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Predicting chronic kidney disease using machine learning

Problem Definition and Proposed Solution:

Chronic kidney disease (CKD) is one of the major public health issues with rising need of early detection for successful and sustainable care. There are many factors such as blood pressure, diabetes, and other disorders contribute to gradual loss of kidney function over time. CKD is gradual progression hence, it has many stages for criticality of disease. Given medical historical data and diagnostic data of a patient, Machine learning and Data Discovery approach can help identify risk of CKD at early stage. This is a binary classification problem.

Abstract:

A condition characterised by a gradual loss of kidney function. Early stages can be asymptomatic. Disease progression occurs slowly over a period of time. Treatment in the initial stages aims to manage signs and symptoms, and slow the progression of disease. Advanced stage treatment includes dialysis and kidney transplant.

Introduction:

Early Prediction of Chronic Kidney Disease Using Machine Learning. Predictive analytics for healthcare using machine learning is a challenged task to help doctors decide the exact treatments for saving lives. Four machine learning methods are explored including K-nearest neighbours (KNN), support vector machine (SVM), logistic regression (LR), and decision tree classifiers.

Algorithms Used:

I've used Random Forest Algorithm for prediction.

Random Forest Algorithm:

Random Forest is a popular machine learning **algorithm** that belongs to the supervised learning technique. It can be used for both Classification and Regression problems in ML. It is based on the concept of ensemble learning, which is a process of combining multiple classifiers to solve a complex problem and to improve the performance of the model. The random forest algorithm relies on a parallel ensemble method called "**bagging**" to generate its weak classifiers. Bagging is a colloquial term for bootstrap aggregation. Bootstrap aggregation is a method that allows us to decrease the variance of an estimate by averaging multiple estimates that are measured from random subsamples of a population.

Code:

Data

This dataset is originally from UCI Machine Learning Repository. However, this is a cleaned dataset from Kaggle. https://www.kaggle.com/abhia1999/chronic-kidney-disease

Preparing the tools

```python
#Importing EDA (Exploratory Data Analysis) and other Libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline

#Import Sklearn Models
from sklearn.ensemble import RandomForestClassifier

#Model Evaluations
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.metrics import classification_report
```

Load the Data

```python
df=pd.read_csv("chronic-kidney-disease.csv")
df.head(10)
```

	Bp	Sg	Al	Su	Rbc	Bu	Sc	Sod	Pot	Hemo	Wbcc	Rbcc	Htn	Class
0	80.0	1.020	1.0	0.0	1.0	36.0	1.2	137.53	4.63	15.4	7800.0	5.20	1.0	1
1	50.0	1.020	4.0	0.0	1.0	18.0	0.8	137.53	4.63	11.3	6000.0	4.71	0.0	1
2	80.0	1.010	2.0	3.0	1.0	53.0	1.8	137.53	4.63	9.6	7500.0	4.71	0.0	1
3	70.0	1.005	4.0	0.0	1.0	56.0	3.8	111.00	2.50	11.2	6700.0	3.90	1.0	1
4	80.0	1.010	2.0	0.0	1.0	26.0	1.4	137.53	4.63	11.6	7300.0	4.60	0.0	1
5	90.0	1.015	3.0	0.0	1.0	25.0	1.1	142.00	3.20	12.2	7800.0	4.40	1.0	1
6	70.0	1.010	0.0	0.0	1.0	54.0	24.0	104.00	4.00	12.4	8406.0	4.71	0.0	1
7	76.0	1.015	2.0	4.0	1.0	31.0	1.1	137.53	4.63	12.4	6900.0	5.00	0.0	1
8	100.0	1.015	3.0	0.0	1.0	60.0	1.9	137.53	4.63	10.8	9600.0	4.00	1.0	1
9	90.0	1.020	2.0	0.0	0.0	107.0	7.2	114.00	3.70	9.5	12100.0	3.70	1.0	1

```
df.tail(10)
```

	Bp	Sg	Al	Su	Rbc	Bu	Sc	Sod	Pot	Hemo	Wbcc	Rbcc	Htn	Class
390	80.0	1.025	0.0	0.0	1.0	25.0	0.8	135.0	3.7	15.0	6300.0	5.3	0.0	0
391	80.0	1.025	0.0	0.0	1.0	16.0	1.1	142.0	4.1	15.6	5800.0	6.3	0.0	0
392	80.0	1.020	0.0	0.0	1.0	48.0	1.2	147.0	4.3	14.8	6600.0	5.5	0.0	0
393	60.0	1.025	0.0	0.0	1.0	45.0	0.7	141.0	4.4	13.0	7400.0	5.4	0.0	0
394	80.0	1.020	0.0	0.0	1.0	46.0	0.8	139.0	5.0	14.1	9500.0	4.6	0.0	0
395	80.0	1.020	0.0	0.0	1.0	49.0	0.5	150.0	4.9	15.7	6700.0	4.9	0.0	0
396	70.0	1.025	0.0	0.0	1.0	31.0	1.2	141.0	3.5	16.5	7800.0	6.2	0.0	0
397	80.0	1.020	0.0	0.0	1.0	26.0	0.6	137.0	4.4	15.8	6600.0	5.4	0.0	0
398	60.0	1.025	0.0	0.0	1.0	50.0	1.0	135.0	4.9	14.2	7200.0	5.9	0.0	0
399	80.0	1.025	0.0	0.0	1.0	18.0	1.1	141.0	3.5	15.8	6800.0	6.1	0.0	0

Checking for missing data

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 14 columns):
Bp       400 non-null float64
Sg       400 non-null float64
Al       400 non-null float64
Su       400 non-null float64
Rbc      400 non-null float64
Bu       400 non-null float64
Sc       400 non-null float64
Sod      400 non-null float64
Pot      400 non-null float64
Hemo     400 non-null float64
Wbcc     400 non-null float64
Rbcc     400 non-null float64
Htn      400 non-null float64
Class    400 non-null int64
dtypes: float64(13), int64(1)
memory usage: 43.9 KB
```

Shuffle the data

As we can see the Class=1 means the patient has a chronic kidney disease and the Class=0 means that the patient doesn't have chronic kidney disease. However, the dataset is not shuffled so we need to do that next. Note that we will also reset the index.

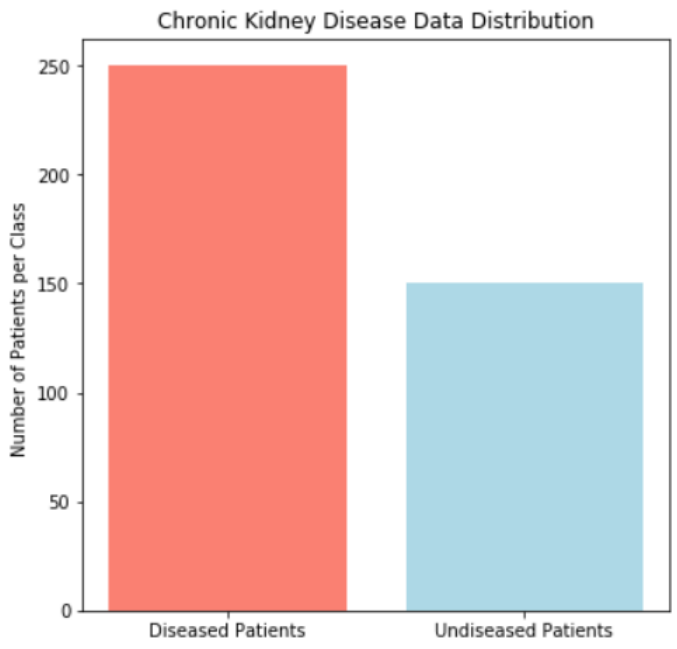
```
np.random.seed(42)
df= df.sample(frac=1).reset_index(drop=True)
```

Another thing we need to look into is that if the sample data is balanced, meaning that it is not biased towards patients with chronic kidney disease or vice versa.

```
CKD={}
CKD['Diseased Patients']= df["Class"].value_counts()[1]
CKD['Undiseased Patients']= df["Class"].value_counts()[0]
CKD
```

```
{'Diseased Patients': 250, 'Undiseased Patients': 150}
```

```
fig, ax = plt.subplots(figsize=(6,6))
ax.bar(CKD.keys(),CKD.values(),color=['salmon','lightblue'])
##Salmon for the diseased patients, lightblue for the undiseased patients.
ax.set(title="Chronic Kidney Disease Data Distribution",ylabel="Number of Patients per Class ");
```



As we can see the dataset is unbalanced, however we will proceed with building the machine learning model in order to see if the model will be biased by this i.e. we will observe if the model favors predicting patient's as being diseased.

Split the data

We will start of by splitting the dataset into training and validation sets. We will do an 70%-30% split.

```
X_train, X_val = train_test_split(df, test_size=0.3, random_state=42)
X_train.shape, X_val.shape
```

```
((280, 14), (120, 14))
```

Separate the features from the target variable

```
y_train = X_train.pop("Class")
y_val = X_val.pop("Class")
X_train.shape,y_train.shape, X_val.shape,y_val.shape
```

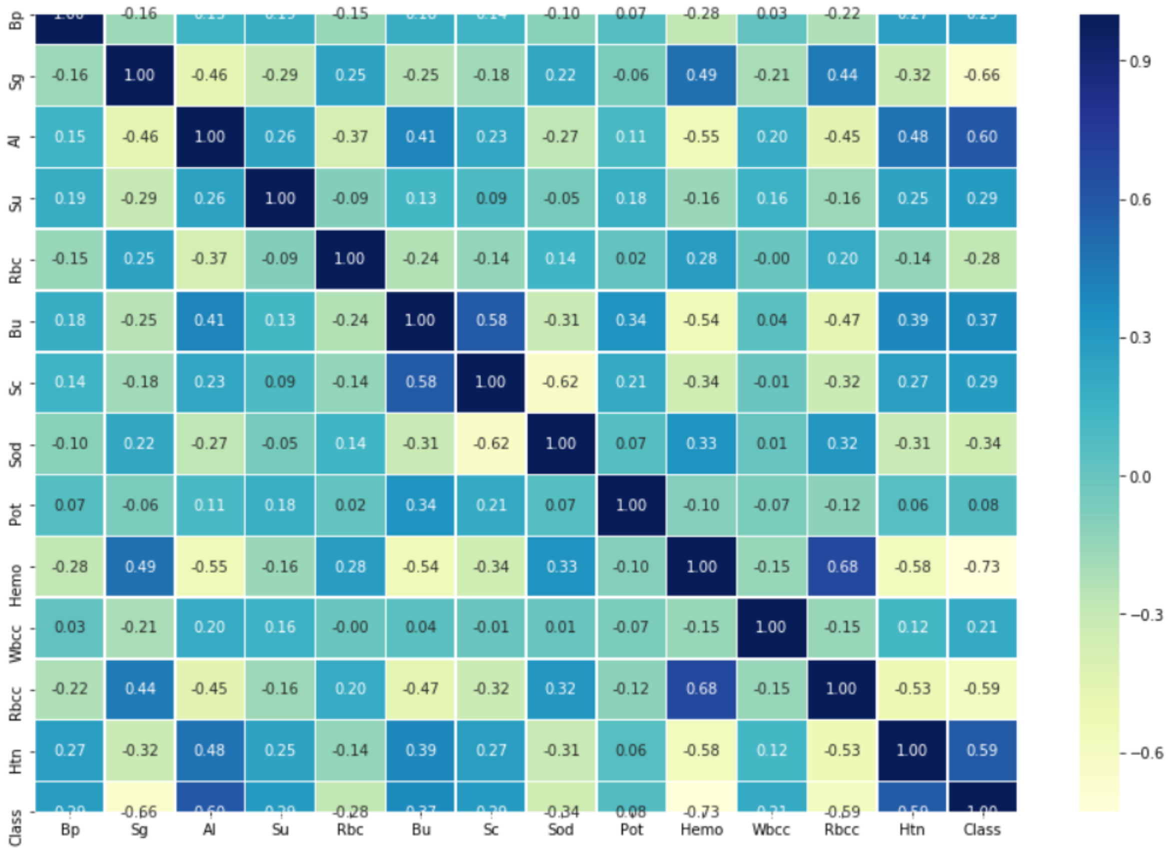
```
((280, 13), (280,), (120, 13), (120,))
```

As you can see, we got a very high score using the Random Forest Classifier.

And the reason for that is:

- 1: We are using a Kaggle data set that is already cleaned and has the appropriate features that have a high correlation with the target "Class". As we can see from the correlation table below a lot of the features have a high correlation with the target "Class".
- 2: We used a Random Forest Classifier for our classification problem which is a powerful ensembled model.
- 3: In addition to the reasons above, we only have 400 records which means that our model was able to fit the data easily, thus the 1.0 score on the training set.

```
corr_matrix = df.corr()
fig, ax= plt.subplots(figsize=(15,10))
ax = sns.heatmap(corr_matrix,
                 annot=True,
                 linewidths=0.5,
                 fmt=".2f",
                 cmap="YlGnBu")
```



Experimenting

However, the model is clearly overfitting the data, and we need to have some generalization. We will use cross validation to see effects of this overfitting. I'm mainly interested in the Accuracy and F1 metrics.

```
X = pd.concat([X_train, X_val])
y = pd.concat([y_train, y_val])
X.shape, y.shape
```

```
((400, 13), (400,))
```

```
cv_acc = np.mean(cross_val_score(model,
                                 X,
                                 y,
                                 cv=5,
                                 scoring="accuracy"))

cv_f1 = np.mean(cross_val_score(model,
                                X,
                                y,
                                cv=5,
                                scoring="f1"))

print("Cross-val-accuracy-score:",cv_acc)
print("Cross-val-F1-score:",cv_f1)
```

```
Cross-val-accuracy-score: 0.985
Cross-val-F1-score: 0.9902143612419494
```

We will change some of the hyperparameters in order to get a regularizing effect, such as the decreasing the max_leaf_nodes, and increasing the n_estimators.

```
from sklearn.ensemble import RandomForestClassifier
np.random.seed(42)
model2 = RandomForestClassifier(n_estimators=200, max_leaf_nodes=10)
model2 = model2.fit(X_train, y_train)

print(model2.score(X_train, y_train))
print(model2.score(X_val, y_val))
```

```
1.0
0.9583333333333334
```

```
X = pd.concat([X_train, X_val])
y = pd.concat([y_train, y_val])
X.shape, y.shape
```

```
((400, 13), (400,))
```

```
np.random.seed(42)
cv_acc = np.mean(cross_val_score(model2,
                                  X,
                                  y,
                                  cv=5,
                                  scoring="accuracy"))

cv_f1 = np.mean(cross_val_score(model2,
                                 X,
                                 y,
                                 cv=5,
                                 scoring="f1"))

print("Cross-val-accuracy-score:",cv_acc)
print("Cross-val-F1-score:",cv_f1)
```

```
Cross-val-accuracy-score: 0.9924999999999999
Cross-val-F1-score: 0.9920792079207921
```

This model generalizes better as observed by the cross validation F1 and Accuracy scores. So, we will be using it.

*Now let's view an evaluation metrics: *

- Classification Report

```
y_preds = model2.predict(X_val)
print(classification_report(y_val, y_preds))
```

```
              precision    recall  f1-score   support

           0       0.97      0.90      0.94        41
           1       0.95      0.99      0.97        79

    accuracy                           0.96       120
   macro avg       0.96      0.94      0.95       120
weighted avg       0.96      0.96      0.96       120
```

Save the model

Finally, we will save this model in case we want to use it later.

```python
from joblib import dump, load
dump(model2, 'chronic-kidney-disease-model.joblib')
```

```
['chronic-kidney-disease-model.joblib']
```

```python
loaded_model = load('chronic-kidney-disease-model.joblib')
```