EARLY PREADICTION FOR CHRONIC KIDNEY DISEASE DETECTION: A PROGRESSIVE APPROCH TO THE HEALTH MANAGEMENT

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1. INTRODUCTION

1.1 overview

Chronic Kidney Disease (CKD) is a major medical problem and can be cured if treated in the early stages. Usually, people are not aware that medical tests we take for different purposes could contain valuable information concerning kidney diseases. Consequently, attributes of various medical tests are investigated to distinguish which attributes may contain helpful information about the disease. The information says that it helps us to measure the severity of the problem, the predicted survival of the patient after the illness, the pattern of the disease and work for curing the disease. In todays world as we know most of the people are facing so many disease and as this can be cured if we treat people in early stages this project can use a pretrained model to predict the Chronic Kidney Disease which can help in treatments of peoples who are suffer from this disease

Requirements

The business requirements for a machine learning model to predict chronic kidney disease include the ability to accurately predict the CKD based on given information, Minimise the number of false positives (predicting diseased) and false negatives (not diseased). Provide an explanation for the model's decision, to comply with regulations and improve transparency.

Literature Survey

Chronic kidney disease (CKD) is a significant public health issue, affecting an estimated 14% of the global population. The disease is characterized by a gradual loss of kidney function over time, leading to a range of serious health complications, including end-stage renal disease (ESRD) requiring dialysis or kidney transplant. Early detection and management of CKD is crucial to prevent progression to E SRD and improve patient outcomes. There have been numerous studies in recent years aimed at developing accurate and efficient methods for predicting CKD progression. These studies have employed a variety of techniques, including machine learning, deep learning, and artificial neural networks.

Impact

On a social level, early detection and prediction of CKD can lead to improved patient outcomes and quality of life. By identifying individuals at risk for CKD, healthcare providers can intervene early and slow the progression of the disease through lifestyle changes, medication management, and other treatments. This can help prevent the need for dialysis or kidney transplantation, which can be costly and life-altering for patients. Additionally, early prediction can also help reduce the overall burden of CKD on the healthcare system by reducing the number of hospitalizations and emergency room visits.

Collect the dataset

In this project we have used .csv data. This data is downloaded from kaggle.com

There are several techniques for understanding the data. But here we have used some of it. In an additional way, you can use multiple techniques.

link: **https://www.kaggle.com/datasets/mansoordaku/ckdisease**

Importing the libraries

Import the necessary libraries as shown in the image.

Importing Libaries

```
import pandas as pd #used for data manipulation
import numpy as np #used for numerical analysis
from collections import Counter as c # return counts of number of classess
import matplotlib.pyplot as plt #used for data Visualization
import seaborn as sns #data visualization library
import missingno as msno #finding missing values
from sklearn.metrics import accuracy_score, confusion_matrix#model performance
from sklearn.model_selection import train_test_split #splits data in random train and test
from sklearn.preprocessing import LabelEncoder #encoding the levels of categorical features
from sklearn.linear_model import LogisticRegression #Classification ML algorithm
import pickle #Python object hierarchy is converted into a byte stream,
```

Read the dataset

Our dataset format might be in .csv, excel files, .txt, .json, etc. We can read the dataset with the help of pandas. In pandas we have a function called data.head() to read the dataset. As a parameter we have to give the directory of the csv file.

```
data=pd.read_csv("chronickidneydisease.csv") #loading the csv data
data.head() #return you the first 5 rows values
```

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	...	44	7800	5.2	yes	yes	no	good	no	no	ckd
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	...	38	6000	NaN	no	no	no	good	no	no	ckd
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31	7500	NaN	no	yes	no	poor	no	yes	ckd
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32	6700	3.9	yes	no	no	poor	yes	yes	ckd
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35	7300	4.6	no	no	no	good	no	no	ckd

5 rows × 26 columns

Data Preparation

As we have understood how the data is, let's pre-process the collected data. The download data set is not suitable for training the machine learning model as it might have so much randomness so we need to clean the dataset properly in order to fetch good results. This activity includes the following steps.

- Rename the columns
- Handling missing values
- Handling categorical data
- Handling Numerical data

Note: These are the general steps of pre-processing the data before using it for machine learning. Depending on the condition of your dataset, you may or may not have to go through all these steps

Rename The Columns

```
data.columns #return all the column names
```

```
Index(['age', 'bp', 'sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'bgr', 'bu',
       'sc', 'sod', 'pot', 'hemo', 'pcv', 'wc', 'rc', 'htn', 'dm', 'cad',
       'appet', 'pe', 'ane', 'classification'],
      dtype='object')
```

```
data.columns=['age','blood_pressure','specific_gravity','albumin',
              'sugar','red_blood_cells','pus_cell','pus_cell_clumps','bacteria',
              'blood glucose random','blood_urea','serum_creatinine','sodium','potassium',
              'hemoglobin','packed_cell_volume','white_blood_cell_count','red_blood_cell_count',
              'hypertension','diabetesmellitus','coronary_artery_disease','appetite',
              'pedal_edema','anemia','class'] # manually giving the name  of the columns
data.columns
```

```
Index(['age', 'blood_pressure', 'specific_gravity', 'albumin', 'sugar',
       'red_blood_cells', 'pus_cell', 'pus_cell_clumps', 'bacteria',
       'blood glucose random', 'blood_urea', 'serum_creatinine', 'sodium',
       'potassium', 'hemoglobin', 'packed_cell_volume',
       'white_blood_cell_count', 'red_blood_cell_count', 'hypertension',
       'diabetesmellitus', 'coronary_artery_disease', 'appetite',
       'pedal_edema', 'anemia', 'class'],
      dtype='object')
```

Handling Missing Values

- Let’s find the shape of our dataset first. To find the shape of our data, the df.shape method is used. To find the data type, df.info() function is used.

```
data.info() #info will give you a summary of dataset
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 25 columns):
 #   Column                  Non-Null Count  Dtype  
---  ------                  --------------  -----  
 0   age                     391 non-null    float64
 1   blood_pressure          388 non-null    float64
 2   specific_gravity        353 non-null    float64
 3   albumin                 354 non-null    float64
 4   sugar                   351 non-null    float64
 5   red_blood_cells         248 non-null    object 
 6   pus_cell                335 non-null    object 
 7   pus_cell_clumps         396 non-null    object 
 8   bacteria                396 non-null    object 
 9   blood glucose random    356 non-null    float64
 10  blood_urea              381 non-null    float64
 11  serum_creatinine        383 non-null    float64
 12  sodium                  313 non-null    float64
 13  potassium               312 non-null    float64
 14  hemoglobin              348 non-null    float64
 15  packed_cell_volume      330 non-null    object 
 16  white_blood_cell_count  295 non-null    object 
 17  red_blood_cell_count    270 non-null    object 
 18  hypertension            398 non-null    object 
 19  diabetesmellitus        398 non-null    object 
 20  coronary_artery_disease 398 non-null    object 
 21  appetite                399 non-null    object 
 22  pedal_edema             399 non-null    object 
 23  anemia                  399 non-null    object 
 24  class                   400 non-null    object 
dtypes: float64(11), object(14)
memory usage: 78.2+ KB
```

Handling Categorical Columns

The below code is used for fetching all the object or categorical type of columns from our data and we are storing it as **set** in variable catcols.

```
catcols=set(data.dtypes[data.dtypes=='O'].index.values) # only fetch the object type columns
print(catcols)
```

```
{'hypertension', 'packed_cell_volume', 'class', 'coronary_artery_disease', 'anemia', 'red_blood_cell_count', 'red_blood_cells', 'bacteri
a', 'pedal_edema', 'appetite', 'pus_cell', 'diabetesmellitus', 'pus_cell_clumps', 'white_blood_cell_count'}
```

As, you can observe that it gives us the same count of columns which we find previously.

```
for i in catcols:
    print("Columns :",i)
    print(c(data[i])) #using counter for checking the number of classess in the column
    print('*'*120+'\n')
```

```
Columns : hypertension
Counter({'no': 251, 'yes': 147, nan: 2})
************************************************************************************************************************

Columns : packed_cell_volume
Counter({nan: 70, '52': 21, '41': 21, '44': 19, '48': 19, '40': 16, '43': 14, '45': 13, '42': 13, '32': 12, '36': 12, '33': 12, '28': 12,
'50': 12, '37': 11, '34': 11, '35': 9, '29': 9, '30': 9, '46': 9, '31': 8, '39': 7, '24': 7, '26': 6, '38': 5, '47': 4, '49': 4, '53': 4,
'51': 4, '54': 4, '27': 3, '22': 3, '25': 3, '23': 2, '19': 2, '16': 1, '\t?': 1, '14': 1, '18': 1, '17': 1, '15': 1, '21': 1, '20': 1,
'\t43': 1, '9': 1})
************************************************************************************************************************

Columns : class
Counter({'ckd': 250, 'notckd': 150})
************************************************************************************************************************

Columns : coronary_artery_disease
Counter({'no': 362, 'yes': 34, '\tno': 2, nan: 2})
************************************************************************************************************************

Columns : anemia
Counter({'no': 339, 'yes': 60, nan: 1})
************************************************************************************************************************

Columns : red_blood_cell_count
Counter({nan: 130, '5.2': 18, '4.5': 16, '4.9': 14, '4.7': 11, '3.9': 10, '4.8': 10, '4.6': 9, '3.4': 9, '3.7': 8, '5.0': 8, '6.1': 8, '5.
5': 8, '5.9': 8, '3.8': 7, '5.4': 7, '5.8': 7, '5.3': 7, '4.3': 6, '4.2': 6, '5.6': 6, '4.4': 5, '3.2': 5, '4.1': 5, '6.2': 5, '5.1': 5,
'6.4': 5, '5.7': 5, '6.5': 5, '3.6': 4, '6.0': 4, '6.3': 4, '4.0': 3, '4': 3, '3.5': 3, '3.3': 3, '5': 2, '2.6': 2, '2.8': 2, '2.5': 2,
'3.1': 2, '2.1': 2, '2.9': 2, '2.7': 2, '3.0': 2, '2.3': 1, '8.0': 1, '3': 1, '2.4': 1, '\t?': 1})
************************************************************************************************************************
```

```
Columns : red_blood_cells
Counter({'normal': 201, nan: 152, 'abnormal': 47})
************************************************************************************************************************

Columns : bacteria
Counter({'notpresent': 374, 'present': 22, nan: 4})
************************************************************************************************************************

Columns : pedal_edema
Counter({'no': 323, 'yes': 76, nan: 1})
************************************************************************************************************************

Columns : appetite
Counter({'good': 317, 'poor': 82, nan: 1})
************************************************************************************************************************

Columns : pus_cell
Counter({'normal': 259, 'abnormal': 76, nan: 65})
************************************************************************************************************************

Columns : diabetesmellitus
Counter({'no': 258, 'yes': 134, '\tno': 3, '\tyes': 2, nan: 2, ' yes': 1})
************************************************************************************************************************

Columns : pus_cell_clumps
Counter({'notpresent': 354, 'present': 42, nan: 4})
************************************************************************************************************************

Columns : white_blood_cell_count
Counter({nan: 105, '9800': 11, '6700': 10, '9600': 9, '9200': 9, '7200': 9, '6900': 8, '11000': 8, '5800': 8, '7800': 7, '9100': 7, '940
0': 7, '7000': 7, '4300': 6, '6300': 6, '10700': 6, '10500': 6, '7500': 5, '8300': 5, '7900': 5, '8600': 5, '5600': 5, '10200': 5, '5000':
5, '8100': 5, '9500': 5, '6000': 4, '6200': 4, '10300': 4, '7700': 4, '5500': 4, '10400': 4, '6800': 4, '6500': 4, '4700': 4, '7300': 3,
'4500': 3, '8400': 3, '6400': 3, '4200': 3, '7400': 3, '8000': 3, '5400': 3, '3800': 2, '11400': 2, '5300': 2, '8500': 2, '14600': 2, '710
0': 2, '13200': 2, '9000': 2, '8200': 2, '15200': 2, '12400': 2, '12800': 2, '8800': 2, '5700': 2, '9300': 2, '6600': 2, '12100': 1, '1220
0': 1, '18900': 1, '21600': 1, '11300': 1, '\t6200': 1, '11800': 1, '12500': 1, '11900': 1, '12700': 1, '13600': 1, '14900': 1, '16300':
1, '\t8400': 1, '10900': 1, '2200': 1, '11200': 1, '19100': 1, '\t?': 1, '12300': 1, '16700': 1, '2600': 1, '26400': 1, '4900': 1, '1200
0': 1, '15700': 1, '4100': 1, '11500': 1, '10800': 1, '9900': 1, '5200': 1, '5900': 1, '9700': 1, '5100': 1})
************************************************************************************************************************
```

In the above we are looping with each categorical column and printing the classes of each categorical columns using counter function so that we can detect which columns are categorical and which are not.

If you observe some columns have a few classes and some have many, those columns are having many classes can be considered as numerical column and we have to remove it and add it to the continuous columns.

```
catcols.remove('red_blood_cell_count') # remove is used for removing a particular column
catcols.remove('packed_cell_volume')
catcols.remove('white_blood_cell_count')
print(catcols)
```

```
{'hypertension', 'class', 'coronary_artery_disease', 'anemia', 'red_blood_cells', 'bacteria', 'pedal_edema', 'appetite', 'pus_cell', 'diab
etesmellitus', 'pus_cell_clumps'}
```

As we store our columns as set, we can make use of **remove** function which is used to remove the element in our case we can take it as columns.

Label Encoding For Categorical Columns

Typically, any structured dataset includes multiple columns with combination of numerical as well as categorical variables. A machine can only understand the numbers. It cannot understand the text. That's essentially the case with Machine Learning algorithms too.We need to convert each text category to numbers in order for the machine to process those using mathematical equations.

How should we handle categorical variables? There are Multiple way to handle, but will see one of it is LabelEncoding.

Label Encoding is a popular encoding technique for handling categorical variables. In this technique, each label is assigned a unique integer based on alphabetical ordering.

Let's see how to implement label encoding in Python using the scikit-learn library.

we have to convert only the text class category columns; we first select it then we will implement Label Encoding to it.

Labeling Encoding of Categorical Column

```
#'specific_gravity','albumin', 'sugar'(as these columns are  numerical it is removed)
catcols=['anemia','pedal_edema','appetite','bacteria','class','coronary_artery_disease','diabetesmellit
 'hypertension','pus_cell','pus_cell_clumps','red_blood_cells'] #only considered the text class columns
```

```
from sklearn.preprocessing import LabelEncoder #imorting the LabelEncoding from sklearn
for i in catcols: #looping through all the categorical columns
    print("LABEL ENCODING OF:",i)
    LEi = LabelEncoder() # creating an object of LabelEncoder
    print(c(data[i])) #getting the classes values before transformation
    data[i] = LEi.fit_transform(data[i])# trannsforming our text classes to numerical values
    print(c(data[i])) #getting the classes values after transformation
    print("*"*100)
```

In the above code we are looping through all the selected text class categorical columns and performing label encoding.

```
LABEL ENCODING OF: anemia
Counter({'no': 340, 'yes': 60})
Counter({0: 340, 1: 60})
****************************************************************************************************
LABEL ENCODING OF: pedal_edema
Counter({'no': 324, 'yes': 76})
Counter({0: 324, 1: 76})
****************************************************************************************************
LABEL ENCODING OF: appetite
Counter({'good': 318, 'poor': 82})
Counter({0: 318, 1: 82})
****************************************************************************************************
LABEL ENCODING OF: bacteria
Counter({'notpresent': 378, 'present': 22})
Counter({0: 378, 1: 22})
****************************************************************************************************
LABEL ENCODING OF: class
Counter({'ckd': 250, 'notckd': 150})
Counter({0: 250, 1: 150})
****************************************************************************************************
LABEL ENCODING OF: coronary_artery_disease
Counter({'no': 366, 'yes': 34})
Counter({0: 366, 1: 34})
****************************************************************************************************
LABEL ENCODING OF: diabetesmellitus
Counter({'no': 263, 'yes': 137})
Counter({0: 263, 1: 137})
****************************************************************************************************
LABEL ENCODING OF: hypertension
Counter({'no': 253, 'yes': 147})
Counter({0: 253, 1: 147})
****************************************************************************************************
LABEL ENCODING OF: pus_cell
Counter({'normal': 324, 'abnormal': 76})
Counter({1: 324, 0: 76})
****************************************************************************************************
LABEL ENCODING OF: pus_cell_clumps
Counter({'notpresent': 358, 'present': 42})
Counter({0: 358, 1: 42})
****************************************************************************************************
LABEL ENCODING OF: red_blood_cells
Counter({'normal': 353, 'abnormal': 47})
```

As you can see here, after performing label encoding alphabetical classes is converted to numeric.

Handling Numerical Columns

```
contcols=set(data.dtypes[data.dtypes!='0'].index.values)# only fetech the float and int type columns
#contcols=pd.DataFrame(data,columns=contcols)
print(contcols)
```

```
{'blood_urea', 'serum_creatinine', 'albumin', 'blood_pressure', 'blood glucose random', 'sugar', 'sodium', 'hemoglobin', 'specific_gravit
y', 'age', 'potassium'}
```

Same as we did with categorical columns, we are majing use of **dtypes** for finding the continuous columns

```
for i in contcols:
    print("Continous Columns :",i)
    print(c(data[i]))
    print('*'*120+'\n')
```

If we observe the output of the above code we can observe that some columns have few values or you can say classes which can be considered as categorical columns. So , let's remove it and add the columns which we observed into their respective variables.

```
contcols.remove('specific_gravity')
contcols.remove('albumin')
contcols.remove('sugar')
print(contcols)

```

With the help of add() function we can add an element.

```
contcols.add('red_blood_cell_count') # using add we can add the column
contcols.add('packed_cell_volume')
contcols.add('white_blood_cell_count')
print(contcols)
```

```
{'blood_urea', 'serum_creatinine', 'packed_cell_volume', 'blood_pressure', 'blood glucose random', 'sodium', 'hemoglobin', 'red_blood_cell
_count', 'age', 'potassium', 'white_blood_cell_count'}
```

```
catcols.add('specific_gravity')
catcols.add('albumin')
catcols.add('sugar')
print(catcols)
```

```
{'hypertension', 'class', 'albumin', 'coronary_artery_disease', 'anemia', 'sugar', 'red_blood_cells', 'specific_gravity', 'bacteria', 'ped
al_edema', 'appetite', 'pus_cell', 'diabetesmellitus', 'pus_cell_clumps'}
```

In our data some columns some unwanted classes so we have to rectify that also for that we simply use **replace()**

```
data['coronary_artery_disease'] = data.coronary_artery_disease.replace('\tno','no') # replacing \tno wi
c(data['coronary_artery_disease'])
```

```
Counter({'no': 364, 'yes': 34, nan: 2})
```

```
data['diabetesmellitus'] = data.diabetesmellitus.replace(to_replace={'\tno':'no','\tyes':'yes',' yes':'
c(data['diabetesmellitus'])
```

```
Counter({'yes': 137, 'no': 261, nan: 2})
```

1.2 Purpose

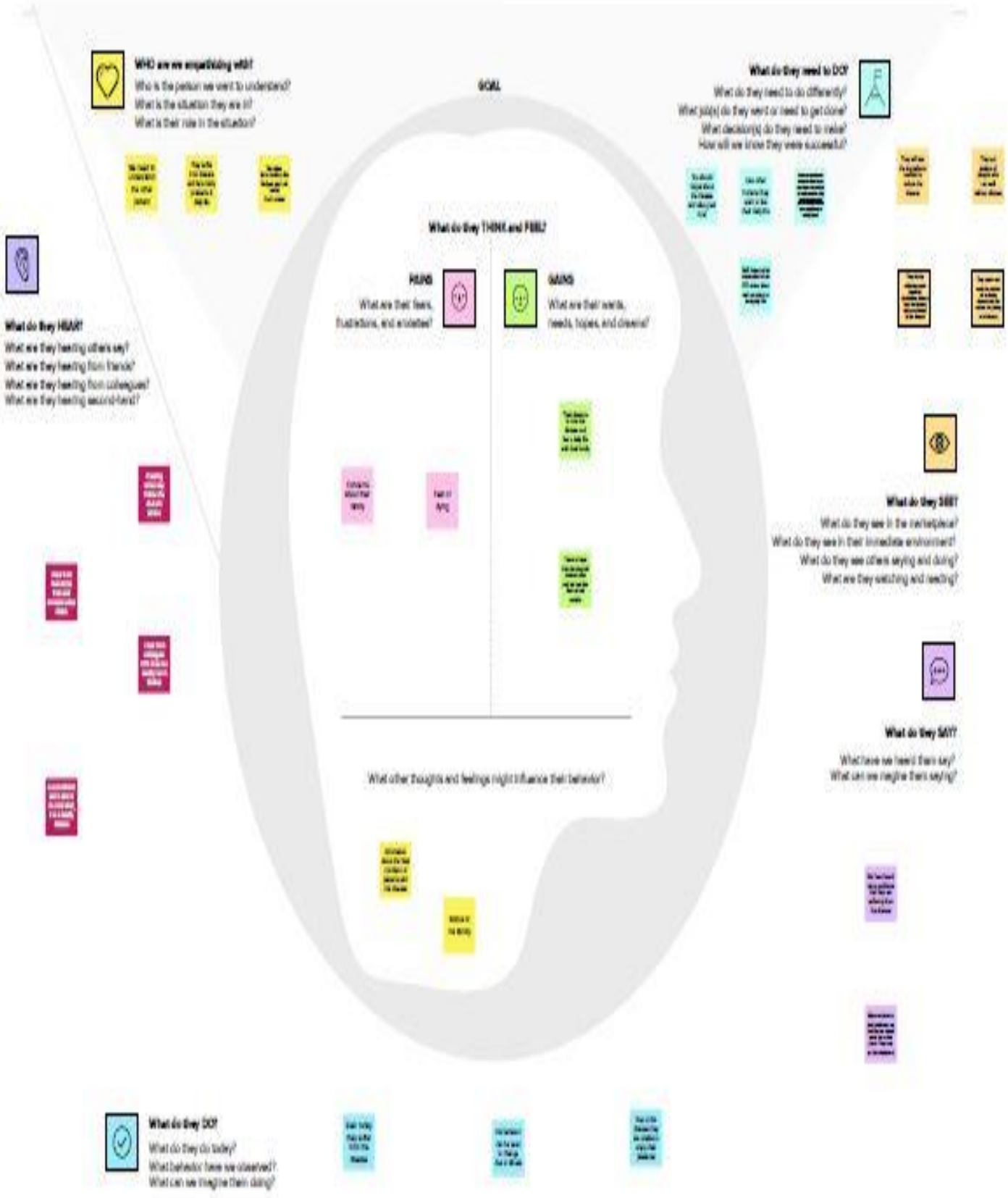
Chronic kidney disease (CKD) is one of the most life-threatening disorders. To improve survivability, early discovery and good management are encouraged. In this paper, CKD was diagnosed using multiple optimized neural networks against traditional neural networks on the UCI machine learning dataset, to identify the most efficient model for the task. The study works on the binary classification of CKD from 24 attributes. For classification, optimized CNN (OCNN), ANN (OANN), and LSTM (OLSTM) models were used as well as traditional CNN, ANN, and LSTM models. With various performance matrixes, error measures, loss values, AUC values, and compilation time, the implemented models are compared to identify the most competent model for the classification of CKD. It is observed that, overall, the optimized models have better performance compared to the traditional models. The highest validation accuracy among the tradition models were achieved from CNN with 92.71%, whereas OCNN, OANN, and OLSTM have higher accuracies of 98.75%, 96.25%, and 98.5%, respectively. Additionally, OCNN has the highest AUC score of 0.99 and the lowest compilation time for classification with 0.00447 s, making it the most efficient model for the diagnosis of CKD.

Despite the absence of precise epidemiological data, we know there are a great many patients in the conservative phase of chronic kidney disease (CKD). The incidence and prevalence of renal replacement therapy (RRT) is increasing worldwide. As well as being a large and growing clinical problem, CKD is of an economic and organizational concern, since RRT consumes a considerable proportion of health care resources. In this context, any medical intervention that may prevent the progression of CKD towards end-stage renal disease (ESRD) is extremely important. Improving the patients' cardiovascular status is also a major objective in the management of this population, as cardiovascular disease (CVD) is the

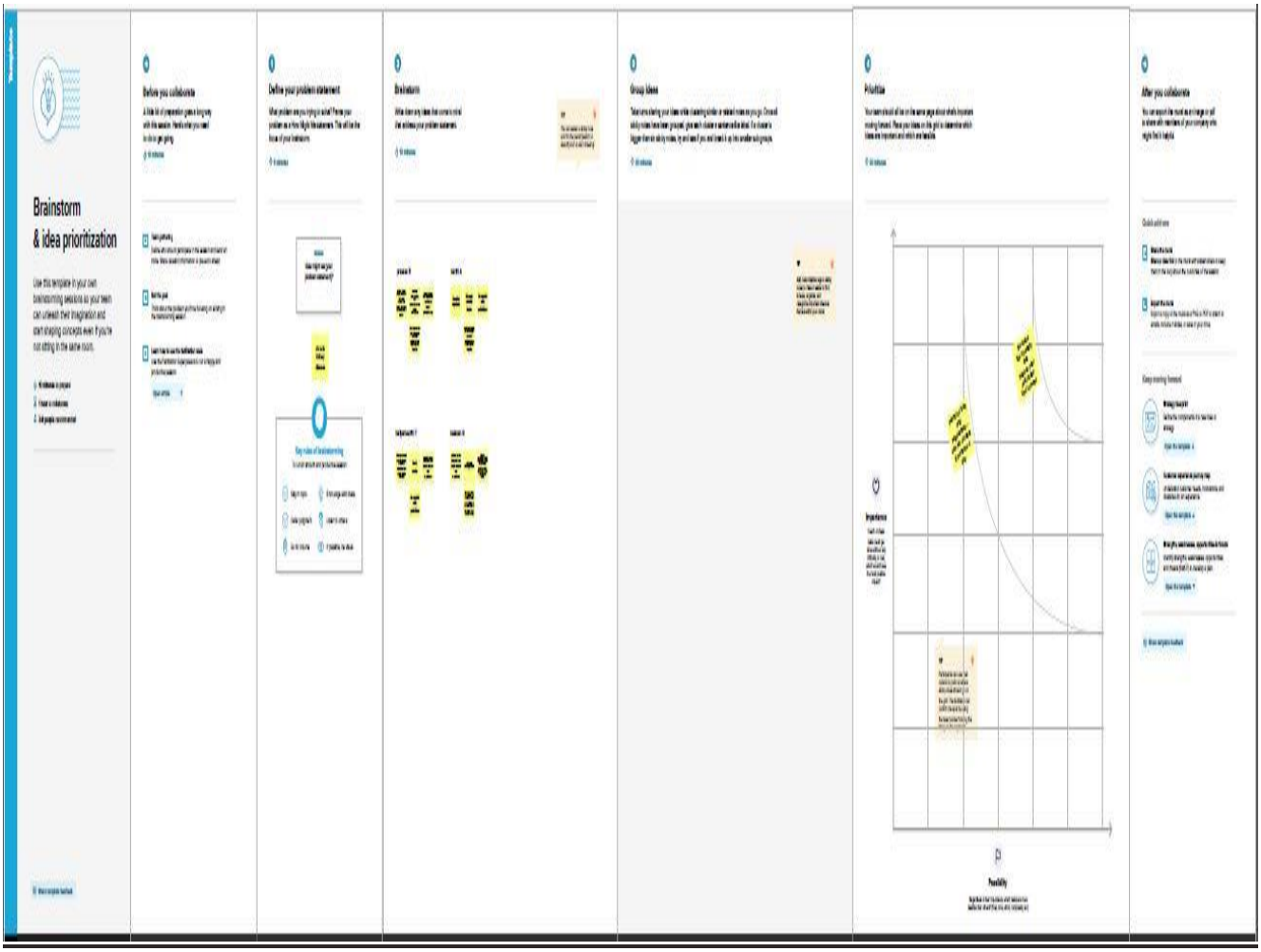
leading cause of morbidity and mortality for dialysis patients. Several interventions to delay the progressive loss of renal function and/or to prevent the development of CVD are now available. These include low-protein diets; correction of calcium-phosphate disorders and anaemia; blood pressure and proteinuria control; and smoking cessation. Other interventions, such as the administration of lipid-lowering agents, anti-inflammatory drugs, and anti-oxidant agents are emerging as particularly promising therapeutic approaches, although prospective, controlled, randomized clinical trials are needed to demonstrate their clinical usefulness. Intervention in the conservative phase of CKD is likely to be more effective if performed as early as possible in the course of the disease, since it has been widely demonstrated that early and regular nephrology specialist care is associated with decreased morbidity and mortality.

2. Problem definition & Design Thinking

2.1 Empathy map



2.2 Ideation & Brainstroming Map



3. Result

The Best Model

Saving the best model after comparing its performance using different evaluation metrics means selecting the model with the highest performance and saving its weights and configuration. This can be useful in avoiding the need to retrain the model every time it is needed and to be able to use it in the future.

```
pickle.dump(lgr, open('CKD.pkl','wb'))
```

Integrate With Web Framework

In this section, we will be building a web application that is integrated to the model we built. A UI is provided for the uses where he has to enter the values for predictions. The enter values are given to the saved model and prediction is showcased on the UI.

This section has the following tasks

- Building HTML Pages
- Building server-side script
- Run the web application

Building Html Pages

For this project create four HTML files namely

- home.html
- index1.html
- indexnew.html
- result.html

and save them in the templates folder

Build Python Code

Import the libraries

```
from flask import Flask, render_template, request
import numpy as np
import pickle
```

Load the saved model. Importing the flask module in the project is mandatory. An object of Flask class is our WSGI application.

Flask constructor takes the name of the current module (__name__) as argument.

```
app = Flask(__name__) # initializing a flask app
model = pickle.load(open('CKD.pkl', 'rb')) #loading the model
```

Render HTML page:

```
@app.route('/')# route to display the home page
def home():
    return render_template('home.html') #rendering the home page
```

Here we will be using a declared constructor to route to the HTML page which we have created earlier.

In the above example, '/' URL is bound with the home.html function. Hence, when the home page of the web server is opened in the browser, the html page will be rendered. Whenever you enter the values from the html page the values can be retrieved using POST Method.

Retrieves the value from UI:

```
@app.route('/Prediction',methods=['POST','GET'])

def prediction():
    return render_template('indexnew.html')
@app.route('/Home',methods=['POST','GET'])
def my_home():
    return render_template('home.html')

@app.route('/predict',methods=['POST'])# route to show the predictions in a web UI
def predict():

    #reading the inputs given by the user
    input_features = [float(x) for x in request.form.values()]
    features_value = [np.array(input_features)]

    features_name = ['blood_urea', 'blood glucose random', 'anemia',
       'coronary_artery_disease', 'pus_cell', 'red_blood_cells',
       'diabetesmellitus', 'pedal_edema']

    df = pd.DataFrame(features_value, columns=features_name)

    # predictions using the loaded model file
    output = model.predict(df)
```

Here we are routing our app to predict() function. This function retrieves all the values from the HTML page using Post request. That is stored in an array. This array is passed to the model.predict() function. This function returns the prediction. And this prediction value will be rendered to the text that we have mentioned in the submit.html page earlier.

```
# showing the prediction results in a UI# showing the prediction results in a UI
return render_template('result.html', prediction_text=output)
```

Main Function:

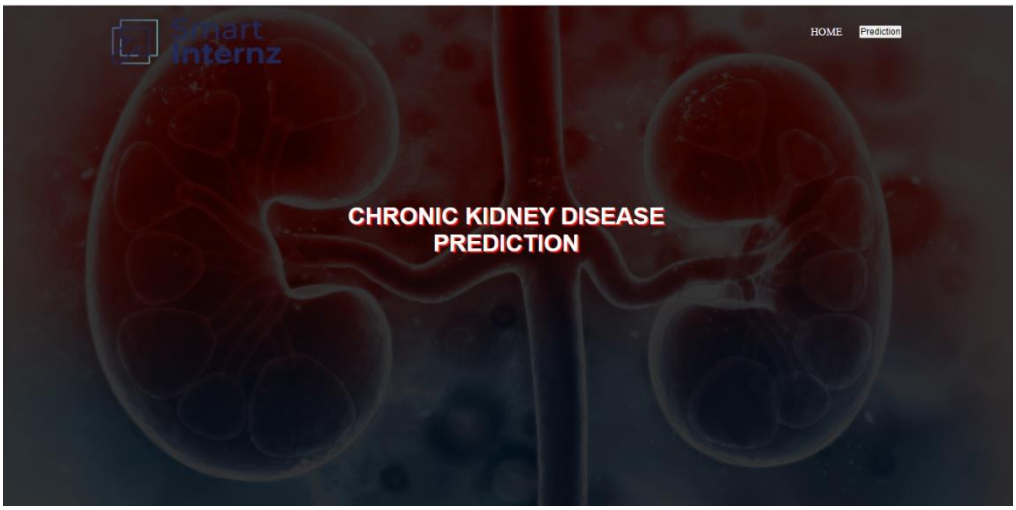
```
if __name__ == '__main__':
    # running the app
    app.run(debug=True)
```

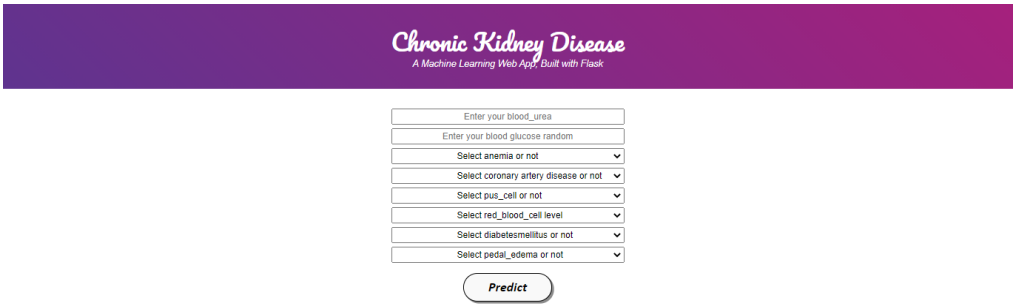
Run The Web Application

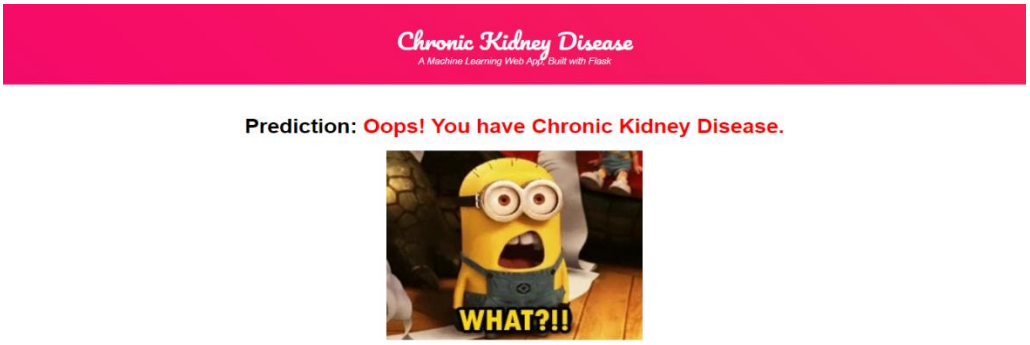
- Open anaconda prompt from the start menu
- Navigate to the folder where your python script is.
- Now type “python app.py” command
- Navigate to the localhost where you can view your web page.
- Click on the predict button from the top left corner, enter the inputs, click on the submit button, and see the result/prediction on the web.

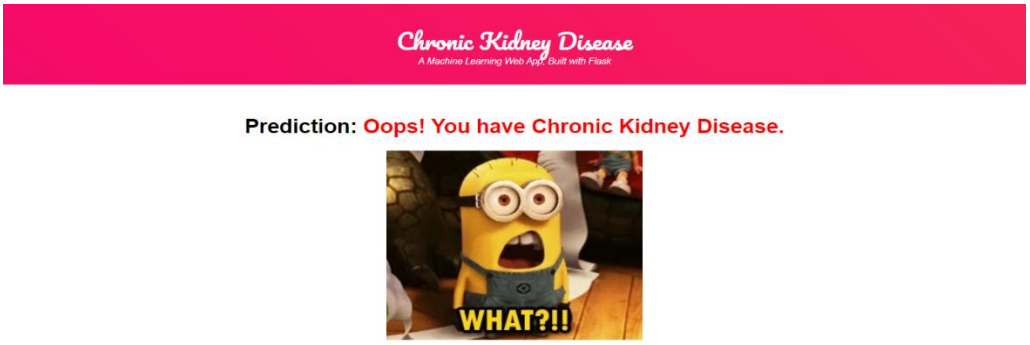
```
(base) D:\SmartBridge\Chronic Kidney Disease>python app.py
 * Serving Flask app "app" (lazy loading)
 * Environment: production
   WARNING: This is a development server. Do not use it in a production deployment.
   Use a production WSGI server instead.
 * Debug mode: off
 * Running on http://127.0.0.1:5000/ (Press CTRL+C to quit)
```

Now,Go the web browser and write the localhost url (http://127.0.0.1:5000) to get the below result

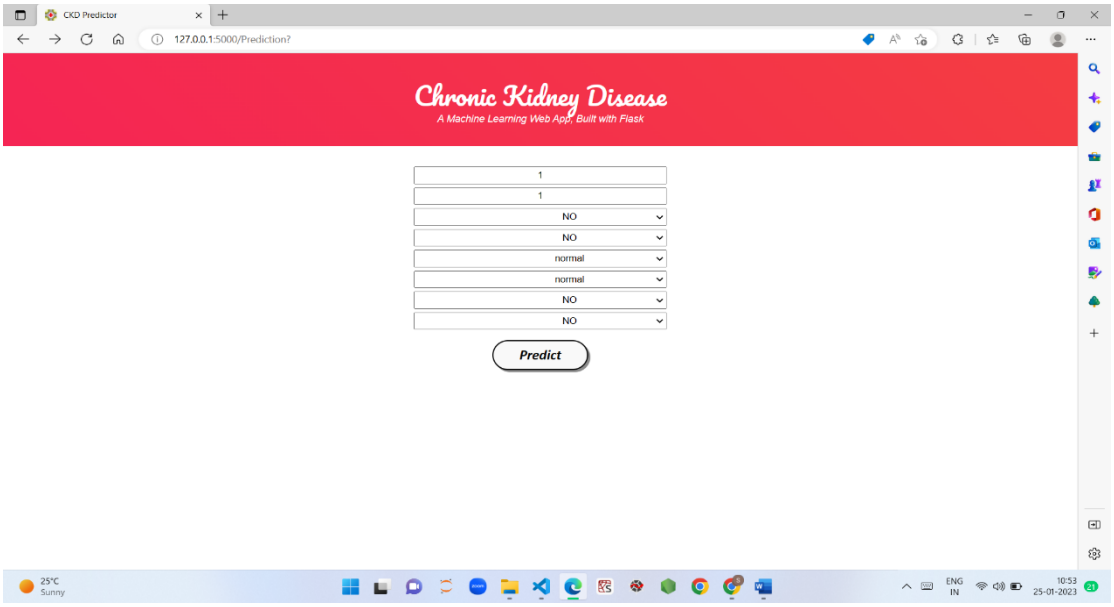


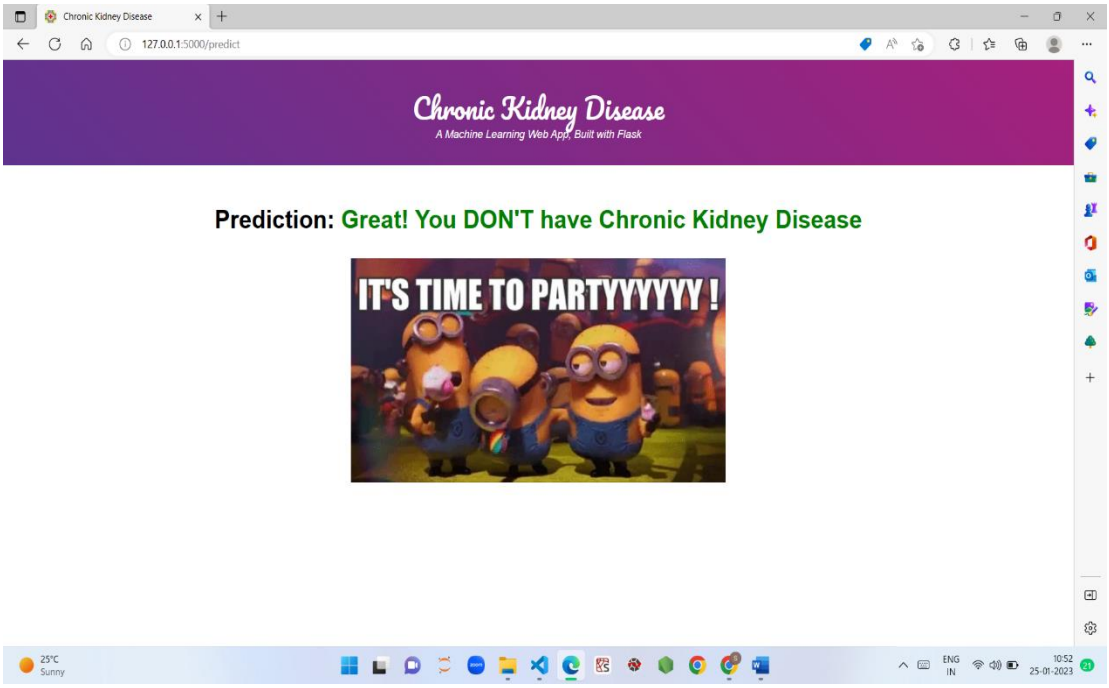






Input - Now, the user will give inputs to get the predicted result after clicking onto the submit button.





4 .Advantages and disadvantages

Advantages

Early prediction and proper treatments can possibly stop, or slow the progression of this chronic disease to end-stage, where dialysis or kidney transplantation is the only way to save patient’s life.

Disadvantages

It is necessary to educate primary care physicians about CKD, its risk factors and associated co-morbidities. Although multiple benefits of screening for CKD are doubtless, the results obtained by screening should be interpreted with caution, bearing in mind that screening detects only markers of kidney disease but not the disease itself.

5. Application

Chronic kidney disease (CKD) includes all clinical features and complications during the progression of various kidney conditions towards end-stage renal disease (ESRD). These conditions include immune and inflammatory disease such as: primary and hepatitis C virus (HCV)-related glomerulonephritis; infectious disease such as pyelonephritis with or without reflux and tuberculosis; vascular disease such as chronic ischemic nephropathy; hereditary and congenital disease such as polycystic disease and congenital cystic dysplasia; metabolic disease including diabetes and hyperuricemia; and systemic disease (collagen disease, vasculitis, myeloma). During the progression of CKD, ultrasound imaging and color Doppler imaging (US–CDI) can differentiate the etiology of the renal damage in only 50–70% of cases. Indeed, the end-stage kidney appears shrunken, reduced in volume (Ø < 9 cm), unstructured, amorphous, and with acquired cystic degeneration (small and multiple cysts involving the cortex and medulla) or nephrocalcinosis, but there are rare exceptions, such as polycystic kidney disease, diabetic nephropathy, and secondary inflammatory nephropathies. The main difficulties in the differential diagnosis are encountered in multifactorial CKD, which is commonly presented to the nephrologist at stage 4–5, when the kidney is shrunken, unstructured and amorphous. As in acute renal injury and despite the lack of sensitivity, US–CDI is essential for assessing the progression of renal damage and related complications, and for evaluating all conditions that increase the risk of CKD, such as lithiasis, recurrent urinary tract infections, vesicoureteral reflux, polycystic kidney disease and obstructive nephropathy. The timing and frequency of ultrasound scans in CKD patients should be evaluated case by case. In this review, we will consider the morpho-functional features of the kidney in all nephropathies that may lead to progressive CKD.

6. Conclusion

Technological development, including machine learning, has huge impact on health through an effective analysis of various chronic kidney disease is major chronic disease

associated with aging, hypertension and diabetes, affecting people 60 and over. Its major cause is the malfunctioning of the kidney disease using machine learning techniques based on a chronic kidney disease(CKD).

7. Future scope

This study used a supervised machine-learning algorithm, feature selection methods to select the best subset features to develop the models. It is better to see the difference in performance results using unsupervised or deep learning algorithms models. The proposed model supports the experts to give the fast decision, it is better to make it a mobile-based system that enables the experts to follow the status of the patients and help the patients to use the system to know their status.

8.Appendix

Source code

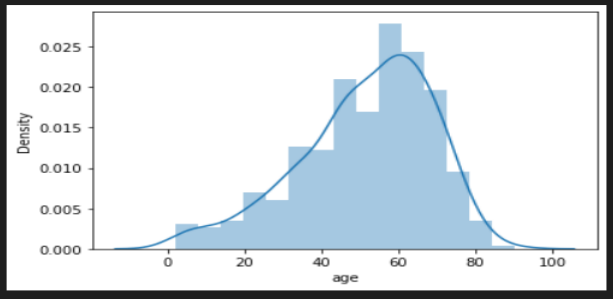
```
data.describe() # computes summary values for continous column data
```

	age	blood_pressure	specific_gravity	albumin	sugar	blood glucose random	blood_urea	serum_creatinine	sodium
count	391.000000	388.000000	353.000000	354.000000	351.000000	356.000000	381.000000	383.000000	313.000000
mean	51.483376	76.469072	1.017408	1.016949	0.450142	148.036517	57.425722	3.072454	137.528754
std	17.169714	13.683637	0.005717	1.352679	1.099191	79.281714	50.503006	5.741126	10.408752
min	2.000000	50.000000	1.005000	0.000000	0.000000	22.000000	1.500000	0.400000	4.500000
25%	42.000000	70.000000	1.010000	0.000000	0.000000	99.000000	27.000000	0.900000	135.000000
50%	55.000000	80.000000	1.020000	0.000000	0.000000	121.000000	42.000000	1.300000	138.000000
75%	64.500000	80.000000	1.020000	2.000000	0.000000	163.000000	66.000000	2.800000	142.000000
max	90.000000	180.000000	1.025000	5.000000	5.000000	490.000000	391.000000	76.000000	163.000000

Age distribution

```
[236] sns.distplot(data.age)
```

```
C:\Users\Saumya\Anaconda3\lib\site-packages\seaborn\distributions.py:2557: FutureWa
your code to use either `displot` (a figure-level function with similar flexibility
  warnings.warn(msg, FutureWarning)

<AxesSubplot:xlabel='age', ylabel='Density'>
```

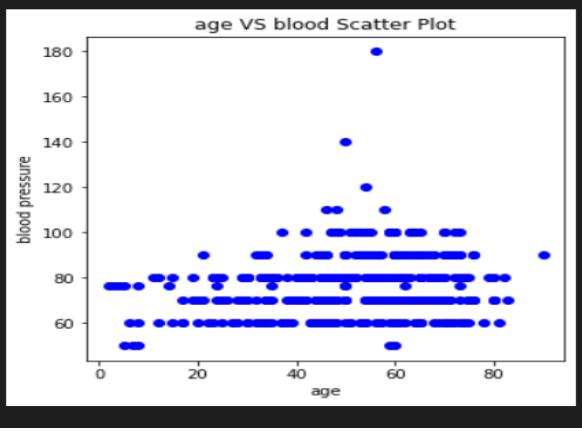


Bivariate Analysis

Age vs Blood Pressure

```
import matplotlib.pyplot as plt # import the matplotlib libaray
fig=plt.figure(figsize=(5,5)) #plot size
plt.scatter(data['age'],data['blood_pressure'],color='blue')
plt.xlabel('age') #set the label for x-axis
plt.ylabel('blood pressure') #set the label for y-axis
plt.title("age VS blood Scatter Plot") #set a title for the axes
```

```
Text(0.5, 1.0, 'age VS blood Scatter Plot')
```

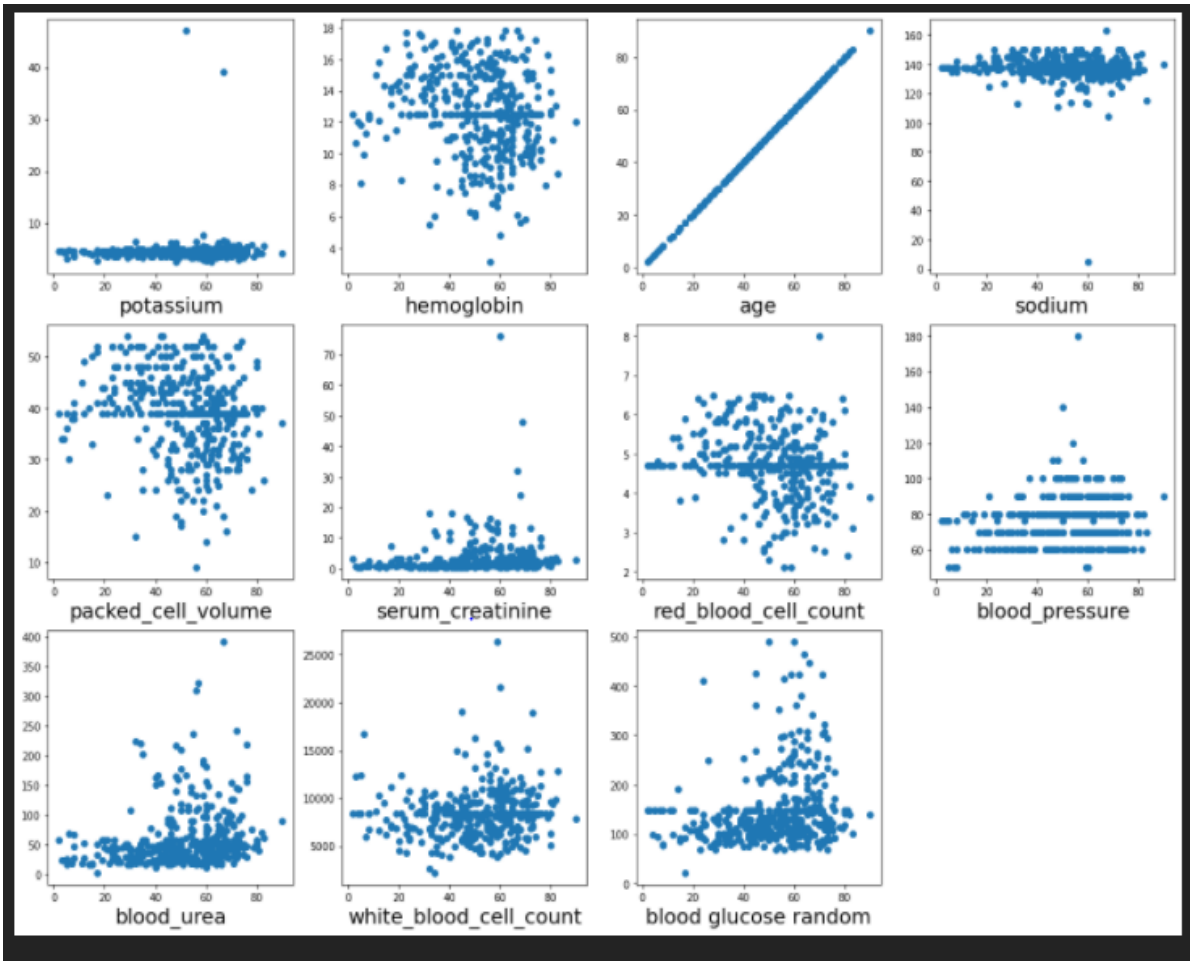


Multivariate Analysis

Age vs all continuous columns

Age vs all continous columns

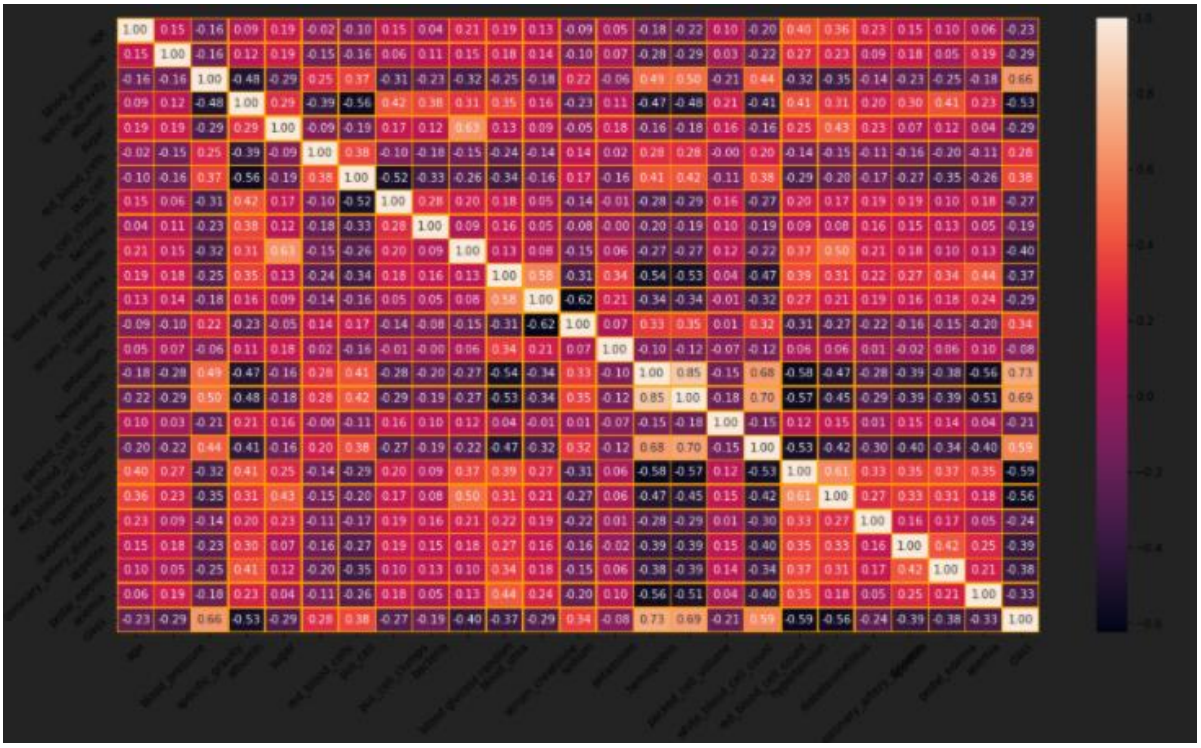
```
plt.figure(figsize=(20,15), facecolor='white')
plotnumber = 1

for column in contcols:
    if plotnumber<=11 :     # as there are 11 continous columns in the data
        ax = plt.subplot(3,4,plotnumber) # 3,4 is refer to 3X4 matrix
        plt.scatter(data['age'],data[column]) #plotting scatter plot
        plt.xlabel(column,fontsize=20)
        #plt.ylabel('Salary',fontsize=20)
    plotnumber+=1
plt.show()
```



As you can observe with the scatter plot many of features are correlated with age.

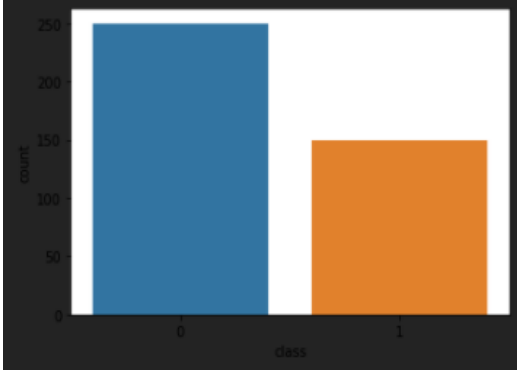
Finding correlation between the independent Columns

```
#HEAT MAP #correlation of parameters
f,ax=plt.subplots(figsize=(18,10))
sns.heatmap(data.corr(),annot=True,fmt=".2f",ax=ax,linewidths=0.5,linecolor="orange")
plt.xticks(rotation=45)
plt.yticks(rotation=45)
plt.show()
```



```
sns.countplot(data['class'])
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x20c1d390d30>
```




```
# perfroming feature Scaling op[eration using standard scaller on X part of the dataset because
# there different type of values in the columns
from sklearn.preprocessing import StandardScaler
sc=StandardScaler()
x_bal=sc.fit_transform(x)
```

Creating Independent and Dependent

```
selcols=['red_blood_cells','pus_cell', 'blood glucose random','blood_urea',
           'pedal_edema', 'anemia','diabetesmellitus','coronary_artery_disease']
x=pd.DataFrame(data,columns=selcols)
y=pd.DataFrame(data,columns=['class'])
print(x.shape)
print(y.shape)
```

```
(400, 8)
(400, 1)
```

Splitting the data into train and test

```
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2,random_state=2)#train test split
```

ANN Model

```
# Importing the Keras libraries and packages
import tensorflow
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense
```

```
# Creating ANN skleton view

classification = Sequential()
classification.add(Dense(30,activation='relu'))
classification.add(Dense(128,activation='relu'))
classification.add(Dense(64,activation='relu'))
classification.add(Dense(32,activation='relu'))
classification.add(Dense(1,activation='sigmoid'))
```

```
# Compiling the ANN model

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

```
# Training the model

classification.fit(x_train,y_train,batch_size=10,validation_split=0.2,epochs=100)
```

```
Output exceeds the size limit. Open the full output data in a text editor
Epoch 1/100
26/26 [==============================] - 0s 6ms/step - loss: 0.1151 - accuracy: 0.9531 - val_loss: 0.2476 - val_accuracy: 0.9062
Epoch 2/100
26/26 [==============================] - 0s 4ms/step - loss: 0.1171 - accuracy: 0.9570 - val_loss: 0.2498 - val_accuracy: 0.9062
Epoch 3/100
26/26 [==============================] - 0s 4ms/step - loss: 0.1146 - accuracy: 0.9531 - val_loss: 0.2317 - val_accuracy: 0.9219
Epoch 4/100
26/26 [==============================] - 0s 4ms/step - loss: 0.1305 - accuracy: 0.9531 - val_loss: 0.2855 - val_accuracy: 0.8906
Epoch 5/100
26/26 [==============================] - 0s 4ms/step - loss: 0.1387 - accuracy: 0.9492 - val_loss: 0.2068 - val_accuracy: 0.9219
Epoch 6/100
26/26 [==============================] - 0s 4ms/step - loss: 0.1230 - accuracy: 0.9492 - val_loss: 0.2576 - val_accuracy: 0.9062
Epoch 7/100
26/26 [==============================] - 0s 4ms/step - loss: 0.1241 - accuracy: 0.9531 - val_loss: 0.2688 - val_accuracy: 0.8906
Epoch 8/100
26/26 [==============================] - 0s 4ms/step - loss: 0.1128 - accuracy: 0.9570 - val_loss: 0.2334 - val_accuracy: 0.9219
Epoch 9/100
26/26 [==============================] - 0s 4ms/step - loss: 0.1180 - accuracy: 0.9531 - val_loss: 0.2435 - val_accuracy: 0.9062
Epoch 10/100
```

```
[==============================] - 0s 4ms/step - loss: 0.1139 - accuracy: 0.9531 - val_loss: 0.2799 - val_accuracy: 0.8906 Ep
...
Epoch 99/100 26/26 [==============================] - 0s 3ms/step - loss: 0.1074 - accuracy: 0.9570 - val_loss: 0.2439 - va
[==============================] - 0s 4ms/step - loss: 0.1062 - accuracy: 0.9570 - val_loss: 0.2572 - val_accuracy: 0.9062

<tensorflow.python.keras.callbacks.History at 0x1fdf3ca7b20>
```

```
from sklearn.ensemble import RandomForestClassifier
rfc = RandomForestClassifier(n_estimators=10,criterion='entropy')
```

```
rfc.fit(x_train,y_train)
```

```
<ipython-input-255-b87bb2ba9825>:1: DataConversionWarning: A column-vector y wa
(n_samples,), for example using ravel().
  rfc.fit(x_train,y_train)

RandomForestClassifier(criterion='entropy', n_estimators=10)
```

```
y_predict = rfc.predict(x_test)
```

+ Code

```
y_predict_train = rfc.predict(x_train)
```

```
from sklearn.tree import DecisionTreeClassifier

dtc = DecisionTreeClassifier(max_depth=4,splitter='best',criterion='entropy')
```

```
dtc.fit(x_train,y_train)
```

```
DecisionTreeClassifier(criterion='entropy', max_depth=4)
```

```
y_predict= dtc.predict(x_test)
y_predict
```

```
array([0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 1, 0, 0, 0, 1, 1, 0, 1, 1,
       0, 1, 0, 1, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0,
       0, 1, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 0,
       0, 1, 0, 1, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0])
```

```
y_predict_train = dtc.predict(x_train)
```

```
from sklearn.linear_model import LogisticRegression
lgr = LogisticRegression()
lgr.fit(x_train,y_train)
```

```
C:\Users\Saumya\Anaconda3\lib\site-packages\sklearn\utils\validation.py:72: DataConversionWar
Please change the shape of y to (n_samples, ), for example using ravel().
  return f(**kwargs)

LogisticRegression()
```

Predicting our output with the model which we build

```
from sklearn.metrics import accuracy_score,classification_report

y_predict = lgr.predict(x_test)
```

```
# logistic Regression

y_pred = lgr.predict([[1,1,121.000000,36.0,0,0,1,0]])

print(y_pred)
(y_pred)
```

```
[0]

array([0])
```

```
# DecisionTree classifier

y_pred = dtc.predict([[1,1,121.000000,36.0,0,0,1,0]])

print(y_pred)
(y_pred)
```

```
[0]

array([0])
```

```
# Random Forest Classifier
y_pred = rfc.predict([[1,1,121.000000,36.0,0,0,1,0]])

print(y_pred)
(y_pred)
```

```
[0]

array([0])
```

```
classification.save("ckd.h5")
```

```
# Testing the model

y_pred = classification.predict(x_test)
```

```
y_pred
```

```
Output exceeds the size limit. Open the full output data in a text editor
array([[2.07892948e-12],
       [7.16007332e-13],
       [0.00000000e+00],
       [6.47086192e-23],
       [9.99349952e-01],
       [1.47531908e-22],
       [0.00000000e+00]
```

```
    y_pred = (y_pred > 0.5)
    y_pred
272]
```

```
Output exceeds the size limit. Open the full output data in a te
array([[False],
       [False],
       [False],
       [False],
       [ True],
       [False],
       [False],
```

```
def predict_exit(sample_value):

  # Convert list to numpy array
    sample_value = np.array(sample_value)

  # Reshape because sample_value contains only 1 record
    sample_value = sample_value.reshape(1, -1)

  # Feature Scaling
    sample_value = sc.transform(sample_value)

    return classifier.predict(sample_value)
98]
```

```
test=classification.predict([[1,1,121.000000,36.0,0,0,1,0]])
if test==1:
    print('Prediction: High chance of CKD!')
else:
    print('Prediction: Low chance of CKD.')
00]
```

```
Prediction: Low chance of CKD.
```

Compare the model

```
from sklearn import model_selection
```

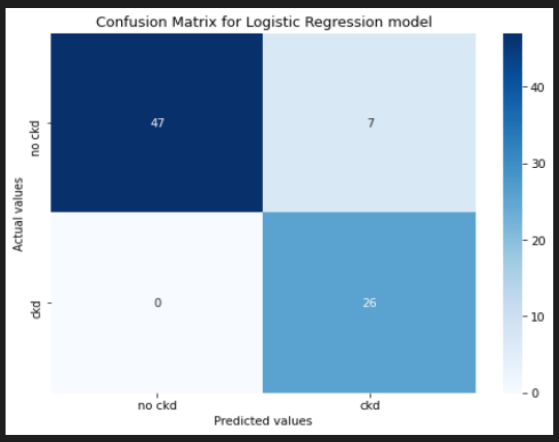
```
    dfs = []
models = [
            ('LogReg', LogisticRegression()),
            ('RF', RandomForestClassifier()),
            ('DecisionTree',DecisionTreeClassifier()),

        ]
results = []
    names = []
    scoring = ['accuracy', 'precision_weighted', 'recall_weighted', 'f1_weighted', 'roc_auc']
    target_names = ['NO CKD', 'CKD']
    for name, model in models:
        kfold = model_selection.KFold(n_splits=5, shuffle=True, random_state=90210)
        cv_results = model_selection.cross_validate(model, x_train, y_train, cv=kfold, scoring=scoring)
        clf = model.fit(x_train, y_train)
        y_pred = clf.predict(x_test)
        print(name)
        print(classification_report(y_test, y_pred, target_names=target_names))
        results.append(cv_results)
        names.append(name)
        this_df = pd.DataFrame(cv_results)
        this_df['model'] = name
        dfs.append(this_df)
final = pd.concat(dfs, ignore_index=True)
return final
```

```
LogReg
              precision    recall  f1-score   support

      NO CKD       1.00      0.87      0.93        54
         CKD       0.79      1.00      0.88        26

    accuracy                           0.91        80
   macro avg       0.89      0.94      0.91        80
weighted avg       0.93      0.91      0.91        80
```

```python
# Making the Confusion Matrix
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_predict)
cm
```

```
array([[47,  7],
       [ 0, 26]], dtype=int64)
```

```python
# Plotting confusion matrix
plt.figure(figsize=(8,6))
sns.heatmap(cm, cmap='Blues', annot=True, xticklabels=['no ckd', 'ckd'], yticklabels=['no ckd', 'ckd'])
plt.xlabel('Predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for Logistic Regression model')
plt.show()
```



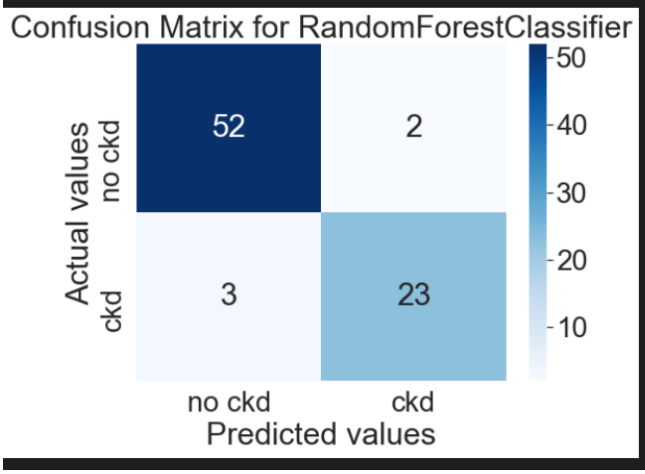
RF

	precision	recall	f1-score	support
NO CKD	0.96	0.96	0.96	54
CKD	0.92	0.92	0.92	26
accuracy			0.95	80
macro avg	0.94	0.94	0.94	80
weighted avg	0.95	0.95	0.95	80

```python
# Making the Confusion Matrix
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_predict)
cm
```

```
array([[52,  2],
       [ 3, 23]], dtype=int64)
```

```python
# Plotting confusion matrix
plt.figure(figsize=(8,6))
sns.heatmap(cm, cmap='Blues', annot=True, xticklabels=['no ckd', 'ckd'], yticklabels=['no ckd', 'ckd'])
plt.xlabel('Predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for RandomForestClassifier')
plt.show()
```



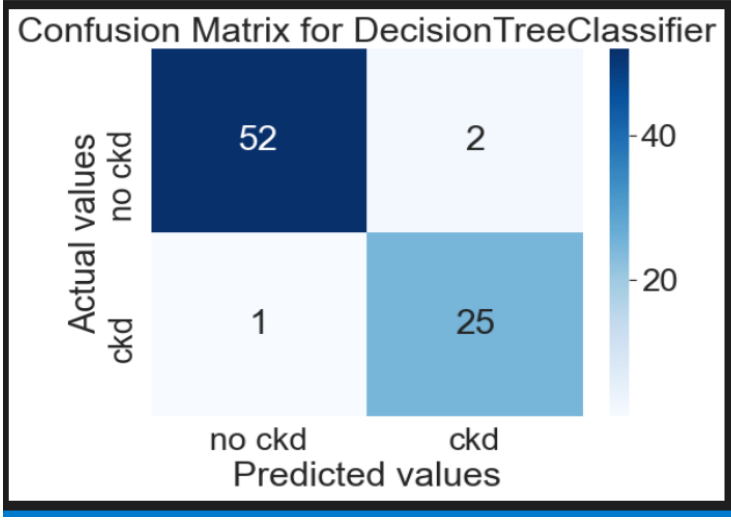
DecisionTree

	precision	recall	f1-score	support
NO CKD	0.93	0.94	0.94	54
CKD	0.88	0.85	0.86	26
accuracy			0.91	80
macro avg	0.90	0.90	0.90	80
weighted avg	0.91	0.91	0.91	80

```python
# Making the Confusion Matrix
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_predict)
cm
```

```
array([[52,  2],
       [ 1, 25]], dtype=int64)
```

```python
# Plotting confusion matrix
plt.figure(figsize=(8,6))
sns.heatmap(cm, cmap='Blues', annot=True, xticklabels=['no ckd', 'ckd'], yticklabels=['no ckd', 'ckd'])
plt.xlabel('Predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for DecisionTreeClassifier')
plt.show()
```



[201]

```python
print (classification_report(y_test, y_pred))
```

```
              precision    recall  f1-score   support

           0       0.96      0.96      0.96        54
           1       0.92      0.92      0.92        26

    accuracy                           0.95        80
   macro avg       0.94      0.94      0.94        80
weighted avg       0.95      0.95      0.95        80
```

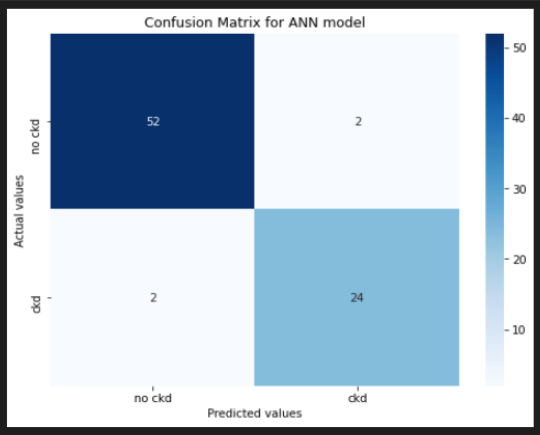
```
# Making the Confusion Matrix
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_pred)
cm
```

92]

```
array([[52,  2],
       [ 2, 24]], dtype=int64)
```

```
# Plotting confusion matrix
plt.figure(figsize=(8,6))
sns.heatmap(cm, cmap='Blues', annot=True, xticklabels=['no ckd', 'ckd'], yticklabels=['no ckd', 'ckd'])
plt.xlabel('Predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for ANN model')
plt.show()
```

95]




```
bootstraps = []
for model in list(set(final.model.values)):
    model_df = final.loc[final.model == model]
    bootstrap = model_df.sample(n=30, replace=True)
    bootstraps.append(bootstrap)

bootstrap_df = pd.concat(bootstraps, ignore_index=True)
results_long = pd.melt(bootstrap_df,id_vars=['model'],var_name='metrics', value_name='values')
time_metrics = ['fit_time','score_time'] # fit time metrics
## PERFORMANCE METRICS
results_long_nofit = results_long.loc[~results_long['metrics'].isin(time_metrics)] # get df without fit data
results_long_nofit = results_long_nofit.sort_values(by='values')
## TIME METRICS
results_long_fit = results_long.loc[results_long['metrics'].isin(time_metrics)] # df with fit data
results_long_fit = results_long_fit.sort_values(by='values')
```

1]

```
import matplotlib.pyplot as plt
import seaborn as sns
plt.figure(figsize=(20, 12))
sns.set(font_scale=2.5)
g = sns.boxplot(x="model", y="values", hue="metrics", data=results_long_nofit, palette="Set3")
plt.legend(bbox_to_anchor=(1.05, 1), loc=2, borderaxespad=0.)
plt.title('Comparison of Model by Classification Metric')
plt.savefig('./benchmark_models_performance.png',dpi=300)
```