STATS 3DA3

Homework Assignment 6

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(Rubini and Eswaran 2015)

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.metrics import mean_squared_error, confusion_matrix, classification_report
from sklearn.tree import DecisionTreeClassifier, DecisionTreeRegressor, plot_tree
from patsy import dmatrices, dmatrix
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.linear_model import LinearRegression
from sklearn.preprocessing import PolynomialFeatures
from sklearn.metrics import accuracy_score
import statsmodels.api as sm
```

```
pip install ucimlrepo
```

```
Requirement already satisfied: ucimlrepo in /Users/dailing/Desktop/3da-assignment6/.conda/lib/p
Note: you may need to restart the kernel to use updated packages.
```

```
from ucimlrepo import fetch_ucirepo

# fetch dataset
chronic_kidney_disease = fetch_ucirepo(id=336)

# data (as pandas dataframes)
X = chronic_kidney_disease.data.features
y = chronic_kidney_disease.data.targets

# metadata
```

```
print(chronic_kidney_disease.metadata)


# variable information
print(chronic_kidney_disease.variables)
```

```
{'uci_id': 336, 'name': 'Chronic Kidney Disease', 'repository_url': 'https://archive.ics.uci.e
     name     role         type demographic              description  \
0     age  Feature      Integer         Age                     None
1      bp  Feature      Integer        None           blood pressure
2      sg  Feature  Categorical        None         specific gravity
3      al  Feature  Categorical        None                  albumin
4      su  Feature  Categorical        None                    sugar
5     rbc  Feature       Binary        None          red blood cells
6      pc  Feature       Binary        None                 pus cell
7     pcc  Feature       Binary        None          pus cell clumps
8      ba  Feature       Binary        None                 bacteria
9     bgr  Feature      Integer        None     blood glucose random
10     bu  Feature      Integer        None               blood urea
11     sc  Feature   Continuous        None         serum creatinine
12    sod  Feature      Integer        None                   sodium
13    pot  Feature   Continuous        None                potassium
14   hemo  Feature   Continuous        None               hemoglobin
15    pcv  Feature      Integer        None        packed cell volume
16   wbcc  Feature      Integer        None   white blood cell count
17   rbcc  Feature   Continuous        None     red blood cell count
18    htn  Feature       Binary        None             hypertension
19     dm  Feature       Binary        None        diabetes mellitus
20    cad  Feature       Binary        None  coronary artery disease
21  appet  Feature       Binary        None                 appetite
22     pe  Feature       Binary        None              pedal edema
23    ane  Feature       Binary        None                   anemia
24  class   Target       Binary        None           ckd or not ckd
```

```
           units missing_values
0           year            yes
1          mm/Hg            yes
2           None            yes
3           None            yes
4           None            yes
5           None            yes
6           None            yes
7           None            yes
8           None            yes
9         mgs/dl            yes
10        mgs/dl            yes
11        mgs/dl            yes
12         mEq/L            yes
13         mEq/L            yes
14           gms            yes
15          None            yes
16     cells/cmm            yes
17  millions/cmm            yes
18          None            yes
19          None            yes
20          None            yes
21          None            yes
22          None            yes
23          None            yes
24          None             no
```

```
X
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	pcv	w
0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	...	15.4	44.0	78
1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	...	11.3	38.0	60
2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	423.0	...	9.6	31.0	75
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	117.0	...	11.2	32.0	67
4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	106.0	...	11.6	35.0	73
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	140.0	...	15.7	47.0	67
396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	75.0	...	16.5	54.0	78
397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	100.0	...	15.8	49.0	66
398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	114.0	...	14.2	51.0	72
399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	131.0	...	15.8	53.0	68

```
y
```

	class
0	ckd
1	ckd
2	ckd
3	ckd
4	ckd
...	...
395	notckd
396	notckd
397	notckd
398	notckd
399	notckd

```
X.dtypes
```

```
age       float64
```

```
bp       float64
sg       float64
al       float64
su       float64
rbc       object
pc        object
pcc       object
ba        object
bgr      float64
bu       float64
sc       float64
sod      float64
pot      float64
hemo     float64
pcv      float64
wbcc     float64
rbcc     float64
htn       object
dm        object
cad       object
appet     object
pe        object
ane       object
dtype: object
```

```
y.dtypes
```

```
class    object
dtype: object
```

```
#to see if "rbc" is binary, since from the website inormation I found that this variable shoul
X['rbc'].value_counts()
```

```
rbc
normal      201
abnormal     47
Name: count, dtype: int64
```

```python
#to see if "pc" is binary, since from the website inormation I found that this variable should
X['pc'].value_counts()
```

```
pc
normal      259
abnormal     76
Name: count, dtype: int64
```

```python
#to see if "pcc" is binary, since from the website inormation I found that this variable shoul
X['pcc'].value_counts()
```

```
pcc
notpresent    354
present        42
Name: count, dtype: int64
```

```python
#to see if "ba" is binary, since from the website inormation I found that this variable should
X['ba'].value_counts()
```

```
ba
notpresent    374
present        22
Name: count, dtype: int64
```

```python
#to see if "htn" is binary, since from the website inormation I found that this variable shoul
X['htn'].value_counts()
```

```
htn
no     251
yes    147
Name: count, dtype: int64
```

```
#to see if "dm" is binary, since from the website inormation I found that this variable should
X['dm'].value_counts()
```

```
dm
no      260
yes     137
\tno      1
Name: count, dtype: int64
```

```
#find that "dm" is not binary, but it should be binary.
X_cat = set(X["dm"])
X_cat
```

```
{'\tno', nan, 'no', 'yes'}
```

```
#make "dm" become binary
X['dm'] = X['dm'].replace('\tno', 'no')
X_cat = set(X["dm"])
X_cat
```

```
{nan, 'no', 'yes'}
```

```
#to double check if "dm" is binary now.
X['dm'].value_counts()
```

```
dm
no     261
yes    137
Name: count, dtype: int64
```

```
#to see if "cad" is binary, since from the website inormation I found that this variable shoul
X['cad'].value_counts()
```

```
cad
no     364
yes     34
Name: count, dtype: int64
```

```
#to see if "appet" is binary, since from the website inormation I found that this variable sho
X['appet'].value_counts()
```

```
appet
good    317
poor     82
Name: count, dtype: int64
```

```
#to see if "pe" is binary, since from the website inormation I found that this variable should
X['pe'].value_counts()
```

```
pe
no     323
yes     76
Name: count, dtype: int64
```

```
#to see if "ane" is binary, since from the website inormation I found that this variable shoul
X['ane'].value_counts()
```

```
ane
no     339
yes     60
Name: count, dtype: int64
```

```python
#to see if "class" is binary, since from the website inormation I found that this variable shou
y['class'].value_counts()
```

```
class
ckd        248
notckd     150
ckd\t        2
Name: count, dtype: int64
```

```python
#find "class" is not binary, but it should be ninary.
y_cat = set(y["class"])
y_cat
```

```
{'ckd', 'ckd\t', 'notckd'}
```

```python
# make itbecome binary
y['class'] = y['class'].replace('ckd\t', 'ckd')
y_cat = set(y["class"])
y_cat
```

```
{'ckd', 'notckd'}
```

```python
#To double check if it is binary now.
y['class'].value_counts()
```

```
class
ckd        250
notckd     150
Name: count, dtype: int64
```

```
# number of missing values in X
X.isnull().sum()
```

```
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
dtype: int64
```

```
# number of missing values in y
y.isnull().sum()
```

```
class    0
dtype: int64
```

1. **Classification Problem Identification:** Define and describe a classification problem based on the dataset.

There are 400 observations and 25 variables in Chronic Kidney Disease dataset. There are 14 float64 type variables, and they are "age", "bp", "sg", "al", "su", "bgr", "bu", "sc", "sod", "pot", "hemo", "pcv", "wbcc", "rbcc". There are 11 object type vaariables, and they are "rbc", "pc", "pcc", "ba", "htn", "dm", "cad", "appet", "pe", "ane", "calss". In these 25 variables, all variables in X are covariates (consists 14 floats and 10 object) and the variable in y is the response (the variable "class" which is an object variable). Moreover, the response is "class" contains only 2 category:"ckd" or "not ckd", so the response is binary.

There are 9 missing values in "age", 12 missing values in "bp", 47 missing values in "sg", 46 missing values in "al", 49 missing values in "su", 152 missing values in "rbc", 65 missing values in "pc", 4 missing values in "pcc", 4 missing values in "ba", 44 missing values in "bgr", 19 missing values in "bu", 17 missing values in "sc", 87 missing values in "sod", 88 missing values in "pot", 52 missing values in "hemo", 71 missing values in "pcv", 106 missing values in "wbcc", 131 missing values in "rbcc", 2 missing values in "htn", 2 missing values in "dm", 2 missing values in "cad", 1 missing value in "appet", 1 missing value in "pe" and 1 missing value in "ane".

0 missing value in "class".

2. **Variable Transformation:** Implement any transformations chosen or justify the absence of such modifications.

```
X1 = X.copy()
columns_to_convert = ['sg', 'al','su']
for col in columns_to_convert:
    X1[col] = pd.Categorical(X1[col])


object_convert =["rbc", "pc", "pcc", "ba", "htn", "dm", "cad", "appet", "pe", "ane"]
for col in object_convert:
    X1[col] = X1[col].astype('category').cat.codes
X1.dtypes
```

```
age       float64
bp        float64
sg       category
al       category
su       category
rbc          int8
pc           int8
pcc          int8
ba           int8
bgr       float64
bu        float64
sc        float64
sod       float64
pot       float64
hemo      float64
pcv       float64
wbcc      float64
rbcc      float64
htn          int8
dm           int8
cad          int8
appet        int8
pe           int8
ane          int8
dtype: object
```

```
#cat = ['sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'htn', 'dm', 'cad', 'appet', 'pe', 'ane']
#X = pd.get_dummies(X,columns=cat)
#caty = ['class']
```

```
#y = pd.get_dummies(y,columns=caty)
```

```
X1
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	pcv	wbcc	rbcc	htn	dm
0	48.0	80.0	1.020	1.0	0.0	-1	1	0	0	121.0	...	15.4	44.0	7800.0	5.2	1	1
1	7.0	50.0	1.020	4.0	0.0	-1	1	0	0	NaN	...	11.3	38.0	6000.0	NaN	0	0
2	62.0	80.0	1.010	2.0	3.0	1	1	0	0	423.0	...	9.6	31.0	7500.0	NaN	0	1
3	48.0	70.0	1.005	4.0	0.0	1	0	1	0	117.0	...	11.2	32.0	6700.0	3.9	1	0
4	51.0	80.0	1.010	2.0	0.0	1	1	0	0	106.0	...	11.6	35.0	7300.0	4.6	0	0
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
395	55.0	80.0	1.020	0.0	0.0	1	1	0	0	140.0	...	15.7	47.0	6700.0	4.9	0	0
396	42.0	70.0	1.025	0.0	0.0	1	1	0	0	75.0	...	16.5	54.0	7800.0	6.2	0	0
397	12.0	80.0	1.020	0.0	0.0	1	1	0	0	100.0	...	15.8	49.0	6600.0	5.4	0	0
398	17.0	60.0	1.025	0.0	0.0	1	1	0	0	114.0	...	14.2	51.0	7200.0	5.9	0	0
399	58.0	80.0	1.025	0.0	0.0	1	1	0	0	131.0	...	15.8	53.0	6800.0	6.1	0	0

```
X1['sg'].value_counts()
```

```
sg
1.020    106
1.010     84
1.025     81
1.015     75
1.005      7
Name: count, dtype: int64
```

```
#why 3 categories?
X1['rbc'].value_counts()
```

```
rbc
 1    201
```

```
-1    152
 0     47
Name: count, dtype: int64
```

```python
X1['pe'].value_counts()
```

```
pe
 0    323
 1     76
-1      1
Name: count, dtype: int64
```

```python
float_col = X1.select_dtypes(include=['float64']).columns
object_col = X1.select_dtypes(include=['object']).columns
```

```python
#way2
binary = {'rbc':{'normal':1,'abnormal':0},
          'pc':{'normal':1,'abnormal':0},
          'pcc':{'present':1,'notpresent':0},
          'ba':{'present':1,'notpresent':0},
          'htn':{'yes':1,'no':0},
          'dm':{'yes':1,'no':0},
          'cad':{'yes':1,'no':0},
          'appet':{'good':1,'poor':0},
          'pe':{'yes':1,'no':0},
          'ane':{'yes':1,'no':0}


          }


for i,j in binary.items():
    X1[i] = X1[i].replace(j)


X1
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	pcv	wbcc	rbcc	htn	dm
0	48.0	80.0	1.020	1.0	0.0	-1	1	0	0	121.0	...	15.4	44.0	7800.0	5.2	1	1
1	7.0	50.0	1.020	4.0	0.0	-1	1	0	0	NaN	...	11.3	38.0	6000.0	NaN	0	0
2	62.0	80.0	1.010	2.0	3.0	1	1	0	0	423.0	...	9.6	31.0	7500.0	NaN	0	1
3	48.0	70.0	1.005	4.0	0.0	1	0	1	0	117.0	...	11.2	32.0	6700.0	3.9	1	0
4	51.0	80.0	1.010	2.0	0.0	1	1	0	0	106.0	...	11.6	35.0	7300.0	4.6	0	0
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
395	55.0	80.0	1.020	0.0	0.0	1	1	0	0	140.0	...	15.7	47.0	6700.0	4.9	0	0
396	42.0	70.0	1.025	0.0	0.0	1	1	0	0	75.0	...	16.5	54.0	7800.0	6.2	0	0
397	12.0	80.0	1.020	0.0	0.0	1	1	0	0	100.0	...	15.8	49.0	6600.0	5.4	0	0
398	17.0	60.0	1.025	0.0	0.0	1	1	0	0	114.0	...	14.2	51.0	7200.0	5.9	0	0
399	58.0	80.0	1.025	0.0	0.0	1	1	0	0	131.0	...	15.8	53.0	6800.0	6.1	0	0

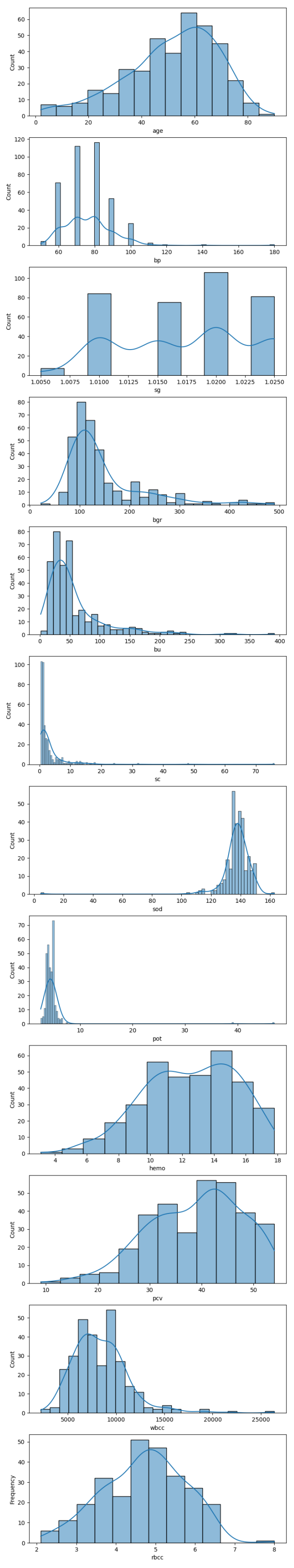
```
scale = StandardScaler()
X1[float_col] = scale.fit_transform(X1[float_col])
X1
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	pcv	wb
0	-0.203139	0.258373	1.020	1.0	0.0	-1	1	0	0	-0.341498	...	0.988022	0.569881	-0.2
1	-2.594124	-1.936857	1.020	4.0	0.0	-1	1	0	0	NaN	...	-0.421688	-0.098536	-0.8
2	0.613295	0.258373	1.010	2.0	3.0	1	1	0	0	3.473064	...	-1.006202	-0.878356	-0.3
3	-0.203139	-0.473370	1.005	4.0	0.0	1	0	1	0	-0.392022	...	-0.456071	-0.766953	-0.5
4	-0.028189	0.258373	1.010	2.0	0.0	1	1	0	0	-0.530963	...	-0.318538	-0.432744	-0.3
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
395	0.205078	0.258373	1.020	0.0	0.0	1	1	0	0	-0.101509	...	1.091172	0.904090	-0.5
396	-0.553039	-0.473370	1.025	0.0	0.0	1	1	0	0	-0.922524	...	1.366237	1.683910	-0.2
397	-2.302541	0.258373	1.020	0.0	0.0	1	1	0	0	-0.606749	...	1.125555	1.126896	-0.6
398	-2.010957	-1.205114	1.025	0.0	0.0	1	1	0	0	-0.429915	...	0.575424	1.349701	-0.4
399	0.380028	0.258373	1.025	0.0	0.0	1	1	0	0	-0.215188	...	1.125555	1.572507	-0.5

3. **Dataset Overview:** Provide a detailed description of the dataset, covering variables, sum-

maries, observation counts, data types, and distributions (at least three statements).

```
def plot_dist(data,features):
    fig,axes=plt.subplots(nrows=len(features),ncols=1,figsize=(8,4*len(features)))
    if len(features) == 1:
        axes = [axes]
    for ax,feature in zip(axes,features):
        sns.histplot(data[feature],kde=True,ax=ax)
    ax.set_xlabel(feature)
    ax.set_ylabel('Frequency')


numerical_cols = ["age","bp","sg","bgr","bu","sc","sod","pot","hemo","pcv","wbcc","rbcc"]
plt.show()
plot_dist(X,numerical_cols)
```


Count
age
Count
bp
Count
sg
Count
bgr
Count
bu
Count
sc
Count
sod
Count
pot
Count
hemo
Count
pcv
Count
wbcc
Frequency
rbcc

```
X1.describe()
```

	age	bp	rbc	pc	pcc	ba	bgr	bu
count	3.910000e+02	3.880000e+02	400.00000	400.000000	400.000000	400.000000	3.560000e+02	3.
mean	9.994847e-17	-2.380684e-16	0.12250	0.485000	0.095000	0.045000	-1.796316e-16	-3
std	1.001281e+00	1.001291e+00	0.93256	0.759089	0.325946	0.251262	1.001407e+00	1.
min	-2.885708e+00	-1.936857e+00	-1.00000	-1.000000	-1.000000	-1.000000	-1.591967e+00	-1
25%	-5.530393e-01	-4.733701e-01	-1.00000	0.000000	0.000000	0.000000	-6.193803e-01	-6
50%	2.050779e-01	2.583733e-01	1.00000	1.000000	0.000000	0.000000	-3.414983e-01	-3
75%	7.590867e-01	2.583733e-01	1.00000	1.000000	0.000000	0.000000	1.890038e-01	1.
max	2.246163e+00	7.575807e+00	1.00000	1.000000	1.000000	1.000000	4.319341e+00	6.

```
X1.dtypes
```

```
age          float64
bp           float64
sg          category
al          category
su          category
rbc             int8
pc              int8
pcc             int8
ba              int8
bgr          float64
bu           float64
sc           float64
sod          float64
pot          float64
hemo         float64
pcv          float64
wbcc         float64
```

```
rbcc      float64
htn          int8
dm           int8
cad          int8
appet        int8
pe           int8
ane          int8
dtype: object
```

Since there are 25 variables and 400 observations in Chronic Kidney Disease dataset.

1).There are 14 float64 type variables, and they are “age”, “bp”, “sg”, “al”, “su”, “bgr”, “bu”, “sc”, “sod”, “pot”, “hemo”, “pcv”, “wbcc”, “rbcc”. There are 11 object type vaariables, and they are “rbc”, “pc”, “pcc”, “ba”, “htn”, “dm”, “cad”, “appet”, “pe”, “ane”, “calss”. In these 25 variables, all variables in X are covariates (consists 14 floats and 10 object) and the variable in y is the response (the variable “class” which is an object variable). Moreover, the response is “class” contains only 2 category:“ckd” or “not ckd”, so the response is binary.

2).The number of features is 24, and they are: “age”, “bp”, “sg”, “al”, “su”, “bgr”, “bu”, “sc”, “sod”, “pot”, “hemo”, “pcv”, “wbcc”, “rbcc”,“rbc”, “pc”, “pcc”, “ba”, “htn”, “dm”, “cad”, “appet”, “pe”, “ane”, “calss”.

3).The number of observations is 400. But we can see that the count of some variables is less than 400, for example: the count of age is 391 which is less than 400. This means there are missing values in some varibales in this dataset.

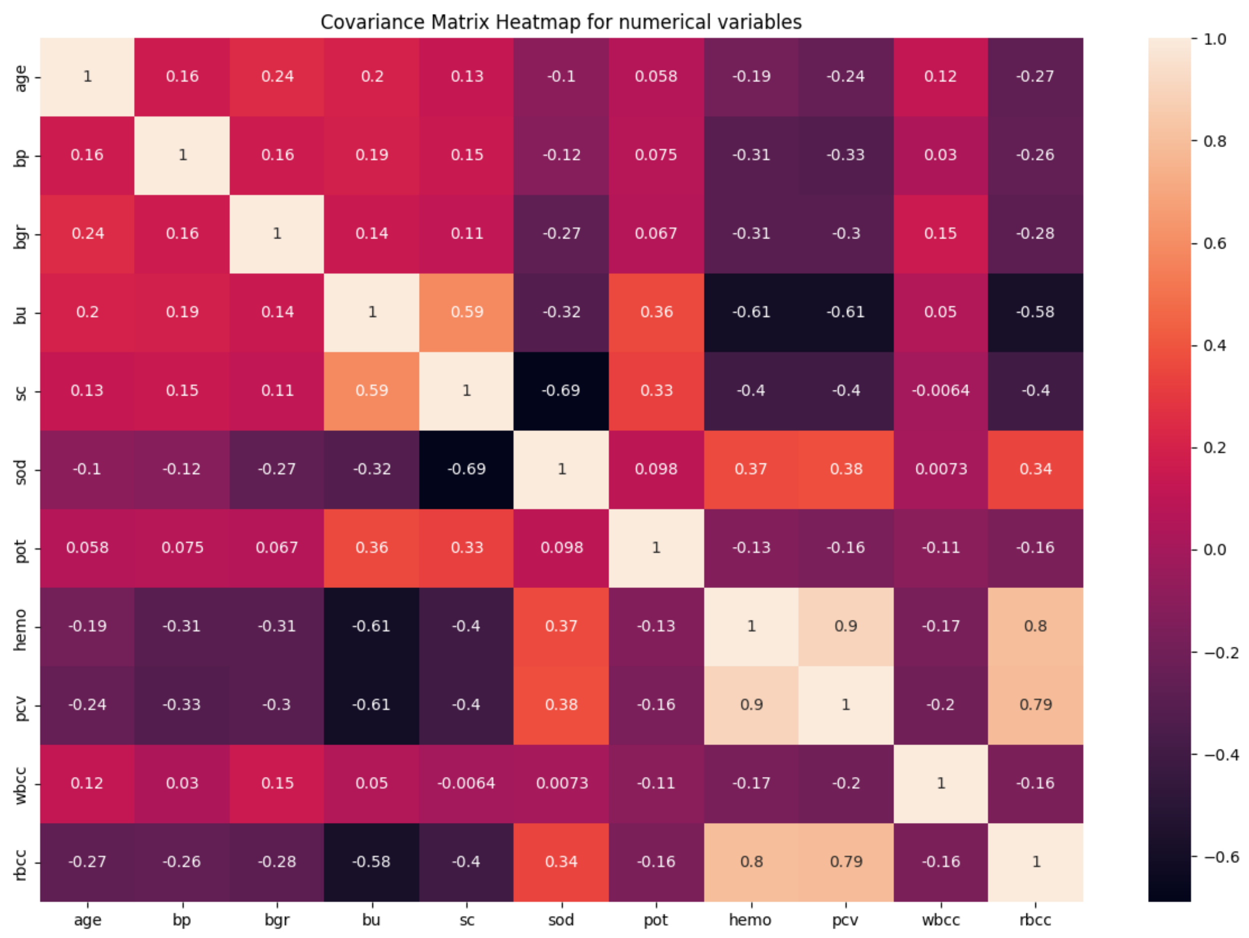
4). The type of variables: There are 14 float64 type variables, and they are “age”, “bp”, “sg”, “al”, “su”, “bgr”, “bu”, “sc”, “sod”, “pot”, “hemo”, “pcv”, “wbcc”, “rbcc”. There are 11 object type vaariables, and they are “rbc”, “pc”, “pcc”, “ba”, “htn”, “dm”, “cad”, “appet”, “pe”, “ane”, “calss”. In these 25 variables, all variables in X are covariates (consists 14 floats and 10 object) and the variable in y is the response (the variable “class” which is an object variable). Moreover, the response is “class” contains only 2 category:“ckd” or “not ckd”, so the respnse is binary.

5). Missing values: There are 9 missing values in “age”, 12 missing values in “bp”, 47 missing values in “sg”, 46 missing values in “al”, 49 missing values in “su”, 152 missing values in “rbc”, 65 missing values in “pc”, 4 missing values in “pcc”, 4 missing values in “ba”, 44 missing values in “bgr”, 19 missing values in “bu”, 17 missing values in “sc”, 87 missing values in “sod”, 88 missing values in “pot”, 52 missing values in “hemo”, 71 missing values in “pcv”, 106 missing values in “wbcc”, 131 missing values in “rbcc”, 2 missing values in “htn”, 2 missing values in “dm”, 2 missing values in “cad”, 1 missing value in “appet”, 1 missing value in “pe” and 1 missing value in “ane”.

0 missing value in “class”.

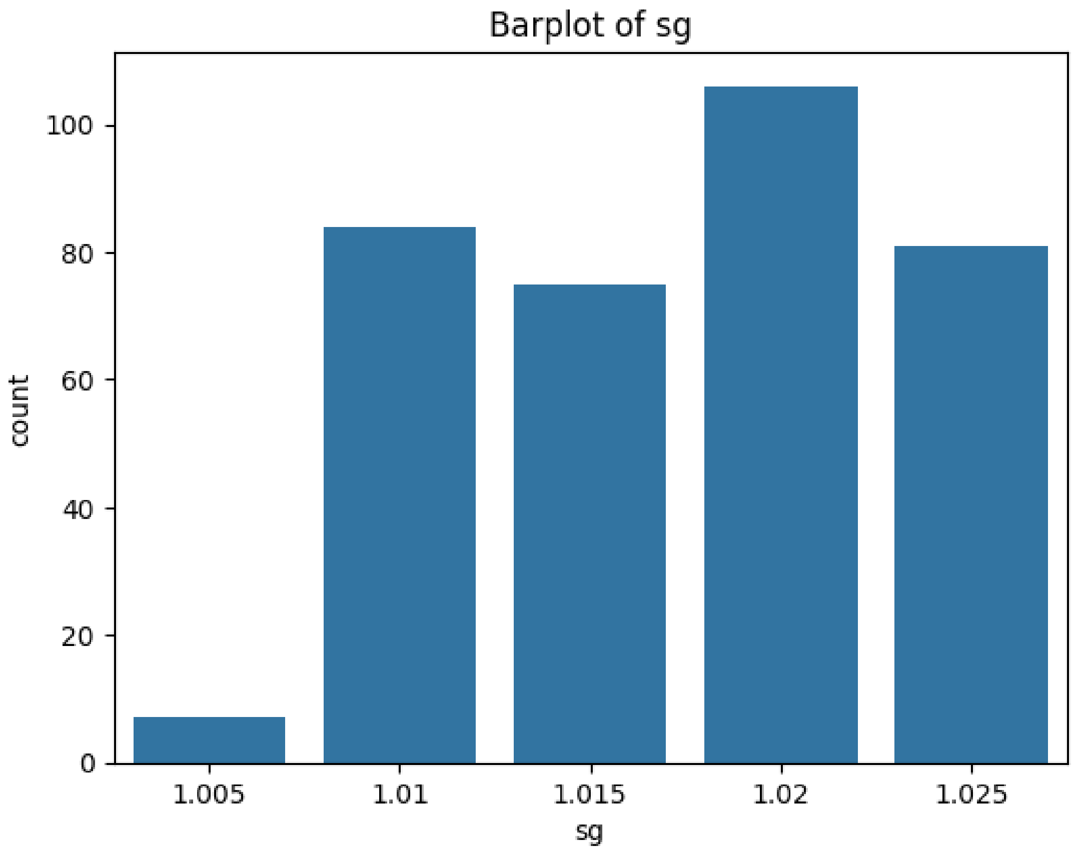
4. **Association Between Variables:** Analyze variable relationships and their implications for feature selection or extraction (at least three statements).

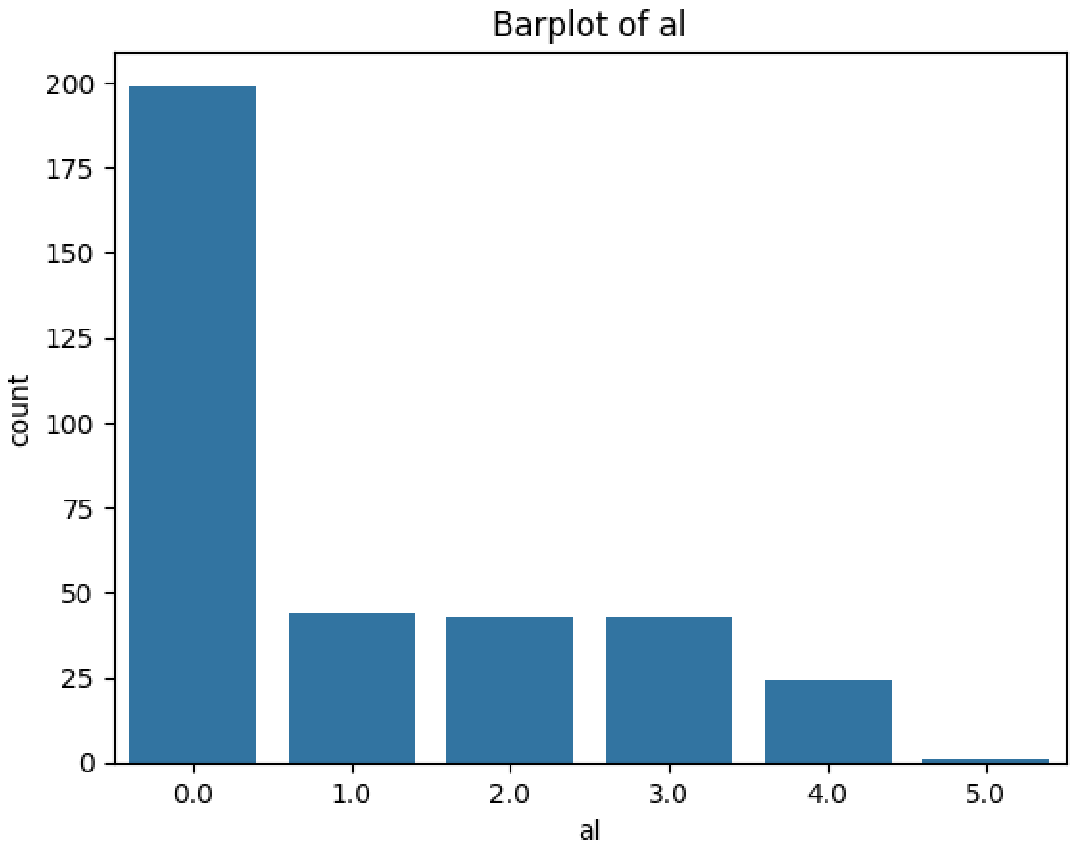
```
# prof says numerical variables shuold use heatmap, categorical variables should use use barpl
#
#
#
#
#numerical variables:
float64=X1.select_dtypes(include=['float64'])
plt.figure(figsize=(15, 10))
sns.heatmap(float64.corr(),
        annot=True)
plt.title('Covariance Matrix Heatmap for numerical variables')
plt.show()
```

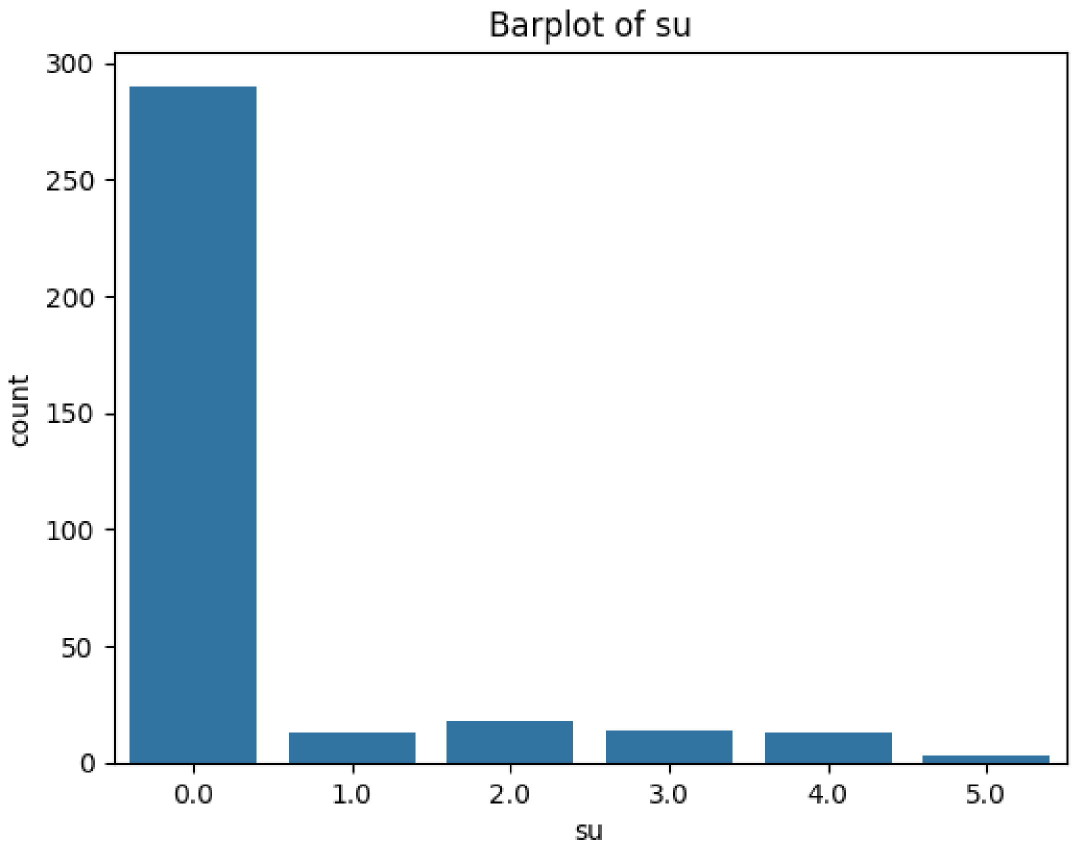


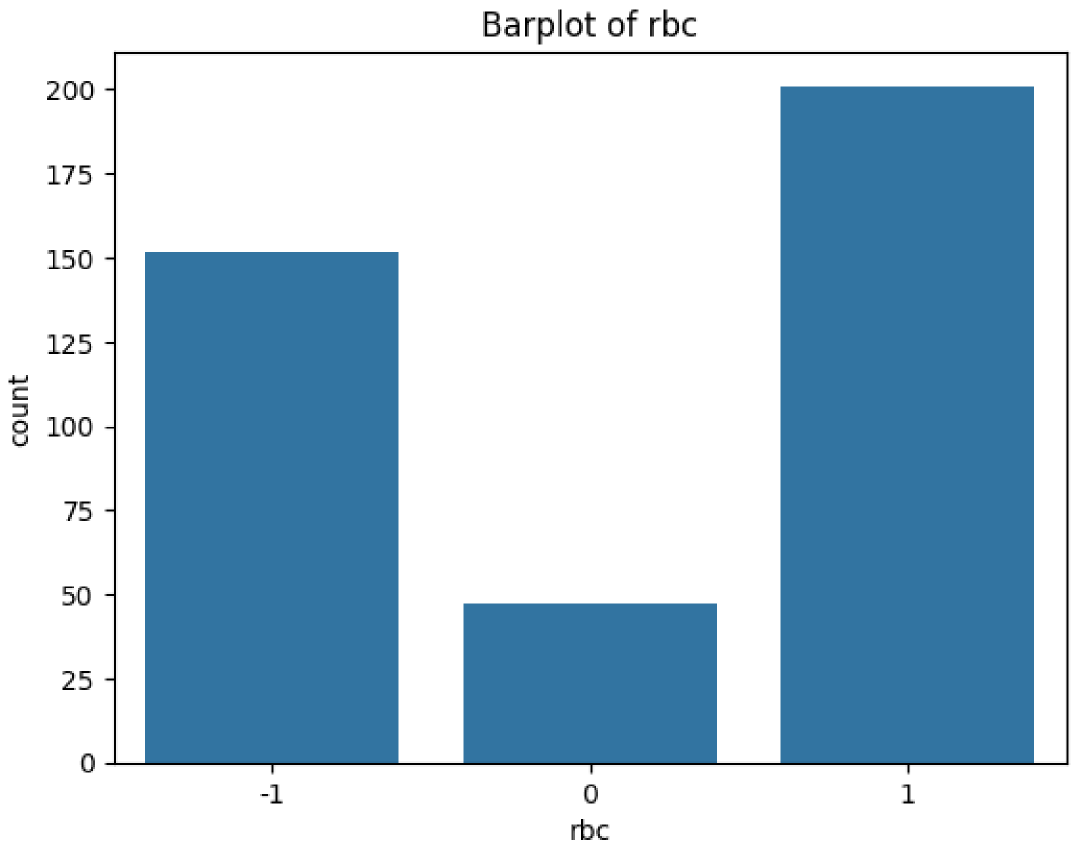
	age	bp	bgr	bu	sc	sod	pot	hemo	pcv	wbcc	rbcc
age	1	0.16	0.24	0.2	0.13	-0.1	0.058	-0.19	-0.24	0.12	-0.27
bp	0.16	1	0.16	0.19	0.15	-0.12	0.075	-0.31	-0.33	0.03	-0.26
bgr	0.24	0.16	1	0.14	0.11	-0.27	0.067	-0.31	-0.3	0.15	-0.28
bu	0.2	0.19	0.14	1	0.59	-0.32	0.36	-0.61	-0.61	0.05	-0.58
sc	0.13	0.15	0.11	0.59	1	-0.69	0.33	-0.4	-0.4	-0.0064	-0.4
sod	-0.1	-0.12	-0.27	-0.32	-0.69	1	0.098	0.37	0.38	0.0073	0.34
pot	0.058	0.075	0.067	0.36	0.33	0.098	1	-0.13	-0.16	-0.11	-0.16
hemo	-0.19	-0.31	-0.31	-0.61	-0.4	0.37	-0.13	1	0.9	-0.17	0.8
pcv	-0.24	-0.33	-0.3	-0.61	-0.4	0.38	-0.16	0.9	1	-0.2	0.79
wbcc	0.12	0.03	0.15	0.05	-0.0064	0.0073	-0.11	-0.17	-0.2	1	-0.16
rbcc	-0.27	-0.26	-0.28	-0.58	-0.4	0.34	-0.16	0.8	0.79	-0.16	1

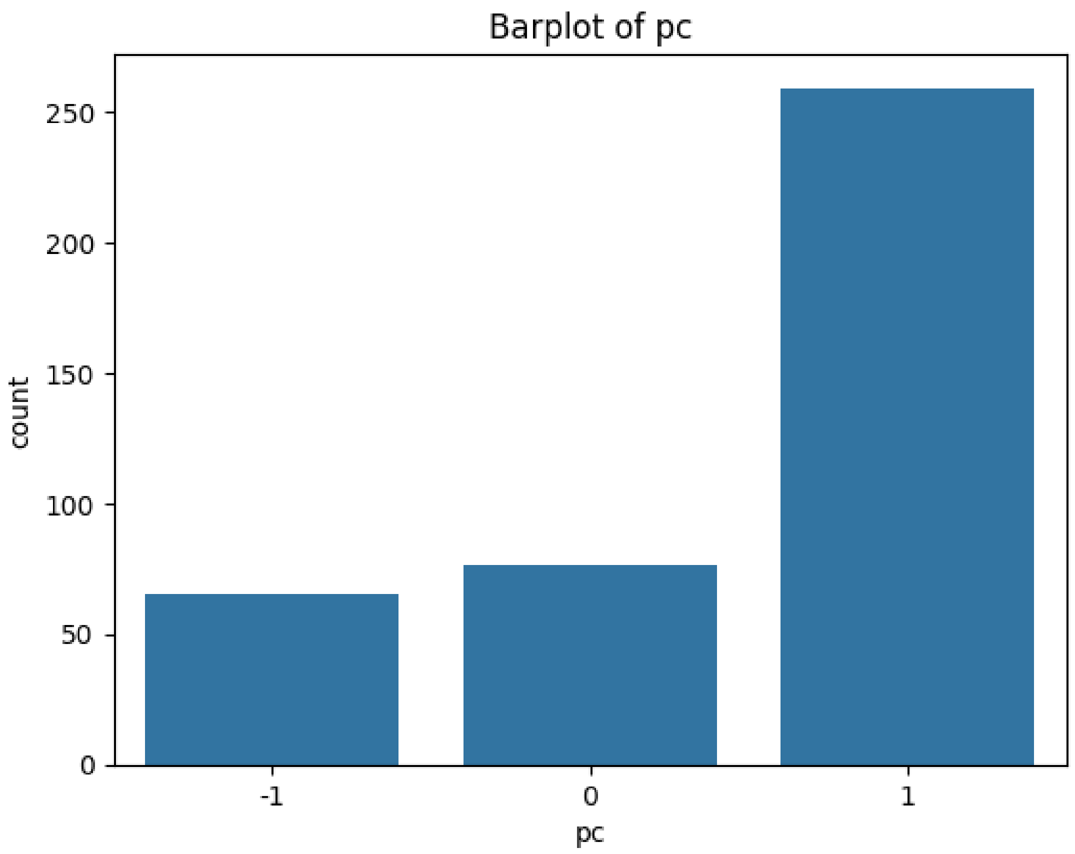
```python
#categorical variables
categorical=X1.select_dtypes(include=['category','int8'])
for column in categorical.columns:
    plt.figure()
    sns.countplot(x=column, data=categorical)
    plt.title(f'Barplot of {column}')
    plt.show()
```

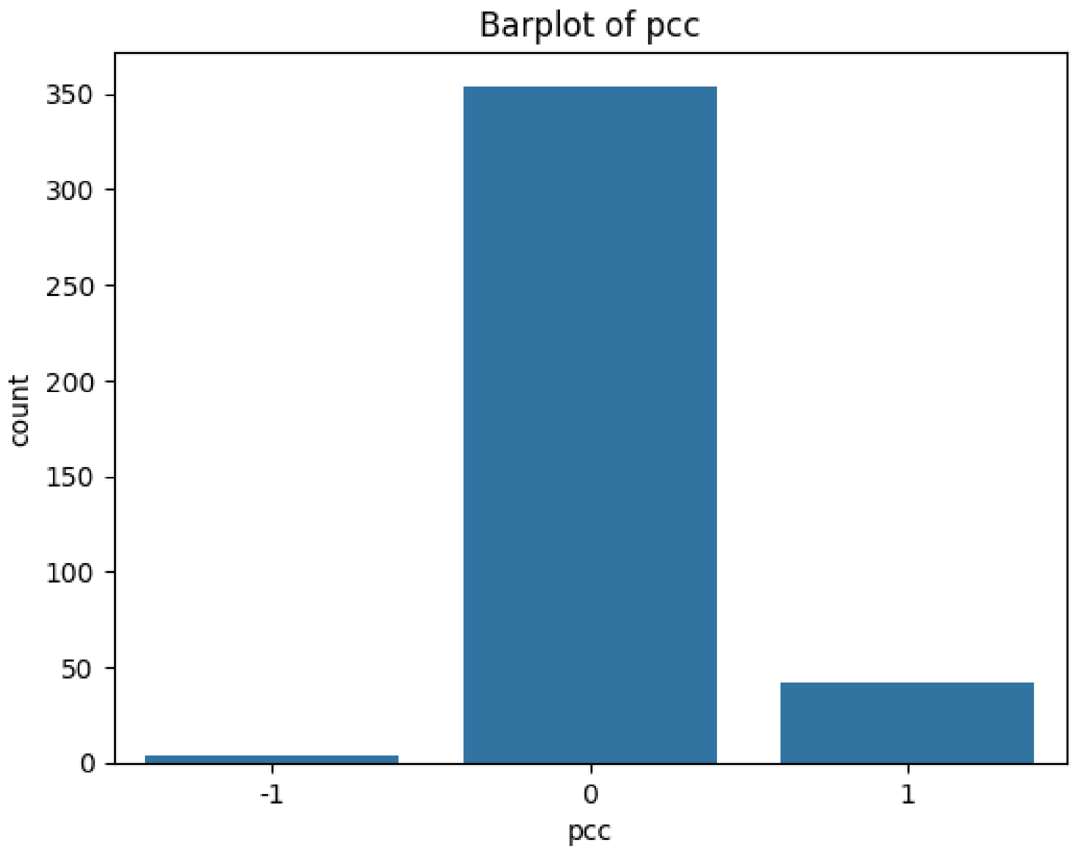

Barplot of sg
count
100
80
60
40
20
0
1.005
1.01
1.015
1.02
1.025
sg

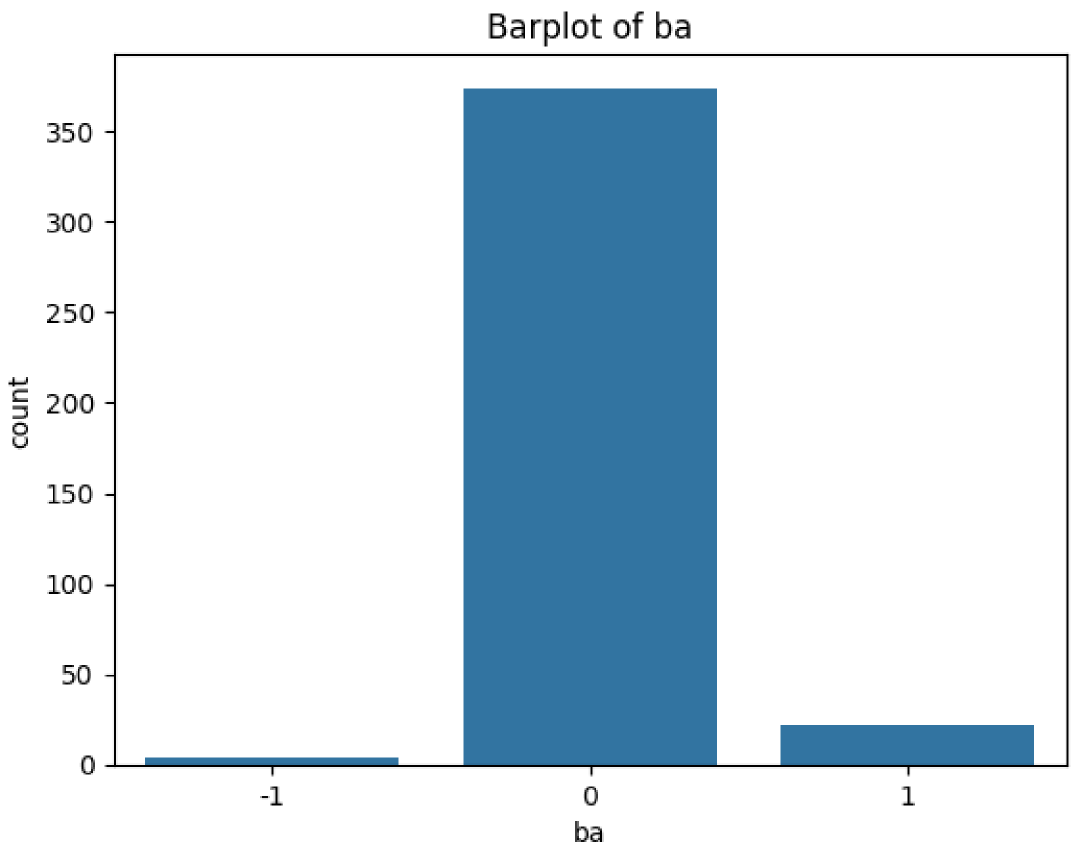

Barplot of al
count
200
175
150
125
100
75
50
25
0
0.0
1.0
2.0
3.0
4.0
5.0
al

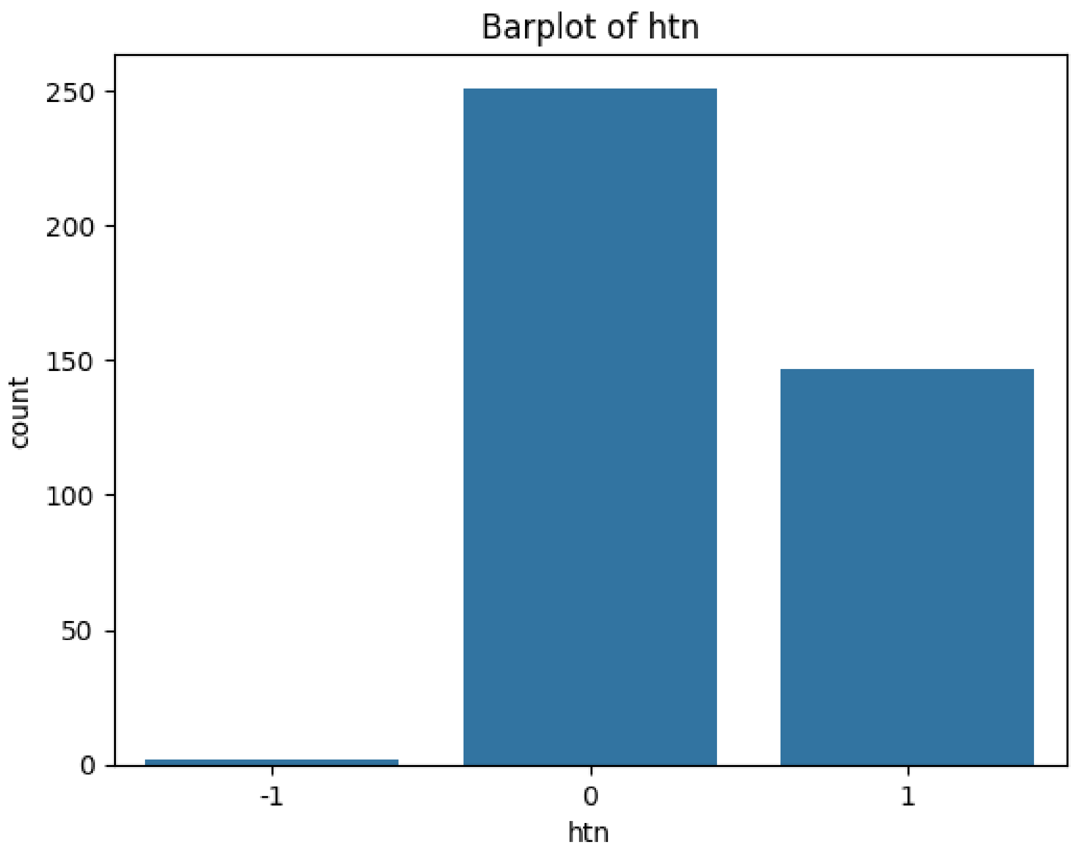

Barplot of su
count
300
250
200
150
100
50
0
0.0
1.0
2.0
3.0
4.0
5.0
su

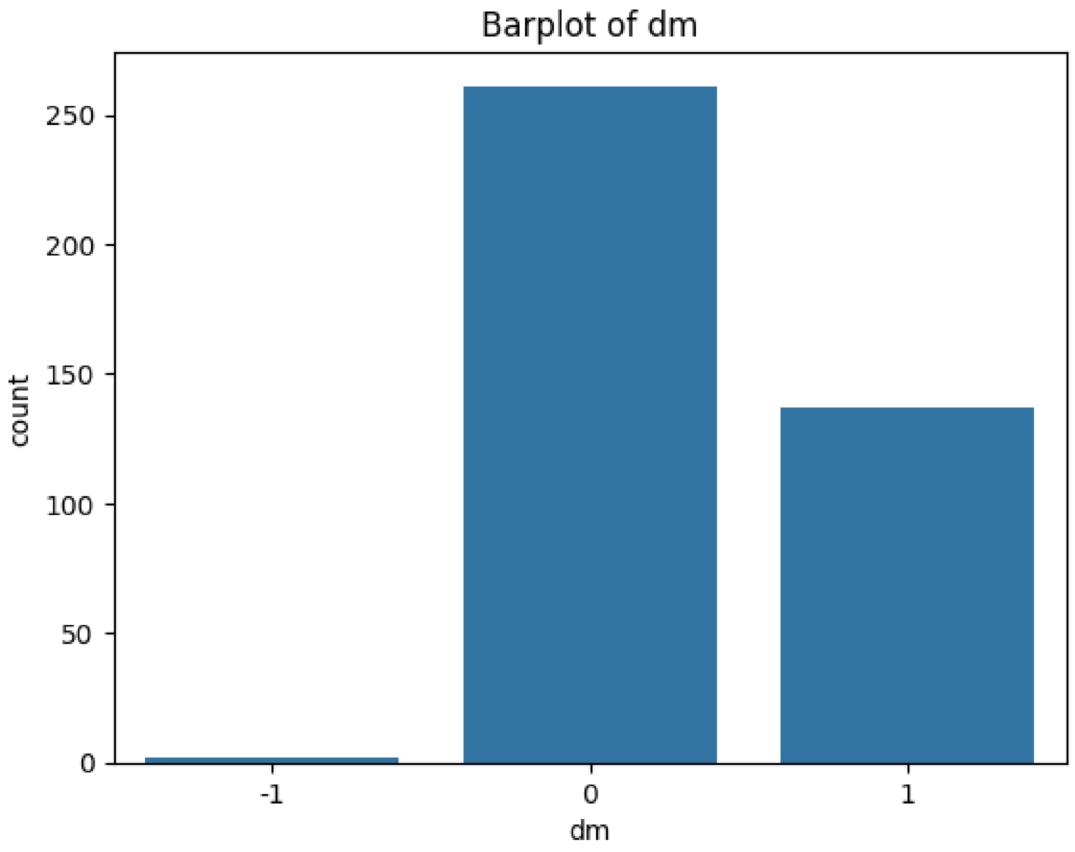

Barplot of rbc
count
200
175
150
125
100
75
50
25
0
-1
0
1
rbc

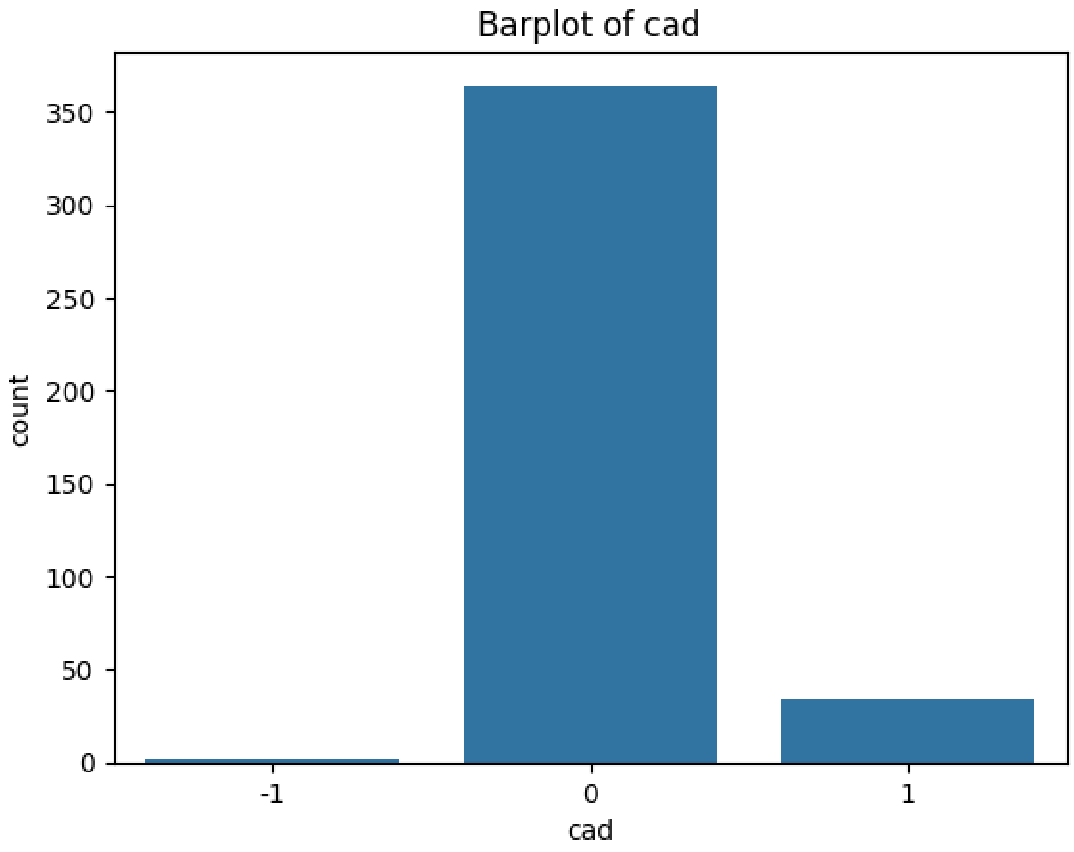

Barplot of pc
count
250
200
150
100
50
0
-1
0
1
pc

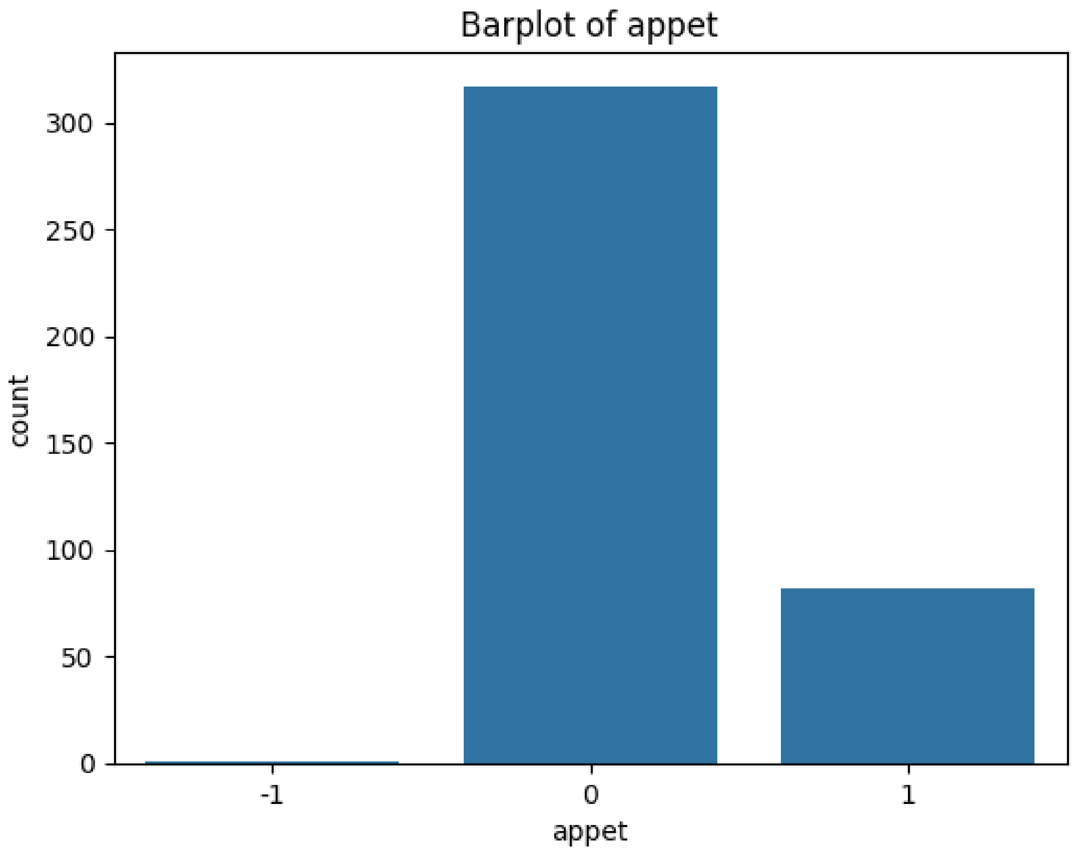

Barplot of pcc
count
350
300
250
200
150
100
50
0
-1
0
1
pcc

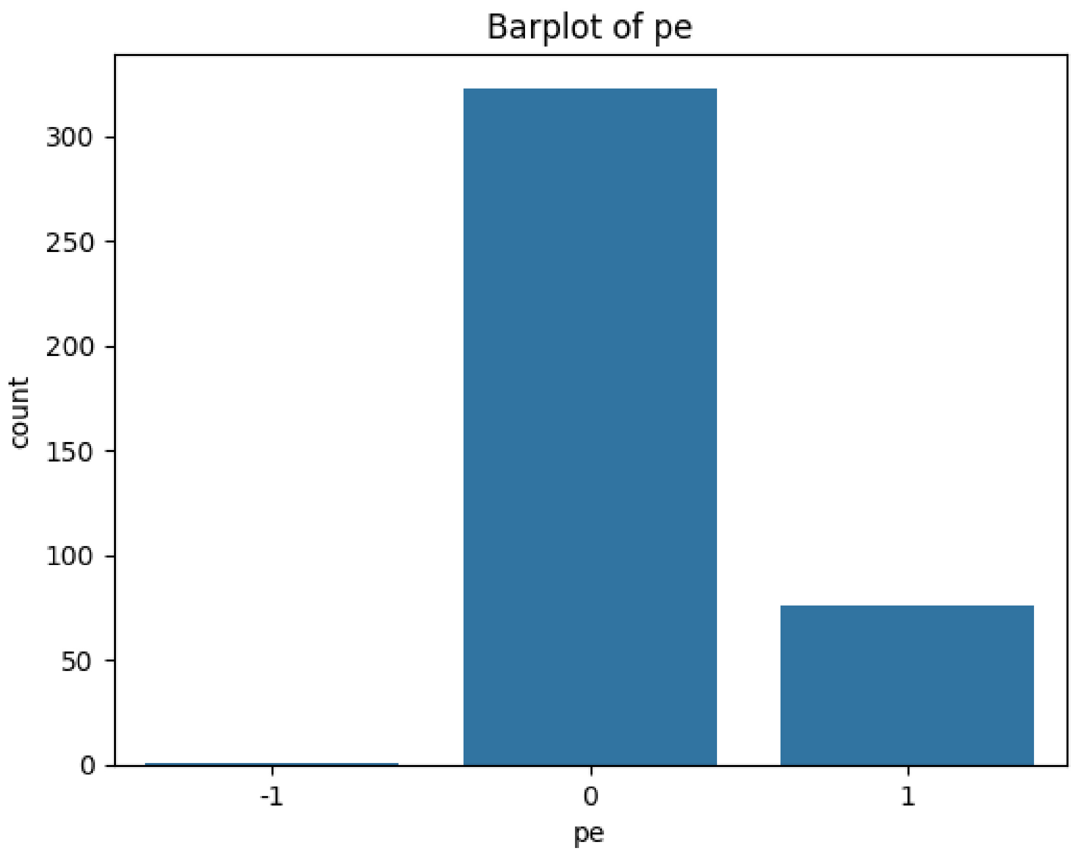

Barplot of ba
count
350
300
250
200
150
100
50
0
-1
0
1
ba

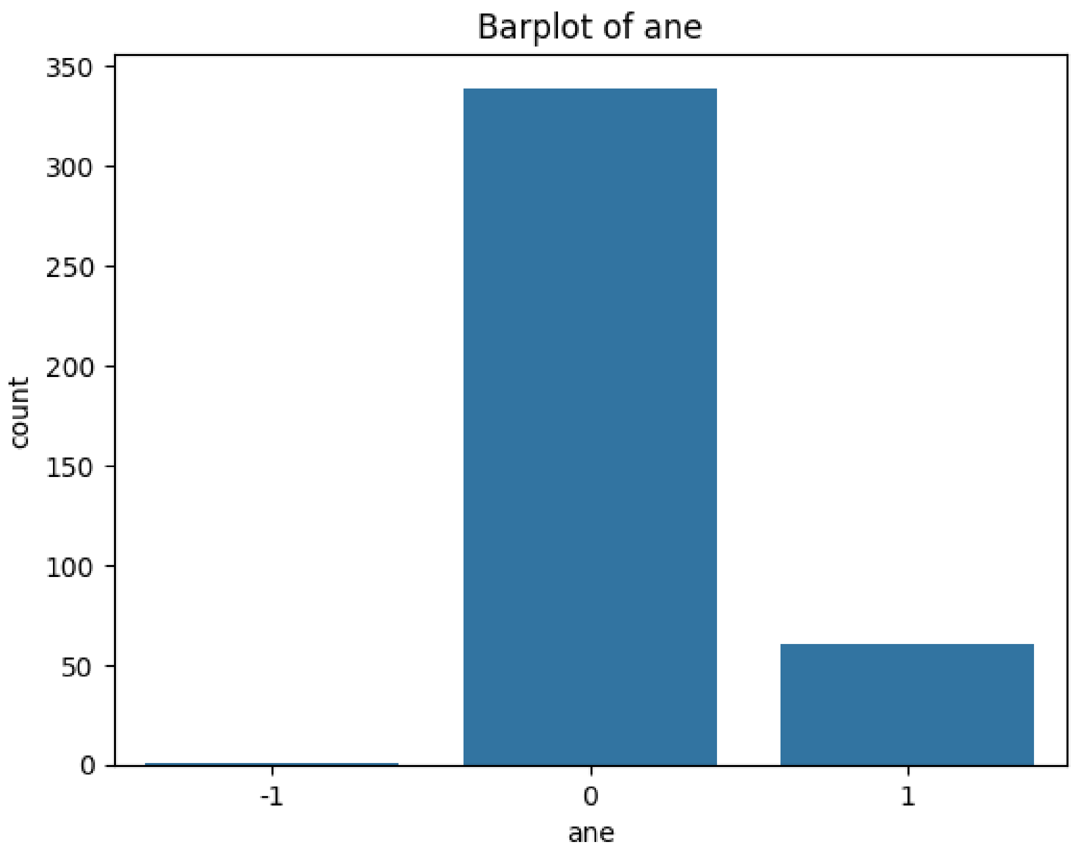

Barplot of htn
count
250
200
150
100
50
0
-1
0
1
htn


Barplot of dm
count
dm
250
200
150
100
50
0
-1
0
1


Barplot of cad
count
350
300
250
200
150
100
50
0
-1
0
1
cad


Barplot of appet
count
300
250
200
150
100
50
0
-1
0
1
appet


Barplot of pe
count
pe
-1
0
1
0
50
100
150
200
250
300



We use heatmap for numerical variables and barplot for categorical variables.

For heatmap:

1). This is a symmetric matrix and the elements on the diagonal are the variance. The diagonal of the correlation matrix is 1.

2). The elements not on the diagonal are the covariance.

3). The smallest number in the matrix is -0.69 which means “sod” and “sc” are neagtively correlated.

4). The largest number in the matrix is 1 (the diagonal).

5). The largest number other than 1 is 0.9 which means “hemo” and “pcv” are positively correlated.

For barplots:

1). In those binary variables, the category “-1” could suggest missing values.

2). For example, in “pe” (pedal edema), the most common category is “0”, which could imply the absence of pedal edema, and the second most common category is “1”, which could imply the presence of pedal edema, and the least category “-1” are missing values.

3). “htn” (hypertension) and “dm” (diabetes mellitus) are not good since the diistribution is not extreme.

5. **Missing Value Analysis and Handling:** Implement your strategy for identifying and addressing missing values in the dataset, or provide reasons for not addressing them.

```
X.isnull().sum()
```

```
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
dtype: int64
```

```
y.isnull().sum()
```

```
class    0
dtype: int64
```

```
#way2
float_na=X1[float_col].isna()
float_nasum=float_na.sum()
print(float_nasum)

cat_na=X1[columns_to_convert].isna()
cat_nasum=cat_na.sum()
print(cat_nasum)

binary_na = (X1[object_convert] == -1)
binary_nasum=binary_na.sum()
print(binary_nasum)
```

```
age      9
bp      12
bgr     44
bu      19
sc      17
sod     87
pot     88
hemo    52
pcv     71
```

```
wbcc    106
rbcc    131
dtype: int64
sg    47
al    46
su    49
dtype: int64
rbc      152
pc        65
pcc        4
ba         4
htn        2
dm         2
cad        2
appet      1
pe         1
ane        1
dtype: int64
```

Missing values: There are 9 missing values in “age”, 12 missing values in “bp”, 47 missing values in “sg”, 46 missing values in “al”, 49 missing values in “su”, 152 missing values in “rbc”, 65 missing values in “pc”, 4 missing values in “pcc”, 4 missing values in “ba”, 44 missing values in “bgr”, 19 missing values in “bu”, 17 missing values in “sc”, 87 missing values in “sod”, 88 missing values in “pot”, 52 missing values in “hemo”, 71 missing values in “pcv”, 106 missing values in “wbcc”, 131 missing values in “rbcc”, 2 missing values in “htn”, 2 missing values in “dm”, 2 missing values in “cad”, 1 missing value in “appet”, 1 missing value in “pe” and 1 missing value in “ane”.

0 missing value in “class”.

```
#the stragegy for addressing missing values
X1_drop= X1.dropna()
X1_drop
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	pcv	wb
3	-0.203139	-0.473370	1.005	4.0	0.0	1	0	1	0	-0.392022	...	-0.456071	-0.766953	-0.5
5	0.496661	0.990117	1.015	3.0	0.0	-1	-1	0	0	-0.935155	...	-0.112239	0.012867	-0.2
9	0.088445	0.990117	1.020	2.0	0.0	0	0	1	0	-0.985679	...	-1.040585	-1.101161	1.25
11	0.671612	-0.473370	1.010	3.0	0.0	0	0	1	0	2.929931	...	-0.593604	-0.766953	-1.3
12	0.963195	-0.473370	1.015	3.0	1.0	-1	1	1	0	0.757399	...	-0.971819	-1.212564	1.29
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
395	0.205078	0.258373	1.020	0.0	0.0	1	1	0	0	-0.101509	...	1.091172	0.904090	-0.5
396	-0.553039	-0.473370	1.025	0.0	0.0	1	1	0	0	-0.922524	...	1.366237	1.683910	-0.2
397	-2.302541	0.258373	1.020	0.0	0.0	1	1	0	0	-0.606749	...	1.125555	1.126896	-0.6
398	-2.010957	-1.205114	1.025	0.0	0.0	1	1	0	0	-0.429915	...	0.575424	1.349701	-0.4
399	0.380028	0.258373	1.025	0.0	0.0	1	1	0	0	-0.215188	...	1.125555	1.572507	-0.5

dropped the columns if the missing value of this variable is greater than 44.

```
missing_values_count = X1.isna().sum()
columns_to_drop = missing_values_count[missing_values_count > 50].index
columns_to_drop
```

```
Index(['sod', 'pot', 'hemo', 'pcv', 'wbcc', 'rbcc'], dtype='object')
```

```
X1_dropped = X1.drop(columns=columns_to_drop)
X1_dropped
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	bu	sc	htn	d
0	-0.203139	0.258373	1.020	1.0	0.0	-1	1	0	0	-0.341498	-0.424804	-0.326574	1	1
1	-2.594124	-1.936857	1.020	4.0	0.0	-1	1	0	0	NaN	-0.781687	-0.396338	0	0
2	0.613295	0.258373	1.010	2.0	3.0	1	1	0	0	3.473064	-0.087748	-0.221928	0	1
3	-0.203139	-0.473370	1.005	4.0	0.0	1	0	1	0	-0.392022	-0.028268	0.126891	1	0
4	-0.028189	0.258373	1.010	2.0	0.0	1	1	0	0	-0.530963	-0.623073	-0.291692	0	0
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	bu	sc	htn	dı
395	0.205078	0.258373	1.020	0.0	0.0	1	1	0	0	-0.101509	-0.167055	-0.448661	0	0
396	-0.553039	-0.473370	1.025	0.0	0.0	1	1	0	0	-0.922524	-0.523939	-0.326574	0	0
397	-2.302541	0.258373	1.020	0.0	0.0	1	1	0	0	-0.606749	-0.623073	-0.431220	0	0
398	-2.010957	-1.205114	1.025	0.0	0.0	1	1	0	0	-0.429915	-0.147229	-0.361456	0	0
399	0.380028	0.258373	1.025	0.0	0.0	1	1	0	0	-0.215188	-0.781687	-0.344015	0	0

```
numerical_cols = X1_dropped.select_dtypes(include=['number']).columns
column_means = X1_dropped[numerical_cols].mean()

X1_filled = X1_dropped.copy()
X1_filled[numerical_cols] = X1_filled[numerical_cols].fillna(column_means)
```

Replacing the missing value by the mean of the variables for numerical variables.

```
from sklearn.impute import SimpleImputer
```

```
obj_col = X1_filled.select_dtypes(include=['category']).columns.tolist()
cat_imputer = SimpleImputer(strategy='most_frequent',missing_values=np.nan)
X1_filled.loc[:, obj_col] = cat_imputer.fit_transform(X1_filled.loc[:, obj_col])
```

Replacing the missing value by the most frequency input of the variables for categorical variables.

```
X1_filled.isna().sum()
```

```
age        0
bp         0
sg         0
al         0
su         0
rbc        0
pc         0
```

```
pcc      0
ba       0
bgr      0
bu       0
sc       0
htn      0
dm       0
cad      0
appet    0
pe       0
ane      0
dtype: int64
```

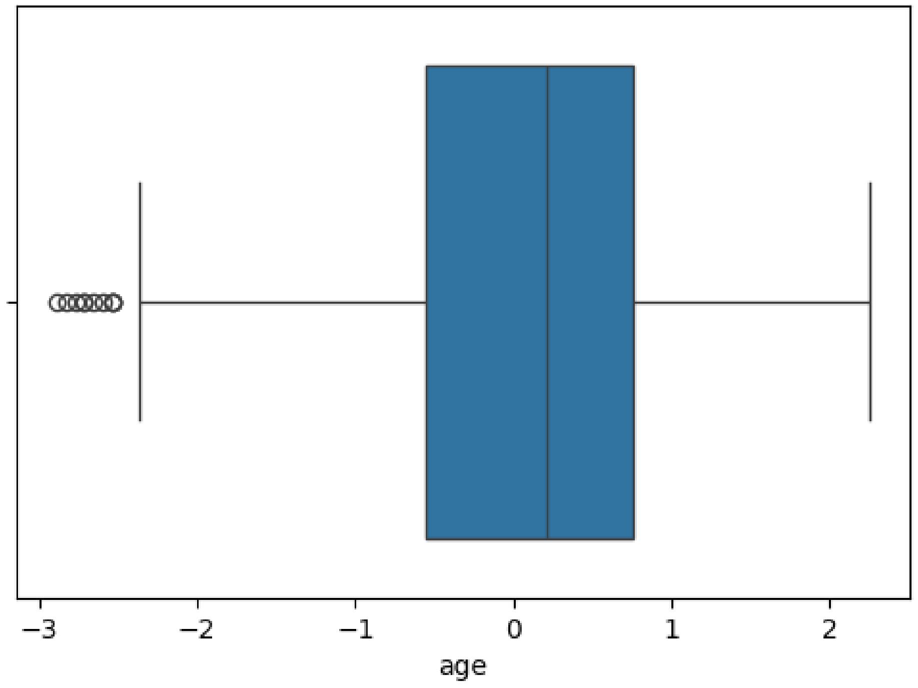
The strategy we used for addressing the missing value is: 1. Replacing the missing value of the numerical variables by its variable means. 2. Using the most frequent input to replaced the missing value for categorical variables.

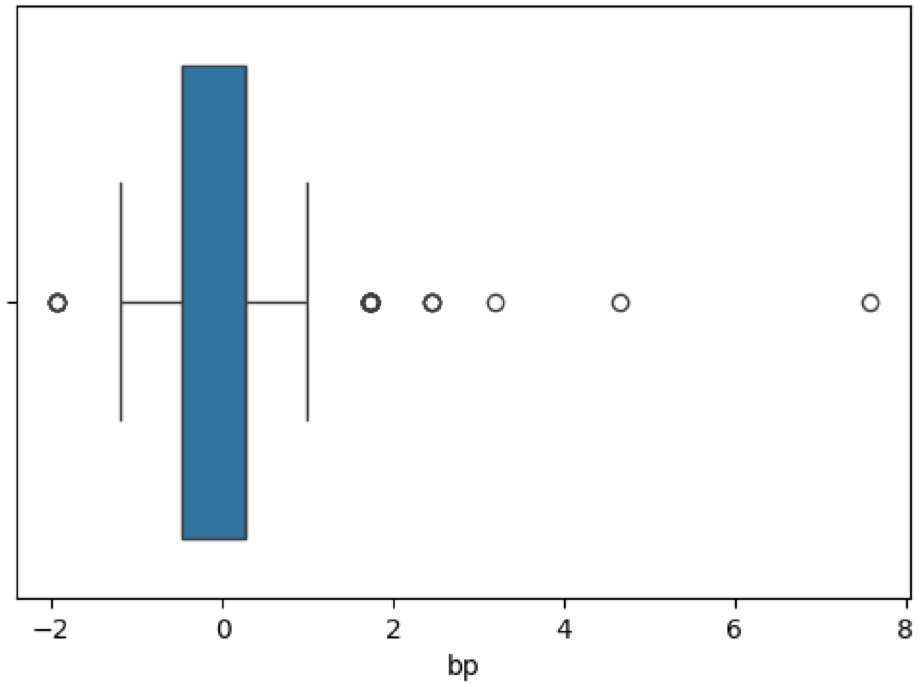
The reason we delete the variables which have missing value size greater than 50 is becasue that large missing value may indicate problems in data qualities. If we using the above stategy to addressing the missing value, the value we replaced may cause 100% accuracy when classified the model. Thus, the most value this variable has missed, the most inaccuracy that the variable will cause when we classified it. Also when the missing vlues is too large, lets say in “rbc”, there are 152 missing vlues out of 400, then even though we train them and use althorithm to work on them, we will learn nothing from it.

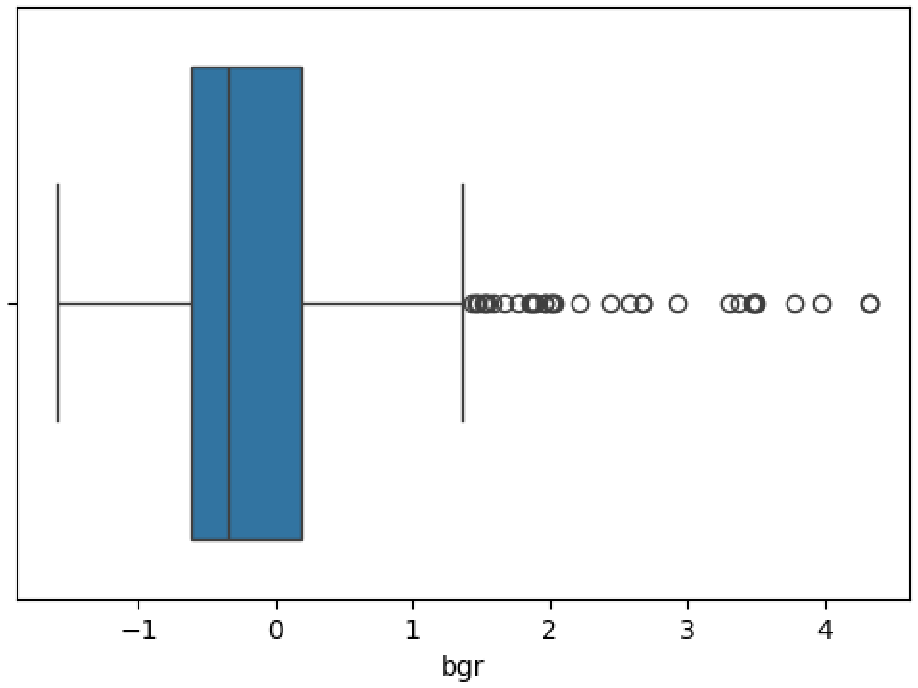
In some algorithms, the missing values can be seen as a seperate category. For instance, in decision tree, KNN, etc. Moreover, when using the KNN classifier, the code can not train on “NA” response values.

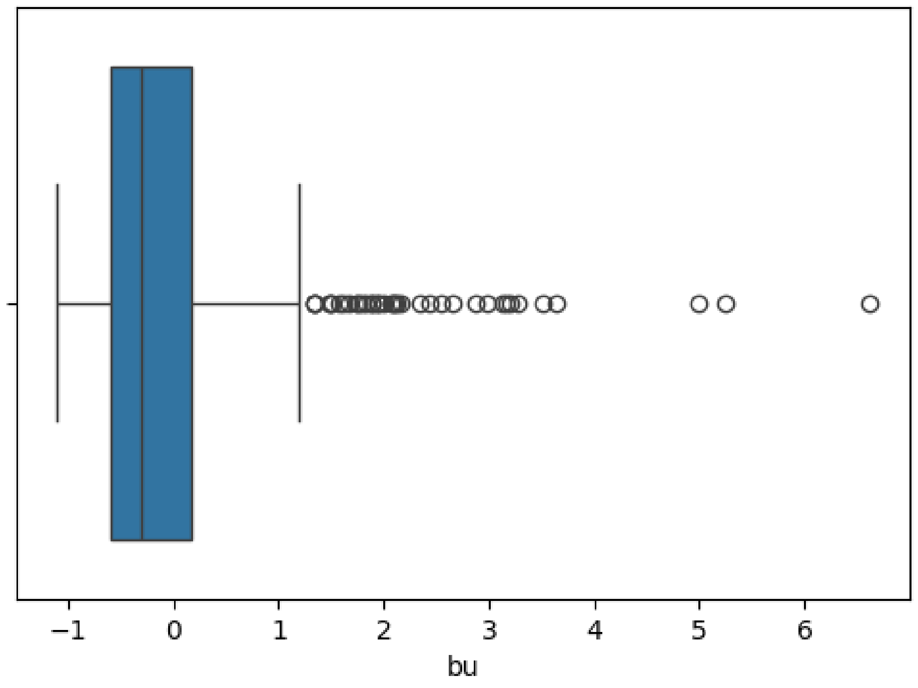
6. **Outlier Analysis:** Implement your approach for identifying and managing outliers, or provide reasons for not addressing them.

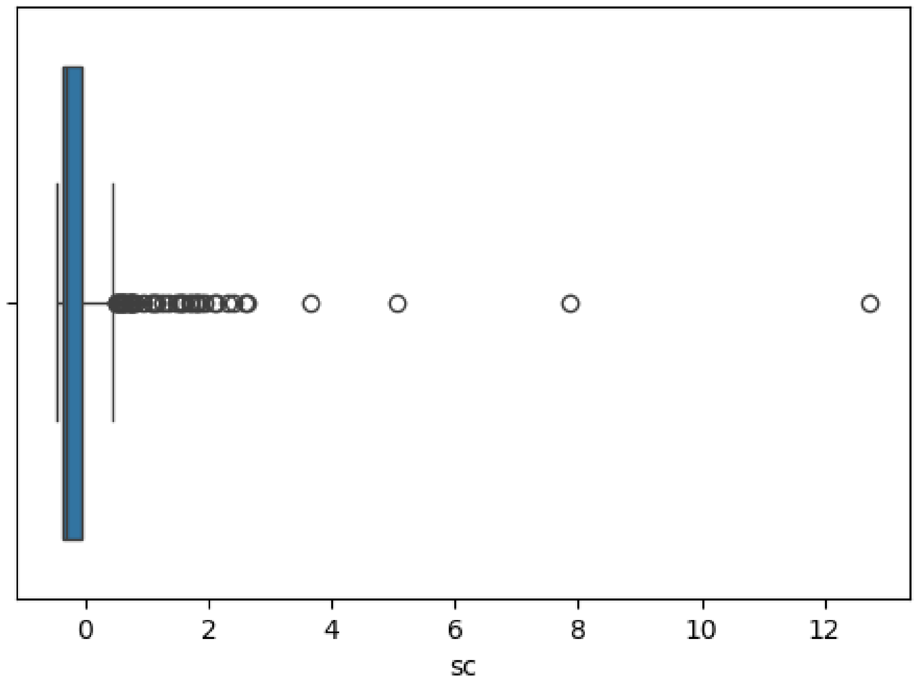
```
for col in float_col:
    plt.figure(figsize=(6, 4))
    sns.boxplot(x=X1.select_dtypes(include=['float64'])[col])
    plt.xlabel(col)
    plt.show()
```

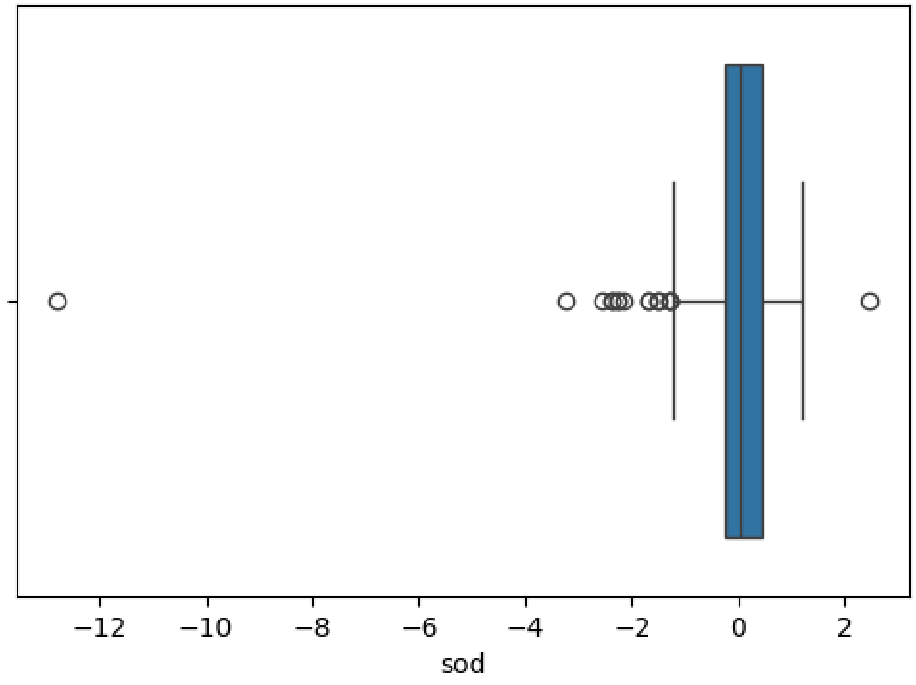


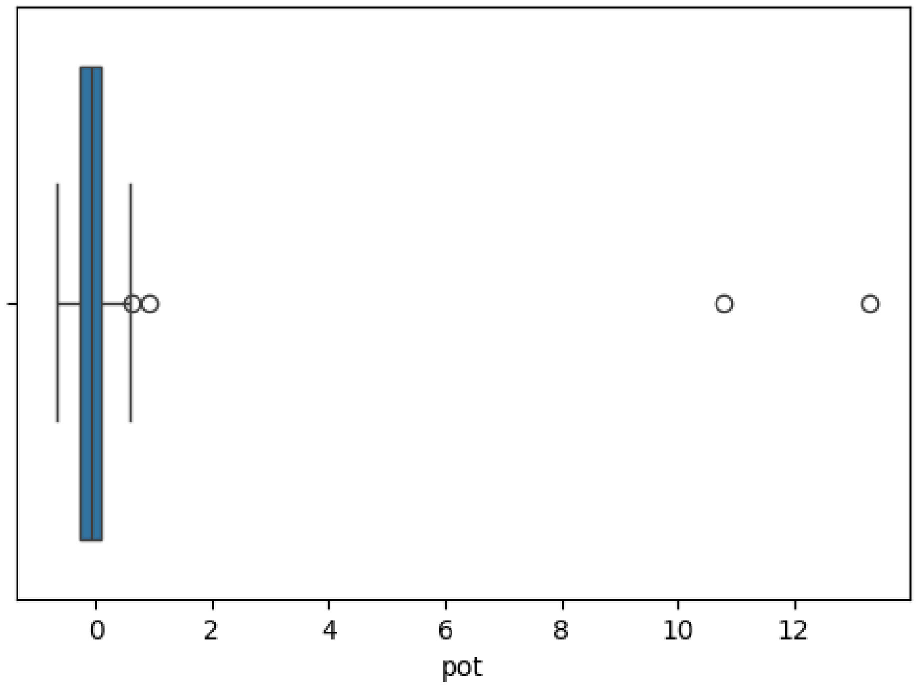


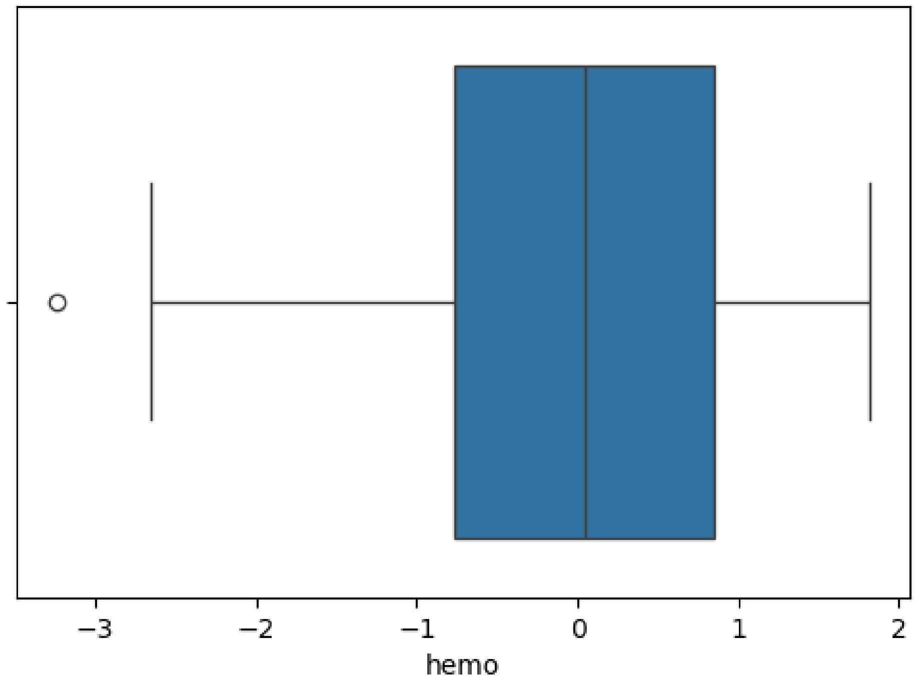

−1
0
1
2
3
4
bgr

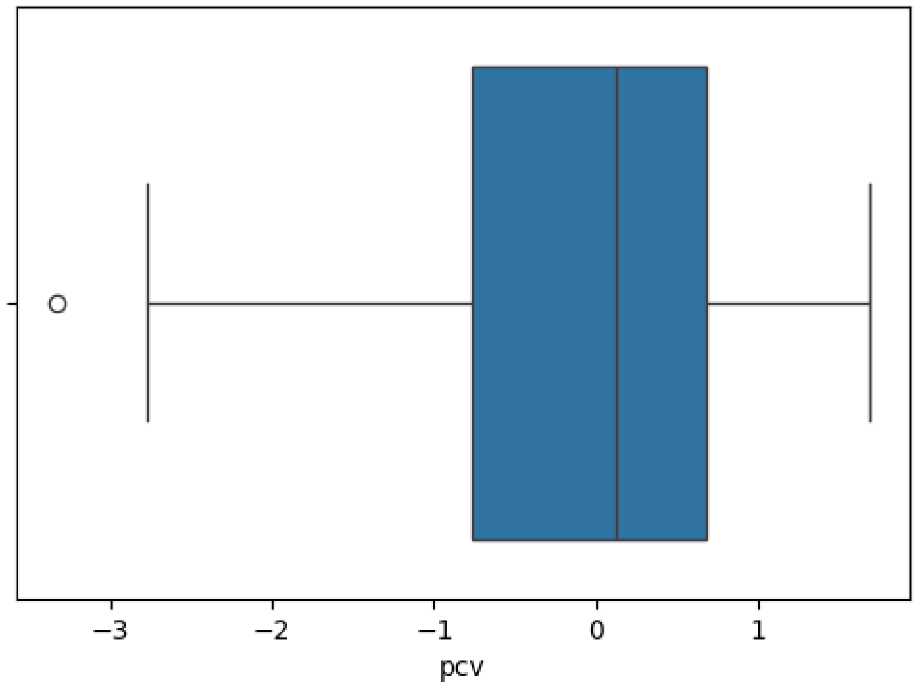

−1
0
1
2
3
4
5
6
bu

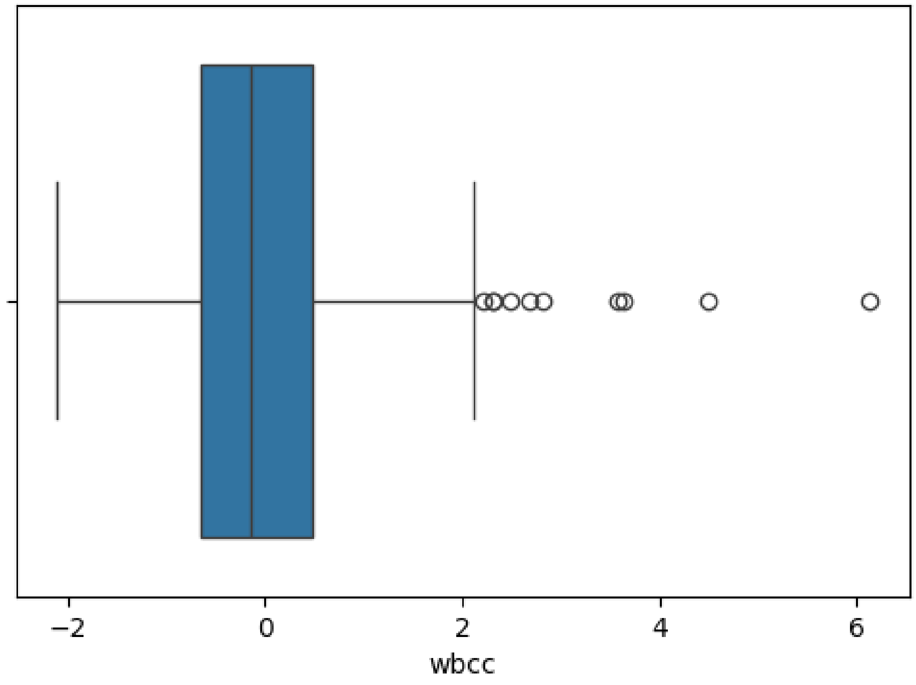

0
2
4
6
8
10
12
sc

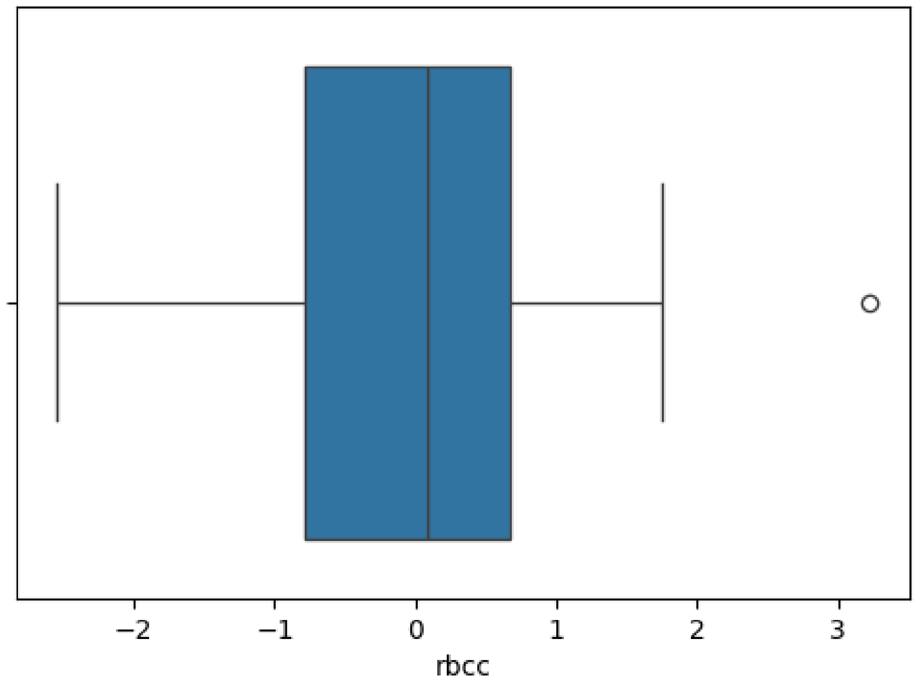

−12
−10
−8
−6
−4
−2
0
2
sod


0
2
4
6
8
10
12
pot


−3
−2
−1
0
1
2
hemo


−3
−2
−1
0
1
pcv


−2
0
2
4
6
wbcc



7. **Sub-group Analysis:** Explore potential sub-groups within the data, employing appropriate data science methods to find the sub-groups of patients and visualize the sub-groups. The sub-group analysis must not include the labels (for CKD patients and healthy controls).

```
#prof says use K-means
from sklearn.preprocessing import scale
from sklearn.decomposition import PCA, TruncatedSVD
from sklearn.cluster import KMeans
from scipy.cluster import hierarchy
from sklearn.cluster import AgglomerativeClustering
from sklearn.metrics import silhouette_samples, silhouette_score
from sklearn.metrics.cluster import rand_score
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import adjusted_rand_score
from sklearn.decomposition import PCA, TruncatedSVD, FactorAnalysis
import matplotlib.pyplot as plt
from sklearn.metrics import silhouette_score, silhouette_samples
from matplotlib import cm
from sklearn.impute import KNNImputer
```

```
y['class'] = y["class"].astype('category').cat.codes
y
```

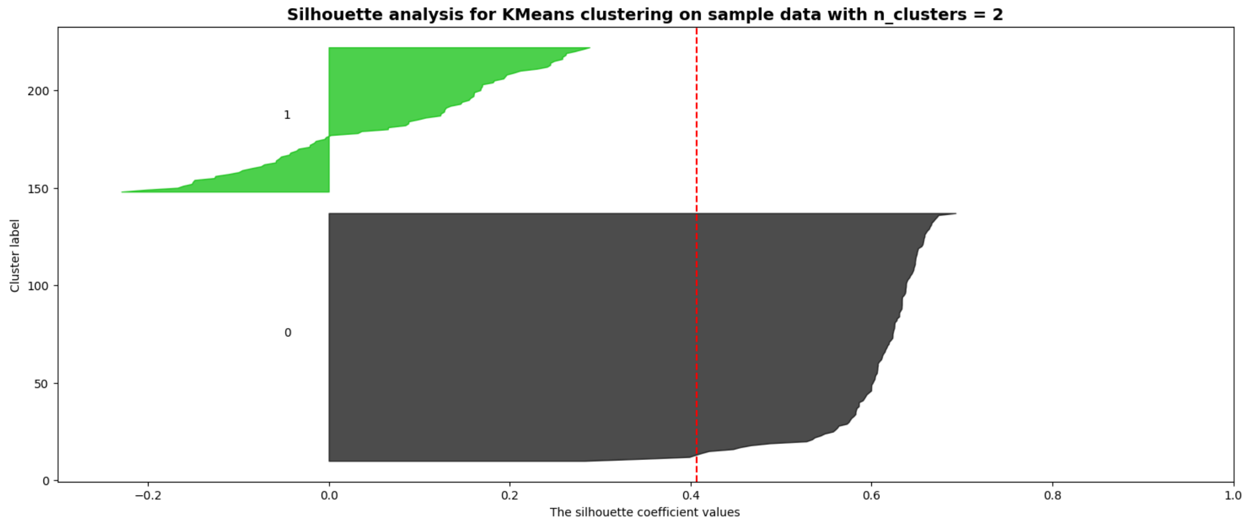
	class
0	0
1	0
2	0
3	0
4	0
...	...
395	1
396	1
397	1
398	1
399	1

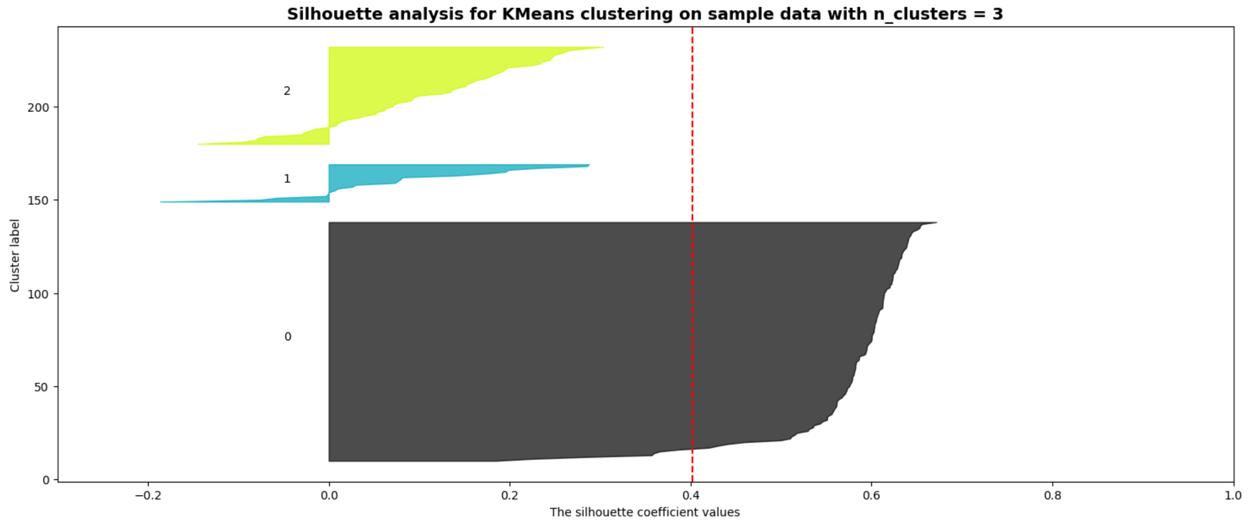
```
km1 = KMeans(n_clusters=2, n_init=20, random_state=0)
km1.fit(y)
km1.labels_
```

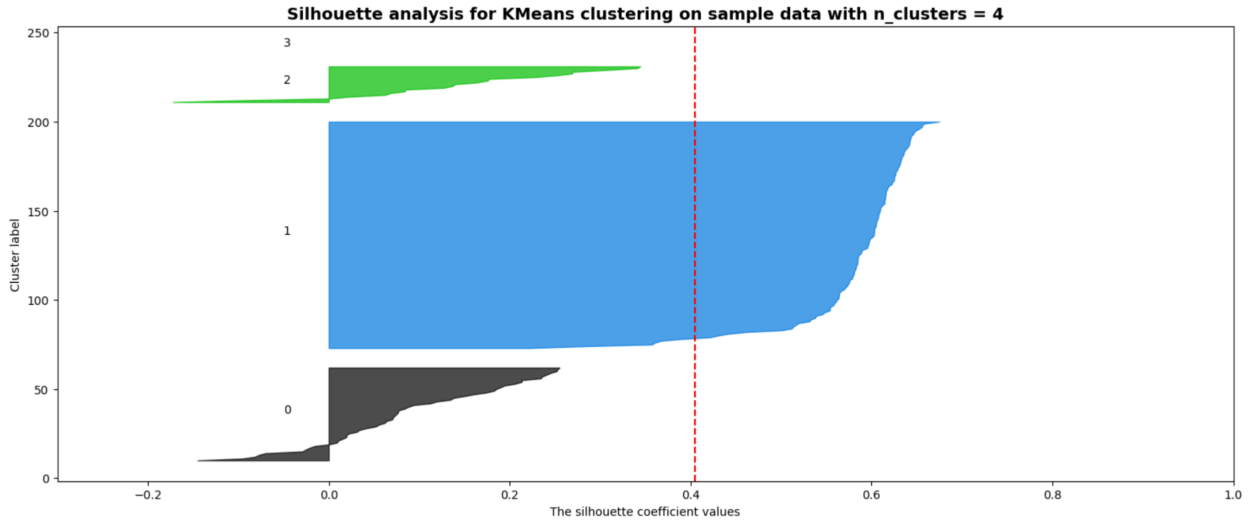
```
array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1], dtype=int32)
```

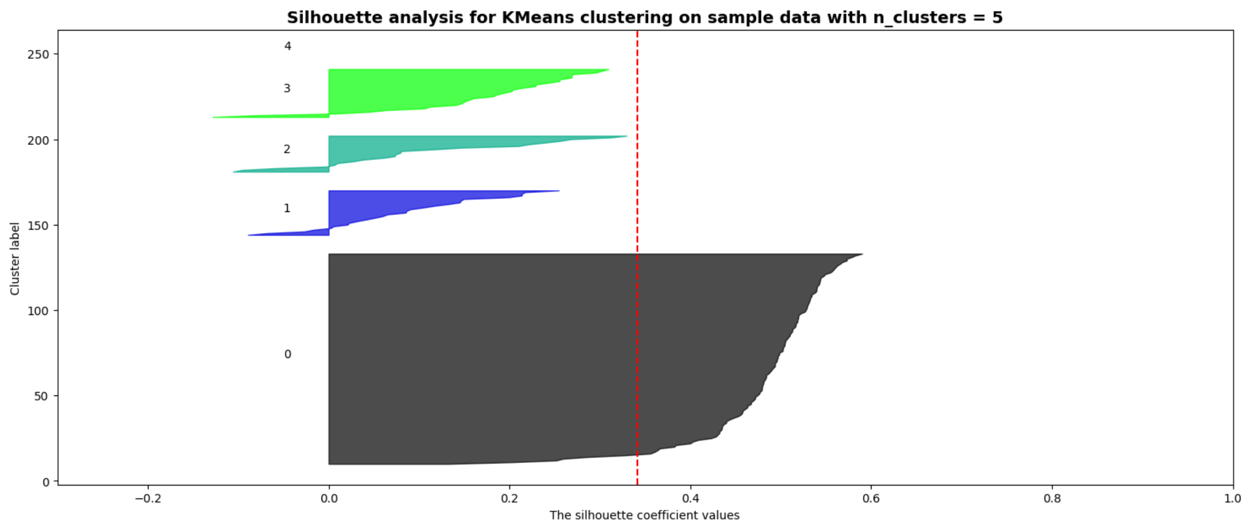
```
# imputer = KNNImputer(n_neighbors=5)
# X_imputed = pd.DataFrame(imputer.fit_transform(X1), columns=X1.columns)
# X_imputed.head()
# X_imputed.isna().sum()
```

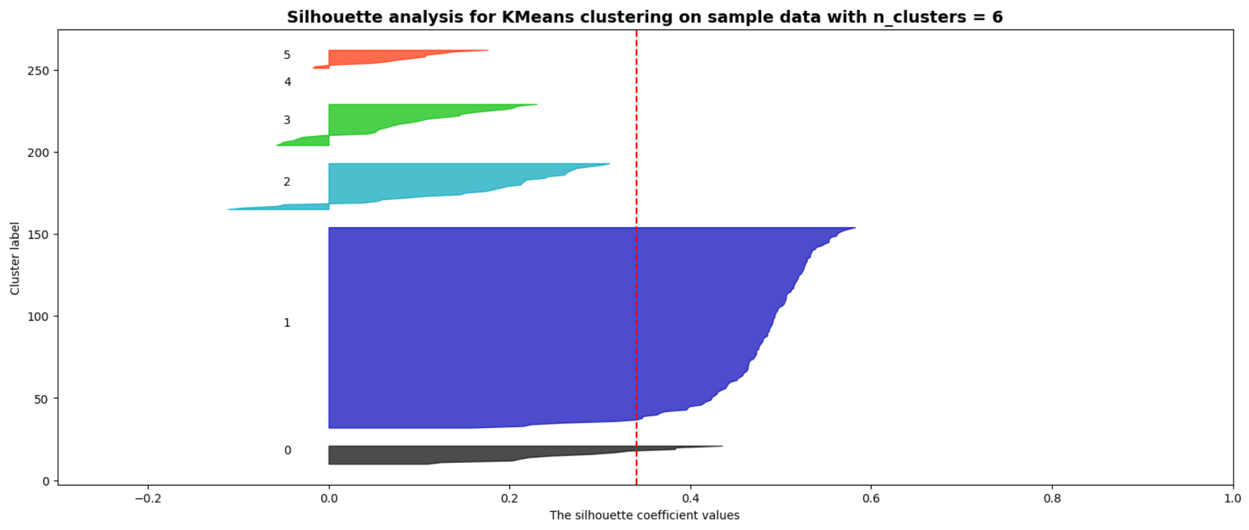
```
range_n_clusters = [2, 3, 4, 5, 6]
for n_clusters in range_n_clusters:
    km = KMeans(n_clusters=n_clusters, n_init=20, random_state=0)
    labels = km.fit_predict(X1_drop)

    silhouette_avg = silhouette_score(X1_drop, labels)
    sample_silhouette_values = silhouette_samples(X1_drop, labels)
    fig, ax1 = plt.subplots(1, 1)
    fig.set_size_inches(18, 7)
    ax1.set_xlim([-0.3, 1])

    y_lower = 10

    for i in range(n_clusters):
        ith_cluster_silhouette_values = sample_silhouette_values[labels == i]
        ith_cluster_silhouette_values.sort()
        size_cluster_i = ith_cluster_silhouette_values.shape[0]
        y_upper = y_lower + size_cluster_i

        # Use the colormap for coloring
        color = cm.nipy_spectral(float(i) / n_clusters)
        ax1.fill_betweenx(
            y=np.arange(y_lower, y_upper),
            x1=0,
            x2=ith_cluster_silhouette_values,
            facecolor=color,
            edgecolor=color,
            alpha=0.7,
        )

        ax1.text(-0.05, y_lower + 0.5 * size_cluster_i, str(i))

        y_lower = y_upper + 10

    ax1.set_title("The silhouette plot for various clusters")
    ax1.set_xlabel("The silhouette coefficient values")
    ax1.set_ylabel("Cluster label")

    ax1.axvline(x=silhouette_avg, color="red", linestyle="--")
    plt.title(
        "Silhouette analysis for KMeans clustering on sample data with n_clusters = %d"
        % n_clusters,
        fontsize=14,
        fontweight="bold",
    )

plt.show()
```


Silhouette analysis for KMeans clustering on sample data with n_clusters = 2
Cluster label
The silhouette coefficient values
0
1


Silhouette analysis for KMeans clustering on sample data with n_clusters = 3
Cluster label
The silhouette coefficient values
0
1
2


Silhouette analysis for KMeans clustering on sample data with n_clusters = 4
Cluster label
The silhouette coefficient values
0
1
2
3





```
kmeans = KMeans(n_clusters=2, n_init=20, random_state=0)
labels = kmeans.fit_predict(y)
labels
```

```
array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1], dtype=int32)
```

```
pca_X = PCA()
X = pd.DataFrame(X1_filled, X1_filled.index, X1_filled.columns)
```

```
pca_loading = pd.DataFrame(pca_X.fit(X).components_.T, index=X1_filled.columns, columns=['pc1'
            'pc11', 'pc12', 'pc13', 'pc14', 'pc15', 'pc16', 'pc17', 'pc18'
           # , 'pc19', 'pc20','pc21', 'pc22', 'pc23', 'pc24']
            ])
pca_loading
```

	pc1	pc2	pc3	pc4	pc5	pc6	pc7	pc8	pc9
age	0.227990	0.230990	0.295718	-0.031051	-0.575582	-0.656010	0.133337	0.002424	0.021785
bp	0.218657	0.195864	0.182461	-0.453550	0.717207	-0.375424	-0.036042	0.093023	0.039444
sg	-0.001662	0.000410	0.000035	0.000870	0.000296	-0.000717	-0.001237	0.000471	0.001026
al	0.553457	-0.487707	-0.482395	-0.347007	-0.140393	0.010337	0.180866	0.053118	0.087756
su	0.357932	-0.308756	0.426065	0.400909	0.206522	0.046562	0.154558	-0.475340	0.349520
rbc	-0.160721	-0.314032	-0.325148	0.422191	0.147226	-0.553442	-0.342586	0.238952	0.237721
pc	-0.174043	-0.281904	-0.051507	0.116840	0.165232	-0.277618	0.505481	-0.186919	-0.676205
pcc	0.071946	-0.044355	-0.032420	-0.030809	-0.042205	-0.030729	-0.036475	0.017117	0.033291
ba	0.043953	-0.029370	-0.034667	-0.031891	0.001018	-0.018845	-0.006731	-0.005783	0.039313

	pc1	pc2	pc3	pc4	pc5	pc6	pc7	pc8	pc9
bgr	0.337320	-0.236555	0.377282	0.237826	0.014970	0.158208	-0.269555	0.548677	-0.422632
bu	0.348920	0.344499	-0.344170	0.250931	0.056552	-0.049455	-0.410254	-0.465145	-0.346444
sc	0.266765	0.457515	-0.264006	0.424086	0.151383	0.091202	0.523546	0.375210	0.133144
htn	0.187133	0.065908	0.030741	-0.085847	-0.078187	-0.009468	-0.061016	0.053573	-0.091387
dm	0.180008	0.035135	0.115632	-0.019354	-0.062214	0.046096	-0.091541	0.012088	-0.044199
cad	0.061433	0.013987	0.014001	0.013954	-0.026179	-0.008642	0.008890	-0.007925	-0.000104
appet	0.094301	0.028995	-0.029747	-0.083728	-0.020176	0.013642	-0.047902	0.015283	-0.123596
pe	0.099282	0.005992	-0.074849	-0.057811	-0.050081	0.052186	-0.058089	-0.086412	0.013031
ane	0.076863	0.059741	-0.053879	-0.025595	0.035715	0.027753	-0.130954	-0.035215	-0.097805

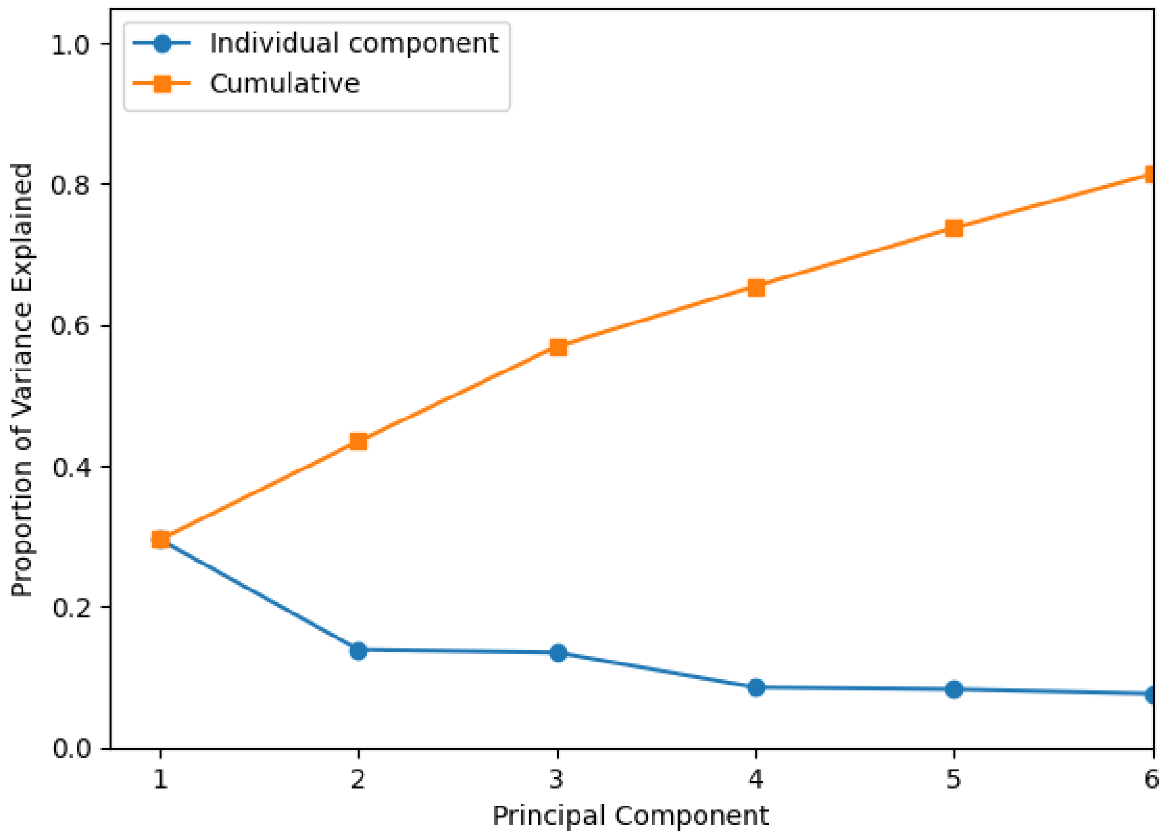
```
pc_scores = pd.DataFrame(pca_X.fit_transform(X), columns=['pc1', 'pc2', 'pc3', 'pc4', 'pc5', '
            'pc11', 'pc12', 'pc13', 'pc14', 'pc15', 'pc16', 'pc17', 'pc18'], index=X.index)
pc_scores
```

	pc1	pc2	pc3	pc4	pc5	pc6	pc7	pc8	pc9
0	-0.159842	0.123121	0.340298	-1.076715	-0.028920	0.446685	0.604284	-0.200452	-0.546039
1	0.080324	-2.658949	-2.090773	-0.980571	-0.533556	2.899035	1.077587	0.010434	-0.315841
2	2.748405	-2.445865	1.908401	1.610708	0.460511	-0.398526	-0.557039	0.808465	-0.761516
3	1.597823	-1.458225	-2.420973	-0.957120	-0.769911	-0.046338	-0.110910	0.412311	0.653469
4	-0.378850	-1.060810	-0.899482	-0.559600	0.156071	-0.818241	0.426550	0.266685	0.309952
...	...	...	...	...	...	...	...	...	...
395	-1.170494	-0.047818	0.180807	0.277176	0.311051	-0.960873	-0.289116	0.125640	-0.220852
396	-1.872246	-0.239130	-0.396054	0.399566	0.208608	-0.289936	0.067806	-0.182926	0.220656
397	-2.067094	-0.656654	-0.599016	0.127848	1.723678	0.628361	-0.291070	0.061005	0.098355
398	-2.076334	-0.721928	-0.895292	0.973608	0.546345	0.997310	-0.405810	-0.172560	-0.183314
399	-1.355503	-0.144376	0.373565	0.134861	0.189736	-1.053690	0.071790	0.388850	0.057877

```
var=pc_scores.var()
var
```

```
pc1     3.011006
pc2     1.418726
pc3     1.376123
pc4     0.871790
pc5     0.843322
pc6     0.780234
pc7     0.413204
pc8     0.356221
pc9     0.333497
pc10    0.193763
pc11    0.135449
pc12    0.107061
pc13    0.098757
pc14    0.082265
pc15    0.071608
pc16    0.058557
pc17    0.044481
pc18    0.000018
dtype: float64
```

```python
plt.figure(figsize=(7,5))

plt.plot([1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18]
, pca_X.explained_variance_ratio_, '-o', label='Individual component')
plt.plot([1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18]
, np.cumsum(pca_X.explained_variance_ratio_), '-s', label='Cumulative')

plt.ylabel('Proportion of Variance Explained')
plt.xlabel('Principal Component')
plt.xlim(0.75,4.25)
plt.ylim(0,1.05)
plt.xticks([1,2,3,4,5,6])
plt.legend(loc=2);
```



```
pca_loading
```

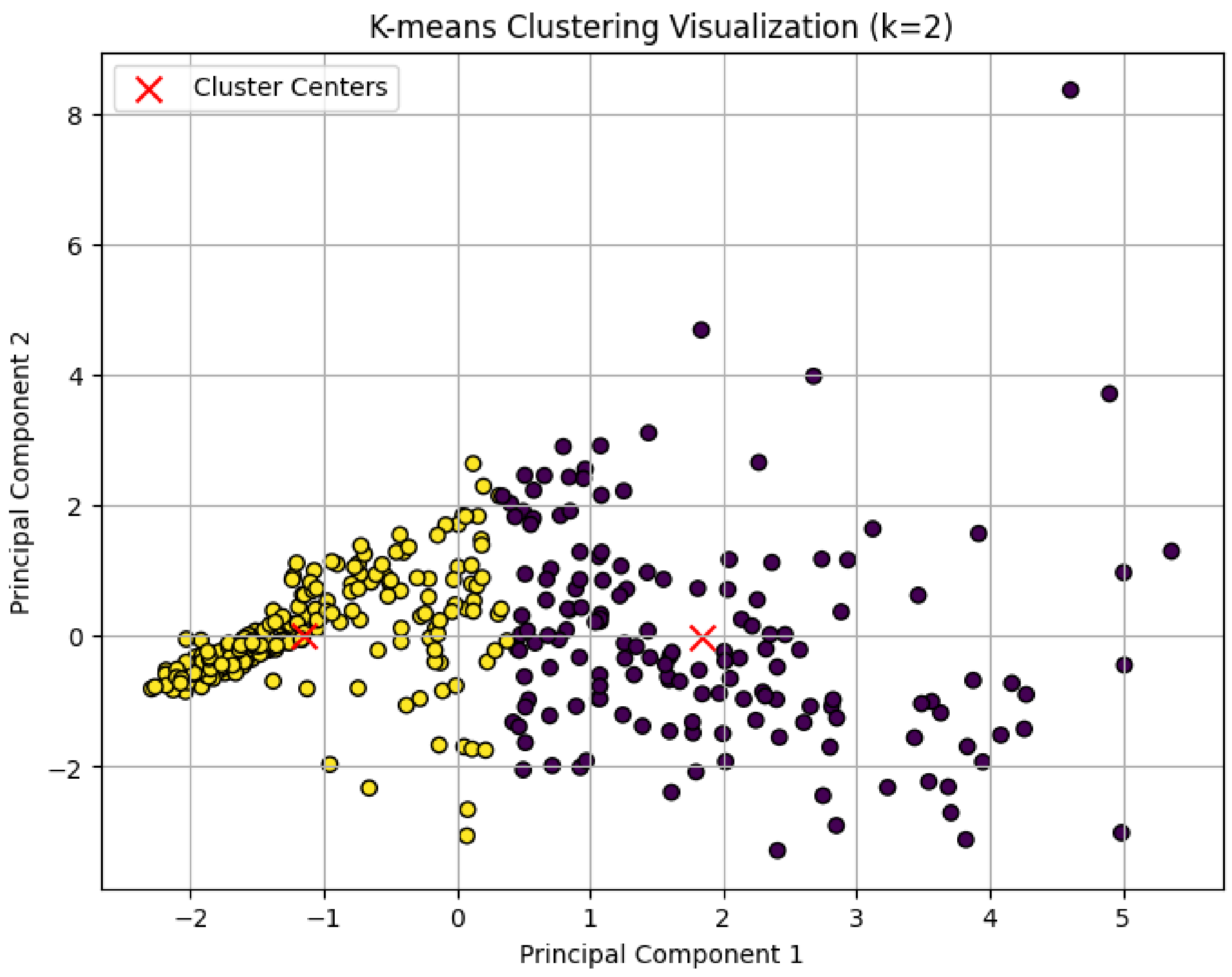
	pc1	pc2	pc3	pc4	pc5	pc6	pc7	pc8	pc9
age	0.227990	0.230990	0.295718	-0.031051	-0.575582	-0.656010	0.133337	0.002424	0.021785
bp	0.218657	0.195864	0.182461	-0.453550	0.717207	-0.375424	-0.036042	0.093023	0.039444
sg	-0.001662	0.000410	0.000035	0.000870	0.000296	-0.000717	-0.001237	0.000471	0.001026
al	0.553457	-0.487707	-0.482395	-0.347007	-0.140393	0.010337	0.180866	0.053118	0.087756
su	0.357932	-0.308756	0.426065	0.400909	0.206522	0.046562	0.154558	-0.475340	0.349520
rbc	-0.160721	-0.314032	-0.325148	0.422191	0.147226	-0.553442	-0.342586	0.238952	0.237721
pc	-0.174043	-0.281904	-0.051507	0.116840	0.165232	-0.277618	0.505481	-0.186919	-0.676205
pcc	0.071946	-0.044355	-0.032420	-0.030809	-0.042205	-0.030729	-0.036475	0.017117	0.033291
ba	0.043953	-0.029370	-0.034667	-0.031891	0.001018	-0.018845	-0.006731	-0.005783	0.039313
bgr	0.337320	-0.236555	0.377282	0.237826	0.014970	0.158208	-0.269555	0.548677	-0.422632

	pc1	pc2	pc3	pc4	pc5	pc6	pc7	pc8	pc9
bu	0.348920	0.344499	-0.344170	0.250931	0.056552	-0.049455	-0.410254	-0.465145	-0.346444
sc	0.266765	0.457515	-0.264006	0.424086	0.151383	0.091202	0.523546	0.375210	0.133144
htn	0.187133	0.065908	0.030741	-0.085847	-0.078187	-0.009468	-0.061016	0.053573	-0.091387
dm	0.180008	0.035135	0.115632	-0.019354	-0.062214	0.046096	-0.091541	0.012088	-0.044199
cad	0.061433	0.013987	0.014001	0.013954	-0.026179	-0.008642	0.008890	-0.007925	-0.000104
appet	0.094301	0.028995	-0.029747	-0.083728	-0.020176	0.013642	-0.047902	0.015283	-0.123596
pe	0.099282	0.005992	-0.074849	-0.057811	-0.050081	0.052186	-0.058089	-0.086412	0.013031
ane	0.076863	0.059741	-0.053879	-0.025595	0.035715	0.027753	-0.130954	-0.035215	-0.097805

```python
PCA_var=sum(pca_X.explained_variance_ratio_[0:2])
PCA_var
```

```
0.4344542793757311
```

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

principal_components = pca_X.fit_transform(X)
kmeans = KMeans(n_clusters=2, n_init=20, random_state=0)
kmeans.fit(principal_components)
cluster_labels = kmeans.labels_

# Plot data points
plt.scatter(principal_components[:, 0], principal_components[:, 1], c=cluster_labels, cmap='vi

# Plot cluster centers
plt.scatter(kmeans.cluster_centers_[:, 0], kmeans.cluster_centers_[:, 1], marker='x', c='red',

plt.title('K-means Clustering Visualization (k=2)')
plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.legend()
plt.grid(True)
plt.show()
```



```
y_1d = np.ravel(y)

adjusted_Rand_index = adjusted_rand_score(y_1d, cluster_labels)

adjusted_Rand_index
```

```
0.2663417112554181
```

8. **Data Splitting:** Segregate 30% of the data for testing, using a random seed of 1. Use the remaining 70% for training and model selection.

```
X_train, X_test, y_train, y_test = train_test_split(
    X1_filled, y, test_size=0.3, random_state=0, stratify=y) #or test_size=0.7
```

9. **Classifier Choices:** Identify the two classifiers you have chosen and justify your selections.

Algorithm 1: Dicision tree

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.metrics import mean_squared_error, confusion_matrix, classification_report
from sklearn.tree import DecisionTreeClassifier, DecisionTreeRegressor, plot_tree
```

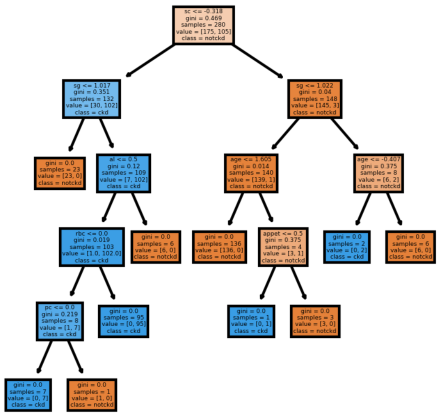
```
cs_dt = DecisionTreeClassifier(
    max_depth =30,
    random_state=1
)
```

```
cs_dt.fit(X_train, y_train)
```

```
DecisionTreeClassifier(max_depth=30, random_state=1)
```

```
fig, axes = plt.subplots(
    nrows = 1,ncols = 1,figsize = (3,3), dpi=300
    )
plot_tree(
    cs_dt,
    max_depth= 30,
    feature_names = X_train.columns.tolist(),
    class_names=['notckd', 'ckd'],
    filled = True
    )
```

```
[Text(0.4642857142857143, 0.9166666666666666, 'sc <= -0.318\ngini = 0.469\nsamples = 280\nvalu
 Text(0.21428571428571427, 0.75, 'sg <= 1.017\ngini = 0.351\nsamples = 132\nvalue = [30, 102]\
 Text(0.14285714285714285, 0.5833333333333334, 'gini = 0.0\nsamples = 23\nvalue = [23, 0]\ncla
 Text(0.2857142857142857, 0.5833333333333334, 'al <= 0.5\ngini = 0.12\nsamples = 109\nvalue =
 Text(0.21428571428571427, 0.4166666666666667, 'rbc <= 0.0\ngini = 0.019\nsamples = 103\nvalue
 Text(0.14285714285714285, 0.25, 'pc <= 0.0\ngini = 0.219\nsamples = 8\nvalue = [1, 7]\nclass
 Text(0.07142857142857142, 0.08333333333333333, 'gini = 0.0\nsamples = 7\nvalue = [0, 7]\nclas
 Text(0.21428571428571427, 0.08333333333333333, 'gini = 0.0\nsamples = 1\nvalue = [1, 0]\nclas
 Text(0.2857142857142857, 0.25, 'gini = 0.0\nsamples = 95\nvalue = [0, 95]\nclass = ckd'),
 Text(0.35714285714285715, 0.4166666666666667, 'gini = 0.0\nsamples = 6\nvalue = [6, 0]\nclass
 Text(0.7142857142857143, 0.75, 'sg <= 1.022\ngini = 0.04\nsamples = 148\nvalue = [145, 3]\ncl
 Text(0.5714285714285714, 0.5833333333333334, 'age <= 1.605\ngini = 0.014\nsamples = 140\nvalu
 Text(0.5, 0.4166666666666667, 'gini = 0.0\nsamples = 136\nvalue = [136, 0]\nclass = notckd'),
 Text(0.6428571428571429, 0.4166666666666667, 'appet <= 0.5\ngini = 0.375\nsamples = 4\nvalue
 Text(0.5714285714285714, 0.25, 'gini = 0.0\nsamples = 1\nvalue = [0, 1]\nclass = ckd'),
 Text(0.7142857142857143, 0.25, 'gini = 0.0\nsamples = 3\nvalue = [3, 0]\nclass = notckd'),
 Text(0.8571428571428571, 0.5833333333333334, 'age <= -0.407\ngini = 0.375\nsamples = 8\nvalue
 Text(0.7857142857142857, 0.4166666666666667, 'gini = 0.0\nsamples = 2\nvalue = [0, 2]\nclass
 Text(0.9285714285714286, 0.4166666666666667, 'gini = 0.0\nsamples = 6\nvalue = [6, 0]\nclass
```



```
pred = cs_dt.predict(X_test)
pred[:5]
```

```
array([0, 0, 0, 0, 0], dtype=int8)
```

```
cm = pd.DataFrame(confusion_matrix(y_test, pred), index=['No', 'Yes'], columns=['No', 'Yes'])
cm.index.name = 'True'
cm.columns.name = 'Predicted'
cm
```

Predicted	No	Yes
True		
No	72	3
Yes	1	44

```
print(classification_report(y_test, pred))
```

```
              precision    recall  f1-score   support

           0       0.99      0.96      0.97        75
           1       0.94      0.98      0.96        45
```

```
    accuracy                           0.97       120
   macro avg       0.96      0.97      0.96       120
weighted avg       0.97      0.97      0.97       120
```

```
path = cs_dt.cost_complexity_pruning_path(
    X_train,
    y_train
)
ccp_alphas, impurities = path.ccp_alphas, path.impurities
```

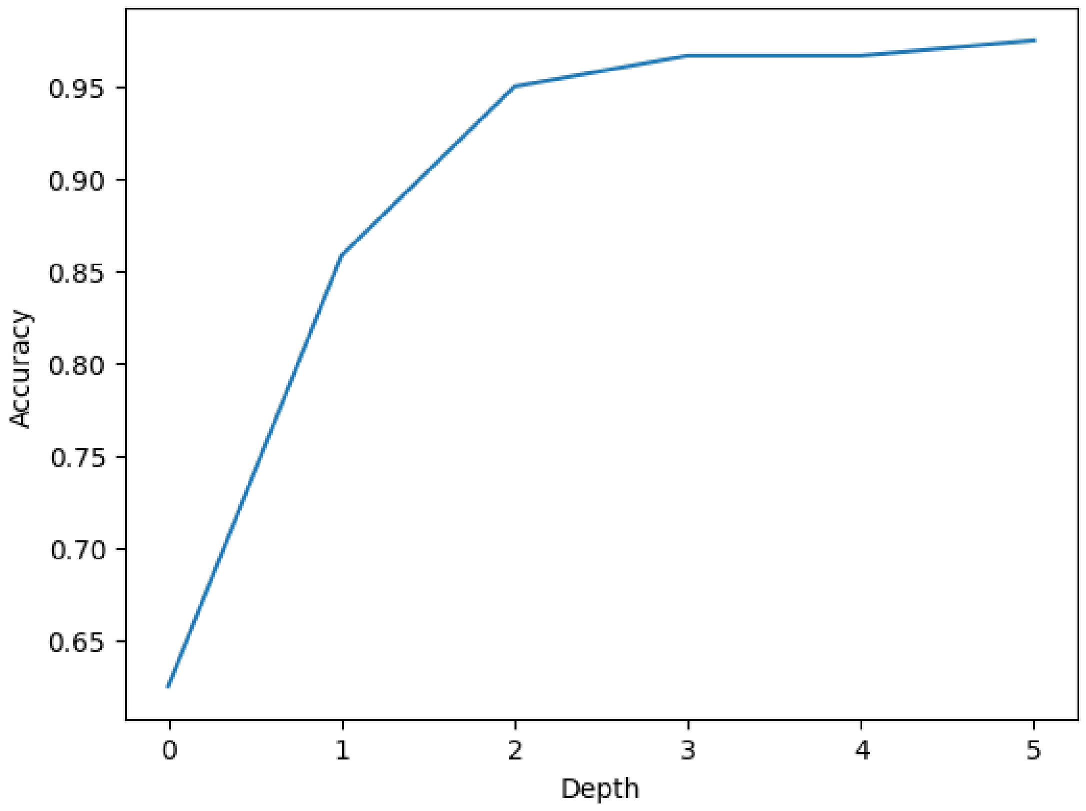
```
clfs = []
for ccp_alpha in ccp_alphas:
    clf = DecisionTreeClassifier(
        random_state=0,
        ccp_alpha=ccp_alpha
        )
    clf.fit(X_train, y_train)
    clfs.append(clf)
```

```
depth = [clf.tree_.max_depth for clf in clfs]
depth
```

```
[5, 4, 3, 3, 2, 1, 0]
```

```
test_score = [clf.score(X_test, y_test) for clf in clfs]
```

```
plt.plot(depth, test_score)
plt.xlabel('Depth')
plt.ylabel('Accuracy')
plt.show()
```



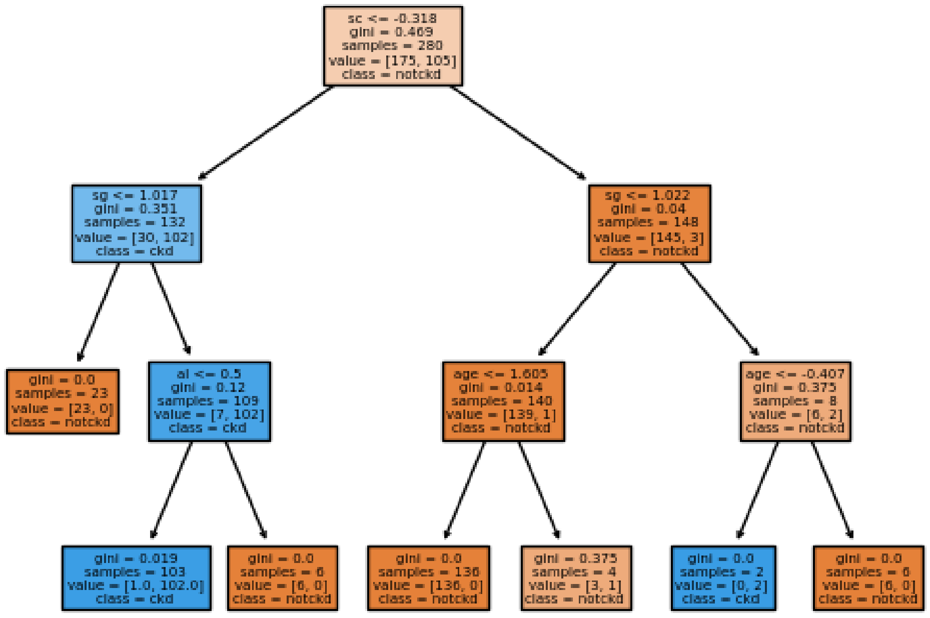
```
cs_dt_new = DecisionTreeClassifier(
    max_depth =3,
    random_state=1
)
```

```
cs_dt_new.fit(X_train, y_train)
```

```
DecisionTreeClassifier(max_depth=3, random_state=1)
```

```
plot_tree(
    cs_dt_new,
    max_depth= 3,
    feature_names = X_train.columns.tolist(),
    class_names=['notckd', 'ckd'],
    filled = True
    )
```

```
[Text(0.4230769230769231, 0.875, 'sc <= -0.318\ngini = 0.469\nsamples = 280\nvalue = [175, 105]
 Text(0.15384615384615385, 0.625, 'sg <= 1.017\ngini = 0.351\nsamples = 132\nvalue = [30, 102]
 Text(0.07692307692307693, 0.375, 'gini = 0.0\nsamples = 23\nvalue = [23, 0]\nclass = notckd')
 Text(0.23076923076923078, 0.375, 'al <= 0.5\ngini = 0.12\nsamples = 109\nvalue = [7, 102]\ncla
 Text(0.15384615384615385, 0.125, 'gini = 0.019\nsamples = 103\nvalue = [1.0, 102.0]\nclass =
 Text(0.3076923076923077, 0.125, 'gini = 0.0\nsamples = 6\nvalue = [6, 0]\nclass = notckd'),
 Text(0.6923076923076923, 0.625, 'sg <= 1.022\ngini = 0.04\nsamples = 148\nvalue = [145, 3]\nc
 Text(0.5384615384615384, 0.375, 'age <= 1.605\ngini = 0.014\nsamples = 140\nvalue = [139, 1]\
 Text(0.46153846153846156, 0.125, 'gini = 0.0\nsamples = 136\nvalue = [136, 0]\nclass = notckd
 Text(0.6153846153846154, 0.125, 'gini = 0.375\nsamples = 4\nvalue = [3, 1]\nclass = notckd'),
 Text(0.8461538461538461, 0.375, 'age <= -0.407\ngini = 0.375\nsamples = 8\nvalue = [6, 2]\ncla
 Text(0.7692307692307693, 0.125, 'gini = 0.0\nsamples = 2\nvalue = [0, 2]\nclass = ckd'),
 Text(0.9230769230769231, 0.125, 'gini = 0.0\nsamples = 6\nvalue = [6, 0]\nclass = notckd')]
```



```python
pred_new = cs_dt_new.predict(X_test)
pred_new[:5]
```

```
array([0, 0, 0, 0, 0], dtype=int8)
```

```
cm_new = pd.DataFrame(confusion_matrix(y_test, pred_new), index=['No', 'Yes'], columns=['No',
cm_new.index.name = 'True'
cm_new.columns.name = 'Predicted'
cm_new
```

Predicted	No	Yes
True		
No	72	3
Yes	1	44

```
print(classification_report(y_test, pred_new))
```

```
              precision    recall  f1-score   support

           0       0.99      0.96      0.97        75
           1       0.94      0.98      0.96        45

    accuracy                           0.97       120
   macro avg       0.96      0.97      0.96       120
weighted avg       0.97      0.97      0.97       120
```

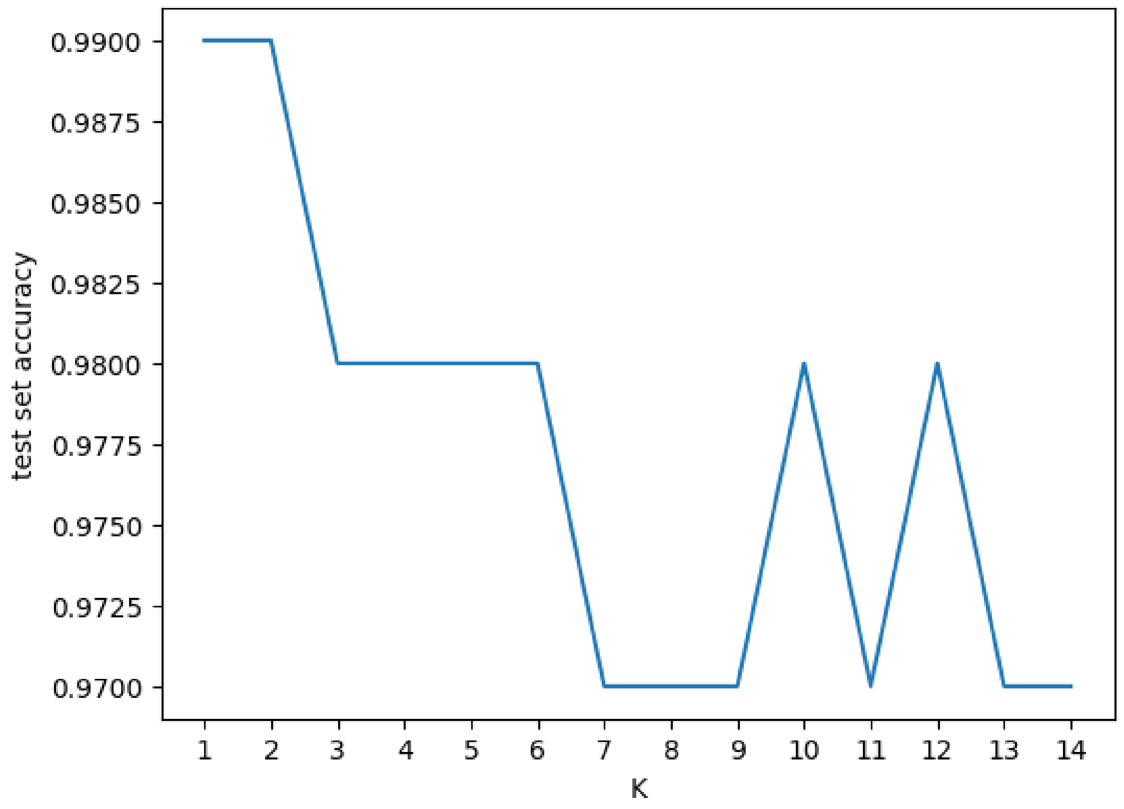
Algorithm 2: KNN

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn import neighbors
from sklearn.preprocessing import scale
from sklearn.model_selection import train_test_split
from sklearn import metrics
```

```
x2_train, x2_test, y2_train, y2_test = train_test_split(
    X1_filled,
    y,
    test_size = 0.3,
    random_state = 0,
    stratify = y
    )
```

```
k_range = range(1, 15)
scores_r = []

for k in k_range:
    knn_r = neighbors.KNeighborsClassifier(n_neighbors=k)
    y_train_flat = np.ravel(y2_train)
    knn_r.fit(x2_train, y_train_flat)
    y_r_pred = knn_r.predict(x2_test.values)
    scores_r.append(round(metrics.accuracy_score(y2_test, y_r_pred), 2))
```

```
plt.plot(k_range, scores_r)
plt.xlabel('K')
plt.ylabel('test set accuracy')
plt.xticks(range(1,15))
plt.show()
```



```
knn3 = neighbors.KNeighborsClassifier(
    n_neighbors = 2,
    algorithm = 'brute'
    )

y_train_flat = np.ravel(y2_train)

knn3.fit(x2_train, y_train_flat)
```

```
KNeighborsClassifier(algorithm='brute', n_neighbors=2)
```

```
pred3 = knn3.predict(x2_test.values)
pred3[1:5]
```

```
array([0, 0, 0, 0], dtype=int8)
```

```
round(metrics.accuracy_score(y2_test, pred3), 2)
```

```
0.99
```

```
conf_matrix = confusion_matrix(y2_test, pred3)
print(conf_matrix)
```

```
[[74  1]
 [ 0 45]]
```

10. **Performance Metrics:** Outline the two metrics for comparing the performance of the classifiers.

```
cm = pd.DataFrame(confusion_matrix(y_test, pred), index=['No', 'Yes'], columns=['No', 'Yes'])
cm.index.name = 'True'
cm.columns.name = 'Predicted'
print('Confusion Matrix of Decision Tree:')
cm
```

```
Confusion Matrix of Decision Tree:
```

Predicted	No	Yes
True		
No	72	3
Yes	1	44

For the desicion tree classifier confusion matrix, there are 72 observations been correctly predicted as No, and 44 variables been predicted as Yes truely. Remindered that the y variable has two input, one is no, means this person do not have chronic kidney disease; the other one is yes, means the person has chronic kidney disease.

```
conf_matrix = pd.DataFrame(confusion_matrix(y2_test, pred3), index=['No', 'Yes'], columns=['No
conf_matrix.index.name = 'True'
conf_matrix.columns.name = 'Predicted'
print('Confusion Matrix of KNN:')
conf_matrix
```

```
Confusion Matrix of KNN:
```

Predicted	No	Yes
True		
No	74	1
Yes	0	45

73 observations without chronic kidney disease in KNN classifier been coreectly predicted as no, and 45 person with chronic kidney disease are correctly predicted as yes.

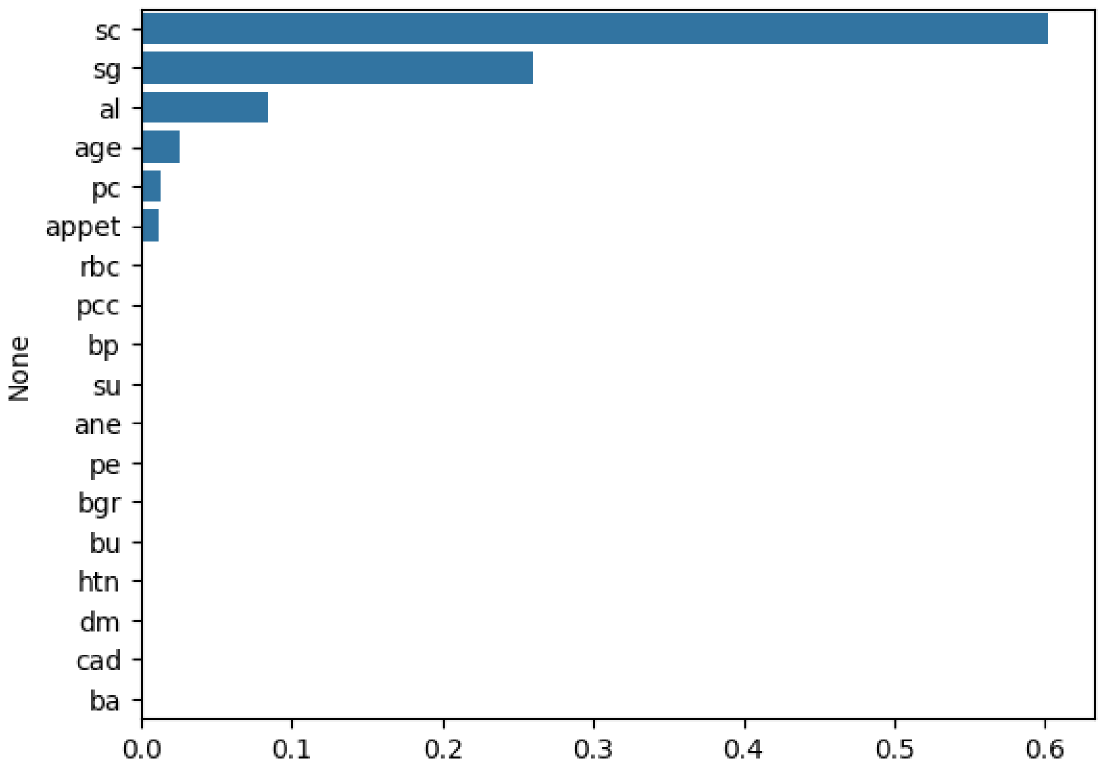
By comparision of these two confussion matrixs, since the KNN classifier has number of observations of both person with chronic kidney disease and person without chronic kidney disease been predicted truely than the number of observations been predicted by the decision tree classifier. Thus, we considered KNN classifier better than decision tree. Moreover, compare the accuracy score of both classifiers, KNN has 98% accuracy which is greater than decision tree with 97% accuracy.

11. **Feature Selection/Extraction:** Implement methods to enhance the performance of at least one classifier in (9). The answer for this question can be included in (12).

We want to do feature selection for decision tree.

```
feature_importances = cs_dt.feature_importances_


sorted_indices = feature_importances.argsort()[::-1]
sorted_feature_names = X_train.columns[sorted_indices]
sorted_importances = feature_importances[sorted_indices]
```

```
sns.barplot(x = sorted_importances, y = sorted_feature_names)
plt.show()
```



12. **Classifier Comparison:** Utilize the selected metrics to compare the classifiers based on the test set. Discuss your findings (at least two statements).

```
conf_matrix = confusion_matrix(y2_test, pred3)
print("KNN Result: ")
print(conf_matrix)



print("Decision Tree Result: " )
cm = pd.DataFrame(confusion_matrix(y_test, pred), index=['No', 'Yes'], columns=['No', 'Yes'])
cm.index.name = 'True'
cm.columns.name = 'Predicted'
print(cm)
```

```
KNN Result:
[[74  1]
 [ 0 45]]
Decision Tree Result:
Predicted  No  Yes
True
No         72    3
Yes         1   44
```

From the above confusion matrix, we can observe that KNN has a better result.

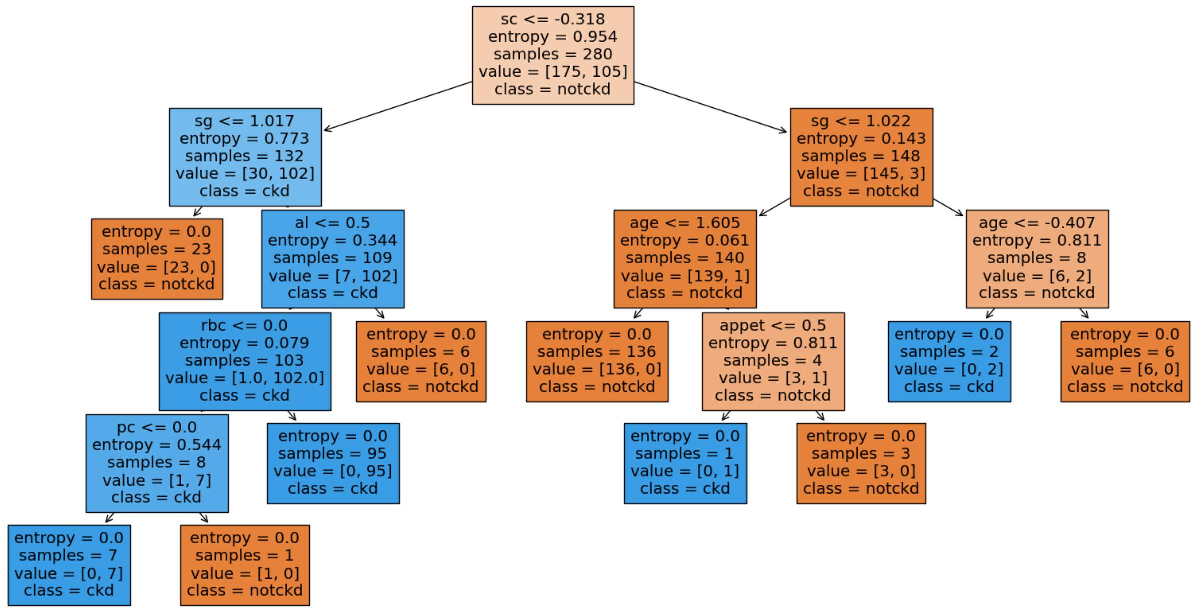
13. **Interpretable Classifier Insight:** After re-training the interpretable classifier with all available data, analyze and interpret the significance of predictor variables in the context of the data and the challenge (at least two statements).

```
clf = DecisionTreeClassifier(max_depth =6,
    random_state=1,criterion='entropy')
clf.fit(X_train, y_train)



y_pred = clf.predict(X_test)
```

```
from sklearn.metrics import accuracy_score, classification_report


print("Accuracy:", accuracy_score(y_test, y_pred))
print(classification_report(y_test, y_pred))



plt.figure(figsize=(20,10))
plot_tree(clf, filled=True,feature_names = X_train.columns.tolist(),class_names=['notckd', 'ck
plt.show()
```

```
Accuracy: 0.9666666666666667
```

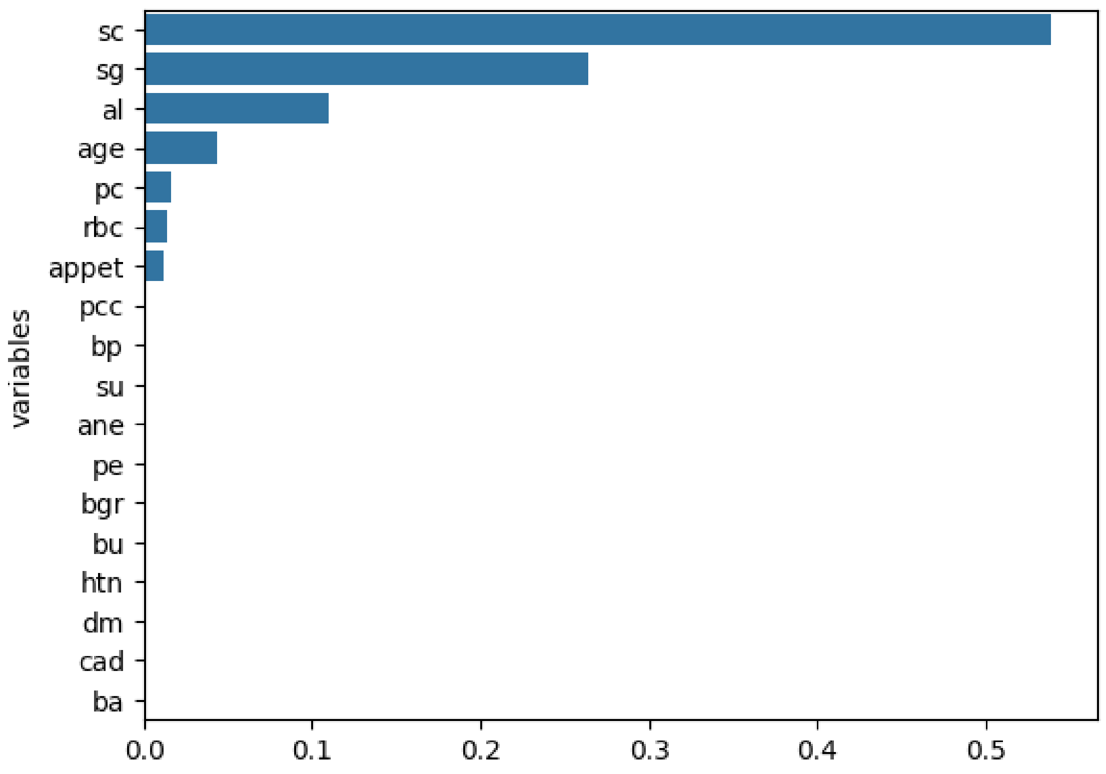
```
              precision    recall  f1-score   support

           0       0.99      0.96      0.97        75
           1       0.94      0.98      0.96        45

    accuracy                           0.97       120
   macro avg       0.96      0.97      0.96       120
weighted avg       0.97      0.97      0.97       120
```



```python
cm = pd.DataFrame(confusion_matrix(y_test, y_pred), index=['No', 'Yes'], columns=['No', 'Yes']
cm.index.name = 'True'
cm.columns.name = 'Predicted'
cm
```

Predicted	No	Yes
True		
No	72	3
Yes	1	44

```
fea_imp = clf.feature_importances_
sorted_indices = fea_imp.argsort()[::-1]
sorted_feature_names = X_train.columns[sorted_indices]
sorted_importances = fea_imp[sorted_indices]
sns.barplot(x = sorted_importances, y = sorted_feature_names)
plt.ylabel("variables")

plt.show()
```



We have retrain the model with a different criteria and less depth. This less complicated model give as a better result. We also find features that are significant to the model.

14. [**Bonus**] Sub-group Improvement Strategy: If sub-groups were identified, propose and implement a method to improve one classifier performance further. Compare the performance of the new classifer with the results in (12).

We can use resampling to improve one classifier performance further, since we have too many missing values in this sample data.

```
poly = PolynomialFeatures(degree=3, interaction_only=True)
X_polytrain = poly.fit_transform(X_train)
X_polytest = poly.transform(X_test)
logit_model = LogisticRegression()
logit_model.fit(X_polytrain, y_train)
y_polypred = logit_model.predict(X_polytest)
accuracy = accuracy_score(y_test, y_polypred)
accuracy
```

```
0.9833333333333333
```

Improved Model Accuracy is 0.9833333333333333.

15. **Team Contributions:** Document each team member's specific contributions related to the questions above.

Ling Dai(400220798): Question Question 1-6,8,9,14

Shujia Zhang(400390028): Question 2, 5, 7,10,11,12,13

Yunxin Li(400323756):3,4, 10, 11, 12, 13

All team memebers are participated in this project actively. We have a lot of disscusion and communication during the projects, so most of the code are actually done together offline in school.

16. **Link** to the public GitHub repository.

https://github.com/dail9/3da-assignment6/blob/main/assignment6.ipynb

Reference

Rubini, Soundarapandian, L., and P. Eswaran. 2015. "Chronic Kidney Disease." UCI Machine Learning Repository.