Abstract

Every year, an increasing number of patients are diagnosed with late stages of renal disease. Chronic Kidney Disease, also known as Chronic Renal Disease, is characterized by abnormal kidney function or a breakdown of renal function that progresses over months or years. Chronic kidney disease is often found during screening of persons who are known to be at risk for kidney issues, such as those with high blood pressure or diabetes, and those with a blood family who has chronic kidney disease (CKD). As a result, early prognosis is critical in battling the disease and providing effective therapy. Only early identification and continuous monitoring can avoid serious kidney damage or renal failure. Machine Learning (ML) plays a significant part in the healthcare system, and it may efficiently aid and help with decision support in medical institutions. The primary goals of this research are to design and suggest a machine learning method for predicting CKD. Random Forest (LR), Artificial Neural Network (ANN), and Decision Tree are three master teaching methodologies investigated (DT). The components are built using chronic kidney disease datasets, and the outcomes of these models are compared to select the optimal model for prediction.

Introduction

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.

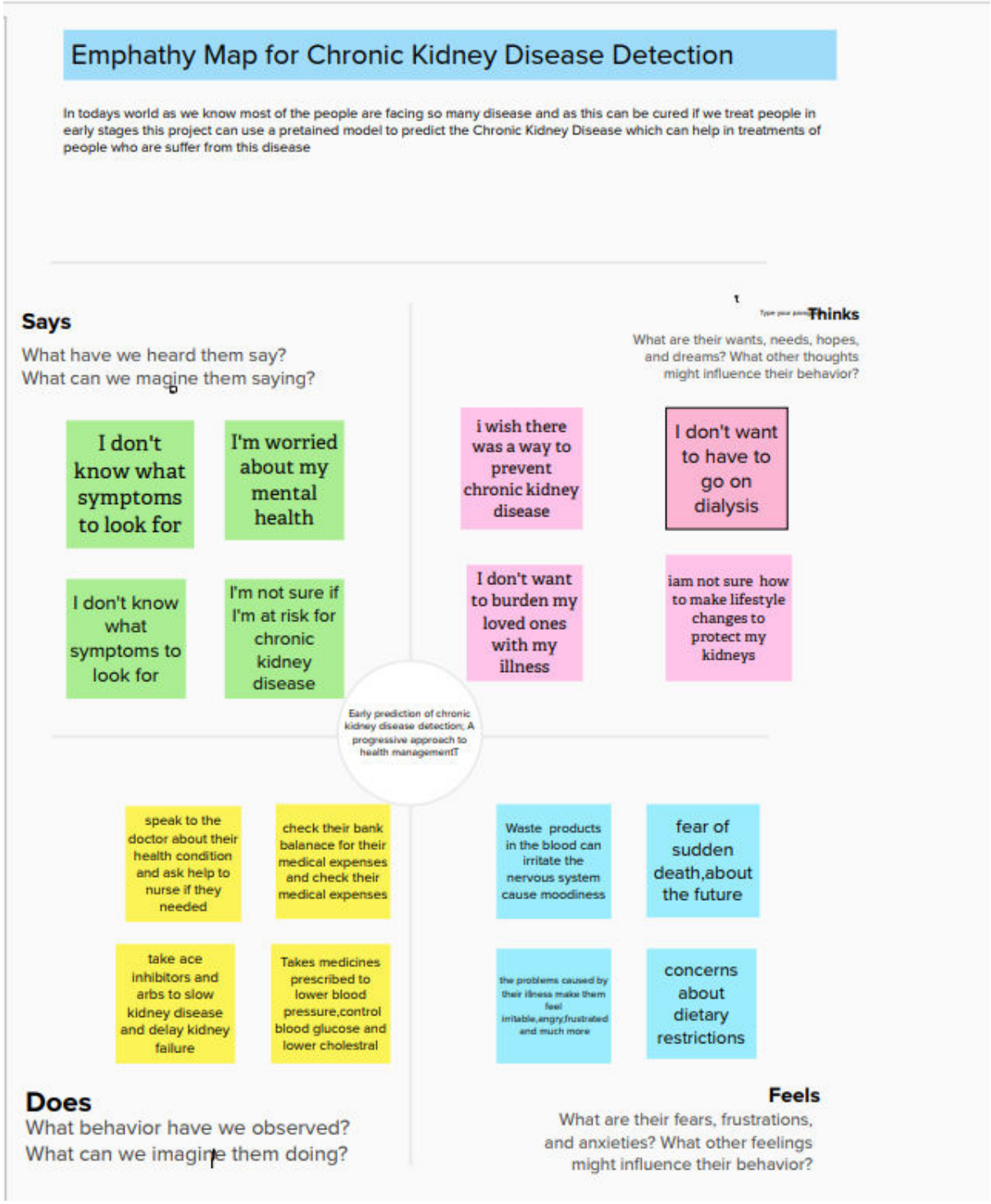
In today world as we know most of the people are facing so many disease and as this can be cured if we treat people in early stages this project can use a pre trained model to predict the Chronic Kidney Disease which can help in treatments of peoples who are suffer from this disease.

Purpose

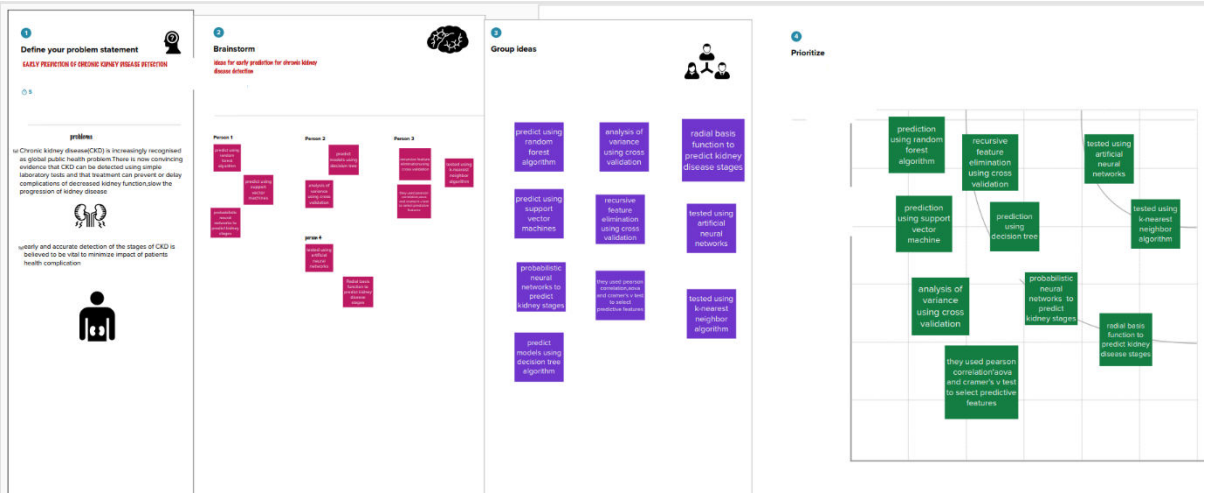
The rationale for testing asymptomatic people for CKD is that earlier detection might allow for the implementation of therapeutic interventions and avoidance of inappropriate exposure to nephrotoxic agents, both of which may slow the progression of CKD to end-stage kidney disease.

Problem Definition & Design Thinking

Empathy Map



Ideation &brainstorming map



Result

The application uses ANN and Naive Bayes Algorithms for classification. The application has Admin module which is the main module to maintain the application. After admin's successful login he can add doctors and receptionists. The receptionist will add the training dataset (old patient) and register's the new patient. Doctor can analyze whether a patient have CKD or not and also determine the CKD stage if patient having CKD. Also, doctors have an option to upload treatment details for particular patient. The patient can view his treatment details by logging in to the application.

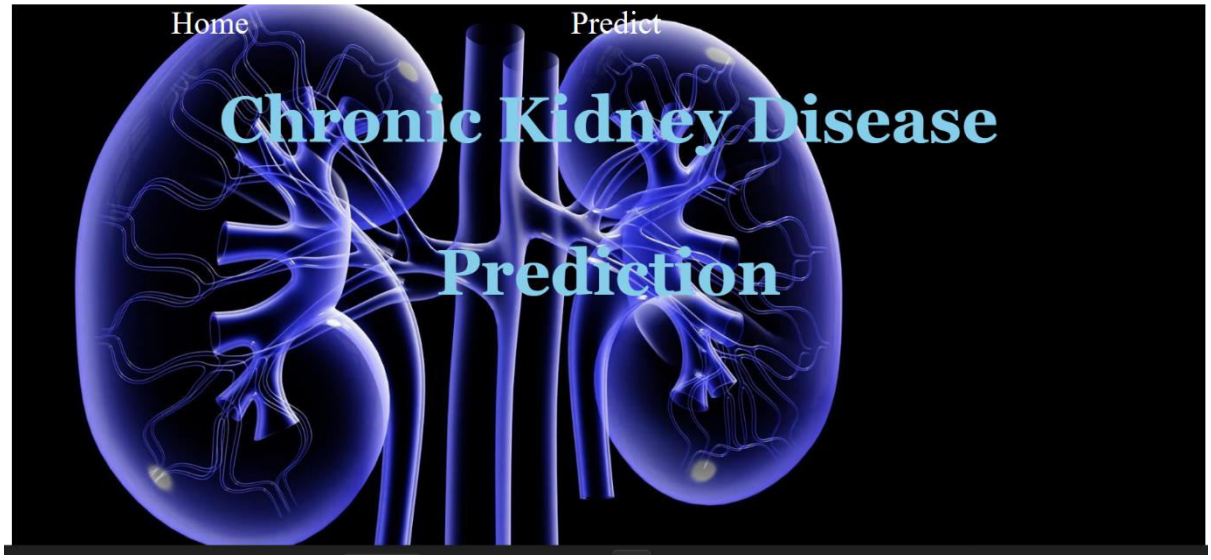
Index.html source code

```
<!DOCTYPE html>
<html lang="en">
<head>
  <meta charset="UTF-8">
  <meta http-equiv="X-UA-Compatible" content="IE=edge">
  <meta name="viewport" content="width=device-width, initial-scale=1.0">
  <title>Home</title>
  <style>
    h1,h2{
      width:100%;
```

```
        height:100px;
        color:skyblue;
        text-align:center;

        text-decoration:none;
        font-family: Georgia, 'Times New Roman', Times, serif;
        font-size: 4em;
      }

      .container{

        background-image: url("https://wallpaperaccess.com/full/5917781.jpg");
        background-size: cover;
        background-position: center;
        height: 100vh;
        width: 100%;

      }
       div a{
        margin: 5em;
       text-align:right;
        font-size: 20px;
        font-size: 2em;
        font-family: 'Times New Roman', Times, serif;
        text-decoration: none;
        color:white;
        min-width:120px;


      }

    </style>
  </head>
```

```
<body>
    <br>


   <div class="container">
      <form action="http://localhost:5000/" method="post">
      <div class="row">
         <div class="col-md-12 bg-light text-right ">
            <a href="home.html" class="home">Home</a>
            <a href="index.html" class="Prediction">Predict</a>
         </div>
      </div>
      <h1 class="head">Chronic Kidney Disease</h1>
      <h2 class="head">Prediction</h2>



   </div>
</body>
</html>
```

OUTPUT



INDEX.HTML SOURCE CODE:

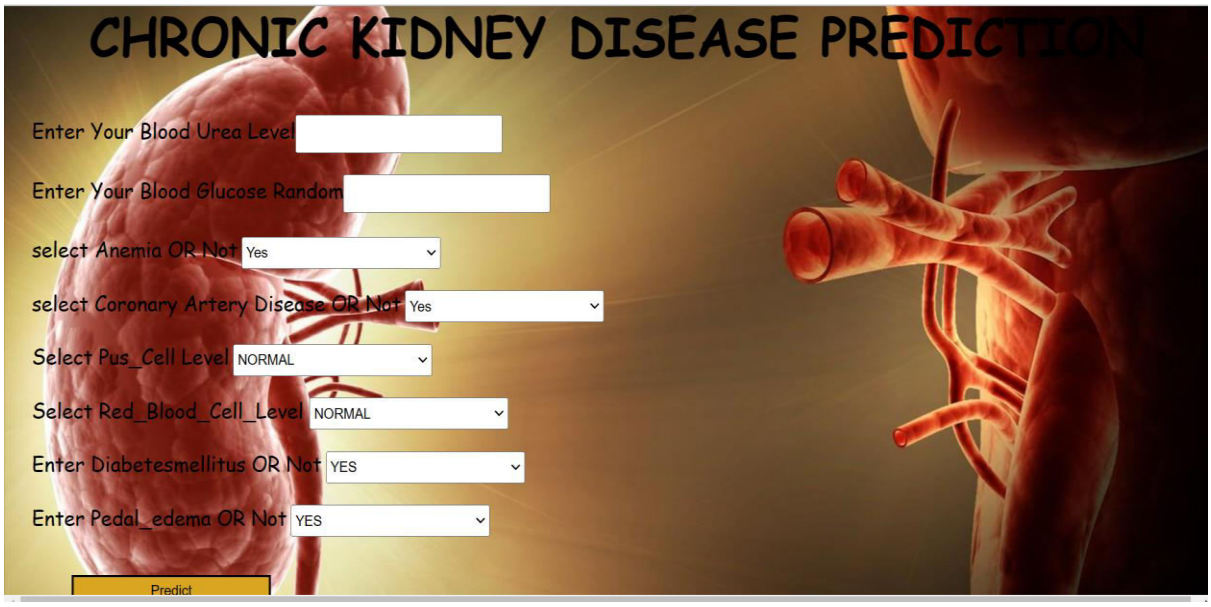
```
<!DOCTYPE html>
<html lang="en">
<head>
    <meta charset="UTF-8">
    <meta http-equiv="X-UA-Compatible" content="IE=edge">
    <meta name="viewport" content="width=device-width, initial-scale=1.0">
    <title>Predict</title>
    <link rel="stylesheet" href="home.html">
    <style>
        body{
            background-image: url("https://wallpaperaccess.com/full/5917783.jpg");
            background-size: cover;
            background-position: center;
            height: 100vh;
            width: 100%;
        }
        .header{
            top: 0;
            width: 100%;
            height: 90px;
            font-family: 'Balsamiq Sans',cursive;
            font-size: 25px;
            font-weight: 800px;
            text-align: center;
        }
        .MAIN p,label{
            font-size: 20px;
            margin-left: 20px;
            font-family: 'Balsamiq Sans',cursive;
```

```
        }
        .MAIN input,select{
            height: 30px;
            width: 200px;
        }
        .MAIN button{
            height: 30px;
            width: 200px;
            margin-left: 60px;
            background-color: #daa520;
        }
        .MAIN b{
            font-size: 20px;
            font-weight: 800px;
            text-align: center;
            font-family: 'Balsamiq Sans',cursive;
            margin-left: 20px;
        }
    </style>
</head>
<body>
    <div class="header">
        <h1>CHRONIC KIDNEY DISEASE PREDICTION</h1>
        </div>
        <div class="MAIN">
            <form action="http://localhost:5000/Prediction" method="post">
                <p> Enter Your Blood Urea Level<span><input type="text" name="urea level"/></span></p>
                <p> Enter Your Blood Glucose Random<span><input type="text"
name="month"/></span></p>


                <label for="anemia or not">select Anemia OR Not</label>
```

```
<select name="anemia or not">
   <option value="1">Yes</option>
   <option value="0">no</option>

</select>
<br><br>
<label for="coronary artery disease or not">select Coronary Artery Disease OR Not</label>
<select name="coronary artery disease or not">
   <option value="1">Yes</option>
   <option value="0">no</option>

</select>
<br><br>
<label for="pus cell ">Select Pus_Cell Level</label>
<select name="pus cell ">
   <option value="0">NORMAL</option>
   <option value="1">ABNORMAL</option>
</select>
<br><br>
<label for="red blood cell level">Select Red_Blood_Cell_Level </label>
<select name="red blood cell level">
   <option value="0">NORMAL</option>
   <option value="1">ABNORMAL</option>


</select>
<br><br>
<label for=" diabetesmellitus or not">Enter Diabetesmellitus OR Not</label>
<select name="diabetesmellitus or not">
   <option value="1">YES</option>
   <option value="0">NO</option>
```

```
            </select>
            <br><br>
            <label for="pedal_edema or not">Enter Pedal_edema OR Not</label>
            <select name="pedal_edema or not">
               <option value="0">YES</option>
               <option value="1">NO</option>

            </select>
            <br>
            <br>
            <br>
            <div class="form-btn">
               <button  href="result.html"class="predict-btn" >Predict</button>
            </div>
         </form>
      </div>
</body>
</html>
```

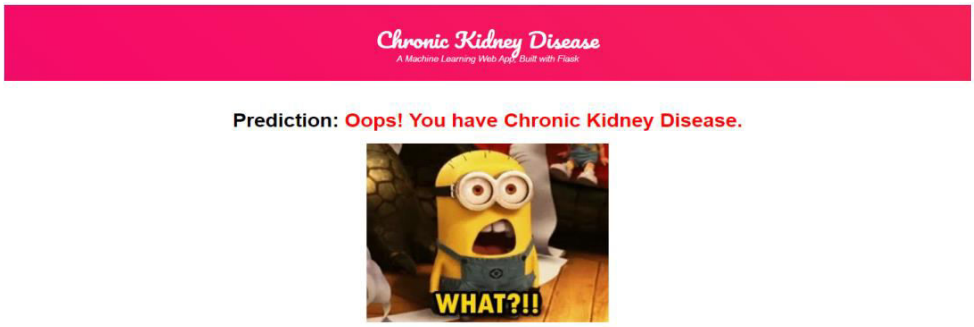
OUTPUT

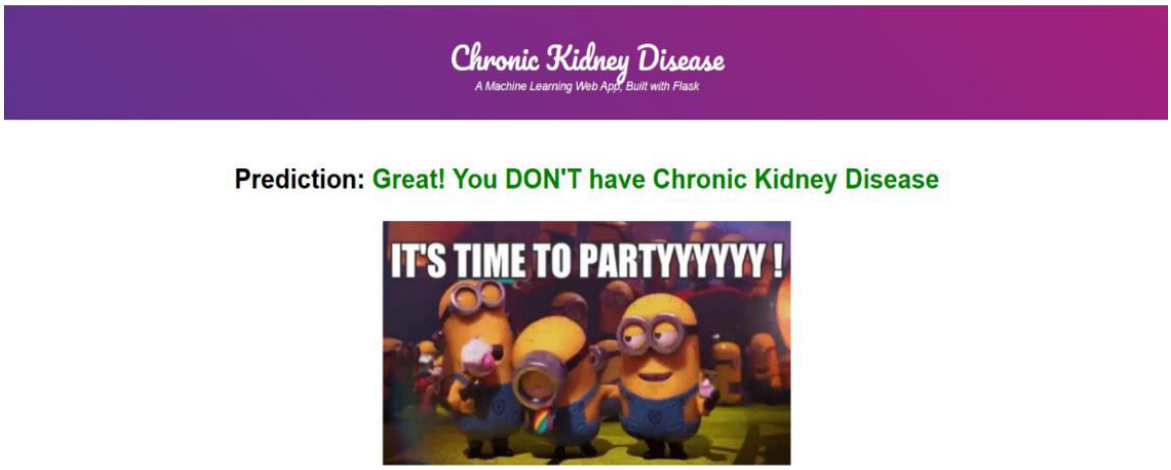


RESULT.HTML SOURCE CODE

```
<html lang ="en" dir="ltr">
  <head>
    <meta charset="utf-8">
    <title>Chronic Kidney Disease</title>
    <link rel="shortcuthref="{{url_for('static',filename='diabetesfavicon.ico') }}">
    <script src="https://kit.fontawesome.com/5f3f547070.js" crossorigin="anonymous"></script>
    <link href="https://fonts.googleapis.com/css2?family=Pacifico&display=swap" rel="stylesheet">
  </head>

  <body>

    <!--Website Title-->
    <div class="container">
      <h2 class='container-heading'><span class="heading_font">Chronic Kidney Disease</span></h2>
      <div class='description'>
        <p>A Machine Learning Web App,Built with Flask</p>
      </div>
    </div>

    <!--Result-->
    <div class="results">
      {% if prediction_text==1 %}
        <h1>Prediction: <span class= 'danger'>Oops! You have Chronic Kidney Disease.</span></h1>
        <img class="gif" src="{{ url_for('static',filename='diabetes.webp') }}" alt="Diabetes Image">
      {%elif prediction_text==0 %}
        <h1>Prediction: <span class= 'safe'>Great! You DON'T have Chronic Kidney Disease</span></h1>
        <img class="gif1" src="{{url_for('static', filename='no-diabetes.webp') }}" alt="Not Diabetes">
      {% endif %}
    </div>
  </body>
 </html>
```

OUTPUT


Chronic Kidney Disease
A Machine Learning Web App, Built with Flask
Prediction: Oops! You have Chronic Kidney Disease.
WHAT?!!


Chronic Kidney Disease
A Machine Learning Web App, Built with Flask
Prediction: Great! You DON'T have Chronic Kidney Disease
IT'S TIME TO PARTYYYYYY !

Advantages

- The early detection of CKD allows patients to receive timely treatment, slowing the disease's progression. Due to its rapid recognition performance and accuracy, machine learning models can effectively assist physicians in achieving this goal.
- Your kidneys act like a filter to remove wastes and extra fluid from your body. Your kidneys filter about 200 quarts of blood each day to make about 1 to 2 quarts of urine. The urine contains wastes and extra fluid. This prevents buildup of wastes and fluid to keep your body healthy.

Disadvantage

- Having CKD increases the chances of having heart disease and stroke.
- Managing high blood pressure, blood sugar, and cholesterol levels—all factors that increase the risk for heart disease and stroke—is very important for people with CKD.

Application

Predictive analytics using machine learning helps detect fraudulent activities in the financial sector. Fraudulent transactions are identified by training machine learning algorithms with past datasets. The models find risky patterns in these datasets and learn to predict and deter fraud.

Conclusion

- This project is a medical sector application which helps the medical practitioners in predicting the CKD disease based on the CKD parameters. It is automation for CKD disease prediction and **it identifies** the disease, its stages in an efficient and economically manner
- It is successfully accomplished by applying the ANN for classification. This classification technique comes under data mining technology. This algorithm takes CKD parameters as input and predicts the disease based on old CKD patient's data.

Future scope

The work will be considered as basement for the healthcare system for CKD patients. Also extension to this work is that implementation of deep learning since deep learning provides high-quality performance than machine learning algorithm.

Appenix

Source Code

Milestone 2:

```
import pandas as pd
import numpy as np
from collections import Counter as c
import matplotlib.pyplot as plt
import seaborn as sns
import missingno as msno
from sklearn.metrics import accuracy_score,confusion_matrix
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.linear_model import LogisticRegression
import pickle
```

Read the data set

```
data=pd.read_csv("/content/kidney_disease.csv")
data.head()
```

	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.columns
```

```
Index(['id', '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=['id','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']
data.columns
```

```
Index(['id', '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')
```

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 26 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   id                        400 non-null    int64
 1   age                       391 non-null    float64
 2   blood_pressure            388 non-null    float64
 3   specific_gravity          353 non-null    float64
 4   albumin                   354 non-null    float64
 5   sugar                     351 non-null    float64
 6   red_blood_cells           248 non-null    object
 7   pus_cell                  335 non-null    object
 8   pus_cell_clumps           396 non-null    object
 9   bacteria                  396 non-null    object
 10  blood glucose random      356 non-null    float64
 11  blood_urea                381 non-null    float64
 12  serum_creatinine          383 non-null    float64
 13  sodium                    313 non-null    float64
 14  potassium                 312 non-null    float64
 15  hemoglobin                348 non-null    float64
 16  packed_cell_volume        330 non-null    object
 17  white_blood_cell_count    295 non-null    object
 18  red_blood_cell_count      270 non-null    object
 19  hypertension              398 non-null    object
 20  diabetesmellitus          398 non-null    object
 21  coronary_artery_disease   398 non-null    object
 22  appetite                  399 non-null    object
 23  pedal_edema               399 non-null    object
 24  anemia                    399 non-null    object
 25  class                     400 non-null    object
dtypes: float64(11), int64(1), object(14)
memory usage: 81.4+ KB
```

```
data.isnull().any()
```

```
id                          False
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'].mode()[0],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['potassium'].fillna(data['potassium'].mean(),inplace=True)
data['packed_cell_volume'].fillna(data['packed_cell_volume'].mode()[0],inplace=True)
data['red_blood_cell_count'].fillna(data['red_blood_cell_count'].mode()[0],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'].mode()[0],inplace=True)
data['age'].fillna(data['age'].mean(),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'].mean(),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'].mean(),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'].mean(),inplace=True)
```

```
catcols=set(data.dtype[data.dtypes=='O'].index.values)
print(catcols)
```

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

```
for i in catcols:
  print("columns :",i)
  print(c(data[i]))
```

```
print('*'*120+'\n')
```

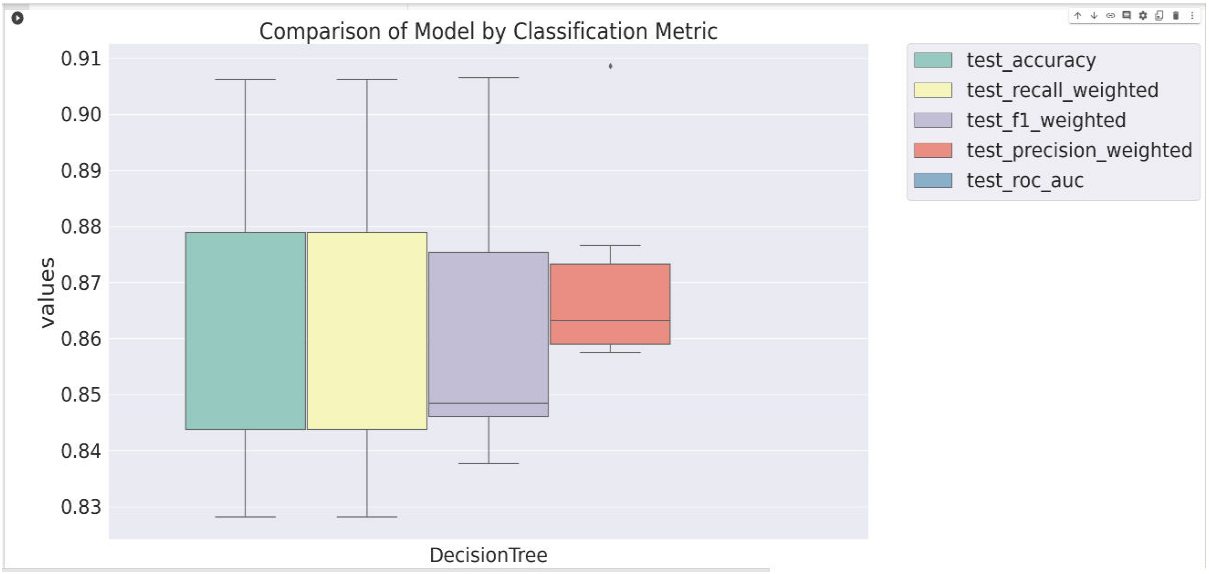
```
columns : diabetesmellitus
Counter({'no': 260, 'yes': 134, '\tno': 3, '\tyes': 2, ' yes': 1})
************************************************************************************************************************

columns : hypertension
Counter({'no': 253, 'yes': 147})
************************************************************************************************************************

columns : coronary_artery_disease
Counter({'no': 364, 'yes': 34, '\tno': 2})
************************************************************************************************************************

columns : pedal_edema
Counter({'no': 324, 'yes': 76})
************************************************************************************************************************

columns : anemia
Counter({'no': 340, 'yes': 60})
************************************************************************************************************************

columns : red_blood_cells
Counter({'normal': 353, 'abnormal': 47})
************************************************************************************************************************
```

```
columns : white_blood_cell_count
Counter({'9800': 116, '6700': 10, '9600': 9, '9200': 9, '7200': 9, '6900': 8, '11000': 8, '5800': 8, '7800': 7, '9100': 7, '9400': 7, '7000': 7, '4300': 6, '6300'
************************************************************************************************************************

columns : packed_cell_volume
Counter({'41': 91, '52': 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
************************************************************************************************************************

columns : red_blood_cell_count
Counter({'5.2': 148, '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':
************************************************************************************************************************

columns : appetite
Counter({'good': 318, 'poor': 82})
************************************************************************************************************************

columns : class
Counter({'ckd': 248, 'notckd': 150, 'ckd\t': 2})
************************************************************************************************************************

columns : bacteria
Counter({'notpresent': 378, 'present': 22})
************************************************************************************************************************

columns : pus_cell
Counter({'normal': 324, 'abnormal': 76})
************************************************************************************************************************
```

```
catcols.remove('red_blood_cell_count')
catcols.remove('packed_cell_volume')
catcols.remove('white_blood_cell_count')
print(catcols)
```

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

```
catcols={'anemia','pedal_edema','appetite','bacteria','class',
'coronary_artery_disease','diabetesmellitus','hypertension','p
us_cell','pus_cell_clumps','red_blood_cells'}
```



Milestone6

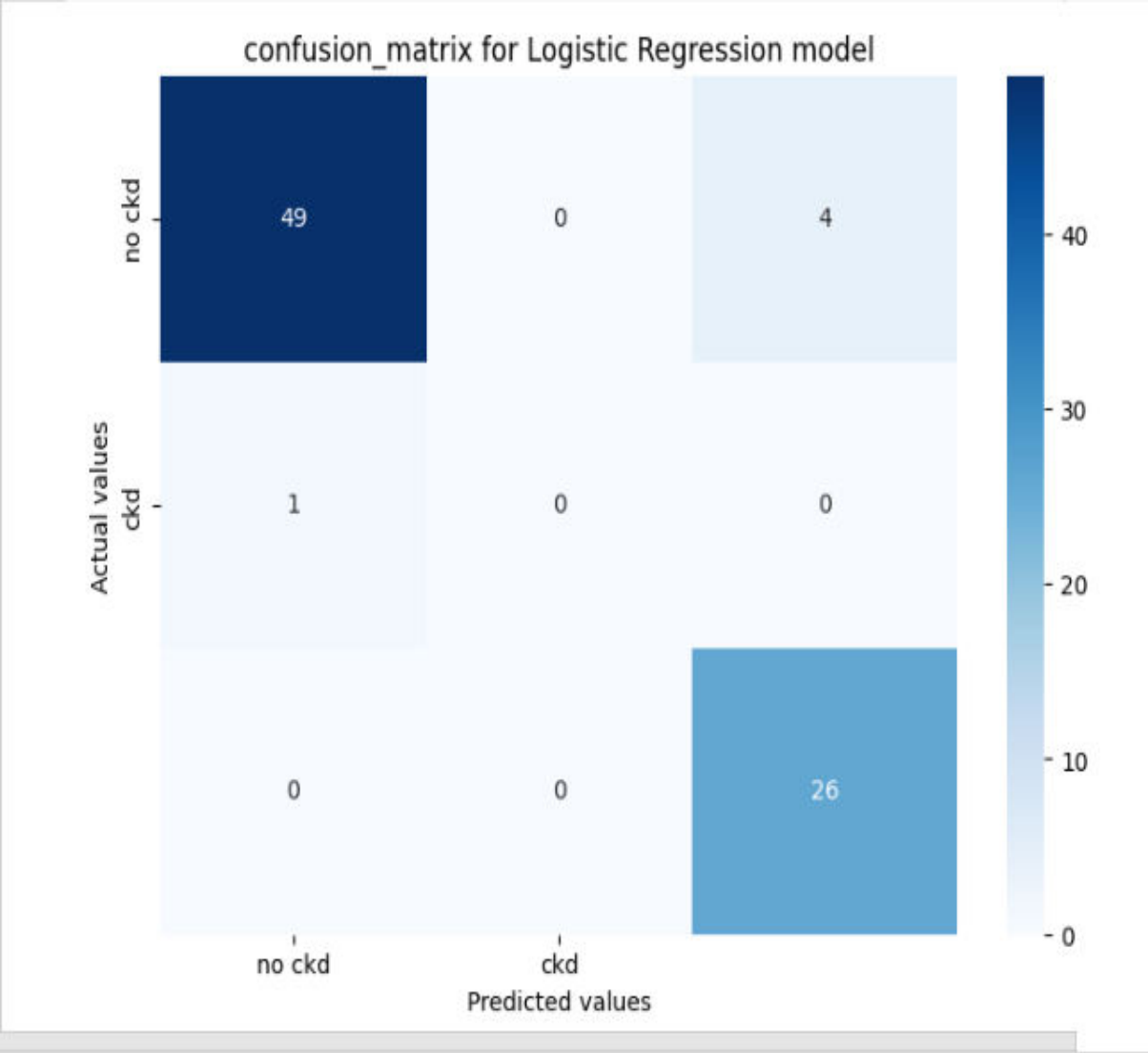
```
pickle.dump(lgr, open('ckd.pkl','wb'))

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

app = Flask('_name_')
model = pickle.load(open('ckd.pkl', 'rb'))

@app.route('/')
def home():
    return render_template('home.html')

@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'])
def predict():
    input_features=[float(x) for x in request.form.values()]
    features_values=[np.array(input_features)]

    features_name=['blood_urea','blood glucose random', 'anemi
a',
                   'coronary_artery_disease', 'pus_cell', 'red
_blood_cells',
                   'diabetesmellitus', 'pedal_edema']
    df=pd.DataFrame(features_value, columns=fetures_name)
    output=model.predict(df)
```

```
[]
              precision    recall  f1-score   support

      NO CKD       0.98      0.92      0.95        53
         CKD       0.00      0.00      0.00         1
         CKD       0.87      1.00      0.93        26

    accuracy                           0.94        80
   macro avg       0.62      0.64      0.63        80
weighted avg       0.93      0.94      0.93        80
```

```
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']

results_long_nofit = results_long.loc[~results_long['metrics'].isin(time_me
trics)]
results_long_nofit = results_long_nofit.sort_values(by='values')

results_long_fit = results_long.loc[results_long['metrics'].
isin(time_metrics)]
results_long_fit = results_long_fit.sort_values(by='values')

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=resul
ts_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)
```

```
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()
```




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

```
          ('LogReg', LogisticRegression()),
          ('RF', RandomForestClassifier()),
          ('DecisionTree', DecisionTreeClassifier()),
         ]
results = []
names = []
scoring = ['accuracy','precision_weighted','recall_weighted','f1_weight
ed','roc_auc']
target_names = ['NO CKD','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_t
rain, cv=kfold, scoring=scoring)
        clf = model.fit(x_train, y_train)
        y_pred = clf.predict(x_test)
        print(names)
        print(classification_report(y_test, y_pred, target_names=target
_names))
        results.append(cv_results)
        names.append(names)
        this_df = pd.DataFrame(cv_results)
        this_df['model'] = name
dfs.append(this_df)
final = pd.concat(dfs, ignore_index=True)
print(final)
```

```
   []
                 precision    recall  f1-score   support

        NO CKD       0.98      0.92      0.95        53
           CKD       0.00      0.00      0.00         1
           CKD       0.87      1.00      0.93        26

      accuracy                           0.94        80
     macro avg       0.62      0.64      0.63        80
  weighted avg       0.93      0.94      0.93        80
```

```
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_predict)
cm
```

```
  array([[49, 0, 4], [ 1, 0, 0], [ 0, 0, 26]])
```

```
plt.figure(figsize=(8,6))
```

```
      array([[ True], [ True], [False], [ True], [ True], [ True],
[False], [False], [ True], [False], [False], [ True], [ True], [ True],
[False], [False], [False], [ True], [ True], [False], [ True], [ True],
[False], [ True], [False], [ True], [False], [ True], [ True], [ True],
[False], [ True], [ True], [False], [False], [ True], [ True], [ True],
[ True], [ True], [ True], [ True], [False], [False], [False], [ True],
[False], [ True], [ True], [ True], [ True], [False], [False], [ True],
[False], [ True], [False], [ True], [ True], [False], [False], [ True],
[ True], [False], [ True], [ True], [ True], [ True], [ True], [ True],
[ True], [False], [ True], [ True], [ True], [False], [False], [ True],
[ True], [ True]])
```

```
def predict_exit(sample_value):
  sample_value = np.array(sample_value)
  sample_value = sample_value.reshape(1,-1)
  sample_value = sc.transform(sample_value)
  return classifier.predict(sample_value)
```

```
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.')
```

```
prediction: High chance of CKD!
```

Milestone5

```
from sklearn import model_selection
```

```
dfs = []
models = [
```

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

[2]
array([2])

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

[2]
array([2])

```
y_pred = rfc.predict([[1,1,121.000000,36.0,0,0,1,0]])
print(y_pred)
(y_pred)
```

[2]
array([2])

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

```
y_pred = classification.predict(x_test)
```

```
y_pred
```

```
   array([[1.], [1.], [0.], [1.], [1.], [1.], [0.], [0.], [1.], [0.],
[0.], [1.], [1.], [1.], [0.], [0.], [0.], [1.], [1.], [0.], [1.], [1.],
[0.], [1.], [0.], [1.], [0.], [1.], [1.], [1.], [0.], [1.], [1.], [0.],
[0.], [1.], [1.], [1.], [1.], [1.], [1.], [1.], [0.], [0.], [0.], [1.],
[0.], [1.], [1.], [1.], [1.], [0.], [0.], [1.], [0.], [1.], [0.], [1.],
[1.], [0.], [0.], [1.], [1.], [0.], [1.], [1.], [1.], [1.], [1.], [1.],
[1.], [0.], [1.], [1.], [1.], [0.], [0.], [1.], [1.], [1.]],
dtype=float32)
```

```
y_pred = (y_pred > 0.5)
y_pred
```

```
from sklearn.tree import DecisionTreeClassifier
dtc = DecisionTreeClassifier(max_depth=4,splitter='best',criterion=
'entropy')
```

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

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

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

```
array([0, 0, 0, 0, 2, 0, 0, 0, 2, 0, 0, 0, 2, 2, 0, 0, 0, 2, 2, 0,
2, 2, 0, 2, 0, 2, 0, 0, 2, 0, 0, 2, 0, 0, 0, 0, 2, 0, 0, 2, 0, 2, 0, 0,
0, 2, 0, 2, 2, 2, 0, 0, 0, 2, 0, 0, 0, 2, 2, 0, 0, 2, 2, 0, 0, 0, 0, 2,
0, 2, 2, 0, 2, 2, 0, 0, 0, 2, 2, 2])
```

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

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

```
LogisticRegression
LogisticRegression()
```

```
from sklearn.metrics import accuracy_score,classification_report
y_predict = lgr.predict(x_test)
```

```
Epoch 90/100
26/26 [==============================] - 0s 4ms/step - loss: -2573623.7500 - accuracy: 0.3281 -
val_loss: -1115827.0000 - val_accuracy: 0.3125
Epoch 91/100
26/26 [==============================] - 0s 4ms/step - loss: -2788516.0000 - accuracy: 0.3281 -
val_loss: -1196266.7500 - val_accuracy: 0.3125
Epoch 92/100
26/26 [==============================] - 0s 4ms/step - loss: -2952012.5000 - accuracy: 0.3047 -
val_loss: -1324442.0000 - val_accuracy: 0.3125
Epoch 93/100
26/26 [==============================] - 0s 4ms/step - loss: -3128123.0000 - accuracy: 0.3516 -
val_loss: -1426936.6250 - val_accuracy: 0.3125
Epoch 94/100
26/26 [==============================] - 0s 4ms/step - loss: -3381758.5000 - accuracy: 0.3164 -
val_loss: -1401845.7500 - val_accuracy: 0.2969
Epoch 95/100
26/26 [==============================] - 0s 4ms/step - loss: -3559427.0000 - accuracy: 0.2891 -
val_loss: -1621283.5000 - val_accuracy: 0.3594
Epoch 96/100
26/26 [==============================] - 0s 4ms/step - loss: -3747214.0000 - accuracy: 0.3398 -
val_loss: -1494436.6250 - val_accuracy: 0.2969
Epoch 97/100
26/26 [==============================] - 0s 4ms/step - loss: -3934591.7500 - accuracy: 0.3086 -
val_loss: -1859112.1250 - val_accuracy: 0.3281
Epoch 98/100
26/26 [==============================] - 0s 4ms/step - loss: -4253708.0000 - accuracy: 0.3242 -
val_loss: -1956884.5000 - val_accuracy: 0.3281
Epoch 99/100
26/26 [==============================] - 0s 4ms/step - loss: -4342637.5000 - accuracy: 0.3008 -
val_loss: -1859389.1250 - val_accuracy: 0.4219
Epoch 100/100
26/26 [==============================] - 0s 4ms/step - loss: -4647518.5000 - accuracy: 0.3086 -
val_loss: -2204960.2500 - val_accuracy: 0.3281
<keras.callbacks.History at 0x7fac27917af0>
```

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

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

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

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

```
Epoch 70/100
26/26 [==============================] - 0s 4ms/step - loss: -476310.2188 - accuracy: 0.3398 -
val_loss: -205862.0469 - val_accuracy: 0.2969
Epoch 71/100
26/26 [==============================] - 0s 5ms/step - loss: -512368.0938 - accuracy: 0.2969 -
val_loss: -248088.7344 - val_accuracy: 0.3750
Epoch 72/100
26/26 [==============================] - 0s 4ms/step - loss: -592021.3125 - accuracy: 0.3281 -
val_loss: -258929.8750 - val_accuracy: 0.2969
Epoch 73/100
26/26 [==============================] - 0s 4ms/step - loss: -630349.8750 - accuracy: 0.2930 -
val_loss: -294555.1250 - val_accuracy: 0.4062
Epoch 74/100
26/26 [==============================] - 0s 4ms/step - loss: -712402.6250 - accuracy: 0.3047 -
val_loss: -323334.4062 - val_accuracy: 0.3438
Epoch 75/100
26/26 [==============================] - 0s 4ms/step - loss: -801394.6875 - accuracy: 0.3398 -
val_loss: -327954.4375 - val_accuracy: 0.2969
Epoch 76/100
26/26 [==============================] - 0s 4ms/step - loss: -861479.0000 - accuracy: 0.3047 -
val_loss: -346356.1562 - val_accuracy: 0.2969
Epoch 77/100
26/26 [==============================] - 0s 4ms/step - loss: -934881.6875 - accuracy: 0.3164 -
val_loss: -435822.5625 - val_accuracy: 0.3281
Epoch 78/100
26/26 [==============================] - 0s 4ms/step - loss: -1051332.7500 - accuracy: 0.3125 -
val_loss: -502227.8125 - val_accuracy: 0.3281
Epoch 79/100
26/26 [==============================] - 0s 4ms/step - loss: -1146265.2500 - accuracy: 0.3086 -
val_loss: -526691.1250 - val_accuracy: 0.3281
Epoch 80/100
26/26 [==============================] - 0s 4ms/step - loss: -1269717.7500 - accuracy: 0.3164 -
val_loss: -534240.1250 - val_accuracy: 0.2969
Epoch 81/100
26/26 [==============================] - 0s 4ms/step - loss: -1367591.5000 - accuracy: 0.2930 -
val_loss: -630709.0625 - val_accuracy: 0.3281
Epoch 82/100
26/26 [==============================] - 0s 4ms/step - loss: -1376455.7500 - accuracy: 0.3594 -
val_loss: -570607.4375 - val_accuracy: 0.2969
Epoch 83/100
26/26 [==============================] - 0s 5ms/step - loss: -1475926.5000 - accuracy: 0.3320 -
val_loss: -733813.8750 - val_accuracy: 0.3281
Epoch 84/100
26/26 [==============================] - 0s 4ms/step - loss: -1736667.2500 - accuracy: 0.2930 -
val_loss: -786050.1875 - val_accuracy: 0.3281
Epoch 85/100
26/26 [==============================] - 0s 4ms/step - loss: -1801545.3750 - accuracy: 0.3125 -
val_loss: -843021.3125 - val_accuracy: 0.3281
Epoch 86/100
26/26 [==============================] - 0s 4ms/step - loss: -2006606.0000 - accuracy: 0.3555 -
val_loss: -761527.0000 - val_accuracy: 0.2969
Epoch 87/100
26/26 [==============================] - 0s 4ms/step - loss: -1988779.5000 - accuracy: 0.2969 -
val_loss: -917298.3125 - val_accuracy: 0.4062
Epoch 88/100
26/26 [==============================] - 0s 4ms/step - loss: -2198979.5000 - accuracy: 0.2891 -
val_loss: -997340.6250 - val_accuracy: 0.4062
Epoch 89/100
26/26 [==============================] - 0s 5ms/step - loss: -2370956.7500 - accuracy: 0.3125 -
val_loss: -1072312.0000 - val_accuracy: 0.3594
```

```
Epoch 50/100
26/26 [==============================] - 0s 4ms/step - loss: -26196.3574 - accuracy: 0.3281 -
val_loss: -12007.9863 - val_accuracy: 0.3281
Epoch 51/100
26/26 [==============================] - 0s 5ms/step - loss: -31911.7598 - accuracy: 0.3125 -
val_loss: -12461.4434 - val_accuracy: 0.4219
Epoch 52/100
26/26 [==============================] - 0s 4ms/step - loss: -41101.1367 - accuracy: 0.3398 -
val_loss: -16585.0547 - val_accuracy: 0.3125
Epoch 53/100
26/26 [==============================] - 0s 4ms/step - loss: -48644.7617 - accuracy: 0.3203 -
val_loss: -18620.9883 - val_accuracy: 0.3125
Epoch 54/100
26/26 [==============================] - 0s 4ms/step - loss: -58008.2969 - accuracy: 0.2852 -
val_loss: -25147.3516 - val_accuracy: 0.3438
Epoch 55/100
26/26 [==============================] - 0s 4ms/step - loss: -69741.4141 - accuracy: 0.3281 -
val_loss: -31293.5098 - val_accuracy: 0.3438
Epoch 56/100
26/26 [==============================] - 0s 4ms/step - loss: -82555.2578 - accuracy: 0.3281 -
val_loss: -30401.0469 - val_accuracy: 0.2812
Epoch 57/100
26/26 [==============================] - 0s 4ms/step - loss: -97163.6406 - accuracy: 0.2930 -
val_loss: -41751.3516 - val_accuracy: 0.3125
Epoch 58/100
26/26 [==============================] - 0s 4ms/step - loss: -115082.7422 - accuracy: 0.3164 -
val_loss: -48524.1133 - val_accuracy: 0.3438
Epoch 59/100
26/26 [==============================] - 0s 4ms/step - loss: -122187.7734 - accuracy: 0.3359 -
val_loss: -60370.7695 - val_accuracy: 0.3750
Epoch 60/100
26/26 [==============================] - 0s 4ms/step - loss: -144334.0625 - accuracy: 0.2969 -
val_loss: -71876.5156 - val_accuracy: 0.3125
Epoch 61/100
26/26 [==============================] - 0s 4ms/step - loss: -159226.1562 - accuracy: 0.3320 -
val_loss: -63945.5625 - val_accuracy: 0.2969
Epoch 62/100
26/26 [==============================] - 0s 4ms/step - loss: -187995.3281 - accuracy: 0.3047 -
val_loss: -81384.0859 - val_accuracy: 0.2969
Epoch 63/100
26/26 [==============================] - 0s 4ms/step - loss: -221094.8125 - accuracy: 0.3125 -
val_loss: -95184.6328 - val_accuracy: 0.3906
Epoch 64/100
26/26 [==============================] - 0s 5ms/step - loss: -235971.0312 - accuracy: 0.3125 -
val_loss: -88253.0938 - val_accuracy: 0.4219
Epoch 65/100
26/26 [==============================] - 0s 4ms/step - loss: -261264.7031 - accuracy: 0.3125 -
val_loss: -102569.3047 - val_accuracy: 0.4219
Epoch 66/100
26/26 [==============================] - 0s 4ms/step - loss: -295232.5312 - accuracy: 0.3320 -
val_loss: -131853.0625 - val_accuracy: 0.3438
Epoch 67/100
26/26 [==============================] - 0s 4ms/step - loss: -346577.7500 - accuracy: 0.3203 -
val_loss: -150731.5469 - val_accuracy: 0.3438
Epoch 68/100
26/26 [==============================] - 0s 5ms/step - loss: -378144.5938 - accuracy: 0.3203 -
val_loss: -173653.5000 - val_accuracy: 0.3438
Epoch 69/100
26/26 [==============================] - 0s 4ms/step - loss: -437493.9062 - accuracy: 0.2969 -
val_loss: -185766.8281 - val_accuracy: 0.4062
```

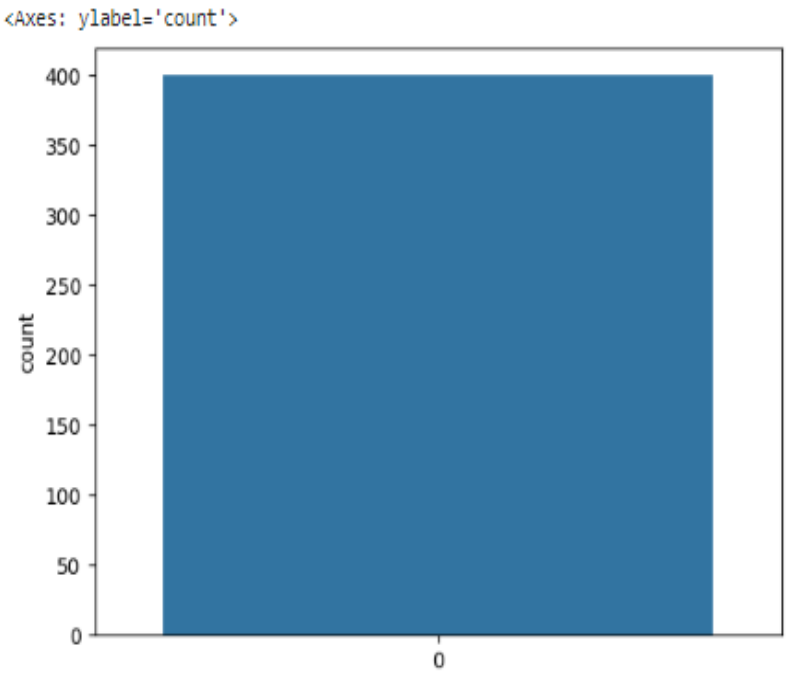
```
Epoch 30/100
26/26 [==============================] - 0s 4ms/step - loss: -32.7403 - accuracy: 0.3359 - val_loss:
4.2639 - val_accuracy: 0.2031
Epoch 31/100
26/26 [==============================] - 0s 4ms/step - loss: -47.5475 - accuracy: 0.2930 - val_loss: -
20.2726 - val_accuracy: 0.3438
Epoch 32/100
26/26 [==============================] - 0s 4ms/step - loss: -35.1881 - accuracy: 0.3242 - val_loss:
13.0977 - val_accuracy: 0.2031
Epoch 33/100
26/26 [==============================] - 0s 5ms/step - loss: -95.2867 - accuracy: 0.3008 - val_loss: -
51.0965 - val_accuracy: 0.3750
Epoch 34/100
26/26 [==============================] - 0s 4ms/step - loss: -167.9017 - accuracy: 0.3008 - val_loss:
-87.6063 - val_accuracy: 0.3438
Epoch 35/100
26/26 [==============================] - 0s 4ms/step - loss: -271.6215 - accuracy: 0.3164 - val_loss:
-101.2619 - val_accuracy: 0.3438
Epoch 36/100
26/26 [==============================] - 0s 4ms/step - loss: -390.8019 - accuracy: 0.3125 - val_loss:
-184.3765 - val_accuracy: 0.3281
Epoch 37/100
26/26 [==============================] - 0s 4ms/step - loss: -676.4297 - accuracy: 0.3203 - val_loss:
-208.3688 - val_accuracy: 0.2969
Epoch 38/100
26/26 [==============================] - 0s 4ms/step - loss: -674.3459 - accuracy: 0.3047 - val_loss:
-285.3145 - val_accuracy: 0.4531
Epoch 39/100
26/26 [==============================] - 0s 4ms/step - loss: -1415.9741 - accuracy: 0.3281 -
val_loss: -602.9527 - val_accuracy: 0.3281
Epoch 40/100
26/26 [==============================] - 0s 4ms/step - loss: -2186.7444 - accuracy: 0.3125 -
val_loss: -626.8016 - val_accuracy: 0.2500
Epoch 41/100
26/26 [==============================] - 0s 4ms/step - loss: -2038.4053 - accuracy: 0.3047 -
val_loss: 224.6841 - val_accuracy: 0.2188
Epoch 42/100
26/26 [==============================] - 0s 5ms/step - loss: -4294.9565 - accuracy: 0.3203 -
val_loss: -773.7548 - val_accuracy: 0.2344
Epoch 43/100
26/26 [==============================] - 0s 4ms/step - loss: -5427.2393 - accuracy: 0.3086 -
val_loss: -1853.7975 - val_accuracy: 0.2812
Epoch 44/100
26/26 [==============================] - 0s 4ms/step - loss: -6827.4507 - accuracy: 0.2930 -
val_loss: -2729.7163 - val_accuracy: 0.4062
Epoch 45/100
26/26 [==============================] - 0s 4ms/step - loss: -7563.3521 - accuracy: 0.3477 -
val_loss: -4681.4121 - val_accuracy: 0.3438
Epoch 46/100
26/26 [==============================] - 0s 4ms/step - loss: -11600.1230 - accuracy: 0.3008 -
val_loss: -5234.6426 - val_accuracy: 0.3906
Epoch 47/100
26/26 [==============================] - 0s 4ms/step - loss: -14210.9482 - accuracy: 0.3125 -
val_loss: -6712.8218 - val_accuracy: 0.3281
Epoch 48/100
26/26 [==============================] - 0s 4ms/step - loss: -19682.2637 - accuracy: 0.3398 -
val_loss: -560.5317 - val_accuracy: 0.2188
Epoch 49/100
26/26 [==============================] - 0s 4ms/step - loss: -17378.3965 - accuracy: 0.2891 -
val_loss: -9983.1055 - val_accuracy: 0.3281
```

```
Epoch 10/100
26/26 [==============================] - 0s 6ms/step - loss: 0.3208 - accuracy: 0.2656 - val_loss:
1.1173 - val_accuracy: 0.1875
Epoch 11/100
26/26 [==============================] - 0s 5ms/step - loss: 0.1900 - accuracy: 0.2656 - val_loss:
0.5179 - val_accuracy: 0.2031
Epoch 12/100
26/26 [==============================] - 0s 5ms/step - loss: -0.0150 - accuracy: 0.2930 - val_loss:
0.5630 - val_accuracy: 0.2031
Epoch 13/100
26/26 [==============================] - 0s 6ms/step - loss: 0.3870 - accuracy: 0.2383 - val_loss:
0.3150 - val_accuracy: 0.2812
Epoch 14/100
26/26 [==============================] - 0s 5ms/step - loss: 0.0302 - accuracy: 0.3008 - val_loss:
0.2780 - val_accuracy: 0.2344
Epoch 15/100
26/26 [==============================] - 0s 5ms/step - loss: -0.2033 - accuracy: 0.2305 - val_loss:
0.1754 - val_accuracy: 0.3125
Epoch 16/100
26/26 [==============================] - 0s 6ms/step - loss: -0.3200 - accuracy: 0.3008 - val_loss:
0.3586 - val_accuracy: 0.2188
Epoch 17/100
26/26 [==============================] - 0s 6ms/step - loss: -0.3454 - accuracy: 0.2656 - val_loss:
0.7526 - val_accuracy: 0.1875
Epoch 18/100
26/26 [==============================] - 0s 5ms/step - loss: -0.2979 - accuracy: 0.2969 - val_loss:
0.0144 - val_accuracy: 0.4375
Epoch 19/100
26/26 [==============================] - 0s 5ms/step - loss: 0.2707 - accuracy: 0.3164 - val_loss: -
0.1211 - val_accuracy: 0.2656
Epoch 20/100
26/26 [==============================] - 0s 6ms/step - loss: -0.6757 - accuracy: 0.2695 - val_loss:
0.5293 - val_accuracy: 0.2344
Epoch 21/100
26/26 [==============================] - 0s 6ms/step - loss: -1.1019 - accuracy: 0.3047 - val_loss: -
0.2022 - val_accuracy: 0.2812
Epoch 22/100
26/26 [==============================] - 0s 5ms/step - loss: -1.7570 - accuracy: 0.2969 - val_loss:
0.5081 - val_accuracy: 0.2188
Epoch 23/100
26/26 [==============================] - 0s 4ms/step - loss: -1.9639 - accuracy: 0.2852 - val_loss: -
0.4449 - val_accuracy: 0.2969
Epoch 24/100
26/26 [==============================] - 0s 4ms/step - loss: -2.9232 - accuracy: 0.2930 - val_loss: -
0.2926 - val_accuracy: 0.3438
Epoch 25/100
26/26 [==============================] - 0s 4ms/step - loss: -3.9678 - accuracy: 0.3164 - val_loss:
0.4535 - val_accuracy: 0.2344
Epoch 26/100
26/26 [==============================] - 0s 4ms/step - loss: -6.0380 - accuracy: 0.2891 - val_loss: -
1.1717 - val_accuracy: 0.3438
Epoch 27/100
26/26 [==============================] - 0s 4ms/step - loss: -8.9568 - accuracy: 0.3398 - val_loss: -
1.0845 - val_accuracy: 0.2344
Epoch 28/100
26/26 [==============================] - 0s 4ms/step - loss: -11.3656 - accuracy: 0.3047 - val_loss: -
5.0146 - val_accuracy: 0.2656
Epoch 29/100
26/26 [==============================] - 0s 4ms/step - loss: -21.1796 - accuracy: 0.3125 - val_loss: -
8.4466 - val_accuracy: 0.3750
```

Milestone 4

```
import tensorflow
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense


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'))



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


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

```
Epoch 1/100
26/26 [==============================] - 3s 19ms/step - loss: 1.9170 - accuracy: 0.2422 - val_loss:
0.5725 - val_accuracy: 0.4688
Epoch 2/100
26/26 [==============================] - 0s 6ms/step - loss: 1.5366 - accuracy: 0.2305 - val_loss:
0.6411 - val_accuracy: 0.2188
Epoch 3/100
26/26 [==============================] - 0s 6ms/step - loss: 0.5509 - accuracy: 0.3164 - val_loss:
0.5074 - val_accuracy: 0.2031
Epoch 4/100
26/26 [==============================] - 0s 6ms/step - loss: 0.3913 - accuracy: 0.2266 - val_loss:
0.4190 - val_accuracy: 0.2031
Epoch 5/100
26/26 [==============================] - 0s 6ms/step - loss: 0.4187 - accuracy: 0.2734 - val_loss:
1.0563 - val_accuracy: 0.1875
Epoch 6/100
26/26 [==============================] - 0s 6ms/step - loss: 0.6825 - accuracy: 0.2891 - val_loss:
1.0657 - val_accuracy: 0.1875
Epoch 7/100
26/26 [==============================] - 0s 6ms/step - loss: 0.6412 - accuracy: 0.2656 - val_loss:
0.5097 - val_accuracy: 0.2344
Epoch 8/100
26/26 [==============================] - 0s 6ms/step - loss: 0.5948 - accuracy: 0.2461 - val_loss:
0.8240 - val_accuracy: 0.1875
Epoch 9/100
26/26 [==============================] - 0s 5ms/step - loss: 0.2572 - accuracy: 0.2930 - val_loss:
0.2896 - val_accuracy: 0.2500
```



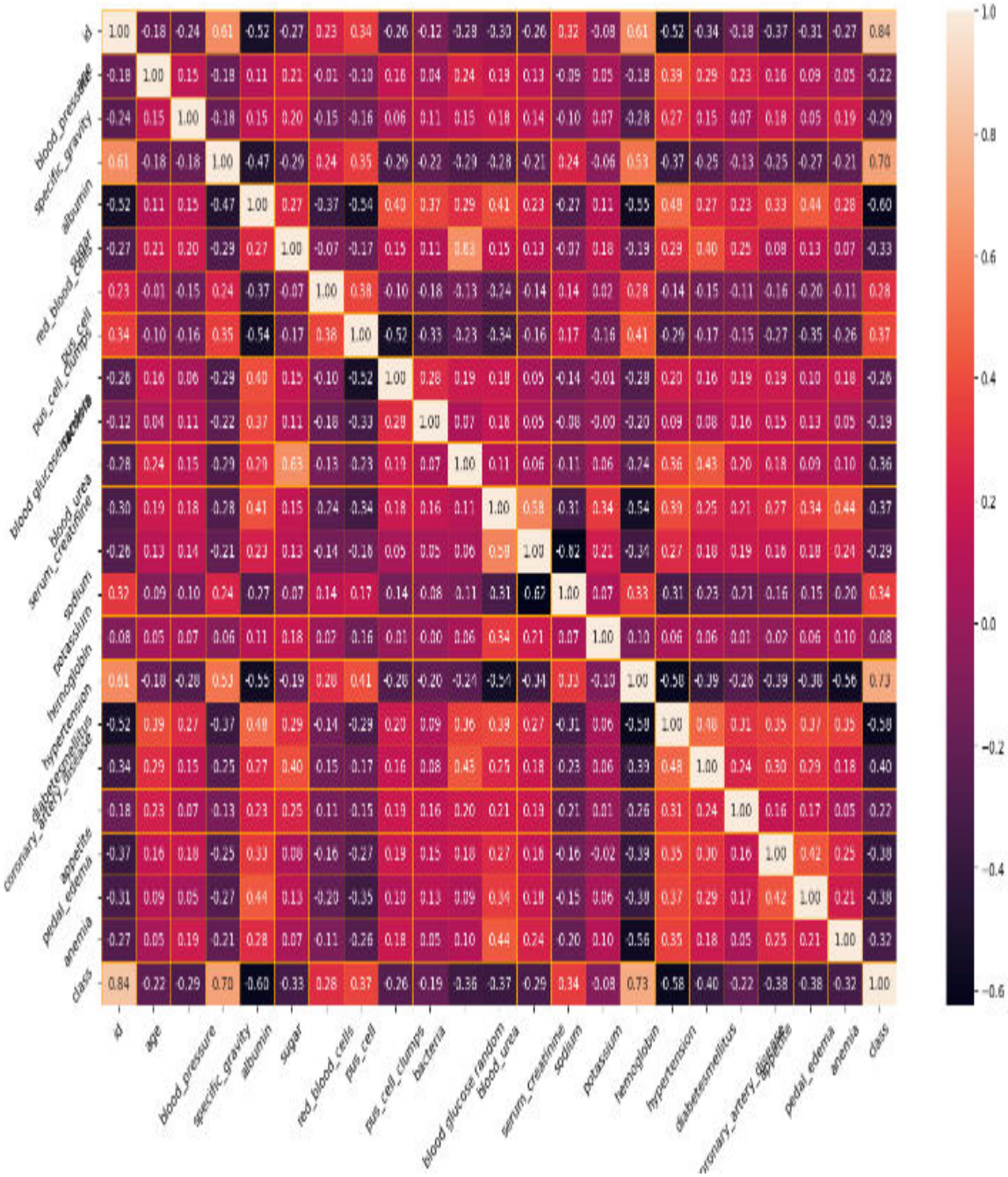

```
from sklearn.preprocessing import StandardScaler
sc=StandardScaler()
```

```
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)
```

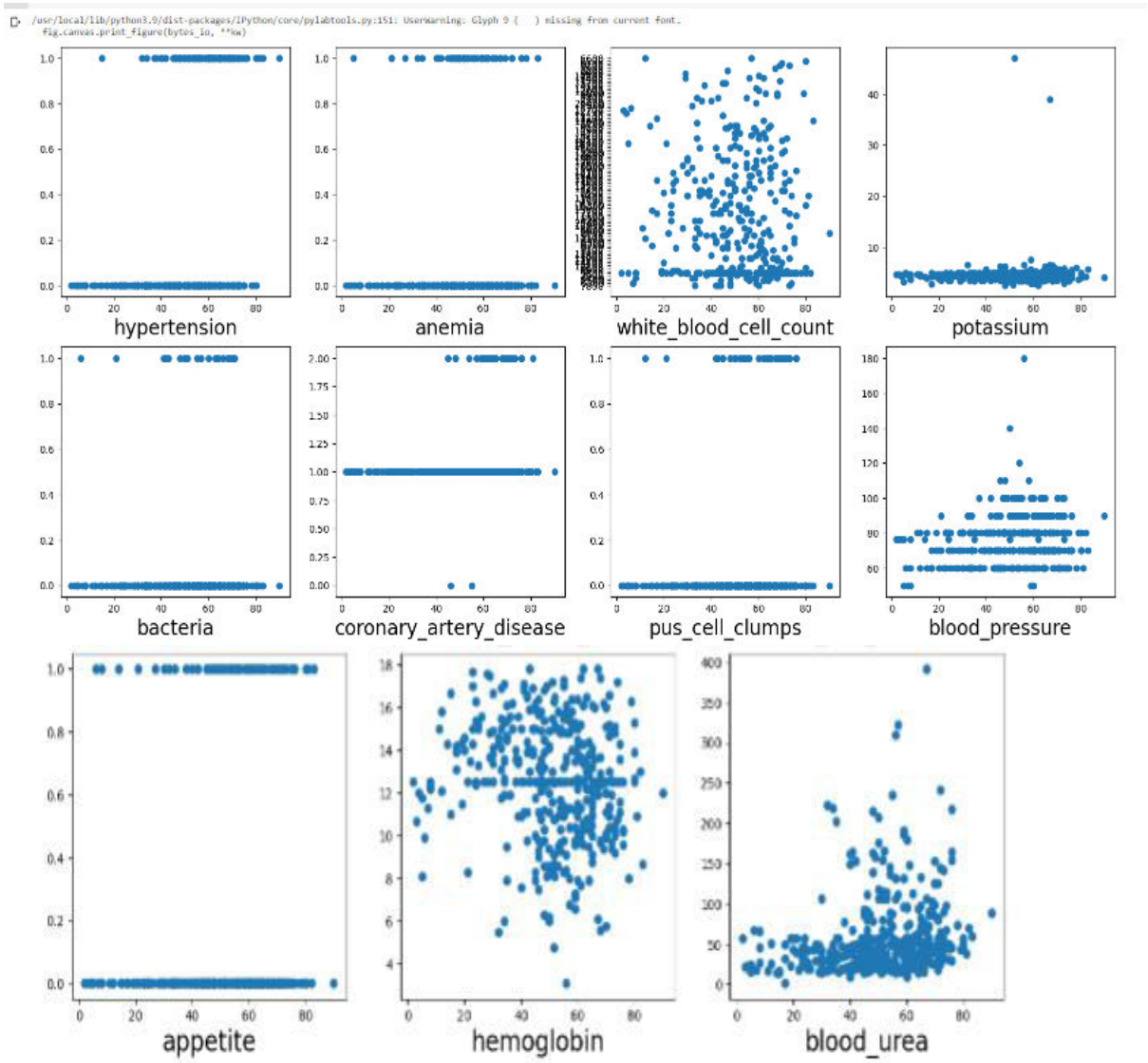
```
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2,random_state=2)
```

```
plt.yticks(rotation=45)
plt.show()
```




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

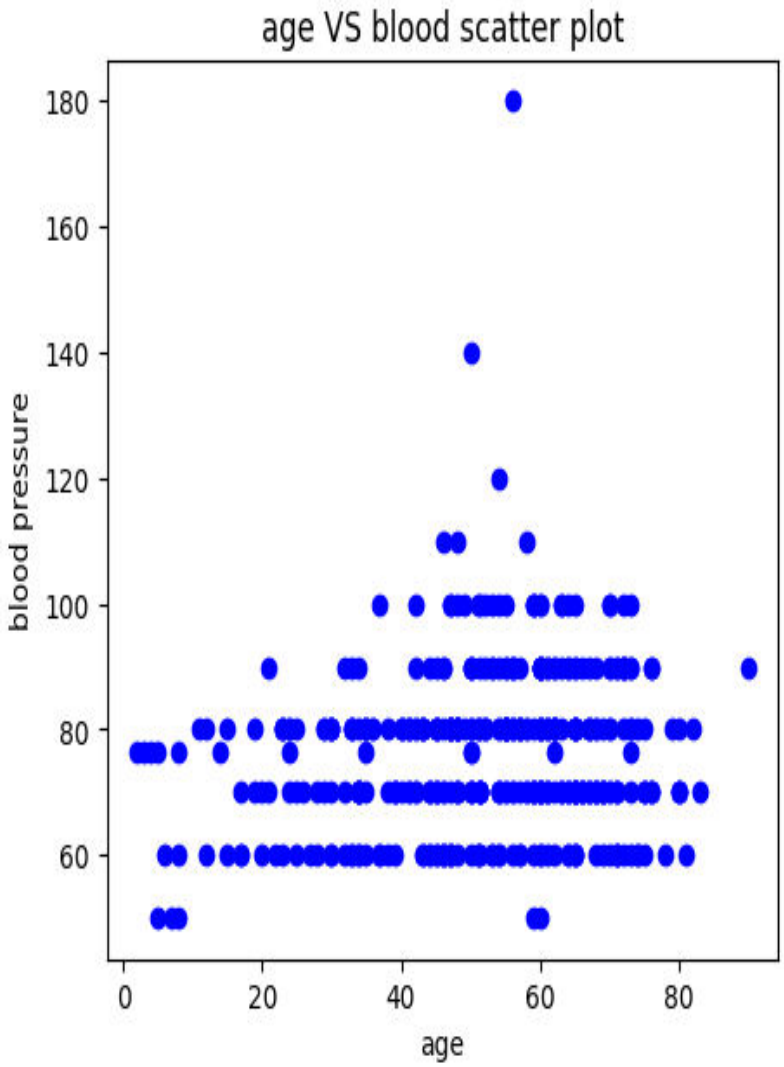
```
  if plotnumber<=11:
    ax = plt.subplot(3,4,plotnumber)
    plt.scatter(data['age'],data[column])
    plt.xlabel(column,fontsize=20)
  plotnumber+=1
plt.show()
```




```
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.ylabel('blood pressure')
plt.title("age VS blood scatter plot")
```

```
Text(0.5, 1.0, 'age VS blood scatter plot')
```




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

for column in contcols:
```

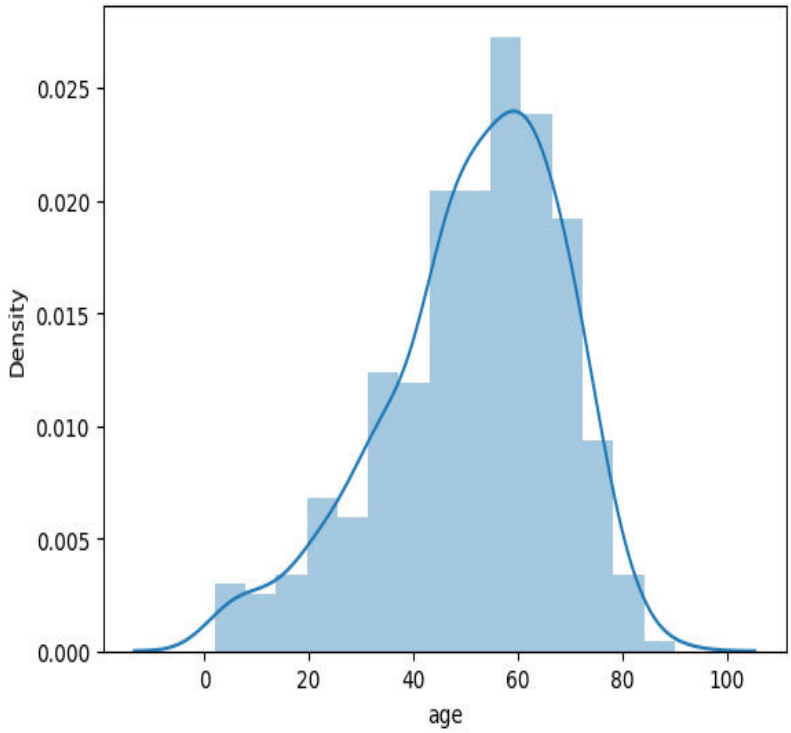
	id	age	blood_pressure	specific_gravity	albumin	sugar	red_blood_cells	pus_cell	pus_cell_clumps	bacteria	...	sodium	p
count	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000	...	400.000000	40
mean	199.500000	51.483376	76.469072	1.017408	1.016949	0.450142	0.882500	0.810000	0.105000	0.055000	...	137.528754	
std	115.614301	16.974966	13.476298	0.005369	1.272318	1.029487	0.322418	0.392792	0.306937	0.228266	...	9.204273	
min	0.000000	2.000000	50.000000	1.005000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	...	4.500000	
25%	99.750000	42.000000	70.000000	1.015000	0.000000	0.000000	1.000000	1.000000	0.000000	0.000000	...	135.000000	
50%	199.500000	54.000000	78.234536	1.017408	1.000000	0.000000	1.000000	1.000000	0.000000	0.000000	...	137.528754	
75%	299.250000	64.000000	80.000000	1.020000	2.000000	0.450142	1.000000	1.000000	0.000000	0.000000	...	141.000000	
max	399.000000	90.000000	180.000000	1.025000	5.000000	5.000000	1.000000	1.000000	1.000000	1.000000	...	163.000000	4

8 rows × 23 columns

```
sns.distplot(data.age)
```

https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

```
sns.distplot(data.age)
<Axes: xlabel='age', ylabel='Density'>
```




```
import matplotlib.pyplot as plt
fig=plt.figure(figsize=(5,5))
plt.scatter(data['age'],data['blood_pressure'],color='blue')
plt.xlabel('age')
```

```
{'hypertension', 'anemia', 'white_blood_cell_count', 'potassium',
'bacteria', 'coronary_artery_disease', 'pus_cell_clumps',
'blood_pressure', 'appetite', 'hemoglobin', 'blood_urea',
'pedal_edema', 'blood glucose random', 'red_blood_cells',
'serum_creatinine', 'packed_cell_volume', 'red_blood_cell_count', 'id',
'diabetesmellitus', 'sodium', 'age', 'class', 'pus_cell'}
```

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

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

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

```
Counter({1: 364, 2: 34, 0: 2})
```

```
data['diabetesmellitus']=data.diabetesmellitus.replace('\tno','no')
c(data['diabetesmellitus'])
```

```
Counter({4: 134, 3: 260, 2: 1, 0: 3, 1: 2})
```

Milestone 3

```
data.describe()
```

```
Continous Columns : sodium
Counter({137.52875399361022: 87, 135.0: 40, 140.0: 25, 141.0: 22,
139.0: 21, 142.0: 20, 138.0: 20, 137.0: 19, 136.0: 17, 150.0: 17,
147.0: 13, 145.0: 11, 132.0: 10, 146.0: 10, 131.0: 9, 144.0: 9, 133.0:
8, 130.0: 7, 134.0: 6, 143.0: 4, 127.0: 3, 124.0: 3, 114.0: 2, 125.0:
2, 128.0: 2, 122.0: 2, 113.0: 2, 120.0: 2, 111.0: 1, 104.0: 1, 4.5: 1,
129.0: 1, 163.0: 1, 126.0: 1, 115.0: 1})
**********************************************************************
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Continous Columns : albumin
Counter({0.0: 199, 1.0169491525423728: 46, 1.0: 44, 2.0: 43, 3.0: 43,
4.0: 24, 5.0: 1})
**********************************************************************
************************************************

Continous Columns : age
Counter({60.0: 19, 65.0: 17, 48.0: 12, 50.0: 12, 55.0: 12, 47.0: 11,
62.0: 10, 45.0: 10, 54.0: 10, 59.0: 10, 56.0: 10, 61.0: 9,
51.48337595907928: 9, 70.0: 9, 46.0: 9, 34.0: 9, 68.0: 8, 73.0: 8,
64.0: 8, 71.0: 8, 57.0: 8, 63.0: 7, 72.0: 7, 67.0: 7, 30.0: 7, 42.0: 6,
69.0: 6, 35.0: 6, 44.0: 6, 43.0: 6, 33.0: 6, 51.0: 5, 52.0: 5, 53.0: 5,
75.0: 5, 76.0: 5, 58.0: 5, 41.0: 5, 66.0: 5, 24.0: 4, 40.0: 4, 39.0: 4,
80.0: 4, 23.0: 4, 74.0: 3, 38.0: 3, 17.0: 3, 8.0: 3, 32.0: 3, 37.0: 3,
25.0: 3, 29.0: 3, 21.0: 2, 15.0: 2, 5.0: 2, 12.0: 2, 49.0: 2, 19.0: 2,
36.0: 2, 20.0: 2, 28.0: 2, 7.0: 1, 82.0: 1, 11.0: 1, 26.0: 1, 81.0: 1,
14.0: 1, 27.0: 1, 83.0: 1, 4.0: 1, 3.0: 1, 6.0: 1, 90.0: 1, 78.0: 1,
2.0: 1, 22.0: 1, 79.0: 1})
**********************************************************************
************************************************
```

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

```
      {'hypertension', 'anemia', 'potassium', 'bacteria',
'coronary_artery_disease', 'pus_cell_clumps', 'blood_pressure',
'appetite', 'hemoglobin', 'blood_urea', 'pedal_edema', 'blood glucose
random', 'red_blood_cells', 'serum_creatinine', 'id',
'diabetesmellitus', 'sodium', 'age', 'class', 'pus_cell'}
```

```
contcols.add('red_blood_cell_count')
contcols.add('packed_cell_volume')
contcols.add('white_blood_cell_count')
print(contcols)
```

```
18.0: 1, 13.0: 1, 48.1: 1, 14.2: 1, 16.4: 1, 2.6: 1, 7.5: 1, 4.3: 1,
18.1: 1, 11.8: 1, 9.3: 1, 6.8: 1, 13.5: 1, 12.8: 1, 11.9: 1, 12.0: 1,
13.4: 1, 15.2: 1, 13.3: 1, 0.4: 1})
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Continous Columns : id
Counter({0: 1, 1: 1, 2: 1, 3: 1, 4: 1, 5: 1, 6: 1, 7: 1, 8: 1, 9: 1,
10: 1, 11: 1, 12: 1, 13: 1, 14: 1, 15: 1, 16: 1, 17: 1, 18: 1, 19: 1,
20: 1, 21: 1, 22: 1, 23: 1, 24: 1, 25: 1, 26: 1, 27: 1, 28: 1, 29: 1,
30: 1, 31: 1, 32: 1, 33: 1, 34: 1, 35: 1, 36: 1, 37: 1, 38: 1, 39: 1,
40: 1, 41: 1, 42: 1, 43: 1, 44: 1, 45: 1, 46: 1, 47: 1, 48: 1, 49: 1,
50: 1, 51: 1, 52: 1, 53: 1, 54: 1, 55: 1, 56: 1, 57: 1, 58: 1, 59: 1,
60: 1, 61: 1, 62: 1, 63: 1, 64: 1, 65: 1, 66: 1, 67: 1, 68: 1, 69: 1,
70: 1, 71: 1, 72: 1, 73: 1, 74: 1, 75: 1, 76: 1, 77: 1, 78: 1, 79: 1,
80: 1, 81: 1, 82: 1, 83: 1, 84: 1, 85: 1, 86: 1, 87: 1, 88: 1, 89: 1,
90: 1, 91: 1, 92: 1, 93: 1, 94: 1, 95: 1, 96: 1, 97: 1, 98: 1, 99: 1,
100: 1, 101: 1, 102: 1, 103: 1, 104: 1, 105: 1, 106: 1, 107: 1, 108: 1,
109: 1, 110: 1, 111: 1, 112: 1, 113: 1, 114: 1, 115: 1, 116: 1, 117: 1,
118: 1, 119: 1, 120: 1, 121: 1, 122: 1, 123: 1, 124: 1, 125: 1, 126: 1,
127: 1, 128: 1, 129: 1, 130: 1, 131: 1, 132: 1, 133: 1, 134: 1, 135: 1,
136: 1, 137: 1, 138: 1, 139: 1, 140: 1, 141: 1, 142: 1, 143: 1, 144: 1,
145: 1, 146: 1, 147: 1, 148: 1, 149: 1, 150: 1, 151: 1, 152: 1, 153: 1,
154: 1, 155: 1, 156: 1, 157: 1, 158: 1, 159: 1, 160: 1, 161: 1, 162: 1,
163: 1, 164: 1, 165: 1, 166: 1, 167: 1, 168: 1, 169: 1, 170: 1, 171: 1,
172: 1, 173: 1, 174: 1, 175: 1, 176: 1, 177: 1, 178: 1, 179: 1, 180: 1,
181: 1, 182: 1, 183: 1, 184: 1, 185: 1, 186: 1, 187: 1, 188: 1, 189: 1,
190: 1, 191: 1, 192: 1, 193: 1, 194: 1, 195: 1, 196: 1, 197: 1, 198: 1,
199: 1, 200: 1, 201: 1, 202: 1, 203: 1, 204: 1, 205: 1, 206: 1, 207: 1,
208: 1, 209: 1, 210: 1, 211: 1, 212: 1, 213: 1, 214: 1, 215: 1, 216: 1,
217: 1, 218: 1, 219: 1, 220: 1, 221: 1, 222: 1, 223: 1, 224: 1, 225: 1,
226: 1, 227: 1, 228: 1, 229: 1, 230: 1, 231: 1, 232: 1, 233: 1, 234: 1,
235: 1, 236: 1, 237: 1, 238: 1, 239: 1, 240: 1, 241: 1, 242: 1, 243: 1,
244: 1, 245: 1, 246: 1, 247: 1, 248: 1, 249: 1, 250: 1, 251: 1, 252: 1,
253: 1, 254: 1, 255: 1, 256: 1, 257: 1, 258: 1, 259: 1, 260: 1, 261: 1,
262: 1, 263: 1, 264: 1, 265: 1, 266: 1, 267: 1, 268: 1, 269: 1, 270: 1,
271: 1, 272: 1, 273: 1, 274: 1, 275: 1, 276: 1, 277: 1, 278: 1, 279: 1,
280: 1, 281: 1, 282: 1, 283: 1, 284: 1, 285: 1, 286: 1, 287: 1, 288: 1,
289: 1, 290: 1, 291: 1, 292: 1, 293: 1, 294: 1, 295: 1, 296: 1, 297: 1,
298: 1, 299: 1, 300: 1, 301: 1, 302: 1, 303: 1, 304: 1, 305: 1, 306: 1,
307: 1, 308: 1, 309: 1, 310: 1, 311: 1, 312: 1, 313: 1, 314: 1, 315: 1,
316: 1, 317: 1, 318: 1, 319: 1, 320: 1, 321: 1, 322: 1, 323: 1, 324: 1,
325: 1, 326: 1, 327: 1, 328: 1, 329: 1, 330: 1, 331: 1, 332: 1, 333: 1,
334: 1, 335: 1, 336: 1, 337: 1, 338: 1, 339: 1, 340: 1, 341: 1, 342: 1,
343: 1, 344: 1, 345: 1, 346: 1, 347: 1, 348: 1, 349: 1, 350: 1, 351: 1,
352: 1, 353: 1, 354: 1, 355: 1, 356: 1, 357: 1, 358: 1, 359: 1, 360: 1,
361: 1, 362: 1, 363: 1, 364: 1, 365: 1, 366: 1, 367: 1, 368: 1, 369: 1,
370: 1, 371: 1, 372: 1, 373: 1, 374: 1, 375: 1, 376: 1, 377: 1, 378: 1,
379: 1, 380: 1, 381: 1, 382: 1, 383: 1, 384: 1, 385: 1, 386: 1, 387: 1,
388: 1, 389: 1, 390: 1, 391: 1, 392: 1, 393: 1, 394: 1, 395: 1, 396: 1,
397: 1, 398: 1, 399: 1})
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Continous Columns : diabetesmellitus
Counter({3: 260, 4: 134, 0: 3, 1: 2, 2: 1})
**********************************************************************
************************************************
```

```
3, 52.0: 3, 106.0: 3, 125.0: 3, 56.0: 2, 54.0: 2, 72.0: 2, 86.0: 2,
90.0: 2, 87.0: 2, 155.0: 2, 153.0: 2, 77.0: 2, 89.0: 2, 111.0: 2, 73.0:
2, 98.0: 2, 82.0: 2, 132.0: 2, 58.0: 2, 10.0: 2, 162.0: 1, 148.0: 1,
180.0: 1, 163.0: 1, 75.0: 1, 65.0: 1, 103.0: 1, 70.0: 1, 202.0: 1,
114.0: 1, 164.0: 1, 142.0: 1, 391.0: 1, 92.0: 1, 139.0: 1, 85.0: 1,
186.0: 1, 217.0: 1, 88.0: 1, 118.0: 1, 50.1: 1, 71.0: 1, 21.0: 1,
219.0: 1, 166.0: 1, 208.0: 1, 176.0: 1, 145.0: 1, 165.0: 1, 322.0: 1,
235.0: 1, 76.0: 1, 113.0: 1, 1.5: 1, 146.0: 1, 133.0: 1, 137.0: 1,
67.0: 1, 115.0: 1, 223.0: 1, 98.6: 1, 158.0: 1, 94.0: 1, 74.0: 1,
150.0: 1, 61.0: 1, 57.0: 1, 95.0: 1, 191.0: 1, 93.0: 1, 241.0: 1, 64.0:
1, 79.0: 1, 215.0: 1, 309.0: 1})
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Continous Columns : pedal_edema
Counter({0: 324, 1: 76})
**********************************************************************
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Continous Columns : blood glucose random
Counter({99.0: 54, 100.0: 9, 93.0: 9, 107.0: 8, 117.0: 6, 140.0: 6,
92.0: 6, 109.0: 6, 131.0: 6, 130.0: 6, 70.0: 5, 114.0: 5, 95.0: 5,
123.0: 5, 124.0: 5, 102.0: 5, 132.0: 5, 104.0: 5, 125.0: 5, 122.0: 5,
121.0: 4, 106.0: 4, 76.0: 4, 91.0: 4, 129.0: 4, 133.0: 4, 94.0: 4,
88.0: 4, 118.0: 4, 139.0: 4, 111.0: 4, 113.0: 4, 120.0: 4, 119.0: 4,
74.0: 3, 108.0: 3, 171.0: 3, 137.0: 3, 79.0: 3, 150.0: 3, 112.0: 3,
127.0: 3, 219.0: 3, 172.0: 3, 89.0: 3, 128.0: 3, 214.0: 3, 105.0: 3,
78.0: 3, 103.0: 3, 82.0: 3, 97.0: 3, 81.0: 3, 138.0: 2, 490.0: 2,
208.0: 2, 98.0: 2, 204.0: 2, 207.0: 2, 144.0: 2, 253.0: 2, 141.0: 2,
86.0: 2, 360.0: 2, 163.0: 2, 158.0: 2, 165.0: 2, 169.0: 2, 210.0: 2,
101.0: 2, 153.0: 2, 213.0: 2, 424.0: 2, 303.0: 2, 192.0: 2, 80.0: 2,
110.0: 2, 96.0: 2, 85.0: 2, 83.0: 2, 75.0: 2, 423.0: 1, 410.0: 1,
380.0: 1, 157.0: 1, 263.0: 1, 173.0: 1, 156.0: 1, 264.0: 1, 159.0: 1,
270.0: 1, 162.0: 1, 246.0: 1, 182.0: 1, 146.0: 1, 425.0: 1, 250.0: 1,
415.0: 1, 251.0: 1, 280.0: 1, 295.0: 1, 298.0: 1, 226.0: 1, 143.0: 1,
115.0: 1, 297.0: 1, 233.0: 1, 294.0: 1, 323.0: 1, 90.0: 1, 308.0: 1,
224.0: 1, 268.0: 1, 256.0: 1, 84.0: 1, 288.0: 1, 273.0: 1, 242.0: 1,
148.0: 1, 160.0: 1, 307.0: 1, 220.0: 1, 447.0: 1, 309.0: 1, 22.0: 1,
261.0: 1, 215.0: 1, 234.0: 1, 352.0: 1, 239.0: 1, 184.0: 1, 252.0: 1,
230.0: 1, 341.0: 1, 255.0: 1, 238.0: 1, 248.0: 1, 241.0: 1, 269.0: 1,
201.0: 1, 203.0: 1, 463.0: 1, 176.0: 1, 116.0: 1, 134.0: 1, 87.0: 1})
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Continous Columns : red_blood_cells
Counter({1: 353, 0: 47})
**********************************************************************
************************************************

Continous Columns : serum_creatinine
Counter({1.2: 40, 1.1: 24, 1.0: 23, 0.5: 23, 0.7: 22, 0.9: 22, 0.6: 18,
0.8: 17, 3.072454308093995: 17, 2.2: 10, 1.5: 9, 1.7: 9, 1.3: 8, 1.6:
8, 1.8: 7, 1.4: 7, 2.5: 7, 2.8: 7, 1.9: 6, 2.7: 5, 2.1: 5, 2.0: 5, 3.2:
5, 3.3: 5, 3.9: 4, 7.3: 4, 4.0: 3, 2.4: 3, 3.4: 3, 2.9: 3, 5.3: 3, 2.3:
3, 7.2: 2, 4.6: 2, 4.1: 2, 5.2: 2, 6.3: 2, 3.0: 2, 6.1: 2, 6.7: 2, 5.6:
2, 6.5: 2, 4.4: 2, 6.0: 2, 3.8: 1, 24.0: 1, 9.6: 1, 76.0: 1, 7.7: 1,
10.8: 1, 5.9: 1, 3.25: 1, 9.7: 1, 6.4: 1, 32.0: 1, 8.5: 1, 15.0: 1,
3.6: 1, 10.2: 1, 11.5: 1, 12.2: 1, 9.2: 1, 13.8: 1, 16.9: 1, 7.1: 1,
```

```
Counter({0: 378, 1: 22})
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Continous Columns : coronary_artery_disease
Counter({1: 364, 2: 34, 0: 2})
**********************************************************************
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Continous Columns : pus_cell_clumps
Counter({0: 358, 1: 42})
**********************************************************************
************************************************

Continous Columns : sugar
Counter({0.0: 290, 0.45014245014245013: 49, 2.0: 18, 3.0: 14, 4.0: 13,
1.0: 13, 5.0: 3})
**********************************************************************
************************************************

Continous Columns : blood_pressure
Counter({80.0: 116, 70.0: 112, 60.0: 71, 90.0: 53, 100.0: 25,
76.46907216494846: 12, 50.0: 5, 110.0: 3, 140.0: 1, 180.0: 1, 120.0:
1})
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Continous Columns : appetite
Counter({0: 318, 1: 82})
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Continous Columns : hemoglobin
Counter({12.526436781609195: 52, 15.0: 16, 10.9: 8, 9.8: 7, 11.1: 7,
13.0: 7, 13.6: 7, 11.3: 6, 10.3: 6, 12.0: 6, 13.9: 6, 15.4: 5, 11.2: 5,
10.8: 5, 9.7: 5, 12.6: 5, 7.9: 5, 10.0: 5, 14.0: 5, 14.3: 5, 14.8: 5,
12.2: 4, 12.4: 4, 12.5: 4, 15.2: 4, 9.1: 4, 11.9: 4, 13.5: 4, 16.1: 4,
14.1: 4, 13.2: 4, 13.8: 4, 13.7: 4, 13.4: 4, 17.0: 4, 15.5: 4, 15.8: 4,
9.6: 3, 11.6: 3, 9.5: 3, 9.4: 3, 12.7: 3, 9.9: 3, 10.1: 3, 8.6: 3,
11.0: 3, 15.6: 3, 8.1: 3, 8.3: 3, 10.4: 3, 11.8: 3, 11.4: 3, 11.5: 3,
15.9: 3, 14.5: 3, 16.2: 3, 14.4: 3, 14.2: 3, 16.3: 3, 16.5: 3, 15.7: 3,
16.4: 3, 14.9: 3, 15.3: 3, 17.8: 3, 12.1: 2, 9.3: 2, 10.2: 2, 10.5: 2,
6.0: 2, 11.7: 2, 8.0: 2, 12.3: 2, 8.7: 2, 13.1: 2, 8.8: 2, 13.3: 2,
14.6: 2, 16.9: 2, 16.0: 2, 14.7: 2, 16.6: 2, 16.7: 2, 16.8: 2, 15.1: 2,
17.1: 2, 17.2: 2, 17.4: 2, 5.6: 1, 7.6: 1, 7.7: 1, 12.9: 1, 6.6: 1,
7.5: 1, 4.8: 1, 7.1: 1, 9.2: 1, 6.2: 1, 8.2: 1, 6.1: 1, 8.4: 1, 9.0: 1,
10.6: 1, 10.7: 1, 5.5: 1, 5.8: 1, 6.8: 1, 8.5: 1, 7.3: 1, 12.8: 1, 6.3:
1, 3.1: 1, 17.3: 1, 17.7: 1, 17.5: 1, 17.6: 1})
**********************************************************************
************************************************

Continous Columns : blood_urea
Counter({57.425721784776904: 19, 46.0: 15, 25.0: 13, 19.0: 11, 40.0:
10, 18.0: 9, 50.0: 9, 15.0: 9, 48.0: 9, 26.0: 8, 27.0: 8, 32.0: 8,
49.0: 8, 36.0: 7, 28.0: 7, 20.0: 7, 17.0: 7, 38.0: 7, 16.0: 7, 30.0: 7,
44.0: 7, 31.0: 6, 45.0: 6, 39.0: 6, 29.0: 6, 24.0: 6, 37.0: 6, 22.0: 6,
23.0: 6, 53.0: 5, 55.0: 5, 33.0: 5, 66.0: 5, 35.0: 5, 42.0: 5, 47.0: 4,
51.0: 4, 34.0: 4, 68.0: 4, 41.0: 4, 60.0: 3, 107.0: 3, 80.0: 3, 96.0:
```

```
LABEL ENCODING OF: bacteria
Counter({'notpresent': 378, 'present': 22})
Counter({0: 378, 1: 22})
**********************************************************************
****************************
LABEL ENCODING OF: pus_cell
Counter({'normal': 324, 'abnormal': 76})
Counter({1: 324, 0: 76})
```

```
contcols=set(data.dtypes[data.dtypes!='O'].index.values)
print(contcols)
```

```
   {'hypertension', 'anemia', 'specific_gravity', 'potassium',
'bacteria', 'coronary_artery_disease', 'pus_cell_clumps', 'sugar',
'blood_pressure', 'appetite', 'hemoglobin', 'blood_urea',
'pedal_edema', 'blood glucose random', 'red_blood_cells',
'serum_creatinine', 'id', 'diabetesmellitus', 'sodium', 'albumin',
'age', 'class', 'pus_cell'}
```

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

```
Continous Columns : hypertension
Counter({0: 253, 1: 147})
**********************************************************************
************************************************

Continous Columns : anemia
Counter({0: 340, 1: 60})
**********************************************************************
************************************************

Continous Columns : specific_gravity
Counter({1.02: 106, 1.01: 84, 1.025: 81, 1.015: 75, 1.0174079320113314:
47, 1.005: 7})
**********************************************************************
************************************************

Continous Columns : potassium
Counter({4.62724358974359: 88, 5.0: 30, 3.5: 30, 4.9: 27, 4.7: 17, 4.8:
16, 4.0: 14, 4.2: 14, 4.1: 14, 3.8: 14, 3.9: 14, 4.4: 14, 4.5: 13, 3.7:
12, 4.3: 12, 3.6: 8, 4.6: 7, 3.4: 5, 5.2: 5, 5.7: 4, 5.3: 4, 3.2: 3,
5.5: 3, 2.9: 3, 5.4: 3, 6.3: 3, 3.3: 3, 2.5: 2, 5.8: 2, 5.9: 2, 5.6: 2,
3.0: 2, 6.5: 2, 6.4: 1, 6.6: 1, 39.0: 1, 7.6: 1, 47.0: 1, 5.1: 1, 2.8:
1, 2.7: 1})
**********************************************************************
************************************************

Continous Columns : bacteria
```

```python
from sklearn.preprocessing import LabelEncoder
for i in catcols:
  print("LABEL ENCODING OF:",i)
  LEi = LabelEncoder()
  print(c(data[i]))
  data[i] = LEi.fit_transform(data[i])
  print(c(data[i]))
  print("*"*100)
```

```
LABEL ENCODING OF: diabetesmellitus
Counter({'no': 260, 'yes': 134, '\tno': 3, '\tyes': 2, ' yes': 1})
Counter({3: 260, 4: 134, 0: 3, 1: 2, 2: 1})
**********************************************************************
****************************
LABEL ENCODING OF: coronary_artery_disease
Counter({'no': 364, 'yes': 34, '\tno': 2})
Counter({1: 364, 2: 34, 0: 2})
**********************************************************************
****************************
LABEL ENCODING OF: hypertension
Counter({'no': 253, 'yes': 147})
Counter({0: 253, 1: 147})
**********************************************************************
****************************
LABEL ENCODING OF: pedal_edema
Counter({'no': 324, 'yes': 76})
Counter({0: 324, 1: 76})
**********************************************************************
****************************
LABEL ENCODING OF: anemia
Counter({'no': 340, 'yes': 60})
Counter({0: 340, 1: 60})
**********************************************************************
****************************
LABEL ENCODING OF: red_blood_cells
Counter({'normal': 353, 'abnormal': 47})
Counter({1: 353, 0: 47})
**********************************************************************
****************************
LABEL ENCODING OF: pus_cell_clumps
Counter({'notpresent': 358, 'present': 42})
Counter({0: 358, 1: 42})
**********************************************************************
****************************
LABEL ENCODING OF: class
Counter({'ckd': 248, 'notckd': 150, 'ckd\t': 2})
Counter({0: 248, 2: 150, 1: 2})
**********************************************************************
****************************
LABEL ENCODING OF: appetite
Counter({'good': 318, 'poor': 82})
Counter({0: 318, 1: 82})
**********************************************************************
****************************
```