Chronic Kidney Disease Prediction

What is Chronic Kidney Disease?

Chronic kidney disease (CKD) is a condition where the kidneys are damaged and can't filter blood properly. This can cause excess fluid and waste to build up in the body, leading to other health problems. CKD is a common condition that often occurs with age, but it can affect anyone. It's more common in people who are Black or of South Asian origin.

[Reference:- Google search (Google's GenAI Search Labs)]

About Dataset

I used the dataset recommended in the task document. The dataset is published at the ***UC Irvine Machine Learning Repository***.

The dataset contains data collected over 2 months of period from nearby hosptials. The Dataset contains around 25 features of which class is the target feature which contains 2 classes either ***ckd*** *(Chronic Kidney Disease) or* ***notckd*** *(not Chronic Kidney Disease)*.

Features Inforamtion

The dataset contains 24 + class = 25 features (11 numeric ,14 nominal)

1. Age(numerical) - age in years
2. Blood Pressure(numerical) - bp in mm/Hg
3. Specific Gravity(nominal) - sg - (1.005,1.010,1.015,1.020,1.025)
4. Albumin(nominal) - al - (0,1,2,3,4,5)
5. Sugar(nominal) - su - (0,1,2,3,4,5)
6. Red Blood Cells(nominal) - rbc - (normal,abnormal)
7. Pus Cell (nominal) - pc - (normal,abnormal)
8. Pus Cell clumps(nominal) - pcc - (present,notpresent)
9. Bacteria(nominal) - ba - (present,notpresent)
10. Blood Glucose Random(numerical) - bgr in mgs/dl
11. Blood Urea(numerical) - bu in mgs/dl
12. Serum Creatinine(numerical) - sc in mgs/dl
13. Sodium(numerical) - sod in mEq/L
14. Potassium(numerical) - pot in mEq/L
15. Hemoglobin(numerical) - hemo in gms
16. Packed Cell Volume(numerical)
17. White Blood Cell Count(numerical) - wc in cells/cumm
18. Red Blood Cell Count(numerical) - rc in millions/cmm
19. Hypertension(nominal) - htn - (yes,no)
20. Diabetes Mellitus(nominal) - dm - (yes,no)
21. Coronary Artery Disease(nominal) - cad - (yes,no)
22. Appetite(nominal) - appet - (good,poor)
23. Pedal Edema(nominal) - pe - (yes,no)
24. Anemia(nominal) - ane - (yes,no)
25. Class (nominal) - class - (ckd,notckd)

[Reference:- https://archive.ics.uci.edu/dataset/336/chronic+kidney+disease - Additional Variable Information]

In this notebook I tried to predict the CKD with the decision tree classifier.

Import necessary packages

I am importing the dataset from the UC *Irvine's Machine Learning Repository*. The data can be directly imported with the help of **ucimlrepo** package. So first I am installing, And then importing it.

In [1]:
```
!pip install ucimlrepo
```

```
DEPRECATION: Configuring installation scheme with distutils config files is deprecated and
will no longer work in the near future. If you are using a Homebrew or Linuxbrew Python, p
lease see discussion at https://github.com/Homebrew/homebrew-core/issues/76621
Requirement already satisfied: ucimlrepo in /usr/local/lib/python3.9/site-packages (0.0.6)
DEPRECATION: ipykernel 6.0.1 has a non-standard dependency specifier matplotlib-inline<0.
2.0appnope,>=0.1.0; platform_system == "Darwin". pip 24.1 will enforce this behaviour chan
ge. A possible replacement is to upgrade to a newer version of ipykernel or contact the au
thor to suggest that they release a version with a conforming dependency specifiers. Discu
ssion can be found at https://github.com/pypa/pip/issues/12063
DEPRECATION: Configuring installation scheme with distutils config files is deprecated and
will no longer work in the near future. If you are using a Homebrew or Linuxbrew Python, p
lease see discussion at https://github.com/Homebrew/homebrew-core/issues/76621
```

In [2]:
```
from ucimlrepo import fetch_ucirepo

import pandas as pd
import numpy as np

import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.preprocessing import LabelEncoder
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import confusion_matrix, classification_report,accuracy_score
from sklearn.tree import plot_tree
```

Fetch Dataset from UCIML Repo

As documented in https://github.com/uci-ml-repo/ucimlrepo UCIML Repo I am directly importing the Chronic Kidney Dataset.

In [3]:
```
# fetch dataset
chronic_kidney_disease = fetch_ucirepo(id=336)

# Convert the data to a Pandas DataFrame
df = pd.DataFrame(chronic_kidney_disease.data.original)
df
```

Out[3]:

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wbcc	rbcc	htn
0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	...	44.0	7800.0	5.2	yes
1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	...	38.0	6000.0	NaN	no
2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	423.0	...	31.0	7500.0	NaN	no

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wbcc	rbcc	htn
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	117.0	...	32.0	6700.0	3.9	yes
4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	106.0	...	35.0	7300.0	4.6	no
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	140.0	...	47.0	6700.0	4.9	no
396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	75.0	...	54.0	7800.0	6.2	no
397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	100.0	...	49.0	6600.0	5.4	no
398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	114.0	...	51.0	7200.0	5.9	no
399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	131.0	...	53.0	6800.0	6.1	no

400 rows × 25 columns

Exploratory Data Analysis

Exploratory Data Analysis or EDA is a way to identify the general patterns in the data. EDA is an important and first step in any data analysis, which helps understand the the features of the dataset. EDA helps in understanding the outliers and the correlations between the features, which ingeneral helps in identifying the patterns.

Describe Dataset

The describe function shows the average , minimum ,standard deviation ,maximum,count 25% of column,50% of column,75% of column of the each column.

In [4]:
```
df.describe(include="all")
```

Out[4]:

	age	bp	sg	al	su	rbc	pc	pcc	ba
count	391.000000	388.000000	353.000000	354.000000	351.000000	248	335	396	396
unique	NaN	NaN	NaN	NaN	NaN	2	2	2	2
top	NaN	NaN	NaN	NaN	NaN	normal	normal	notpresent	notpresent
freq	NaN	NaN	NaN	NaN	NaN	201	259	354	374
mean	51.483376	76.469072	1.017408	1.016949	0.450142	NaN	NaN	NaN	NaN
std	17.169714	13.683637	0.005717	1.352679	1.099191	NaN	NaN	NaN	NaN
min	2.000000	50.000000	1.005000	0.000000	0.000000	NaN	NaN	NaN	NaN
25%	42.000000	70.000000	1.010000	0.000000	0.000000	NaN	NaN	NaN	NaN
50%	55.000000	80.000000	1.020000	0.000000	0.000000	NaN	NaN	NaN	NaN
75%	64.500000	80.000000	1.020000	2.000000	0.000000	NaN	NaN	NaN	NaN
max	90.000000	180.000000	1.025000	5.000000	5.000000	NaN	NaN	NaN	NaN

11 rows × 25 columns

Dataset Information

Pandas.DataFrame.info() returns the detailed the dataframe information like indexed dtypes, columns, non-null values, memory usage etc.

In [5]:
```
df.info()
```

```
<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   bp      388 non-null    float64
 2   sg      353 non-null    float64
 3   al      354 non-null    float64
 4   su      351 non-null    float64
 5   rbc     248 non-null    object 
 6   pc      335 non-null    object 
 7   pcc     396 non-null    object 
 8   ba      396 non-null    object 
 9   bgr     356 non-null    float64
 10  bu      381 non-null    float64
 11  sc      383 non-null    float64
 12  sod     313 non-null    float64
 13  pot     312 non-null    float64
 14  hemo    348 non-null    float64
 15  pcv     329 non-null    float64
 16  wbcc    294 non-null    float64
 17  rbcc    269 non-null    float64
 18  htn     398 non-null    object 
 19  dm      398 non-null    object 
 20  cad     398 non-null    object 
 21  appet   399 non-null    object 
 22  pe      399 non-null    object 
 23  ane     399 non-null    object 
 24  class   400 non-null    object 
dtypes: float64(14), object(11)
memory usage: 78.2+ KB
```

Null Value Check

Pandas.DataFrame.isnull() returns the boolean True for any null value in the dataframe and False for all the other remaining values. And sum() returns the sum of all the true values in a column.

In [6]:
```
df.isnull().sum()
```

Out[6]:
```
age        9
bp        12
sg        47
al        46
su        49
rbc      152
pc        65
pcc        4
ba         4
bgr       44
bu        19
sc        17
sod       87
pot       88
hemo      52
pcv       71
wbcc     106
rbcc     131
htn        2
dm         2
```

```
cad          2
appet        1
pe           1
ane          1
class        0
dtype: int64
```

Correlation Mapping

Pandas.dataframe.corr() helps find the pairwise correlation of all columns in the Pandas Dataframe. Any NaN/None values are automatically excluded.

Pearson, Kendall and Spearman correlation are currently computed using pairwise complete observations as mentioned in pandas documentation [https://pandas.pydata.org/docs/reference/api/pandas.DataFrame.corr.html].

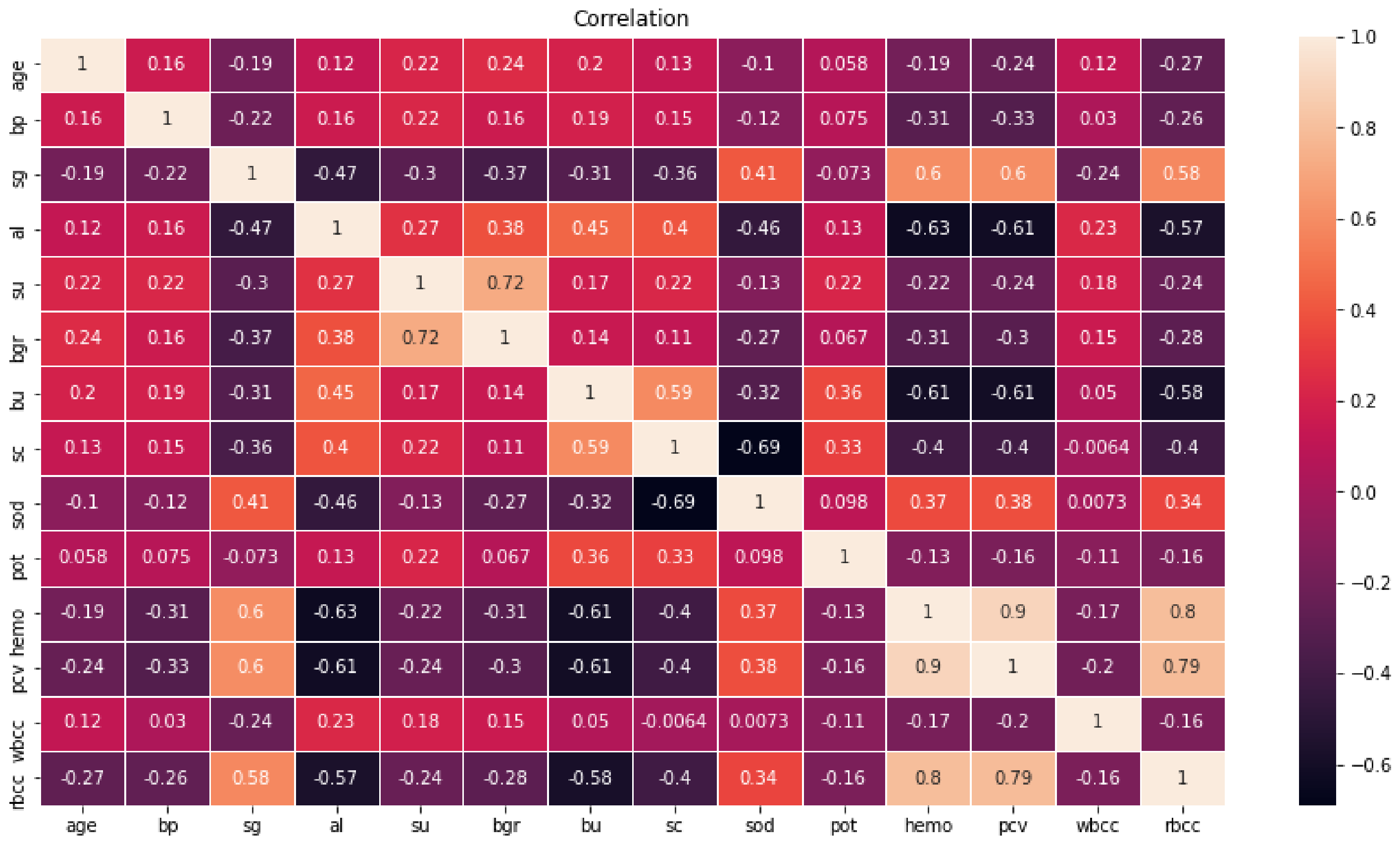
Here I am trying th get the pairwise correlations between the features. By default the Pandas.dataframe.corr() returns pairwise correlation between numeric features of the dataaset.

In [7]:
```python
df_corr = df.corr()
```

Correlation Heatmap

In [8]:
```python
plt.figure(figsize=(15,8));
plt.title("Correlation")
sns.heatmap(df_corr,linewidth=1,annot=True)
```

Out[8]:
```
<AxesSubplot:title={'center':'Correlation'}>
```



Duplicate Value Check

Checking if the dataframe has any duplicate values. To check the same I used duplicated() on dataframe which returns the boolean True/False value and following value_counts() returns the cumulative count of the

Ture and False.

```
In [9]: df.duplicated().value_counts()
```

```
Out[9]: False    400
        dtype: int64
```

Checking the unique classes in the dataframe.

```
In [10]: df['class'].value_counts()
```

```
Out[10]: ckd        248
         notckd     150
         ckd\t        2
         Name: class, dtype: int64
```

```
In [11]: df['class'].unique()
```

```
Out[11]: array(['ckd', 'ckd\t', 'notckd'], dtype=object)
```

There is a duplicate class value with the tab (\t) included as "ckd\t". Checking the number of data points for the calss "ckd\t" in the following cell.

```
In [12]: df[df["class"]=="ckd\t"]
```

Out[12]:

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wbcc	rbcc	htn
37	72.0	80.0	NaN	NaN	NaN	NaN	NaN	notpresent	notpresent	137.0	...	28.0	6900.0	2.5	yes
230	65.0	60.0	1.01	2.0	0.0	normal	abnormal	present	notpresent	192.0	...	NaN	9500.0	NaN	yes

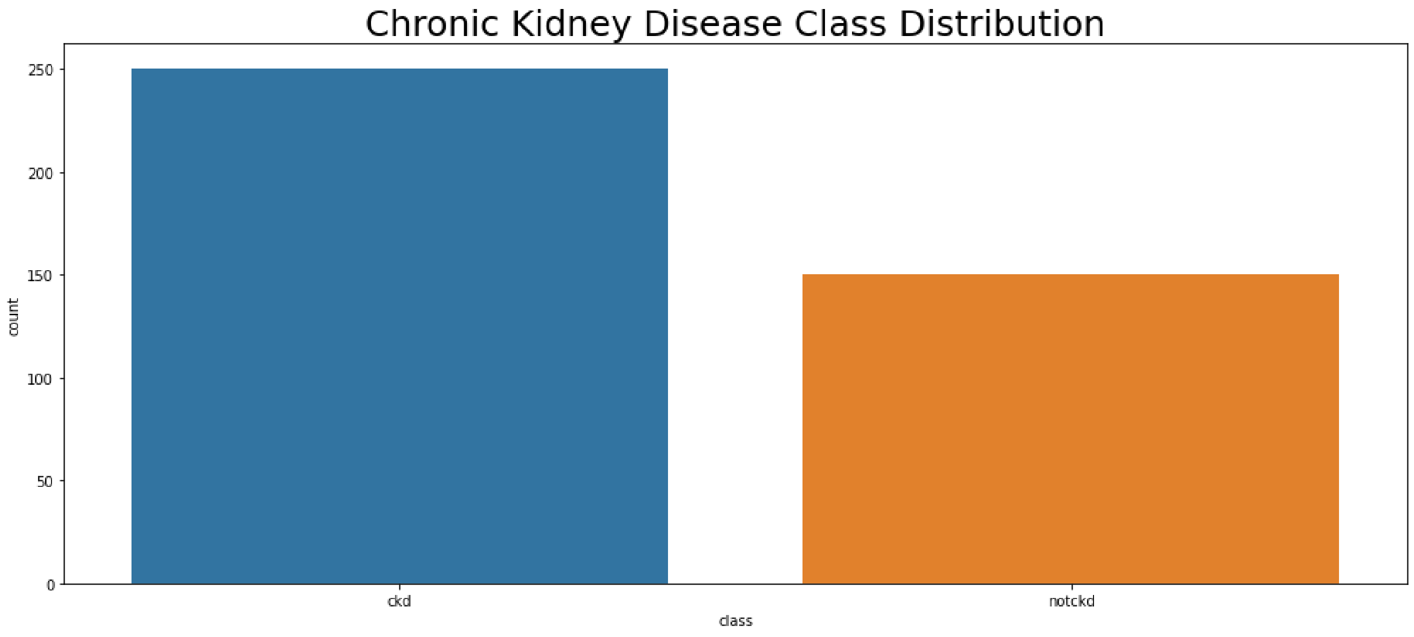
2 rows × 25 columns

Now replacing the "ckd\t" class with "ckd" as it is the valid class value.

```
In [13]: df["class"]=df["class"].replace("ckd\t","ckd",regex=True)
```

Checking the class distribution with the help data visualisation tool matplotlib.

```
In [14]: plt.figure(figsize=(17,7))
         sns.countplot(data=df, x="class")
         plt.title("Chronic Kidney Disease Class Distribution", fontsize=25)
         plt.show()
```



Here I am checking if **age** has any null values. And if find any, filling null value as a mean of all the vlaues in the column.

In [15]:
```
df["age"].isnull().sum()
```

Out[15]:
```
9
```

In [16]:
```
df["age"]=df["age"].fillna(df["age"].mean())
```

In [17]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 25 columns):
 #   Column  Non-Null Count  Dtype  
---  ------  --------------  -----  
 0   age     400 non-null    float64
 1   bp      388 non-null    float64
 2   sg      353 non-null    float64
 3   al      354 non-null    float64
 4   su      351 non-null    float64
 5   rbc     248 non-null    object 
 6   pc      335 non-null    object 
 7   pcc     396 non-null    object 
 8   ba      396 non-null    object 
 9   bgr     356 non-null    float64
 10  bu      381 non-null    float64
 11  sc      383 non-null    float64
 12  sod     313 non-null    float64
 13  pot     312 non-null    float64
 14  hemo    348 non-null    float64
 15  pcv     329 non-null    float64
 16  wbcc    294 non-null    float64
 17  rbcc    269 non-null    float64
 18  htn     398 non-null    object 
 19  dm      398 non-null    object 
 20  cad     398 non-null    object 
 21  appet   399 non-null    object 
 22  pe      399 non-null    object 
 23  ane     399 non-null    object 
 24  class   400 non-null    object 
dtypes: float64(14), object(11)
memory usage: 78.2+ KB
```

Filling Null Values

In following cell I am looking at the numeric columns and filling numeric null values with median of all the available values.

In [18]:
```
numerical=[]
for col in df.columns:
    if df[col].dtype=="float64":
        numerical.append(col)

for col in df.columns:
    if col in numerical:
        df[col].fillna(df[col].median(), inplace=True)
    else:
        df[col].fillna(df[col].mode()[0], inplace=True)
```

Label Encoder

Label Encoding provides the simple and effective way of converting the categorical values to numerical ones. With the scikit-learn's LabelEncoder function we can encode the categorical values efficiently.

In [19]:
```
le = LabelEncoder()
object_col = [col for col in df.columns if df[col].dtype == 'object']
for col in object_col:
    df[col] = le.fit_transform(df[col])
```

In [20]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 25 columns):
 #   Column  Non-Null Count  Dtype  
---  ------  --------------  -----  
 0   age     400 non-null    float64
 1   bp      400 non-null    float64
 2   sg      400 non-null    float64
 3   al      400 non-null    float64
 4   su      400 non-null    float64
 5   rbc     400 non-null    int64  
 6   pc      400 non-null    int64  
 7   pcc     400 non-null    int64  
 8   ba      400 non-null    int64  
 9   bgr     400 non-null    float64
 10  bu      400 non-null    float64
 11  sc      400 non-null    float64
 12  sod     400 non-null    float64
 13  pot     400 non-null    float64
 14  hemo    400 non-null    float64
 15  pcv     400 non-null    float64
 16  wbcc    400 non-null    float64
 17  rbcc    400 non-null    float64
 18  htn     400 non-null    int64  
 19  dm      400 non-null    int64  
 20  cad     400 non-null    int64  
 21  appet   400 non-null    int64  
 22  pe      400 non-null    int64  
 23   ane      400 non-null    int64
 24   class    400 non-null    int64
dtypes: float64(14), int64(11)
memory usage: 78.2 KB
```

In [21]:

```
df
```

Out[21]:

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wbcc	rbcc	htn	dm	cad	appet	pe
0	48.0	80.0	1.020	1.0	0.0	1	1	0	0	121.0	...	44.0	7800.0	5.2	1	2	0	0	0
1	7.0	50.0	1.020	4.0	0.0	1	1	0	0	121.0	...	38.0	6000.0	4.8	0	1	0	0	0
2	62.0	80.0	1.010	2.0	3.0	1	1	0	0	423.0	...	31.0	7500.0	4.8	0	2	0	1	0
3	48.0	70.0	1.005	4.0	0.0	1	0	1	0	117.0	...	32.0	6700.0	3.9	1	1	0	1	1
4	51.0	80.0	1.010	2.0	0.0	1	1	0	0	106.0	...	35.0	7300.0	4.6	0	1	0	0	0
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
395	55.0	80.0	1.020	0.0	0.0	1	1	0	0	140.0	...	47.0	6700.0	4.9	0	1	0	0	0
396	42.0	70.0	1.025	0.0	0.0	1	1	0	0	75.0	...	54.0	7800.0	6.2	0	1	0	0	0
397	12.0	80.0	1.020	0.0	0.0	1	1	0	0	100.0	...	49.0	6600.0	5.4	0	1	0	0	0
398	17.0	60.0	1.025	0.0	0.0	1	1	0	0	114.0	...	51.0	7200.0	5.9	0	1	0	0	0
399	58.0	80.0	1.025	0.0	0.0	1	1	0	0	131.0	...	53.0	6800.0	6.1	0	1	0	0	0

400 rows × 25 columns

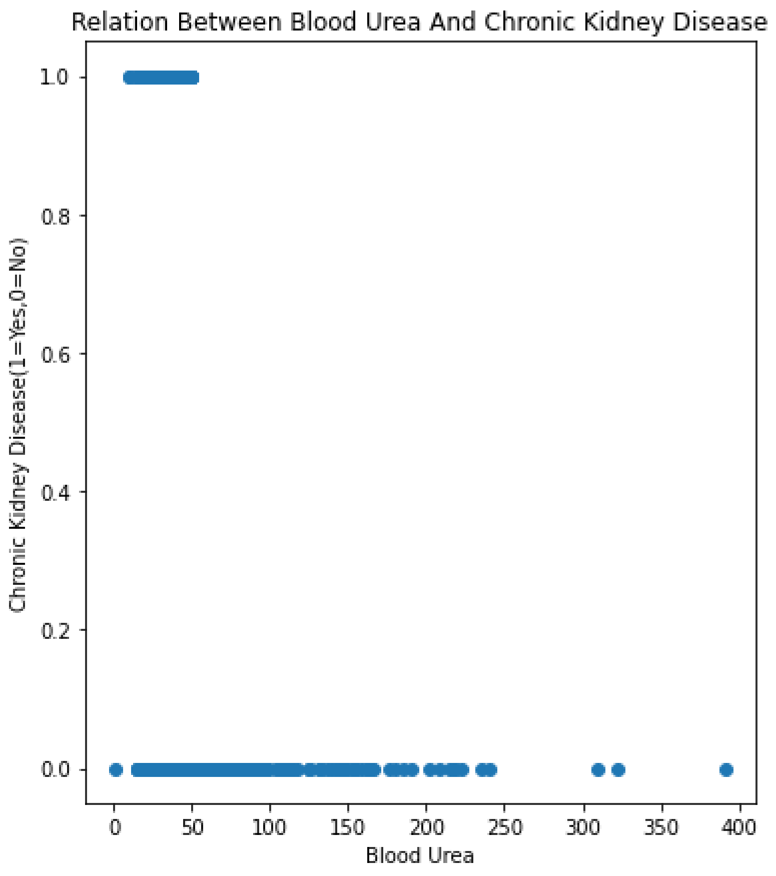
Data Visualisation

Here in following cells I am trying find correlation between the combination of columns.

The normal range of the blood urea is in between 15 to 40 as blood urea goes beyond 40 there might be chances of the kidney failure same can be observed in following scatter plot.

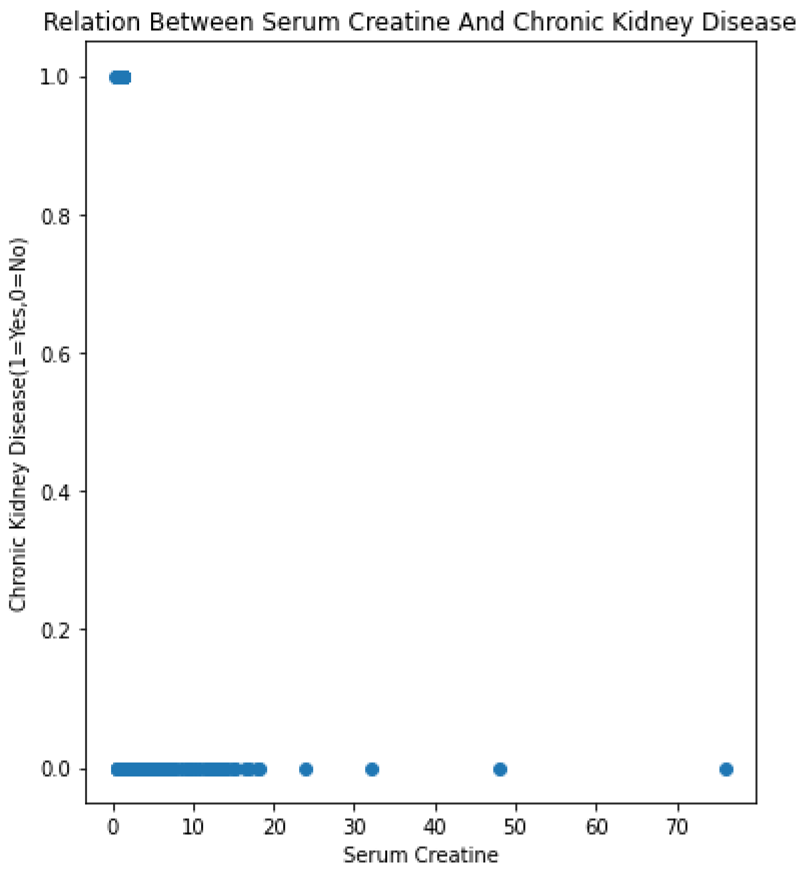
In [22]:

```
fig, ax = plt.subplots(figsize=(6,7))
M=df[['bu']]
N=df[['class']]
plt.title("Relation Between Blood Urea And Chronic Kidney Disease")
plt.xlabel("Blood Urea")
plt.ylabel("Chronic Kidney Disease(1=Yes,0=No)")
ax.scatter(M,N)
plt.show()
```



The normal serum creatine range is inbetween 0.5 to 1.5. If Serum Creatine goes beyond 1.5, there are higher chances of kidney failure and same can be observed in following scatter plot.

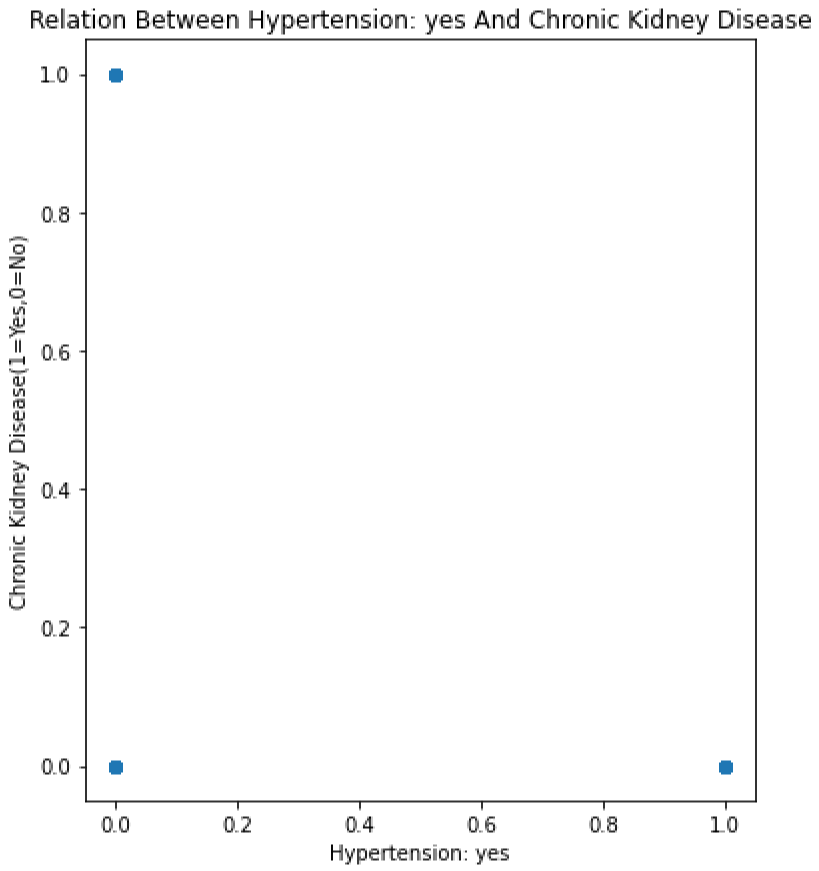
In [23]:
```
fig, ax = plt.subplots(figsize=(6,7))
M=df[['sc']]
N=df[['class']]
plt.title("Relation Between Serum Creatine And Chronic Kidney Disease")
plt.xlabel("Serum Creatine")
plt.ylabel("Chronic Kidney Disease(1=Yes,0=No)")
ax.scatter(M,N)
plt.show()
```



Hypertension is one of the most major factor in Kidney failures and same can be observed in following scatter plot.

In [24]:

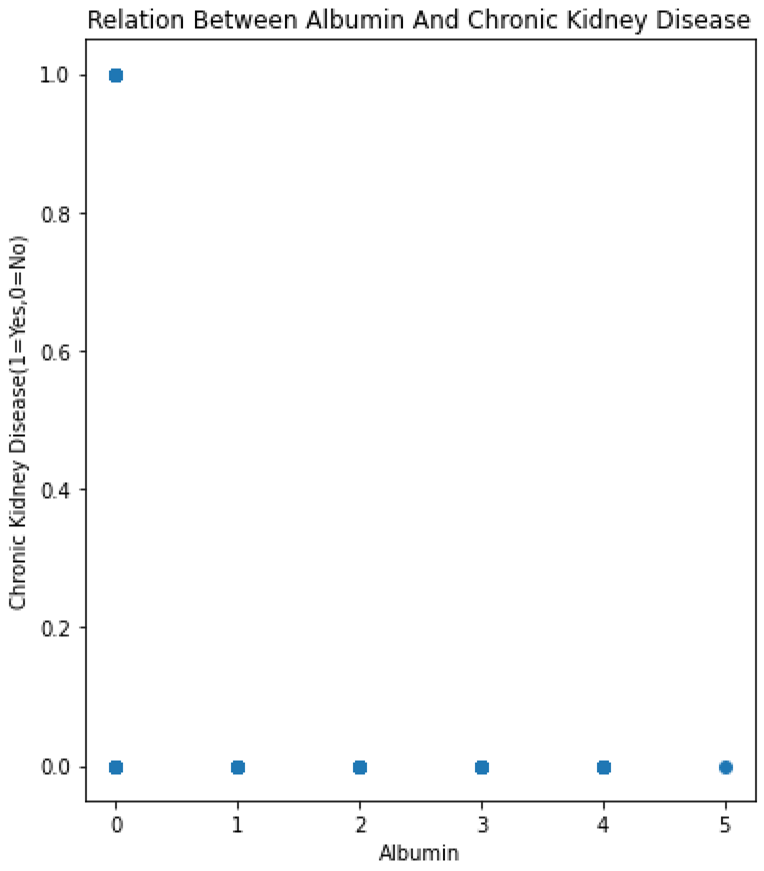
```
fig, ax = plt.subplots(figsize=(6,7))
M=df[['htn']]
N=df[['class']]
plt.title("Relation Between Hypertension: yes And Chronic Kidney Disease")
plt.xlabel("Hypertension: yes")
plt.ylabel("Chronic Kidney Disease(1=Yes,0=No)")
ax.scatter(M,N)
plt.show()
```



If urine albumin goes beyond its normal range it leads to protein leakage which eventually leads to Kidney failure if not dignosed and treated in time.

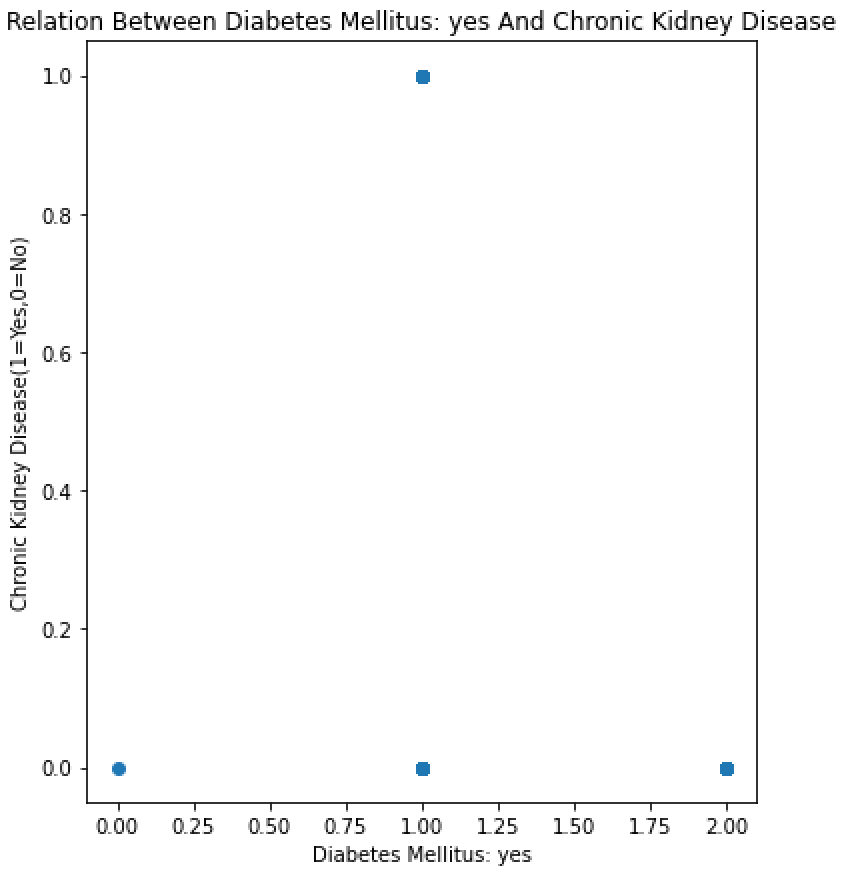
In [25]:

```
fig, ax = plt.subplots(figsize=(6,7))
M=df[['al']]
N=df[['class']]
plt.title("Relation Between Albumin And Chronic Kidney Disease")
plt.xlabel("Albumin")
plt.ylabel("Chronic Kidney Disease(1=Yes,0=No)")
ax.scatter(M,N)
plt.show()
```

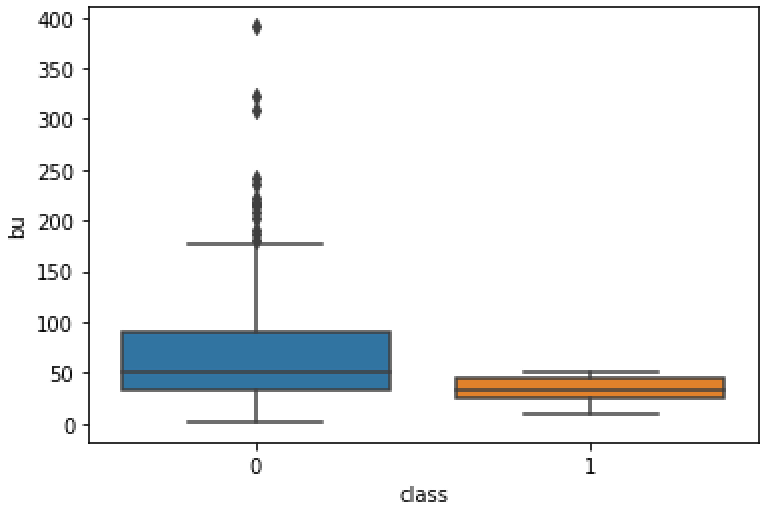


Diabetes as well plays vital role in kidney failures.

In [26]:
```
fig, ax = plt.subplots(figsize=(6,7))
M=df[['dm']]
N=df[['class']]
plt.title("Relation Between Diabetes Mellitus: yes And Chronic Kidney Disease")
plt.xlabel("Diabetes Mellitus: yes")
plt.ylabel("Chronic Kidney Disease(1=Yes,0=No)")
ax.scatter(M,N)
plt.show()
```

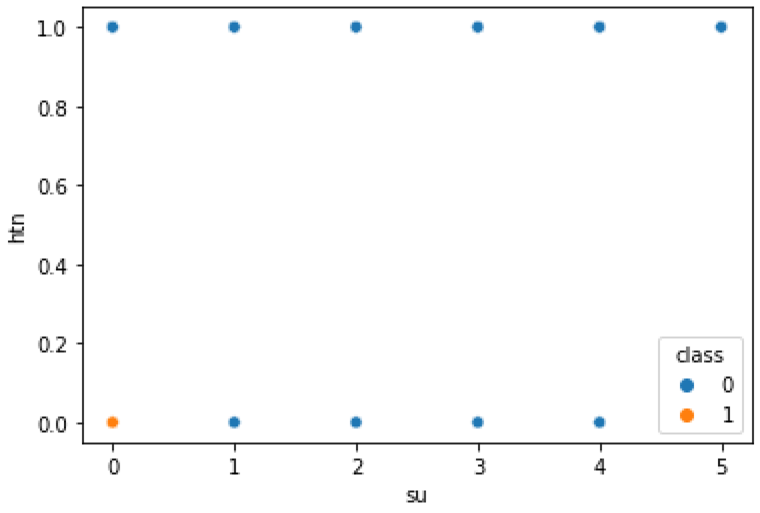


```
In [27]: sns.boxplot(x=df['class'], y=df['bu'])
         plt.show();
```



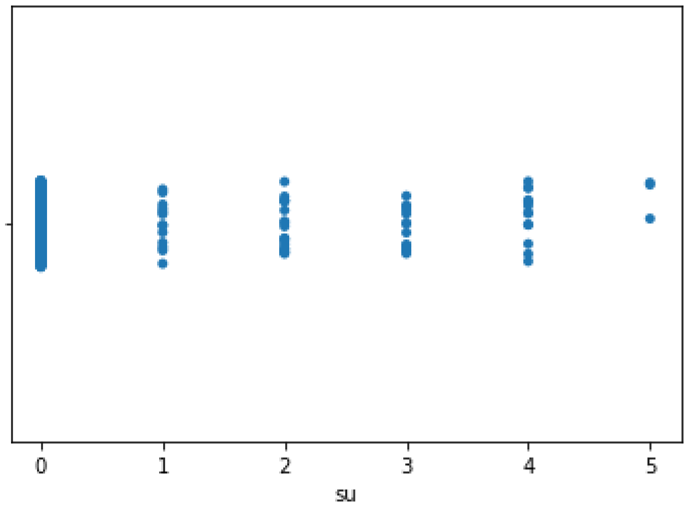
```
In [28]: sns.scatterplot(data=df,x="su",y="htn",hue='class')
```

```
Out[28]: <AxesSubplot:xlabel='su', ylabel='htn'>
```



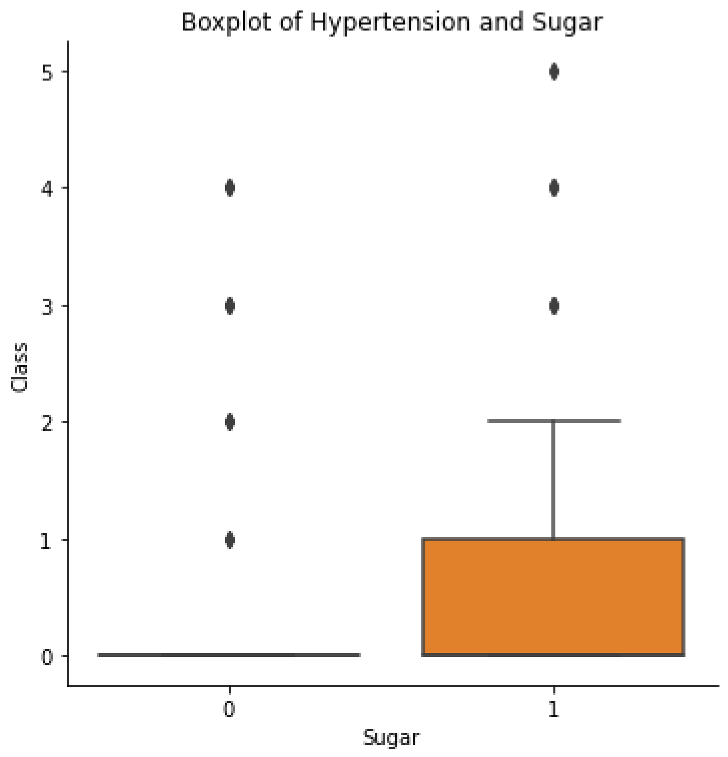
```
In [29]: sns.stripplot(x=df["su"])
```

```
Out[29]: <AxesSubplot:xlabel='su'>
```

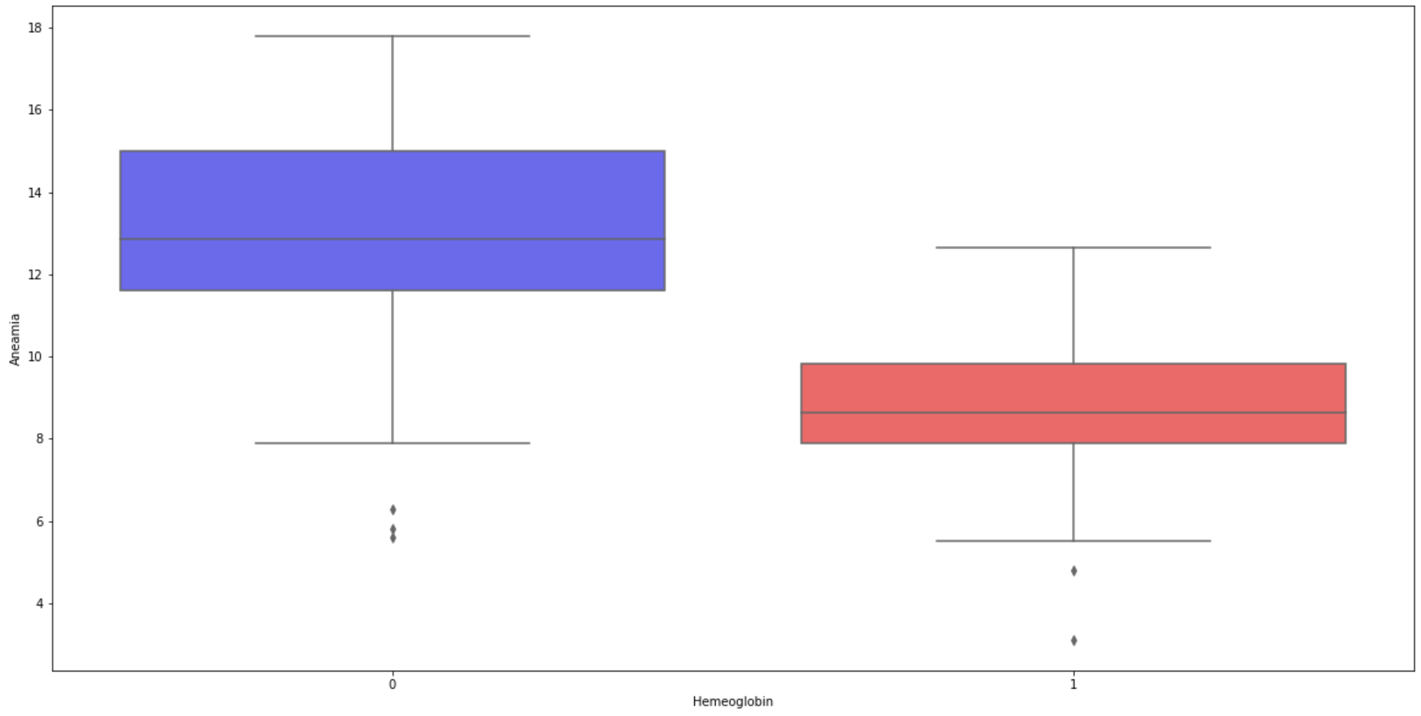


```
In [30]: sns.catplot(x="htn",y="su",data=df,kind="box");
         plt.xlabel("Sugar")
         plt.ylabel("Class")
         plt.title("Boxplot of Hypertension and Sugar")
```

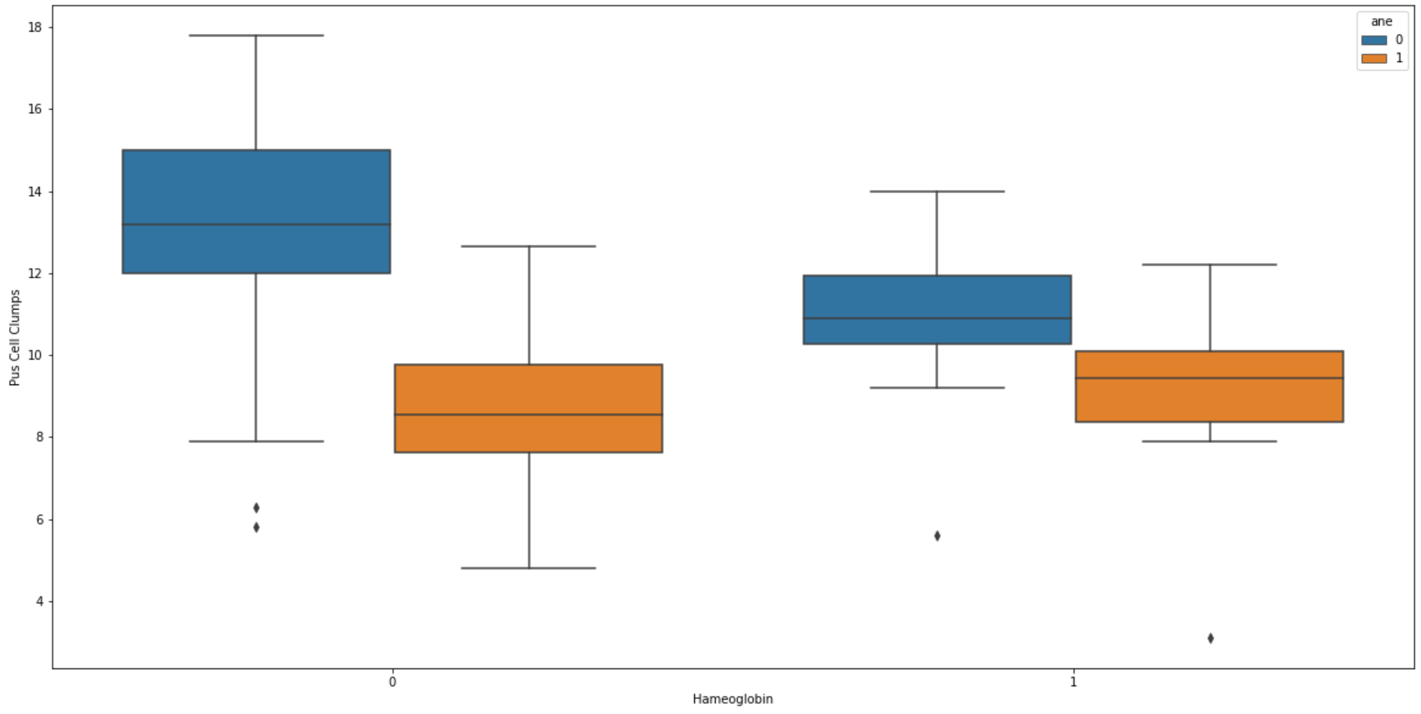
```
Out[30]: Text(0.5, 1.0, 'Boxplot of Hypertension and Sugar')
```



In [31]:
```
plt.figure(figsize=(20,10))
sns.boxplot(data=df, x="ane", y="hemo", palette='seismic')
plt.xlabel("Hemeoglobin")
plt.ylabel("Aneamia")
plt.show()
```



In [32]:
```
plt.figure(figsize=(20,10))
sns.boxplot(data=df, y='hemo', x="pcc", hue="ane")
plt.xlabel("Hameoglobin")
plt.ylabel("Pus Cell Clumps")
plt.show()
```



Understanding the data distribution over a class categories.

In [33]:

```
df.groupby("class").mean()
```

Out[33]:

class	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	
0	54.443468	79.640000	1.014940	1.44	0.632	0.812	0.696	0.168	0.088	167.148000	...	11.016000	3
1	46.549889	71.466667	1.022333	0.00	0.000	1.000	1.000	0.000	0.000	108.253333	...	15.086667	4

2 rows × 24 columns

Defining Target and Independent Variables

Here **class** is the target variable and all the other features independent variables which helps in prediction.

In [34]:

```
X=df.loc[:, df.columns != 'class']
y=df[['class']]
```

Split Data into Train & Test

In [35]:

```
X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.20,random_state=100)
```

In [36]:

```
print("Training Data ::-")
print("X Shape:-" ,X_train.shape)
print("y Shape:-" ,y_train.shape)
```

```
Training Data ::-
X Shape:- (320, 24)
y Shape:- (320, 1)
```

In [37]:

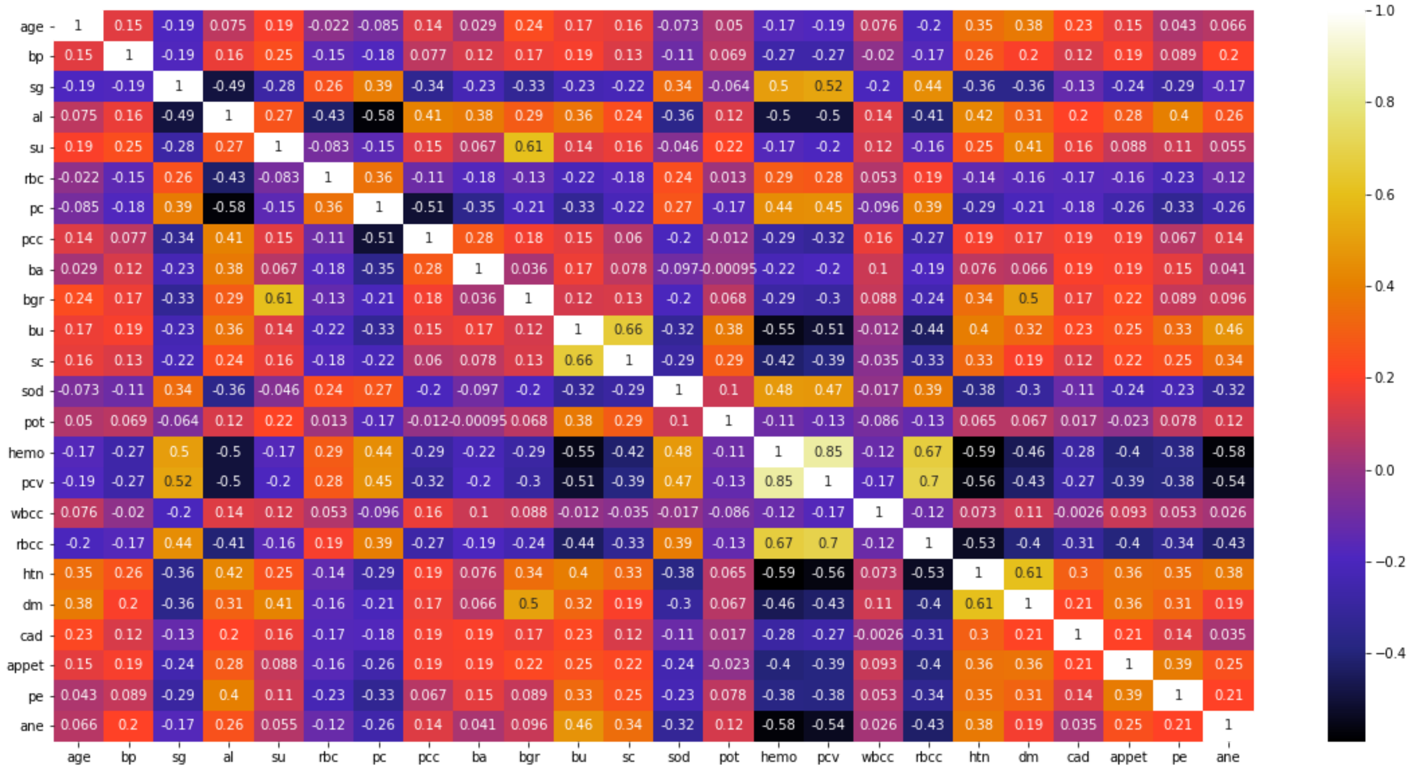
```python
print("Testing Data ::-")
print("X Shape:-" ,X_test.shape)
print("y Shape:-" ,y_test.shape)
```

```
Testing Data ::-
X Shape:- (80, 24)
y Shape:- (80, 1)
```

Pearson Correlation heatmap

In [38]:

```python
plt.figure(figsize=(20,10))
cor = X_train.corr()
sns.heatmap(cor, annot=True, cmap=plt.cm.CMRmap)
plt.show()
```



The following function gets the correlated features. It first removes feature correlated with other features.

In [39]:

```python
def correlated_features(data, corr_threshold):
    col_corr = set()   # Set of all correlated columns
    corr_matrix = data.corr()
    for i in range(len(corr_matrix.columns)):
        for j in range(i):
            if abs(corr_matrix.iloc[i, j]) > corr_threshold: # I am interested in absolute
                col = corr_matrix.columns[i]   # getting the name of column
                col_corr.add(col)
    return col_corr
```

In [40]:

```python
corr_threshold = 0.75
corr_features = correlated_features(X_train, corr_threshold)
len(set(corr_features))
```

Out[40]:

```
1
```

In [41]:

```python
corr_features
```

Out[41]:
```
{'pcv'}
```

Removing the found correlated features in the dataset.

In [42]:
```
X_train.drop(corr_features,axis=1)
X_test.drop(corr_features,axis=1)
```

Out[42]:

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pot	hemo	wbcc	rbcc	htn	dm	cad	app
248	59.0	70.0	1.010	1.0	3.0	0	0	0	0	424.0	...	4.5	12.60	10200.0	4.1	1	2	1	
318	61.0	70.0	1.025	0.0	0.0	1	1	0	0	120.0	...	3.5	17.40	7000.0	5.3	0	1	0	
173	17.0	70.0	1.015	1.0	0.0	0	1	0	0	22.0	...	2.8	13.10	11200.0	4.8	0	1	0	
285	66.0	70.0	1.020	0.0	0.0	1	1	0	0	94.0	...	3.9	16.00	5300.0	5.9	0	1	0	
184	54.0	60.0	1.015	3.0	2.0	1	0	0	0	352.0	...	4.5	11.30	5800.0	3.6	1	2	1	
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
358	47.0	60.0	1.020	0.0	0.0	1	1	0	0	117.0	...	3.5	13.00	5200.0	5.6	0	1	0	
166	27.0	60.0	1.020	0.0	0.0	1	1	0	0	76.0	...	4.3	12.65	8000.0	4.8	0	1	0	
198	59.0	100.0	1.020	4.0	2.0	1	1	0	0	252.0	...	4.7	11.20	26400.0	3.9	1	2	0	
267	48.0	80.0	1.025	0.0	0.0	1	1	0	0	122.0	...	3.9	13.90	9500.0	4.8	0	1	0	
69	26.0	70.0	1.015	0.0	4.0	1	1	0	0	250.0	...	4.4	15.60	6900.0	6.0	0	2	0	

80 rows × 23 columns

Standarlization of X variables

Machine Learning models tend to work better and expectedly when features are relatively on similar scale and close to normal distribution. Although with the real-world data this may be hardly the case. So, it is always advised to standardise the features with the scikit-learn's StandardScaler(). It standardizes a feature by subtracting the mean and then scaling to unit variance. Unit variance means dividing all the values by the standard deviation. StandardScaler does not meet the strict definition of scale I introduced earlier. StandardScaler results in a distribution with a standard deviation equal to 1. The variance is equal to 1 also, because variance = standard deviation squared. And 1 squared is 1. StandardScaler makes the mean of the distribution approximately 0.

[Reference: - https://towardsdatascience.com/scale-standardize-or-normalize-with-scikit-learn-6ccc7d176a02#:~:text=StandardScaler%20is%20the%20industry's%20go,of%20scale%20I%20introduced%2

In [43]:
```
std_scalar=StandardScaler()
X=std_scalar.fit_transform(X)
```

In [44]:
```
X.shape
```

Out[44]:
```
(400, 24)
```

Decision Tree Classifier

Decision tree is one of the Classic supervised learning algorithms which mostly used to solve the classification problems.

A decision tree classifier creates a classification model by building a decision tree. Each node in the tree specifies a test on an attribute, and each branch descending from that node corresponds to one of the possible outcomes for that attribute.

Modeling

In [45]:
```
model=DecisionTreeClassifier(random_state=100)
model.fit(X_train,y_train)
```

Out[45]:
```
DecisionTreeClassifier(random_state=100)
```

In [ ]:
```
```

Model Prediction

In [46]:
```
y_predict=model.predict(X_test)
print(y_predict)
```

```
[0 1 0 1 0 0 0 1 0 0 0 1 1 0 1 1 0 1 0 0 1 0 0 0 1 0 0 1 0 0 0 0 0 0 1 1 1
 1 0 0 0 0 0 1 1 0 0 0 0 0 0 0 0 0 1 1 1 0 1 1 1 0 1 0 0 1 1 0 0 1 0 1 0 0
 1 1 0 0 1 0]
```

Probability of Each Predicted Class

In [47]:
```
print(model.predict_proba(X_test))
```

```
[[1. 0.]
 [0. 1.]
 [1. 0.]
 [0. 1.]
 [1. 0.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [1. 0.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [0. 1.]
 [1. 0.]
 [0. 1.]
 [0. 1.]
 [1. 0.]
 [0. 1.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [1. 0.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [1. 0.]
 [1. 0.]
 [1. 0.]
 [1. 0.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [0. 1.]
 [0. 1.]
 [0. 1.]
 [1. 0.]
 [1. 0.]
 [1. 0.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [0. 1.]
 [1. 0.]
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 [1. 0.]
 [1. 0.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [0. 1.]
 [0. 1.]
 [1. 0.]
 [0. 1.]
 [0. 1.]
 [0. 1.]
 [1. 0.]
 [0. 1.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [0. 1.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [1. 0.]
 [0. 1.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [0. 1.]
 [1. 0.]
 [1. 0.]
 [0. 1.]
 [1. 0.]]
```

Model Evaluation

In [48]:
```
print(confusion_matrix(y_test,y_predict))
```

```
[[49  2]
 [ 0 29]]
```

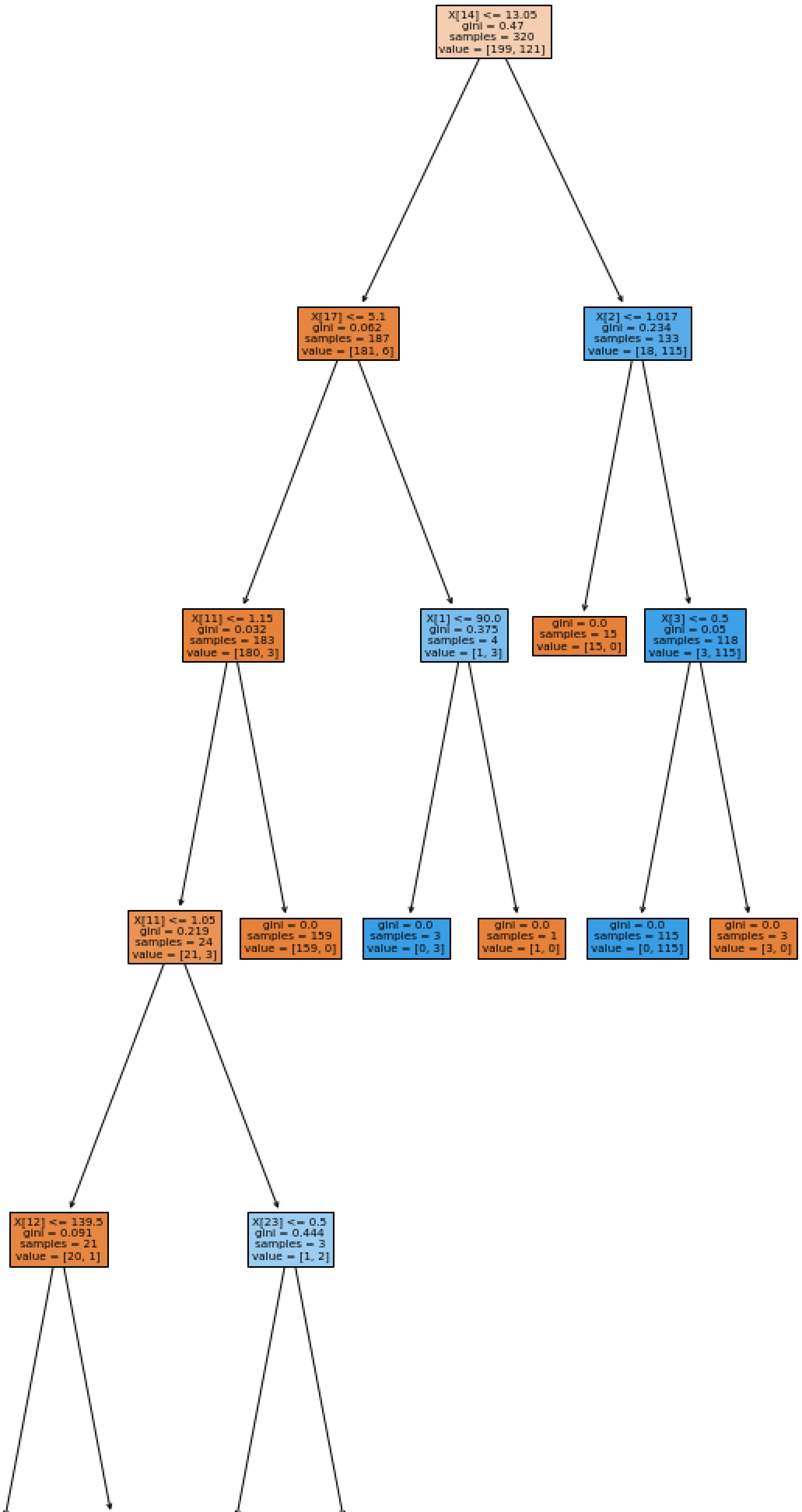
In [49]:
```
print(classification_report(y_test, y_predict))
```

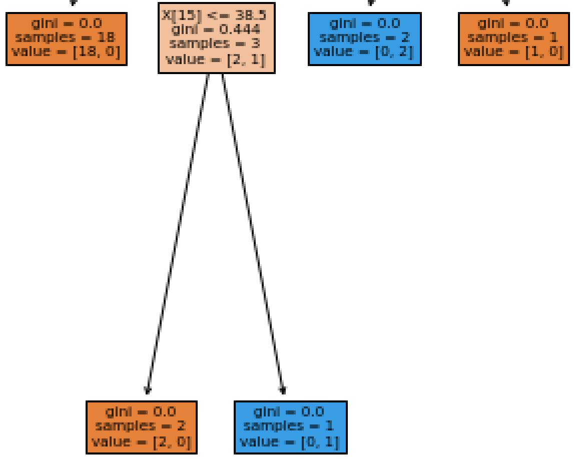
```
              precision    recall  f1-score   support

           0       1.00      0.96      0.98        51
           1       0.94      1.00      0.97        29

    accuracy                           0.97        80
   macro avg       0.97      0.98      0.97        80
weighted avg       0.98      0.97      0.98        80
```

Decision Tree Visualisation

In [50]:

```
plt.figure(figsize=(10,25))
plot_tree(model,filled=True);
```


X[14] <= 13.05
gini = 0.47
samples = 320
value = [199, 121]
X[17] <= 5.1
gini = 0.062
samples = 187
value = [181, 6]
X[2] <= 1.017
gini = 0.234
samples = 133
value = [18, 115]
X[11] <= 1.15
gini = 0.032
samples = 183
value = [180, 3]
X[1] <= 90.0
gini = 0.375
samples = 4
value = [1, 3]
gini = 0.0
samples = 15
value = [15, 0]
X[3] <= 0.5
gini = 0.05
samples = 118
value = [3, 115]
X[11] <= 1.05
gini = 0.219
samples = 24
value = [21, 3]
gini = 0.0
samples = 159
value = [159, 0]
gini = 0.0
samples = 3
value = [0, 3]
gini = 0.0
samples = 1
value = [1, 0]
gini = 0.0
samples = 115
value = [0, 115]
gini = 0.0
samples = 3
value = [3, 0]
X[12] <= 139.5
gini = 0.091
samples = 21
value = [20, 1]
X[23] <= 0.5
gini = 0.444
samples = 3
value = [1, 2]



Zipping the model

In [51]:

```
import pickle
from zipfile import ZipFile

pickle.dump(model, open('Chronic_Kidney_Disease_Prediction_Model.pkl','wb'))

with ZipFile('Chronic_Kidney_Disease_Prediction_Model.zip', 'w') as myzip:
    myzip.write("Chronic_Kidney_Disease_Prediction_Model.pkl")
```

Conclusion

Here I used the **Chronic Kidney Disease** dataset published at **UCIML Repo**. I tried to predict the **Chronic Kidney Disease** using the Decision tree classification approach. As we can see from the model evaluations was able to achieve the accuracy of 97%. We can try to gain more accuracy by refining train-test split ratio or considering more significant features from the dataset with the help of domain experts.