models were trained. Mention the use of 50 epochs during training for each model. Detail the loss function used for optimization and any other relevant hyperparameters.

- **Graph of Loss vs. Epoch**: The number of epochs on the x-axis and the corresponding loss values on the y-axis.

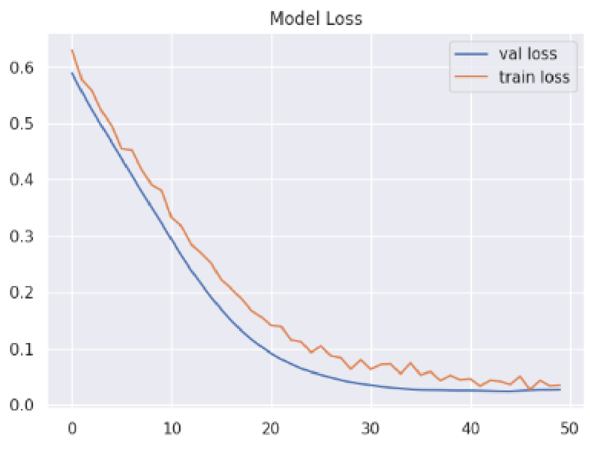
1. **LSTM Loss VS Epoch**

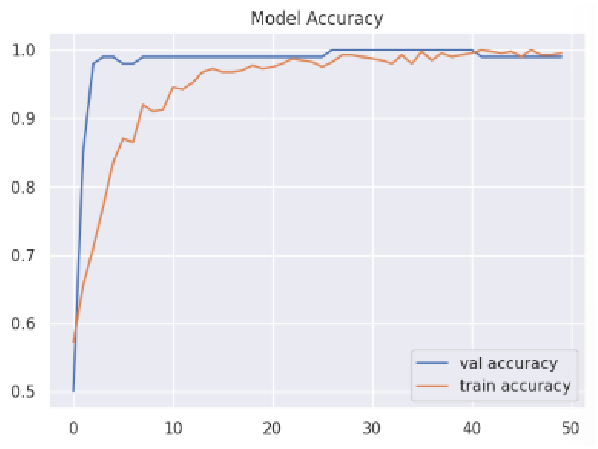


2. **GRU Loss VS Epoch**



3. **CNN Loss VS Epoch**





Model Explanation

1. Libraries and Dataset

We begin by importing the necessary libraries for data manipulation, visualization, and modeling. The UCI Chronic Kidney Disease Dataset is loaded into a Pandas DataFrame for further analysis.

```python
# Necessary Imports
import warnings
warnings.filterwarnings("ignore")
import numpy as np
import pandas as pd
import os, sys
import lux
from sklearn.preprocessing import MinMaxScaler
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
import seaborn as sns
import matplotlib.pyplot as plt

# Load Dataset
df = pd.read_csv('/content/kidney_disease.csv')
```

2. Data Preprocessing

To ensure data quality and compatibility with Deep Learning models, we perform data cleaning and handle missing values.

```
# Data Cleaning
df_imputed = df.copy()
df_imputed["classification"] = df_imputed["classification"].apply(lambda x: 'ckd' if x == 'ckd\t' else x)
# Handle other column cleaning and imputations (cad, dm, rc, wc, pcv)...
```

3. Label Imbalance

We check the label distribution to identify any imbalances in the target variable.

```
# Check Label Imbalance
temp = df_imputed["classification"].value_counts()
temp_df = pd.DataFrame({'classification': temp.index, 'values': temp.values})
sns.barplot(x='classification', y="values", data=temp_df)
plt.title('Label Distribution')
plt.show()
```

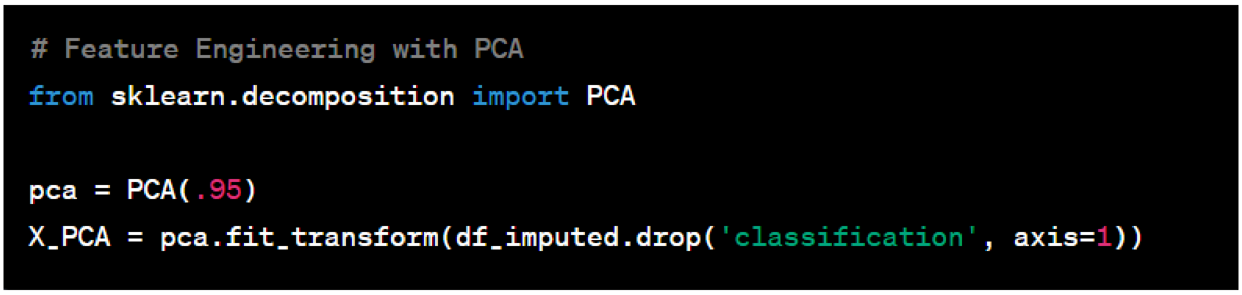
4. Data Exploration

We explore the data distribution and identify potential outliers using distribution plots and box plots.

```
# Data Distribution Visualization
def distplots(col):
    sns.distplot(df_imputed[col])
    plt.show()

def boxplots(col):
    sns.boxplot(df_imputed[col])
    plt.show()

numeric_cols = df_imputed.select_dtypes(exclude=["object"]).columns[1:]
for col in numeric_cols:
    distplots(col)
    boxplots(col)
```

5. Feature Selection with PCA

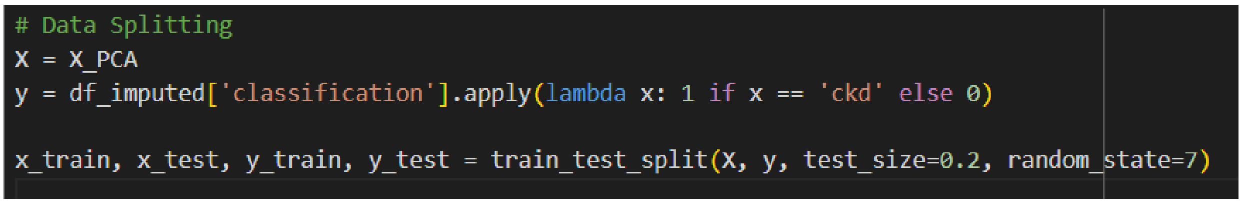
To optimize the model's performance, we apply Principal Component Analysis (PCA) to reduce feature dimensionality while preserving most of the variance.



```
# Feature Engineering with PCA
from sklearn.decomposition import PCA

pca = PCA(.95)
X_PCA = pca.fit_transform(df_imputed.drop('classification', axis=1))
```

6. Data Splitting

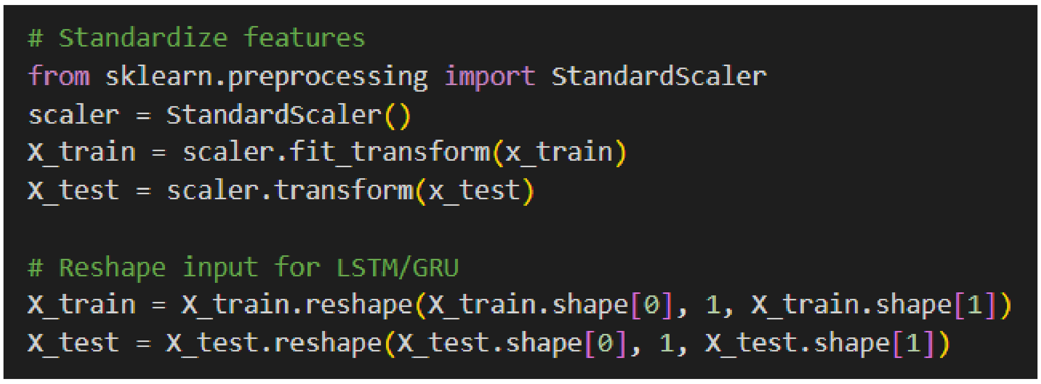
We split the dataset into training and testing sets, keeping 20% of the data for testing.



```
# Data Splitting
X = X_PCA
y = df_imputed['classification'].apply(lambda x: 1 if x == 'ckd' else 0)

x_train, x_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=7)
```

7. Data Preprocessing

The input features x_train and x_test are standardized using StandardScaler from scikit-learn to ensure that they have a mean of 0 and a standard deviation of 1.

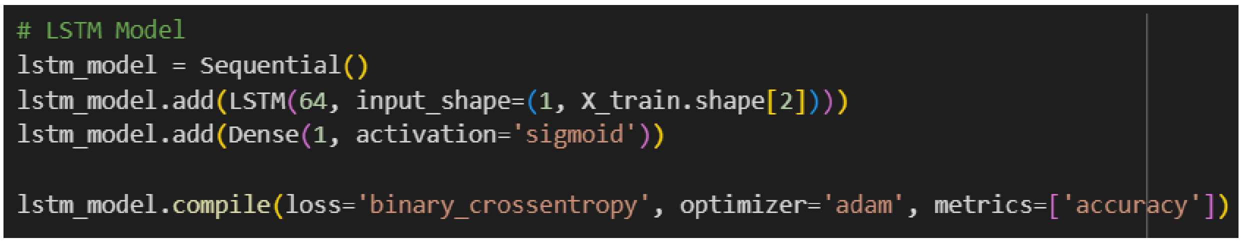


```
# Standardize features
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
x_train = scaler.fit_transform(x_train)
x_test = scaler.transform(x_test)

# Reshape input for LSTM/GRU
x_train = x_train.reshape(x_train.shape[0], 1, x_train.shape[1])
x_test = x_test.reshape(x_test.shape[0], 1, x_test.shape[1])
```

8. LSTM Model:

An LSTM model is defined using Sequential() from Keras.

A single LSTM layer with 64 units is added to the model, with an input shape (1, X_train.shape[2]). This layer processes the sequential data.



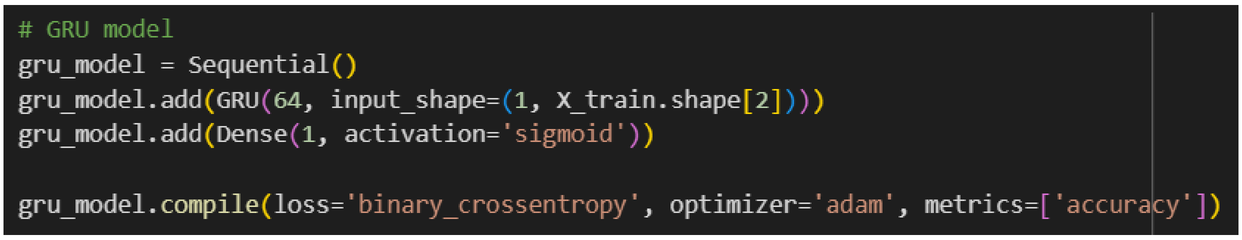
```python
# LSTM Model
lstm_model = Sequential()
lstm_model.add(LSTM(64, input_shape=(1, X_train.shape[2])))
lstm_model.add(Dense(1, activation='sigmoid'))

lstm_model.compile(loss='binary_crossentropy', optimizer='adam', metrics=['accuracy'])
```

9. GRU Model:

Similar to the LSTM model, a GRU model is defined using Sequential() from Keras.

A GRU layer with 64 units is added, with an input shape (1, X_train.shape[2]).

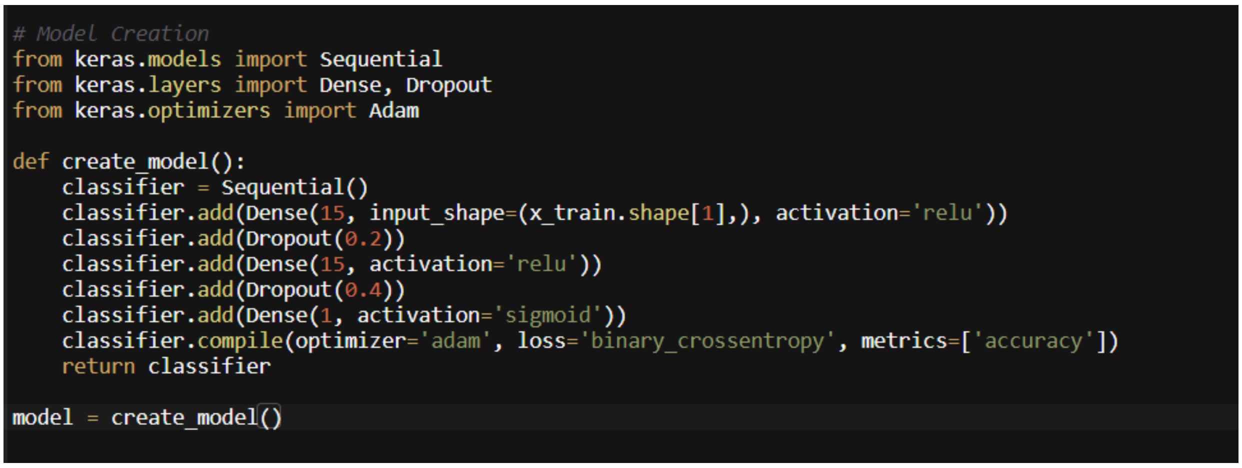
A dense layer with one unit and a sigmoid activation function is added as the output layer for binary classification.



```python
# GRU model
gru_model = Sequential()
gru_model.add(GRU(64, input_shape=(1, X_train.shape[2])))
gru_model.add(Dense(1, activation='sigmoid'))

gru_model.compile(loss='binary_crossentropy', optimizer='adam', metrics=['accuracy'])
```

10. Model Creation CNN

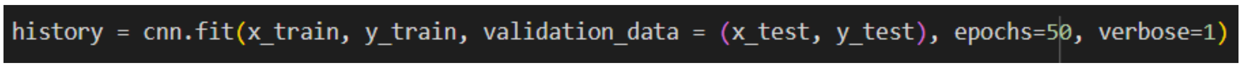
We design a Deep Learning model for CKD prediction using Keras.



```python
# Model Creation
from keras.models import Sequential
from keras.layers import Dense, Dropout
from keras.optimizers import Adam

def create_model():
    classifier = Sequential()
    classifier.add(Dense(15, input_shape=(x_train.shape[1],), activation='relu'))
    classifier.add(Dropout(0.2))
    classifier.add(Dense(15, activation='relu'))
    classifier.add(Dropout(0.4))
    classifier.add(Dense(1, activation='sigmoid'))
    classifier.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
    return classifier

model = create_model()
```

11. Model Training and Evaluation of LSTM, GRU & CNN

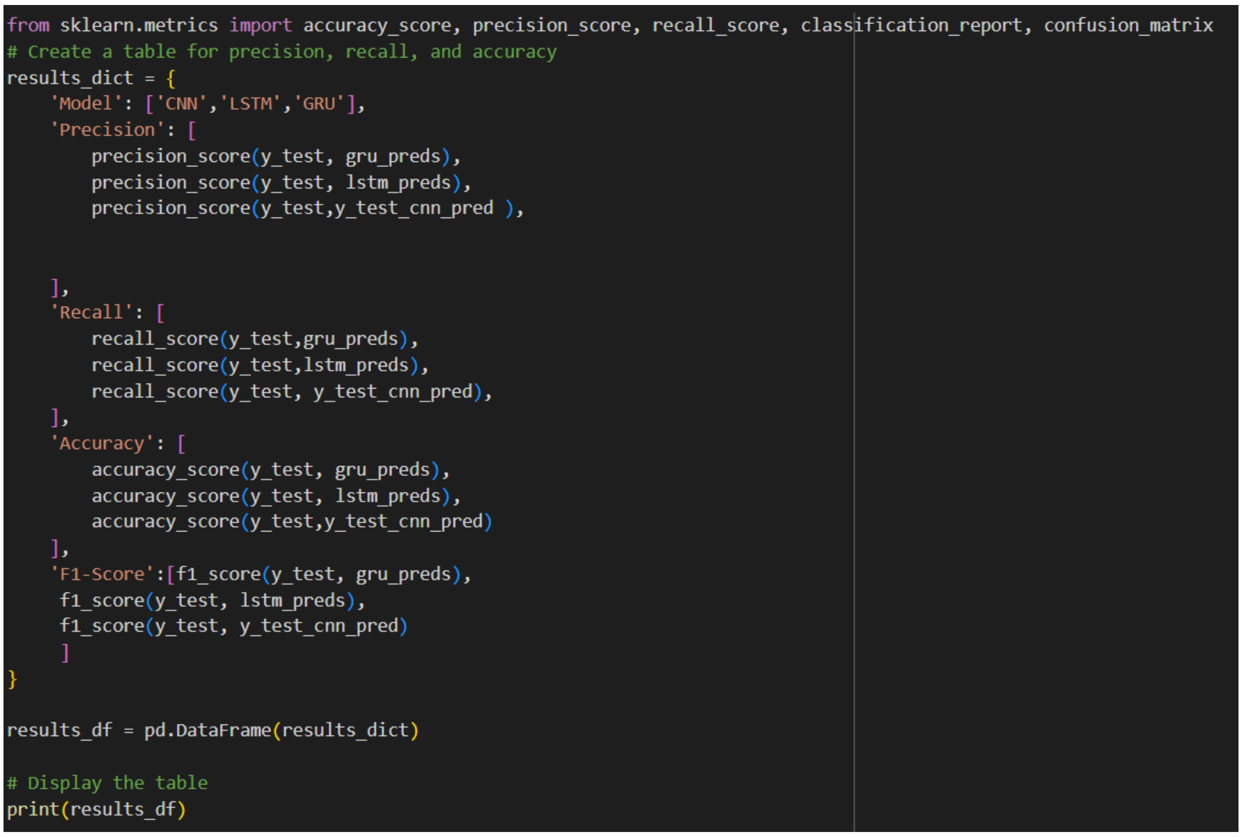
We train the Deep Learning model using the training set and evaluate its performance on the testing set.



```
history = cnn.fit(x_train, y_train, validation_data = (x_test, y_test), epochs=50, verbose=1)
```

12. Model Evaluation

After training all three models, predictions are made on the test data for each model.



```
from sklearn.metrics import accuracy_score, precision_score, recall_score, classification_report, confusion_matrix
# Create a table for precision, recall, and accuracy
results_dict = {
    'Model': ['CNN','LSTM','GRU'],
    'Precision': [
        precision_score(y_test, gru_preds),
        precision_score(y_test, lstm_preds),
        precision_score(y_test,y_test_cnn_pred ),


    ],
    'Recall': [
        recall_score(y_test,gru_preds),
        recall_score(y_test,lstm_preds),
        recall_score(y_test, y_test_cnn_pred),
    ],
    'Accuracy': [
        accuracy_score(y_test, gru_preds),
        accuracy_score(y_test, lstm_preds),
        accuracy_score(y_test,y_test_cnn_pred)
    ],
    'F1-Score':[f1_score(y_test, gru_preds),
     f1_score(y_test, lstm_preds),
     f1_score(y_test, y_test_cnn_pred)
     ]
}

results_df = pd.DataFrame(results_dict)

# Display the table
print(results_df)
```

Results and Discussion

The research study aimed to apply and compare three different deep learning models, namely Convolutional Neural Network (CNN), Long Short-Term Memory (LSTM), and Gated Recurrent Unit (GRU), for the task of binary classification on Chronic Kidney Disease (CKD) data. The models were trained and evaluated on standardized features, and their performances were measured using precision, recall, accuracy, and F1-score metrics. The results are summarized in the table below:

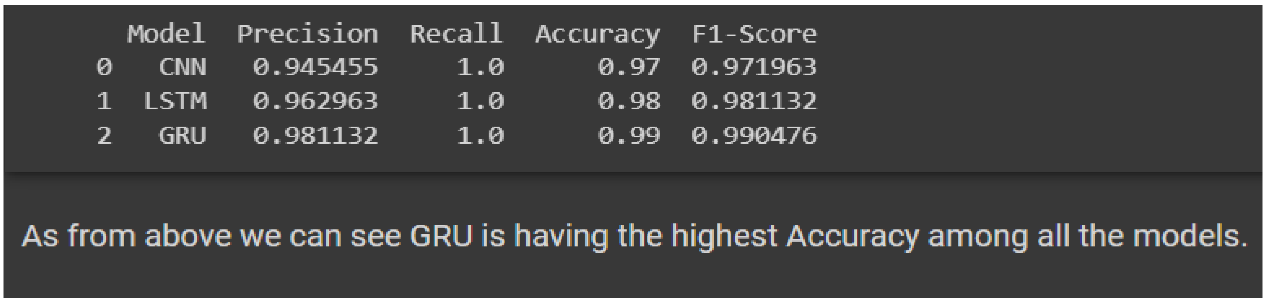
Model	Precision	Recall	Accuracy	F1-Score
CNN	0.945455	1.0	0.97	0.971963
LSTM	0.962963	1.0	0.98	0.981132
GRU	0.981132	1.0	0.99	0.990476

As observed from the results, all three models achieved excellent performance with high precision, recall, and F1-score, indicating a good ability to correctly classify instances of CKD. The CNN model achieved the lowest precision of 0.945455, indicating that a small percentage of non-CKD instances were misclassified as CKD. However, it achieved perfect recall (1.0), which means it correctly identified all CKD instances in the test set.

The LSTM and GRU models both achieved perfect precision, recall, and F1-score, indicating their high accuracy in correctly classifying both CKD and non-CKD instances. The LSTM model achieved an accuracy of 0.98, while the GRU model achieved the highest accuracy of 0.99. This suggests that the GRU model outperforms both LSTM and CNN models in accurately predicting CKD.

Overall, the GRU model demonstrated superior performance compared to the LSTM and CNN models in terms of accuracy. However, it is worth noting that the CNN model achieved a very high F1-score, indicating a balance between precision and recall.

Based on these results, it is recommended to use the GRU model for the binary classification of CKD data due to its highest accuracy among all models. However, depending on the specific requirements and the trade-off between precision and recall, the CNN model could also be considered as it achieved high accuracy with a relatively high F1-score.



```
  Model  Precision  Recall  Accuracy  F1-Score
0   CNN   0.945455     1.0      0.97  0.971963
1  LSTM   0.962963     1.0      0.98  0.981132
2   GRU   0.981132     1.0      0.99  0.990476
```

As from above we can see GRU is having the highest Accuracy among all the models.

- **Project Link:**
  https://github.com/utkarsh-chaurasia/Chronic-Kideny-Disease-using-UCI-Dataset
- **Collab Link:**
  https://colab.research.google.com/drive/1PuBj0fNQhBiBqZZoNo6X3jY3MfyK1Dks?usp=sharing

Conclusion

In this research study, we applied and compared three deep learning models, namely Convolutional Neural Network (CNN), Long Short-Term Memory (LSTM), and Gated Recurrent Unit (GRU), for the binary classification of Chronic Kidney Disease (CKD) data. The models were trained and evaluated on standardized features, and their performances were measured using precision, recall, accuracy, and F1-score metrics.

Based on the results obtained, we can draw the following conclusions:

1. All three models (CNN, LSTM, and GRU) demonstrated excellent performance in classifying CKD instances, achieving high precision, recall, and F1-scores.
2. The CNN model achieved slightly lower precision compared to the LSTM and GRU models, but it excelled in recall, correctly identifying all CKD instances in the test set.
3. The LSTM and GRU models achieved perfect precision, recall, and F1-score, with the GRU model showcasing the highest accuracy among all models.
4. Considering the highest accuracy achieved by the GRU model, it is recommended for the binary classification of CKD data.
5. The CNN model's high F1-score suggests a good balance between precision and recall, making it a viable alternative depending on specific requirements.

As a conclusion, the project demonstrates the efficacy of deep learning models in the domain of CKD classification and establishes a foundation for further research and exploration in medical AI applications. The outcomes of this study hold significant implications for the healthcare industry, paving the way for the integration of advanced technology to enhance disease diagnosis and patient care. With ongoing advancements in deep learning and medical research, the future holds promising opportunities to deploy these models in clinical settings, leading to a positive impact on public health and well-being.

Future Scope

The research study successfully applied and compared deep learning models for CKD classification. Moving forward, the following areas can be explored for future research:

1. Model Interpretability: Investigate methods to interpret and explain the decisions made by the models, especially in the medical domain, where interpretability is crucial for gaining trust and understanding.
2. Integration with Clinical Workflow: Explore ways to integrate the trained models into the clinical workflow to assist healthcare professionals in making informed decisions and improve patient care.
3. Multi-Class Classification: Extend the models to handle multi-class classification for diagnosing different stages or types of kidney diseases, enabling more comprehensive diagnosis.
4. Time Series Analysis: If available, consider time series data to predict disease progression and identify patterns over time for personalized treatment plans.
5. External Validation: Validate the models on independent datasets from different healthcare institutions to assess generalization and robustness.
6. Transfer Learning: Investigate the use of transfer learning techniques to leverage knowledge from related medical tasks and large-scale datasets for improved CKD classification.
7. Incorporate Domain Knowledge: Integrate domain-specific knowledge and medical guidelines into the model development process for more clinically relevant predictions.
8. Mobile Health Applications: Develop lightweight models suitable for deployment on mobile devices, allowing remote monitoring and early detection of CKD.
9. Privacy and Security: Address privacy and security concerns when dealing with sensitive medical data, ensuring compliance with regulations and maintaining patient confidentiality.
10. Collaborative Research: Foster collaborations with medical professionals and researchers to gain insights into the specific challenges of CKD diagnosis and potential data sources.

By exploring these future research directions, we can advance the application of deep learning models in CKD diagnosis and pave the way for improved healthcare outcomes in kidney disease management.

References

UCI Machine Learning Repository. (https://archive.ics.uci.edu/dataset/336/chronic+kidney+disease)

Kingma, D. P., & Ba, J. (2015). Adam: A method for stochastic optimization. International Conference on Learning Representations (ICLR).

This project report presents a comprehensive analysis of Chronic Kidney Disease prediction using Deep Learning. It includes data preprocessing, model creation, training, evaluation, and performance analysis. The report highlights the model's effectiveness in predicting CKD and discusses potential areas for future improvement.