# NAAN MUDHALVAN PROJECT

## EARLY PREDICTION FOR CHRONIC KIDNEY DISEASE DETECTION: A PROGRESSIVE APPROACH TO HEALTH MANAGEMENT

**BACHELOR OF SCIENCE IN COMPUTER SCIENCE**

**TO THE**

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# INTRODUCTION

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.

# Milestone 1: Define Problem / Problem Understanding

## Activity 1: Specify the business problem

Refer Project Description

## Activity 2: Business 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.

## Activity 3: Literature Survey (Student Will Write)

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 ESRD 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.

## Activity 4: Social or Business 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.

## Milestone 2: Data Collection & Preparation

ML depends heavily on data. It is the most crucial aspect that makes algorithm training possible. So this section allows you to download the required dataset.

### Activity 1: Collect the dataset

There are many popular open sources for collecting the data. Eg: kaggle.com, UCI repository, etc.

In this project we have used .csv data. This data is downloaded from kaggle.com. Please refer to the link given below to download the dataset.

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

As the dataset is downloaded. Let us read and understand the data properly with the help of some visualisation techniques and some analysing techniques.

**Note:** 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.

### Activity 1.1: Importing the libraries

Import the necessary libraries as shown in the image. (optional) Here we have used visualisation style as fivethirtyeight.

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 array
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,
```

### Activity 1.2: 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 read_csv() 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

## Activity 2: 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.

## Activity 2.1: 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')
```

### Activity 2.2: Handling missing values

- Let’s find the shape of our dataset first. To find the shape of our data, thedf.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
```

```
data.isnull().any() #it will return true if any columns is having null values
```

```
age                      True
blood_pressure           True
specific_gravity         True
albumin                  True
sugar                    True
red_blood_cells          True
pus_cell                 True
pus_cell_clumps          True
bacteria                 True
blood glucose random     True
blood_urea               True
serum_creatinine         True
sodium                   True
potassium                True
hemoglobin               True
packed_cell_volume       True
white_blood_cell_count   True
red_blood_cell_count     True
hypertension             True
diabetesmellitus         True
coronary_artery_disease  True
appetite                 True
pedal_edema              True
anemia                   True
class                   False
dtype: bool
```

```
data['blood glucose random'].fillna(data['blood glucose random'].mean(),inplace=True)
data['blood_pressure'].fillna(data['blood_pressure'].mean(),inplace=True)
data['blood_urea'].fillna(data['blood_urea'].mean(),inplace=True)
data['hemoglobin'].fillna(data['hemoglobin'].mean(),inplace=True)
data['packed_cell_volume'].fillna(data['packed_cell_volume'].mean(),inplace=True)
data['potassium'].fillna(data['potassium'].mean(),inplace=True)
data['red_blood_cell_count'].fillna(data['red_blood_cell_count'].mean(),inplace=True)
data['serum_creatinine'].fillna(data['serum_creatinine'].mean(),inplace=True)
data['sodium'].fillna(data['sodium'].mean(),inplace=True)
data['white_blood_cell_count'].fillna(data['white_blood_cell_count'].mean(),inplace=True)
```

```
data['age'].fillna(data['age'].mode()[0],inplace=True)
data['hypertension'].fillna(data['hypertension'].mode()[0],inplace=True)
data['pus_cell_clumps'].fillna(data['pus_cell_clumps'].mode()[0],inplace=True)
data['appetite'].fillna(data['appetite'].mode()[0],inplace=True)
data['albumin'].fillna(data['albumin'].mode()[0],inplace=True)
data['pus_cell'].fillna(data['pus_cell'].mode()[0],inplace=True)
data['red_blood_cells'].fillna(data['red_blood_cells'].mode()[0],inplace=True)
data['coronary_artery_disease'].fillna(data['coronary_artery_disease'].mode()[0],inplace=True)
data['bacteria'].fillna(data['bacteria'].mode()[0],inplace=True)
data['anemia'].fillna(data['anemia'].mode()[0],inplace=True)
data['sugar'].fillna(data['sugar'].mode()[0],inplace=True)
data['diabetesmellitus'].fillna(data['diabetesmellitus'].mode()[0],inplace=True)
data['pedal_edema'].fillna(data['pedal_edema'].mode()[0],inplace=True)
data[ 'specific_gravity'].fillna(data[ 'specific_gravity'].mode()[0],inplace=True)
```

Let’s now check the count of null values after filling all null values using

**isnull.sum()**

### Activity 2.3: 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.

**Activity 2.3.1: 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.

## Activity 2.4: Handling Numerical columns

```
contcols=set(data.dtypes[data.dtypes!='O'].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})
```

# Milestone 3: Exploratory Data Analysis

## Activity 1: Descriptive statistical Analysis

Descriptive analysis is to study the basic features of data with the statistical process. Here pandas has a worthy function called describe. With this describe function we can understand the unique, top and frequent values of categorical features. And we can find mean, std, min, max and percentile values of continuous features.

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

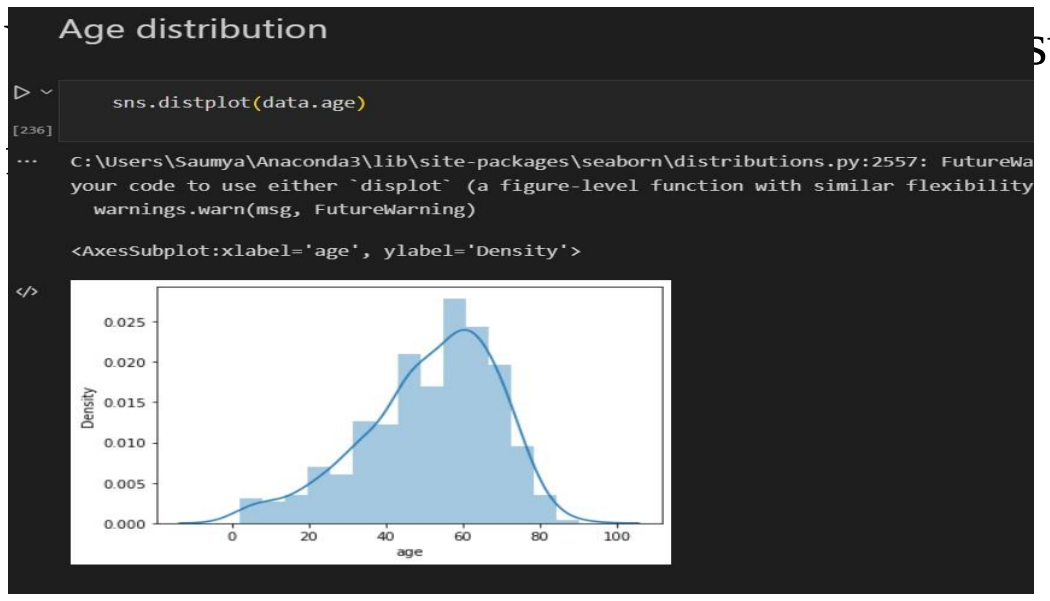
| | age | blood_pressure | specific_gravity | albumin | sugar | blood glucose random | blood_urea | serum_creatinine | sodium |
|---|---|---|---|---|---|---|---|---|---|
| count | 391.000000 | 388.000000 | 353.000000 | 354.000000 | 351.000000 | 356.000000 | 381.000000 | 383.000000 | 313.000000 |
| mean | 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 |

## Activity 2: Visual analysis

Visual analysis is the process of using visual representations, such as charts, plots, and graphs, to explore and understand data. It is a way to quickly identify patterns, trends, and outliers in the data, which can help to gain insights and make informed decisions.

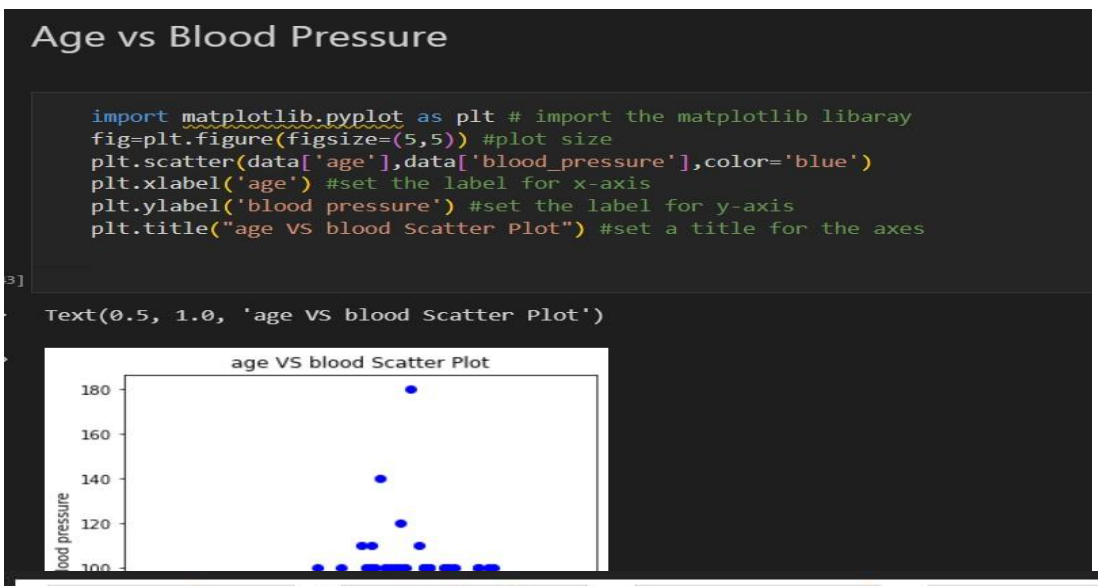
### Activity 2.1: Univariate analysis

In simple words, univariate analysis is understanding the data with a single feature. Here we have displayed two different graphs such as distplot and countplot.
The Seaborn package provides a wonderful function distplot.

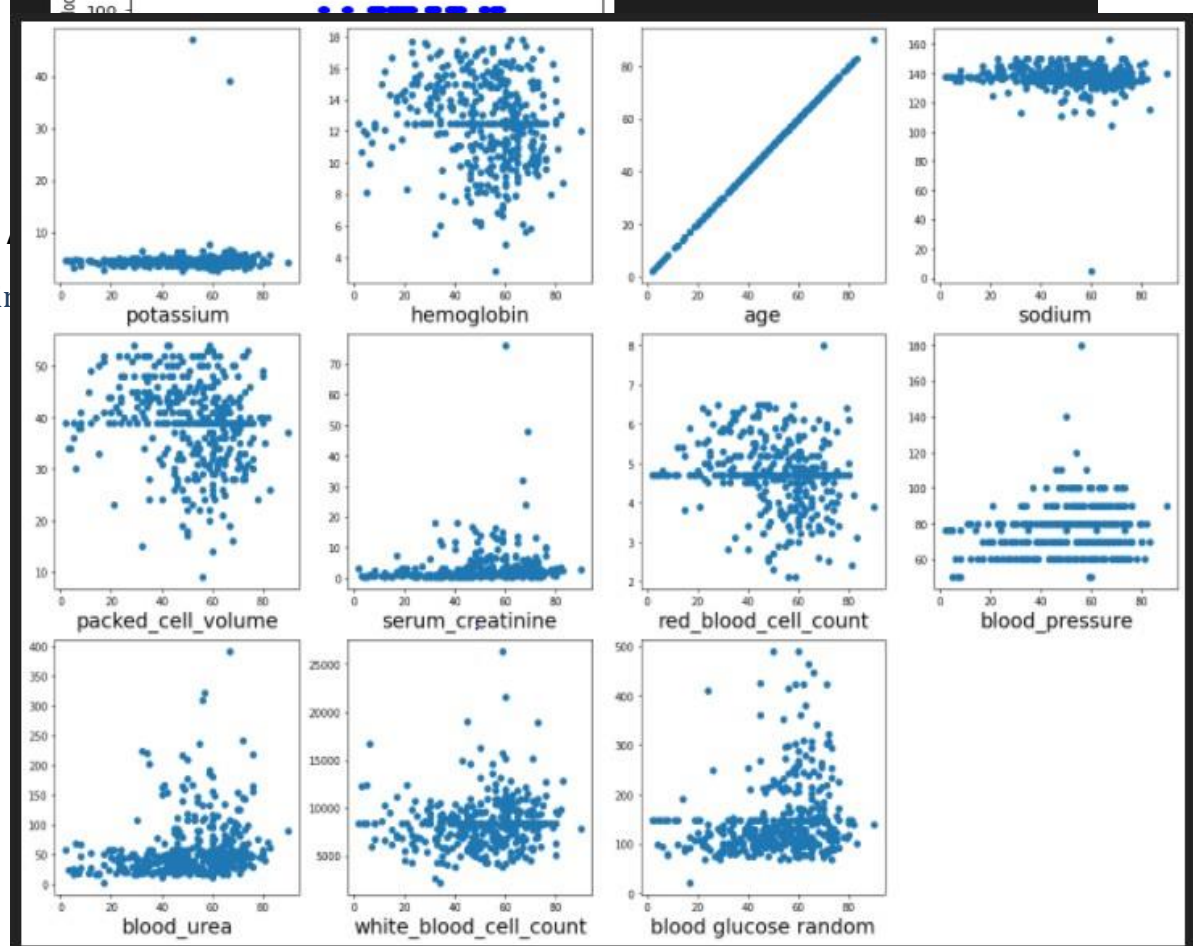



stribution of the

# Activity 2.2: Bivariate analysis




Age vs all contin



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

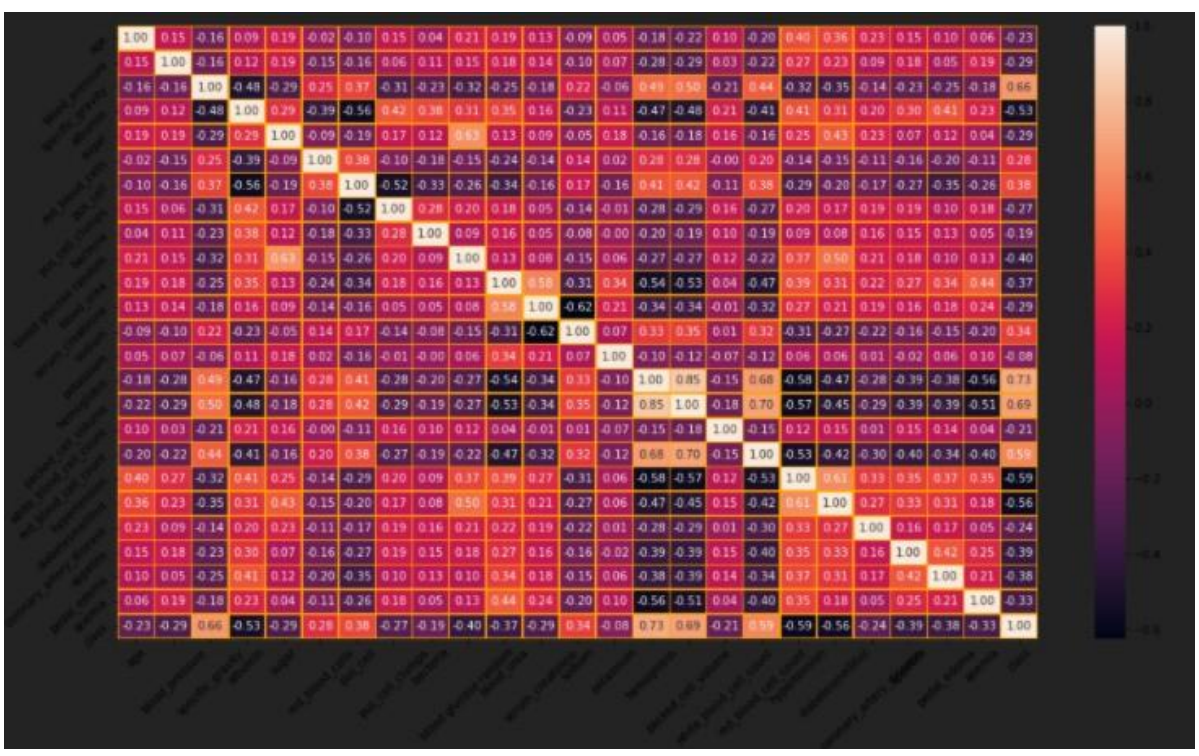
Finding correlation between the independent Columns

Correlation is a statistical relationship between two variables and it could be positive, meaning both variables move in the same direction, or negative, meaning that when one variable's value increases, the other variables' values decrease.

With the help of seaborn heatmap we will be plotting the heatmap and for finding the correlation between variable we have **corr()** available.

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()
```



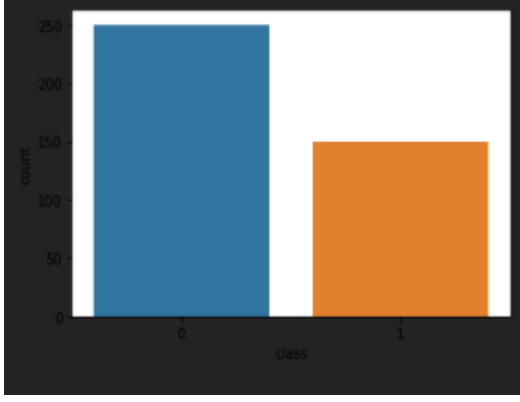
If you observe the heatmap, lighter the colour the correlation between that two variables will be high.

And correlation plays a very important role for extracting the correct features for build our model.

Now, let’s observe the count of our target data classes, by using seaborn countplot

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

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




## Scaling the Data

Scaling is one the important process, we have to perform on the dataset, because of data measures in different ranges can leads to mislead in prediction

Models such as KNN, Logistic regression need scaled data, as they follow distance-based method and Gradient Descent concept.

```
# 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)
```

We will perform scaling only on the input values.Once the dataset is scaled, it will be converted into an array and we need to convert it back to a dataframe.

## Separate independent and dependent variable

Now let’s split the Dataset into train and test sets

Changes: first split the dataset into x and y and then split the data set

Here x and y variables are created. On x variable, df is passed with dropping the target variable. And on y target variable is passed. For splitting training and testing data we are using the train_test_split() function from sklearn. As parameters, we are passing x, y, test_size, random_state.

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)
```

In the above code we are creating DataFrame of the independent variable **x** with our selected columns and for dependent variable

**y** we are only taking the **class** column.

Where **DataFrame is used to** represents a table of data with rows and columns.

Splitting data into train and test

When you are working on a model and you want to train it, you obviously have a dataset. But after training, we have to test the model on some test dataset. For this, you will a dataset which is different from the training set you used earlier. But it might not always be possible to have so much data during the development phase. In such cases, the solution is to split the dataset into two sets, one for training and the other for testing.

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
```

# Milestone 4: Model Building

## Activity 1: Training the model in multiple algorithms

Now our data is cleaned and it's time to build the model. We can train our data on different algorithms. For this project we are applying four classification algorithms. The best model is saved based on its performance.

### Activity 1.1: ANN Model

Building and training an Artificial Neural Network (ANN) using the Keras library with TensorFlow as the backend. The ANN is initialised as an instance of the Sequential class, which is a linear stack of layers. Then, the input layer and two hidden layers are added to the model using the Dense class, where the number of units and activation function are specified. The output layer is also added using the Dense class with a sigmoid activation function. The model is then compiled with the Adam optimizer, binary cross-entropy loss function, and accuracy metric. Finally, the model is fit to the training data with a batch size of 100, 20% validation split, and 100 epochs

```
# 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>
```

# Activity 1.2: Random Forest model

A function named random Forest is created and train and test data are passed as the parameters. Inside the function, Random Forest Classifier algorithm is initialised and training data is passed to the model with .fit() function. Test data is predicted with. predict() function and saved in a new variable. For evaluating the model, a confusion matrix and classification report is done.

```
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)
```

## Activity 1.3: Decision tree model

A function named decision Tree is created and train and test data are passed as the parameters. Inside the function, Decision Tree Classifier algorithm is initialised and training data is passed to the model with the .fit() function. Test data is predicted with. predict() function and saved in a new variable. For evaluating the model, a confusion

matrix and classification report is done.

```
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)
```

# Activity 1.4: Logistic Regression

```
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)
```

### Activity 2: Testing the model

```
# 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])
```

In ANN we first have to save the model to the test the inputs

```
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],
```

```
    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],
```

This code defines a function named "predict_exit" which takes in a sample_value as an input. The function then converts the input sample_value from a list to a numpy array. It reshapes the sample_value array as it contains only one record. Then, it applies feature scaling to the reshaped sample_value array using a scaler object 'sc' that should have been previously defined and fitted. Finally, the function returns the prediction of the classifier on the scaled sample_value.

```
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.
```

# Milestone 5: Performance Testing & Evaluate the results

## Activity 1: Testing model with multiple evaluation metrics

Multiple evaluation metrics means evaluating the model's performance on a test set using different performance measures. This can provide a more comprehensive understanding of the model's strengths and weaknesses. We are using evaluation metrics for classification tasks including accuracy, precision, recall, support and

F1-score.

## Compare the model

```
from sklearn import model_selection
```

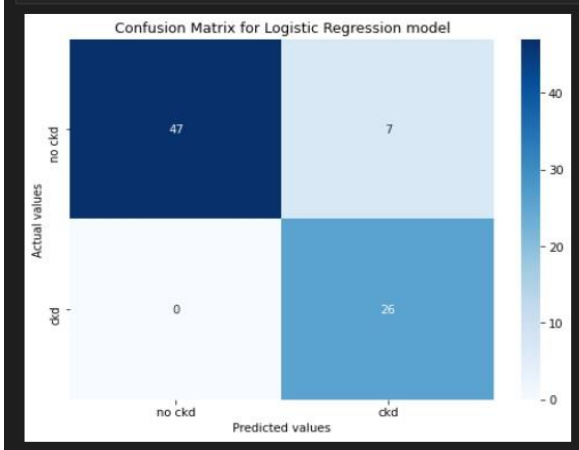
```
    dfs = []
models = [
            ('LogReg', LogisticRegression()),
            ('RF', RandomForestClassifier()),
            ('DecisionTree',DecisionTreeClassifier()),

          ]
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
```

```
# 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)
```

```
# 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()
```

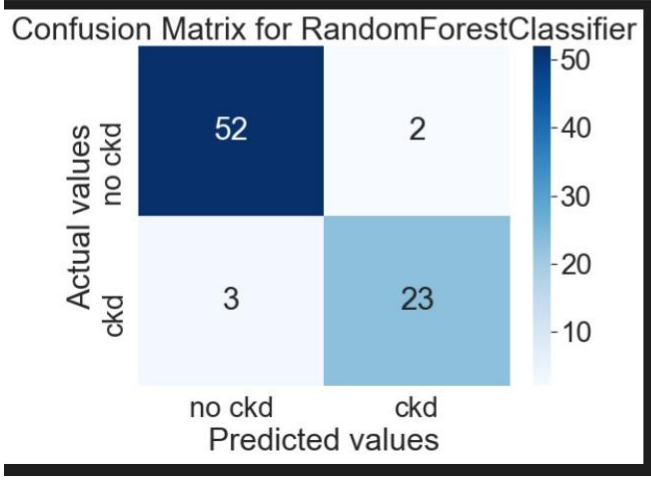



```
RF
              precision    recall  f1-score   support

       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()
```

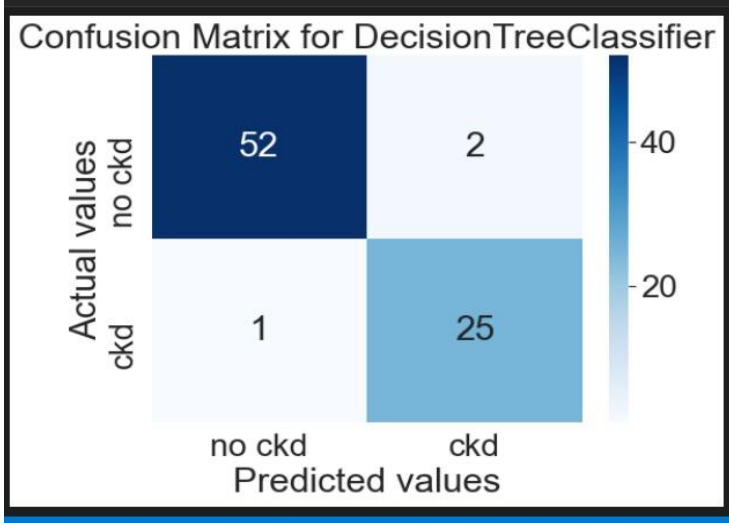



```
DecisionTree
              precision    recall  f1-score   support

      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()
```




For ANN

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

```
[201]
...
              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
```

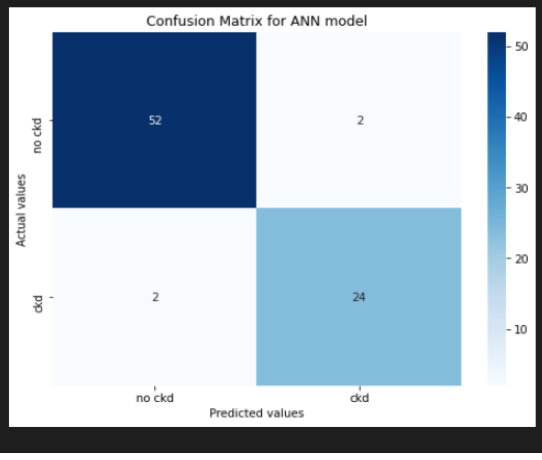
```
# Making the Confusion Matrix
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_pred)
cm
```

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]



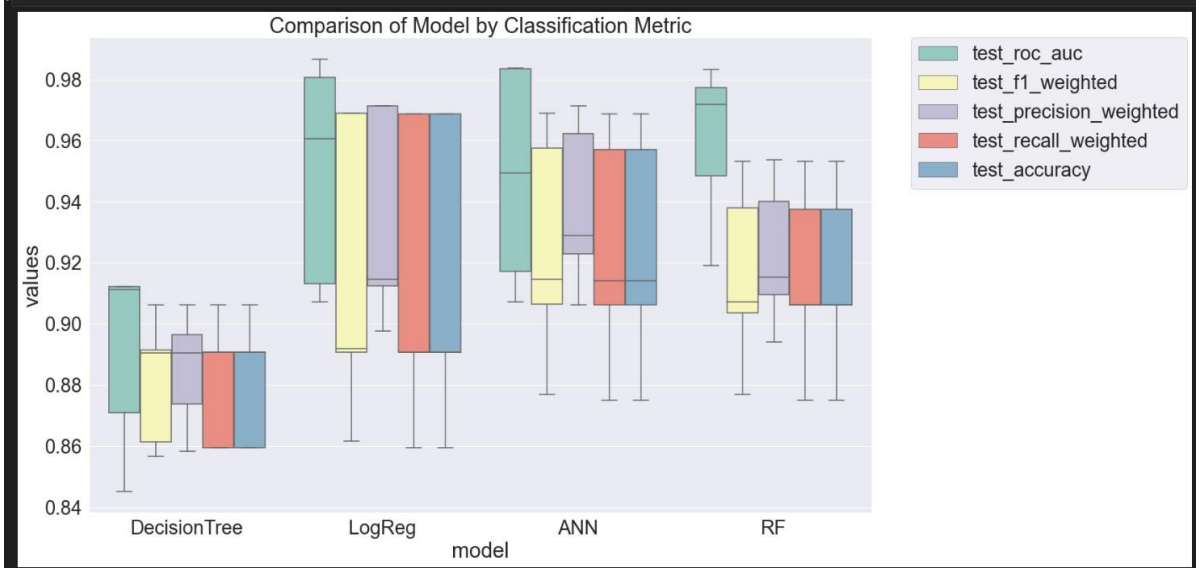

**A**ll above models are performing well for this dataset.

## Activity 2: Evaluate the results

```
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)
```




**A**mong all these 4 models logistic regression has recall 1. So, we are going for logreg model.

## Milestone 6: Model Deployment

### Activity 1: Save 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'))
```

## Activity 2: 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

## Activity 2.1: 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.

## Activity 2.2: 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:

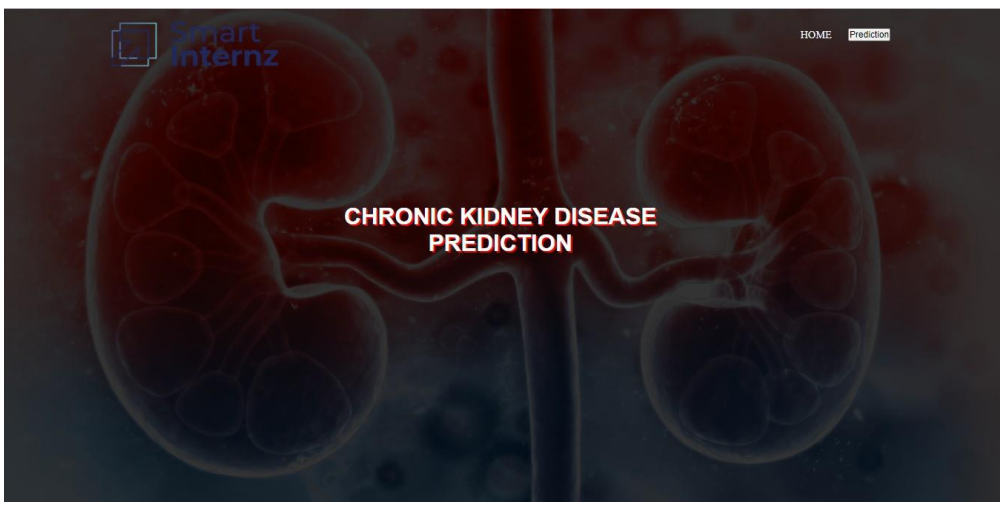
```python
if __name__ == '__main__':
    # running the app
    app.run(debug=True)
```

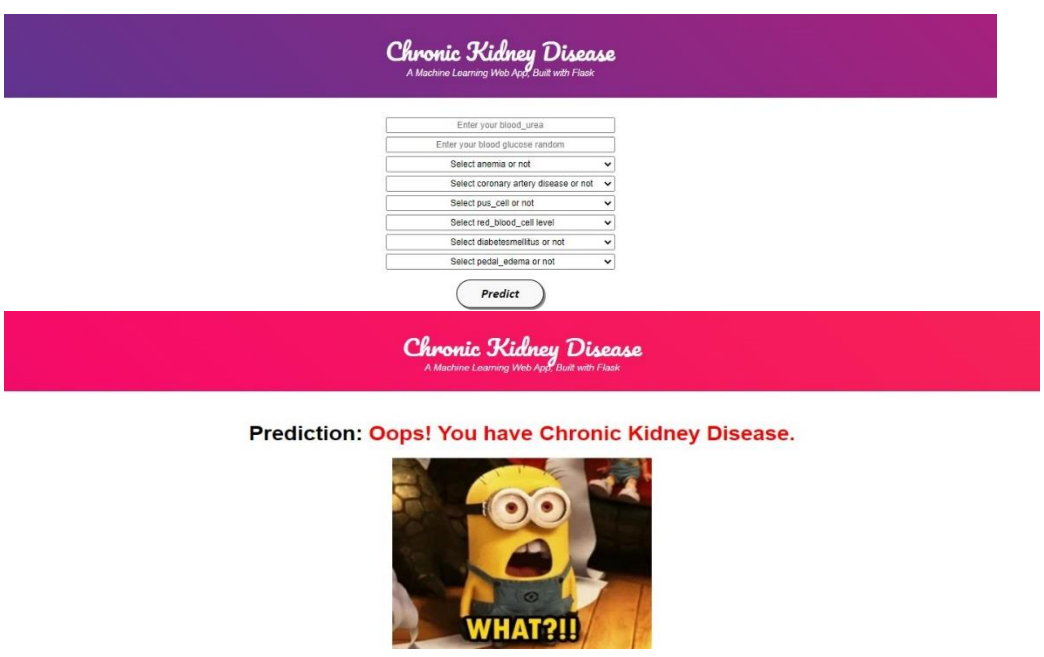
# Activity 2.3: Run the web application

- 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.

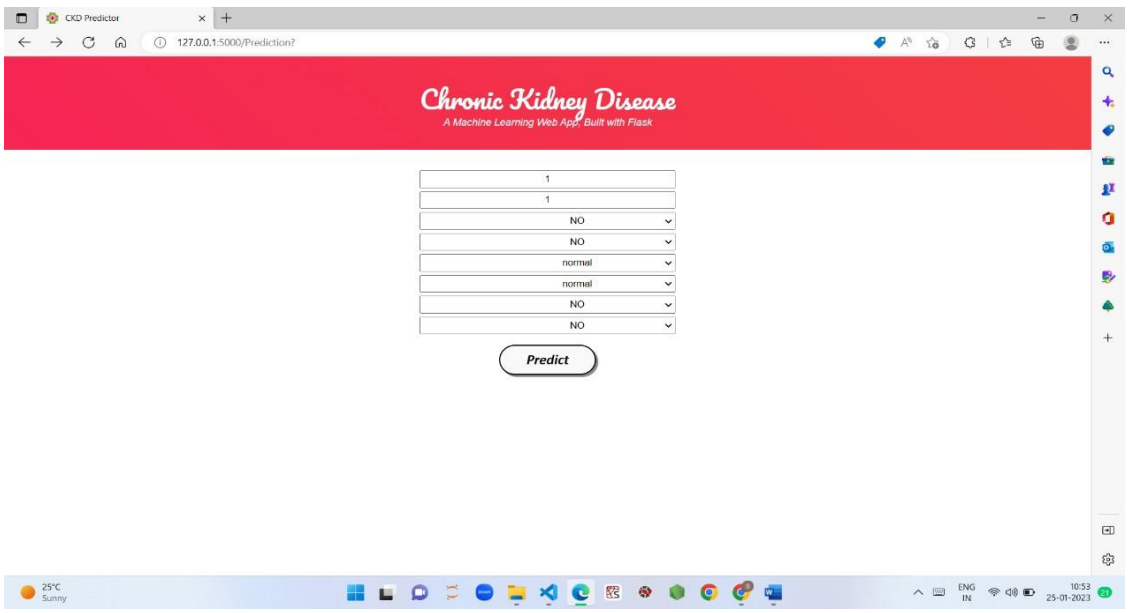
```
(base) D:\SmartBridge\Chronic Kidney Disease>python app.py
 * Serving Flask app "app" (lazy loading)
 * Environment: production
   WARNING: This is a development server. Do not use it in a production deployment.
   Use a production WSGI server instead.
 * Debug mode: off
 * Running on http://127.0.0.1:5000/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

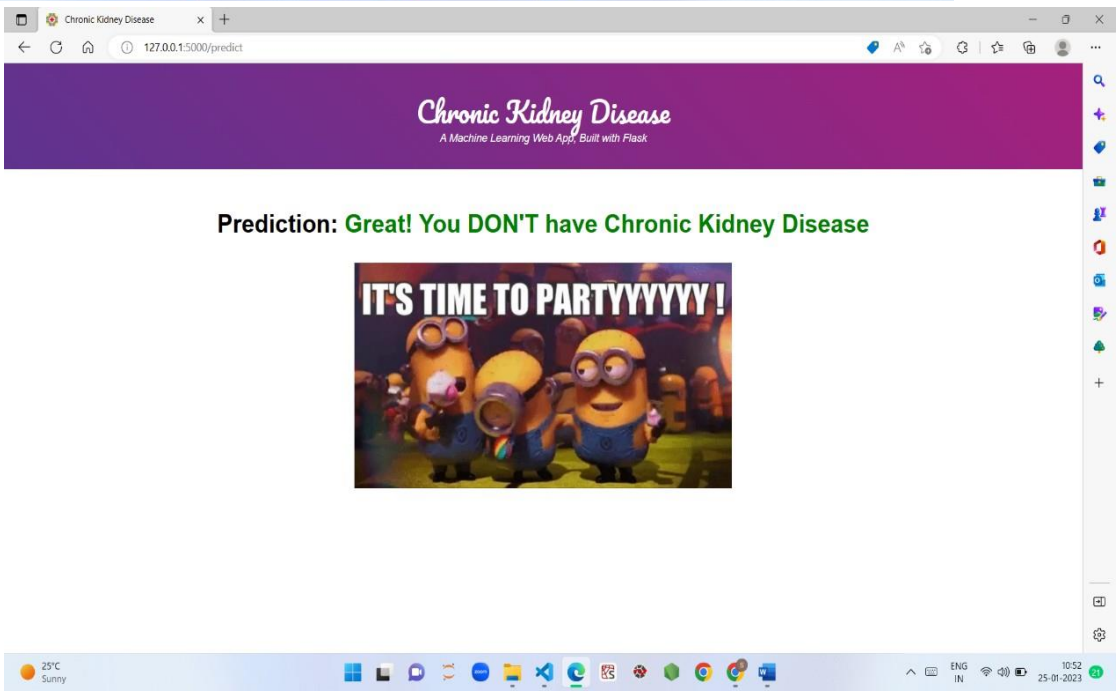
Now,Go the web browser and write the localhost url (http://127.0.0.1:5000) to get the below result




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




# Milestone 7: Project Demonstration & Documentation

Below mentioned deliverables to be submitted along with other deliverables

## Activity 1:- Record explanation Video for project end to end solution

**Activity 2:- Project Documentation-Step by step project developmentprocedure**

Create document as per the template provided