STATS 3DA3

Homework Assignment 6

Haoyuan Chen (400370821), Yincheng Zhu (400371892)

2024-04-04

Submission Deadline

- All submissions must be made before 10:00 PM on Thursday, April 18, 2024.

Submission Guidelines

- Format: Submissions are to be made in PDF format via Avenue to Learn, either individually or as a group of up to three members.
  - GitHub Repository: Your submission must include a link to a public GitHub repository containing the assignment.
  - Team Submissions: For group submissions, Question 15 must detail each member's contributions. Note that while there are no points allocated to Question 15, failure to provide this information will result in the assignment not being graded.

Late Submissions

- 15% will be deducted from assignments each day after the due date (rounding up).
- Assignments won't be accepted after 48 hours after the due date.

Assignment Standards

Please ensure your assignment adheres to the following standards for submission:

- **Title Page Requirements:** Each submission must include a title page featuring your group members' names and student numbers. Assignments lacking a title page will not be considered for grading.
- **Individual Work:** While discussing homework problems with peers and group is permitted, the final written submission must be your group work.
- **Formatting Preferences:** The use of LaTeX for document preparation is highly recommended.
- **Font and Spacing:** Submissions must utilize an eleven-point font (Times New Roman or a similar font) with 1.5 line spacing. Ensure margins of at least 1 inch on all sides.

- **Submission Content:** Do not include the assignment questions within your PDF. Instead, clearly mark each response with the corresponding question number. Screenshots are not an acceptable form of submission under any circumstances.
- **Academic Writing:** Ensure that your writing and any references used are appropriate for an undergraduate level of study.
- **Originality Checks:** Be aware that the instructor may use various tools, including those available on the internet, to verify the originality of submitted assignments.
- Assignment policy on the use of generative AI:
  - Students are not permitted to use generative AI in this assignment. In alignment with McMaster academic integrity policy, it "shall be an offence knowingly to … submit academic work for assessment that was purchased or acquired from another source". This includes work created by generative AI tools. Also state in the policy is the following, "Contract Cheating is the act of"outsourcing of student work to third parties" (Lancaster & Clarke, 2016, p. 639) with or without payment." Using Generative AI tools is a form of contract cheating. Charges of academic dishonesty will be brought forward to the Office of Academic Integrity.

Chronic Kidney Disease Classification Challenge

Overview

Engage with the dataset from the Early Stage of Indians Chronic Kidney Disease (CKD) project, which comprises data on 250 early-stage CKD patients and 150 healthy controls.

For foundational knowledge on the subject, refer to "Predict, diagnose, and treat chronic kidney disease with machine learning: a systematic literature review" by Sanmarchi et al., (2023).

Objectives

Analyze the dataset using two classification algorithms, focusing on exploratory data analysis, feature selection, engineering, and especially on handling missing values and outliers. Summarize your findings with insightful conclusions.

Classifier Requirement: Ensure at least one of the classifiers is interpretable, to facilitate in-depth analysis and inference.

Guidelines

- **Teamwork:** Group submissions should compile the workflow (Python codes and interpretations) into a single PDF, including a GitHub repository link. The contributions listed should reflect the GitHub activity.
- **Content:** Address the following questions in your submission, offering detailed insights and conclusions from your analysis.

Assignment Questions

1. **Classification Problem Identification:** Define and describe a classification problem based on the dataset.
2. **Variable Transformation:** Implement any transformations chosen or justify the absence of such modifications.
3. **Dataset Overview:** Provide a detailed description of the dataset, covering variables, summaries, observation counts, data types, and distributions (at least three statements).

4. **Association Between Variables:** Analyze variable relationships and their implications for feature selection or extraction (at least three statements).
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.
6. **Outlier Analysis:** Implement your approach for identifying and managing outliers, or provide reasons for not addressing them.
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).
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.
9. **Classifier Choices:** Identify the two classifiers you have chosen and justify your selections.
10. **Performance Metrics:** Outline the two metrics for comparing the performance of the classifiers.
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).
12. **Classifier Comparison:** Utilize the selected metrics to compare the classifiers based on the test set. Discuss your findings (at least two statements).
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).
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).
15. **Team Contributions:** Document each team member's specific contributions related to the questions above.
16. **Link** to the public GitHub repository.

Notes

- This assignment encourages you to apply sophisticated machine learning methods to a vital healthcare challenge, promoting the development of critical analytical skills, teamwork, and

practical problem-solving abilities in the context of chronic kidney disease diagnosis and treatment.

- Students can choose one classifer not covered in the lectures.

question 1

```
from ucimlrepo import fetch_ucirepo


import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
from scipy import stats
import matplotlib.cm as cm

from pyampute.exploration.mcar_statistical_tests import MCARTest

from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import scale
from sklearn.decomposition import PCA, TruncatedSVD, FactorAnalysis
from sklearn.impute import SimpleImputer
from sklearn.cluster import KMeans
from sklearn.metrics import silhouette_samples, silhouette_score
from sklearn.impute import KNNImputer
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import confusion_matrix, accuracy_score,classification_report
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier, DecisionTreeClassifier, plot_tree
from sklearn.svm import SVC
from sklearn.model_selection import GridSearchCV
```

```
from sklearn import metrics


sns.set_theme(style="darkgrid")
```

[misc_chronic_kidney_disease_336]

```
# fetch dataset
chronic_kidney_disease = fetch_ucirepo(id=336)


# data (as pandas dataframes)
kidney = pd.DataFrame(chronic_kidney_disease.data.features)
y = pd.DataFrame(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.ec
     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
```

```
kidney.describe()
```

	age	bp	sg	al	su	bgr	bu	sc
count	391.000000	388.000000	353.000000	354.000000	351.000000	356.000000	381.000000	383.000000
mean	51.483376	76.469072	1.017408	1.016949	0.450142	148.036517	57.425722	3.072454
std	17.169714	13.683637	0.005717	1.352679	1.099191	79.281714	50.503006	5.741126
min	2.000000	50.000000	1.005000	0.000000	0.000000	22.000000	1.500000	0.400000
25%	42.000000	70.000000	1.010000	0.000000	0.000000	99.000000	27.000000	0.900000
50%	55.000000	80.000000	1.020000	0.000000	0.000000	121.000000	42.000000	1.300000
75%	64.500000	80.000000	1.020000	2.000000	0.000000	163.000000	66.000000	2.800000
max	90.000000	180.000000	1.025000	5.000000	5.000000	490.000000	391.000000	76.000000

Based on the dataset, the classification problem is whether the patient has chronic kidney disease or not by using the data that was taken over a 2-month period with 25 features (eg, red blood cell count, white blood cell count, etc)

Question 2

```
obj_col = kidney.select_dtypes('object').columns
```

```
for i in obj_col:
    print(f"col_name: {i} value ---> {kidney[i].unique()}")
```

```
col_name: rbc value ---> [nan 'normal' 'abnormal']
col_name: pc value ---> ['normal' 'abnormal' nan]
col_name: pcc value ---> ['notpresent' 'present' nan]
col_name: ba value ---> ['notpresent' 'present' nan]
col_name: htn value ---> ['yes' 'no' nan]
col_name: dm value ---> ['yes' 'no' '\tno' nan]
col_name: cad value ---> ['no' 'yes' nan]
col_name: appet value ---> ['good' 'poor' nan]
col_name: pe value ---> ['no' 'yes' nan]
col_name: ane value ---> ['no' 'yes' nan]
```

```
# fix the typo error
kidney.loc[kidney['dm']== '\tno','dm'] = 'no'
```

```
for i in obj_col:
    print(f"{i}:{kidney[i].unique()},")
```

```
rbc:[nan 'normal' 'abnormal'],
pc:['normal' 'abnormal' nan],
pcc:['notpresent' 'present' nan],
ba:['notpresent' 'present' nan],
htn:['yes' 'no' nan],
dm:['yes' 'no' nan],
cad:['no' 'yes' nan],
appet:['good' 'poor' nan],
pe:['no' 'yes' nan],
ane:['no' 'yes' nan],
```

```
help_map = {
    "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 help_map.items():
    kidney[i] = kidney[i].replace(j)
```

```
print(y['class'].unique())
```

```
['ckd' 'ckd\t' 'notckd']
```

```
#fix typo error
y = y.replace({'ckd': 1, 'notckd': 0, 'ckd\t': 1})
print(y['class'].unique())
```

```
[1 0]
```

```
cate_col = obj_col.to_list()
cate_col.append('sg')
cate_col.append('al')
cate_col.append('su')
```

```
for i in cate_col:
    kidney[i] = pd.Categorical(kidney[i])


float_col = kidney.select_dtypes('float').columns.to_list()
```

```
kidney.dtypes
```

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

```
# scaler = StandardScaler()


# kidney[float_col] = scaler.fit_transform(kidney[float_col])
```

question 3

```
print(kidney.shape)
print(y.shape)
```

```
(400, 24)
(400, 1)
```

```
print(kidney.info())
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 24 columns):
 #   Column  Non-Null Count  Dtype
---  ------  --------------  -----
 0   age     391 non-null    float64
 1   bp      388 non-null    float64
 2   sg      353 non-null    category
 3   al      354 non-null    category
 4   su      351 non-null    category
 5   rbc     248 non-null    category
 6   pc      335 non-null    category
 7   pcc     396 non-null    category
 8   ba      396 non-null    category
 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    category
 19  dm      398 non-null    category
 20  cad     398 non-null    category
 21  appet   399 non-null    category
 22  pe      399 non-null    category
 23  ane     399 non-null    category
dtypes: category(13), float64(11)
memory usage: 41.4 KB
None
```

```
print(y.info())
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 1 columns):
 #   Column  Non-Null Count  Dtype
---  ------  --------------  -----
 0   class   400 non-null    int64
dtypes: int64(1)
memory usage: 3.3 KB
None
```

```
chronic_kidney_disease.data.features.describe()
```

	age	bp	sg	al	su	bgr	bu	sc
count	391.000000	388.000000	353.000000	354.000000	351.000000	356.000000	381.000000	383.000000
mean	51.483376	76.469072	1.017408	1.016949	0.450142	148.036517	57.425722	3.072454
std	17.169714	13.683637	0.005717	1.352679	1.099191	79.281714	50.503006	5.741126
min	2.000000	50.000000	1.005000	0.000000	0.000000	22.000000	1.500000	0.400000
25%	42.000000	70.000000	1.010000	0.000000	0.000000	99.000000	27.000000	0.900000
50%	55.000000	80.000000	1.020000	0.000000	0.000000	121.000000	42.000000	1.300000
75%	64.500000	80.000000	1.020000	2.000000	0.000000	163.000000	66.000000	2.800000
max	90.000000	180.000000	1.025000	5.000000	5.000000	490.000000	391.000000	76.000000

```
chronic_kidney_disease.data.targets.describe()
```

	class
count	400
unique	3
top	ckd
freq	248

```
chronic_kidney_disease.data.features
```

	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	60

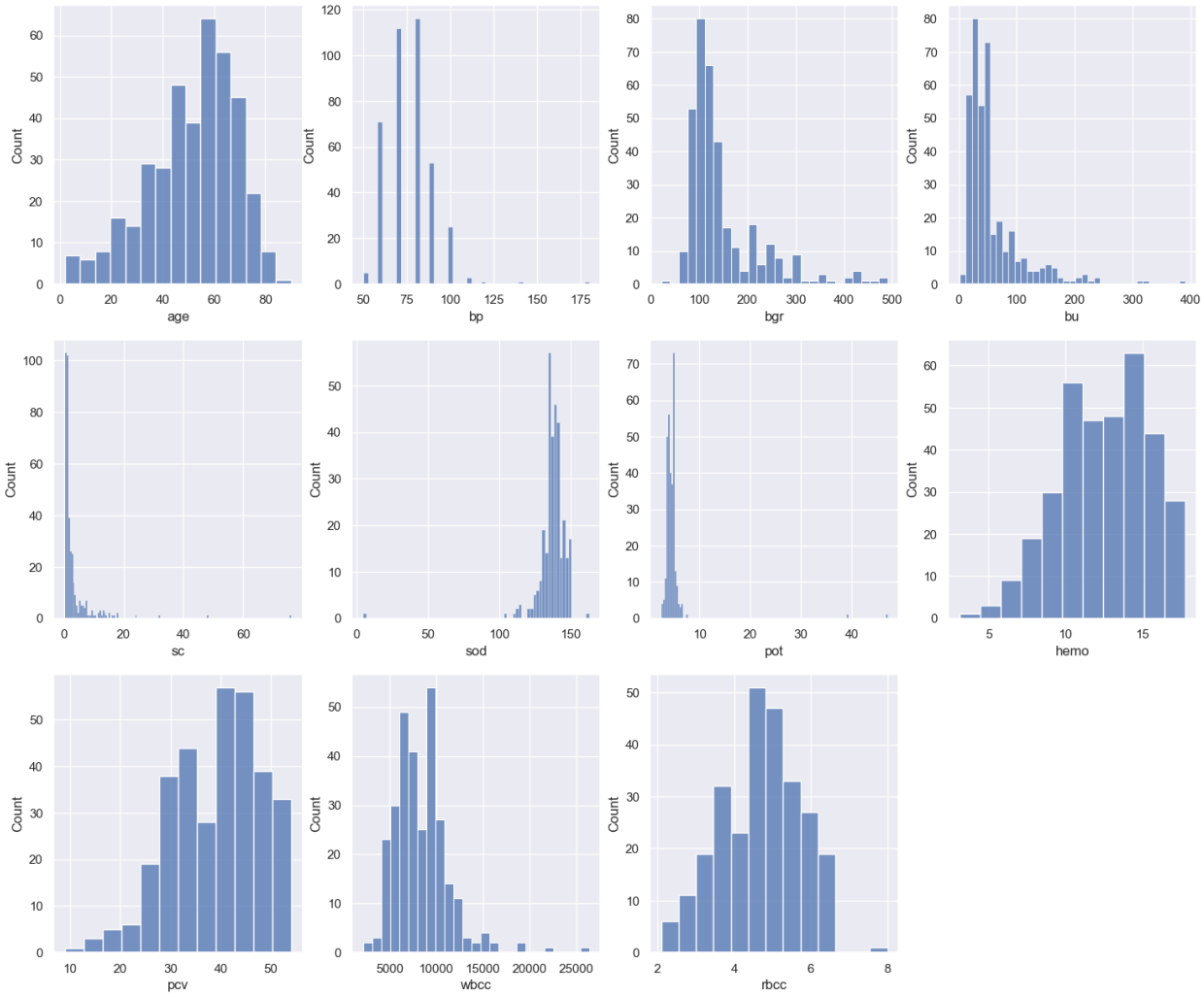
	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	pcv	w
398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	114.0	...	14.2	51.0	72
399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	131.0	...	15.8	53.0	68

```
print(len(float_col))
len(cate_col)
```

```
11
```

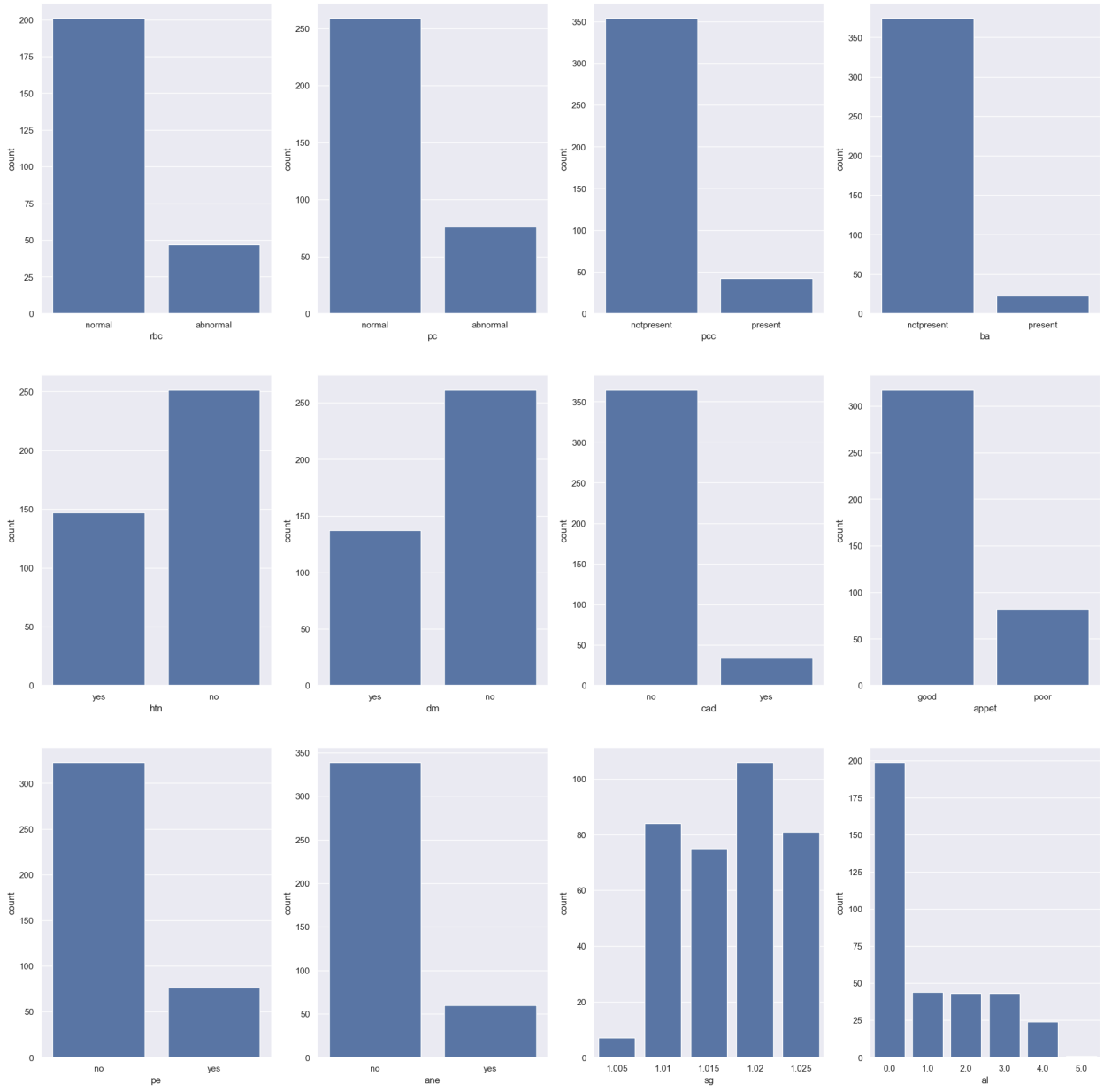
```
13
```

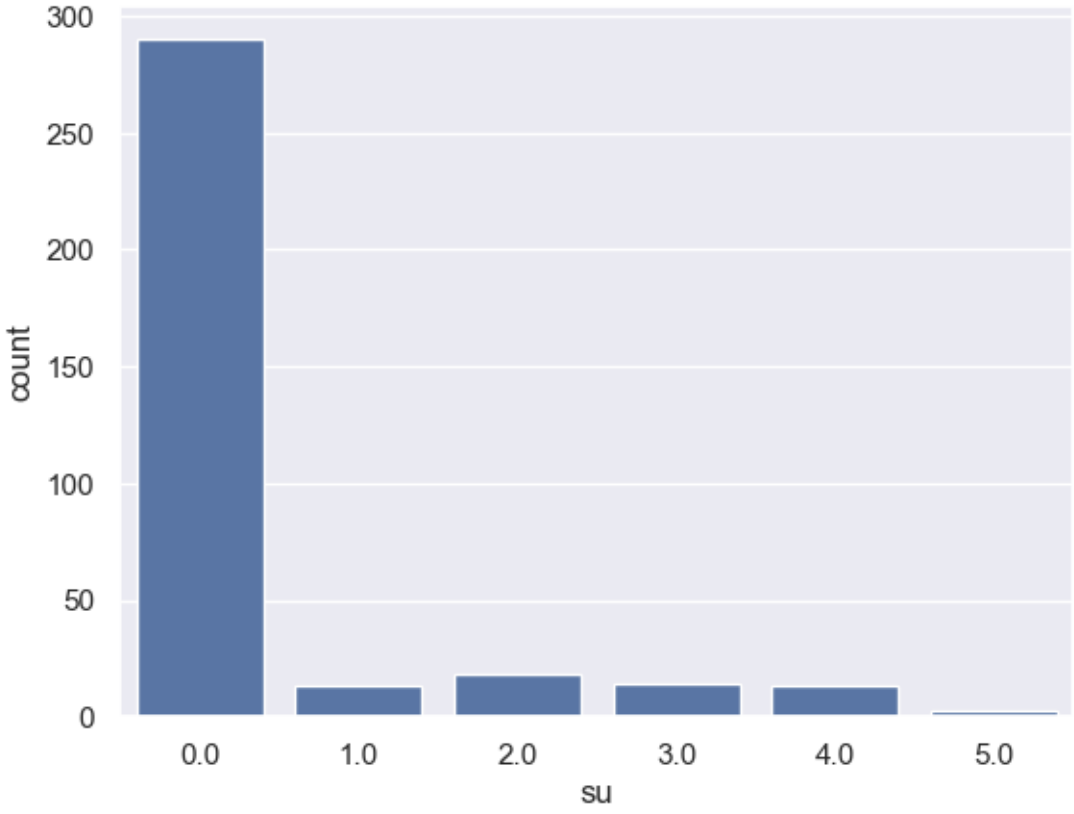
```
plt.figure(figsize = (18, 15))
plotnumber = 1
for i in float_col:
    if plotnumber <= 12:
        ax = plt.subplot(3, 4, plotnumber)
        sns.histplot(x=chronic_kidney_disease.data.features[i])
    plotnumber += 1
plt.show()
```

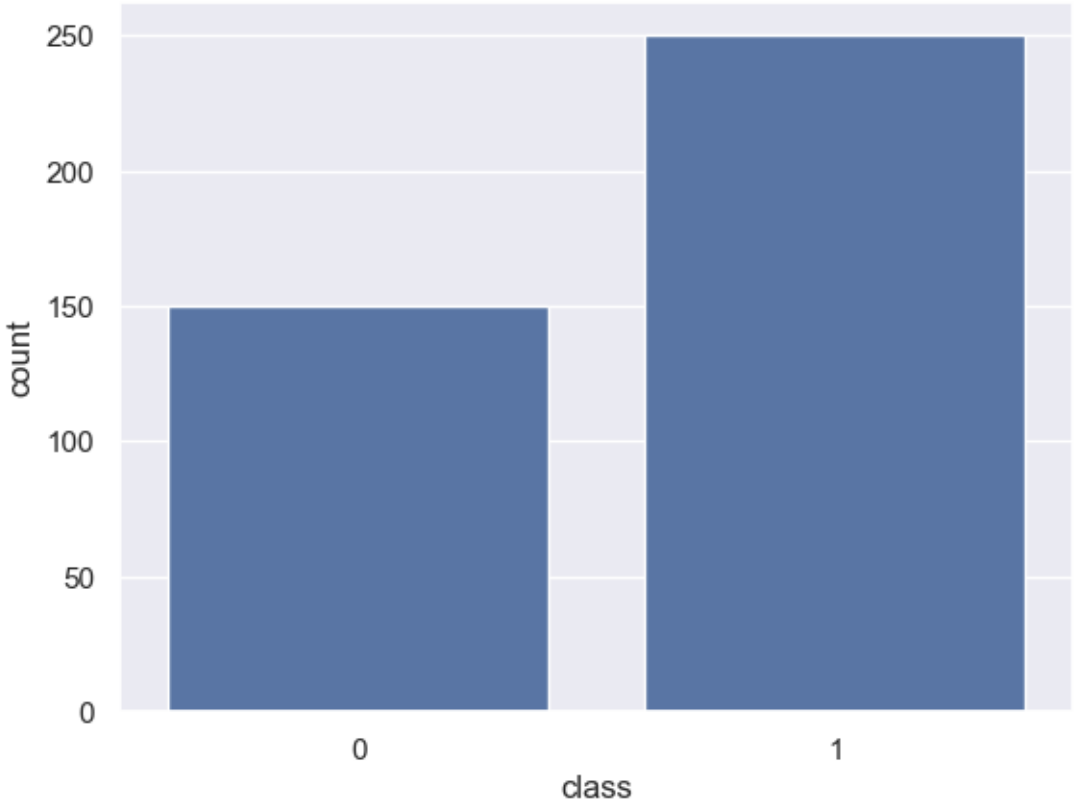



```
plt.figure(figsize = (24, 24))
number = 1

for i in cate_col:
    if number <= 12:
        ax = plt.subplot(3, 4, number)
        sns.countplot(x=chronic_kidney_disease.data.features[i])
    number += 1
plt.show()

sns.countplot(x=chronic_kidney_disease.data.features[cate_col[-1]])
plt.show()
```

```
sns.countplot(x=y['class'])

plt.show()
```




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


250
200
150
100
50
0
count
0
1
class

The dataset contains 400 observations and 24 features, and one target feature. We can see the distributions of all features like the central tendency, dispersion, and shape of the dataset's distribution.

We have Categorical variables 'sg', 'al', 'su', as well as binary data 'rbc', 'pc', 'pcc', 'ba', 'htn', 'dm', 'cad', 'appet', 'pe', 'ane', and binary target 'class'. Discrete variables are 'age', 'bp', 'bgr', 'bu', 'sod', 'pcv', 'wbcc', and continuous variables 'sc', 'pot', 'hemo', 'rbcc'.

there are 24 + class = 25 feature (11 numeric ,14 nominal)

question 4

```
plt.figure(figsize=(20,10))
sns.heatmap(kidney[float_col].corr(), annot = True, fmt=".2f")
plt.title('Correlation Heatmap')
```

```
Text(0.5, 1.0, 'Correlation Heatmap')
```

The packed cell volume (pcv) and hemoglobin (hemo) have the highest positive correlation, which is 0.90. sodium (sod) and serum creatinine (sc) have the highest negative correlation. Positive numbers indicate two predictors are positively correlated and Negative numbers indicate two predictors are negatively correlated. The correlation matrix is symmetric, and the diagonal represents the correlation of each variable with itself, which is always 1

question 5

```
print(f"before dropna length: {len(kidney)}")

# can't not use dropna, since it will cost remove lots of observation
# And target have no missing data
test_dropna = kidney.dropna()
print(f"after dropna length: {len(test_dropna)}")
```

```
before dropna length: 400
after dropna length: 158
```

```
knn_imputer = KNNImputer(n_neighbors=5)
X_knn_imputed = knn_imputer.fit_transform(kidney)

kidney = pd.DataFrame(X_knn_imputed,columns = kidney.columns)

# knn_imputer.set_output(transform='pandas')
# kidney[float_col] = knn_imputer.fit_transform(kidney[float_col])
```

```
# imputer = SimpleImputer(strategy="mean")
# imputer.set_output(transform='pandas')
# kidney[float_col] = imputer.fit_transform(kidney[float_col])

# imputer2 = SimpleImputer(strategy='most_frequent')
# imputer2.set_output(transform='pandas')
```

```
# kidney[cate_col] = imputer2.fit_transform(kidney[cate_col])


for i in cate_col:
    print(f"{i} --> {kidney[i].value_counts()}")
```

```
rbc --> rbc
1.0    204
0.0     60
0.6     40
0.4     37
0.2     30
0.8     29
Name: count, dtype: int64
pc --> pc
1.0    269
0.0     76
0.6     21
0.8     20
0.4      9
0.2      5
Name: count, dtype: int64
pcc --> pcc
0.0    357
1.0     42
0.2      1
Name: count, dtype: int64
ba --> ba
0.0    378
1.0     22
Name: count, dtype: int64
htn --> htn
0.0    252
```

```
1.0    147
0.2      1
Name: count, dtype: int64
dm --> dm
0.0    261
1.0    137
0.4      1
0.2      1
Name: count, dtype: int64
cad --> cad
0.0    365
1.0     34
0.2      1
Name: count, dtype: int64
appet --> appet
1.0    317
0.0     82
0.8      1
Name: count, dtype: int64
pe --> pe
0.0    323
1.0     76
0.2      1
Name: count, dtype: int64
ane --> ane
0.0    340
1.0     60
Name: count, dtype: int64
sg --> sg
1.020    108
1.010     84
1.015     84
```

```
1.025     81
1.005      7
1.018      7
1.013      6
1.014      5
1.014      5
1.012      5
1.016      3
1.016      2
1.019      1
1.019      1
1.015      1
Name: count, dtype: int64
al --> al
0.0    199
1.0     54
2.0     45
3.0     43
4.0     24
1.6      9
1.2      8
1.4      7
0.6      4
1.8      3
0.8      2
2.2      1
5.0      1
Name: count, dtype: int64
su --> su
0.0    304
2.0     19
1.0     16
```

```
0.4     16
3.0     14
4.0     13
1.2      6
0.8      4
5.0      3
1.6      2
1.4      2
0.6      1
Name: count, dtype: int64
```

```
kidney.columns
```

```
Index(['age', 'bp', 'sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'bgr', 'bu',
       'sc', 'sod', 'pot', 'hemo', 'pcv', 'wbcc', 'rbcc', 'htn', 'dm', 'cad',
       'appet', 'pe', 'ane'],
      dtype='object')
```

```
kidney.isnull().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
```

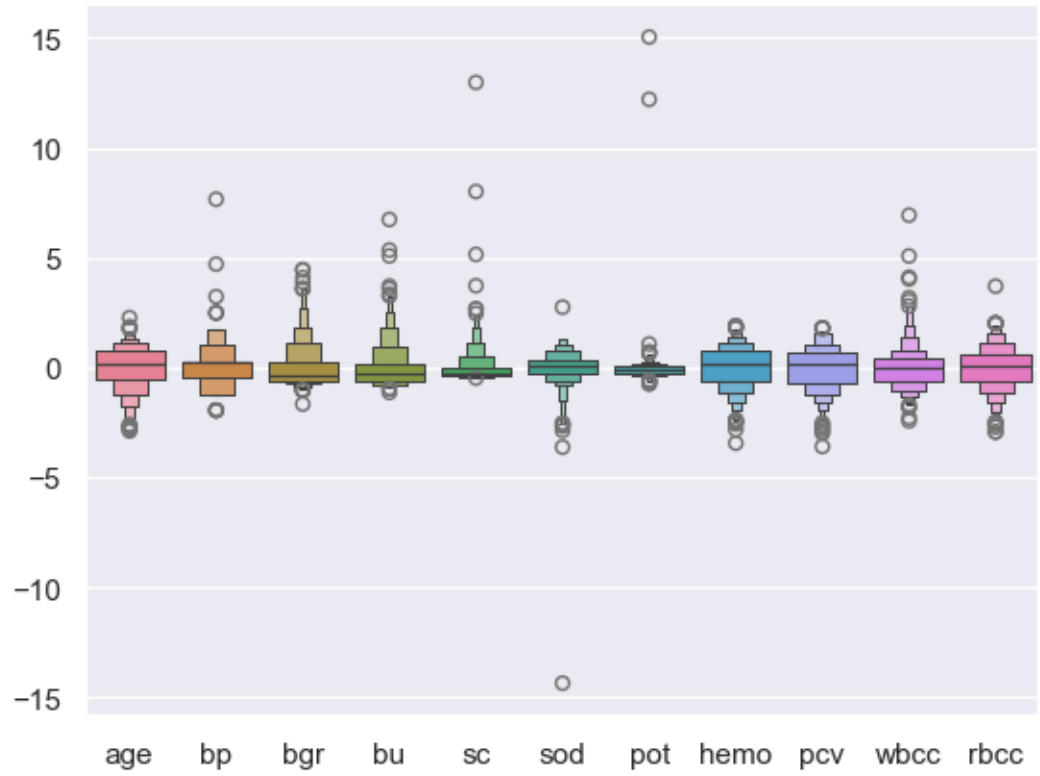
```
sod      0
pot      0
hemo     0
pcv      0
wbcc     0
rbcc     0
htn      0
dm       0
cad      0
appet    0
pe       0
ane      0
dtype: int64
```

question 6

```
z_score = np.abs(stats.zscore(kidney[float_col]))
outliners = np.where(z_score > 3)
outliners
```

```
(array([  2,   6,   6,   7,  10,  11,  21,  21,  48,  49,  61,  61,  61,
         67,  86,  98,  99, 103, 122, 128, 130, 130, 133, 145, 148, 153,
        158, 170, 181, 190, 193, 198, 211, 225, 238, 244, 246, 248, 249,
        249, 249], dtype=int64),
 array([ 2,  4,  5,  2,  2,  2,  4,  5,  9,  9,  3,  4,  6,  2,  2,  1,  1,
         3,  3,  6,  3,  9, 10,  3,  4,  3,  2,  2,  9,  9,  3,  9,  1,  2,
         3,  2,  3,  2,  3,  7,  8], dtype=int64))
```

```
sns.boxenplot(kidney[float_col])
```



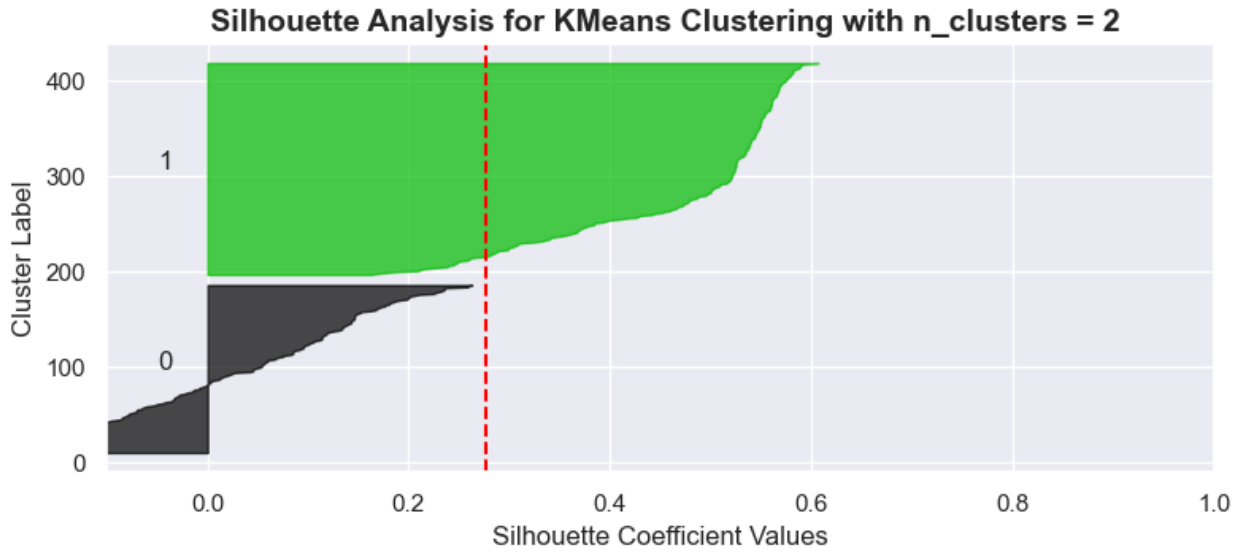
question 7

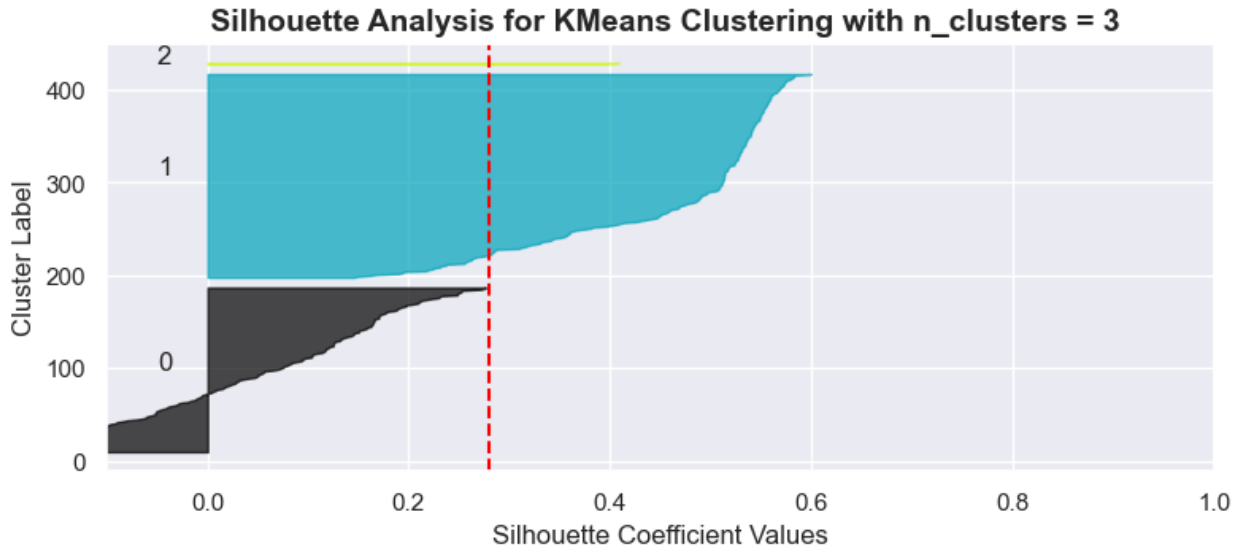
```
# test test
scaler = StandardScaler()
kidney[float_col] = pd.DataFrame(scaler.fit_transform(kidney[float_col]),columns=float_col)



k_values = list(range(2,8))
silhouette_scores = []
X_filled = kidney

for k in k_values:
    km = KMeans(n_clusters = k, n_init = 20, random_state=0)
    cluster_labels = km.fit_predict(X_filled)
    silhouette_avg_km = silhouette_score(X_filled, cluster_labels)
```

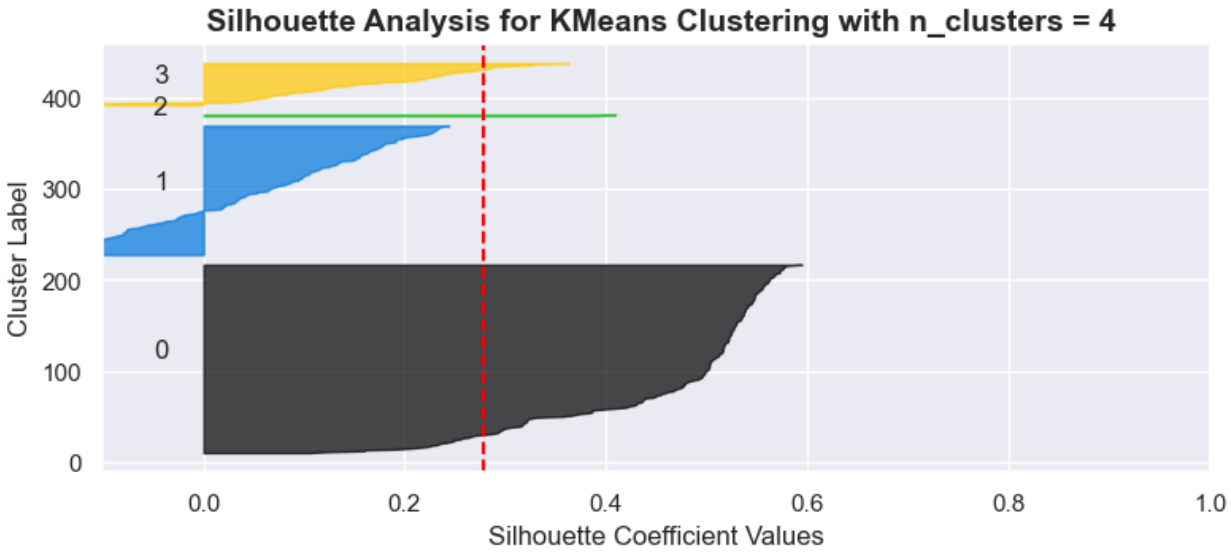
```
    silhouette_scores.append(silhouette_avg_km)

    sample_silhouette_values = silhouette_samples(X_filled, cluster_labels)
    fig, ax1 = plt.subplots(1, 1)
    fig.set_size_inches(18/2, 7/2)
    ax1.set_xlim([-0.1, 1])

    y_lower = 10

    for i in range(k):
        # Aggregate the silhouette scores for samples belonging to
        # cluster i, and sort them
        ith_cluster_silhouette_values = sample_silhouette_values[cluster_labels == i]

        ith_cluster_silhouette_values.sort()

        size_cluster_i = ith_cluster_silhouette_values.shape[0]
        y_upper = y_lower + size_cluster_i

        color = cm.nipy_spectral(float(i) / k)
        ax1.fill_betweenx(
            np.arange(y_lower, y_upper),
            0,
            ith_cluster_silhouette_values,
            facecolor=color,
            edgecolor=color,
            alpha=0.7,
        )

        # Label the silhouette plots with their cluster numbers at the middle
        ax1.text(-0.05, y_lower + 0.5 * size_cluster_i, str(i))
```

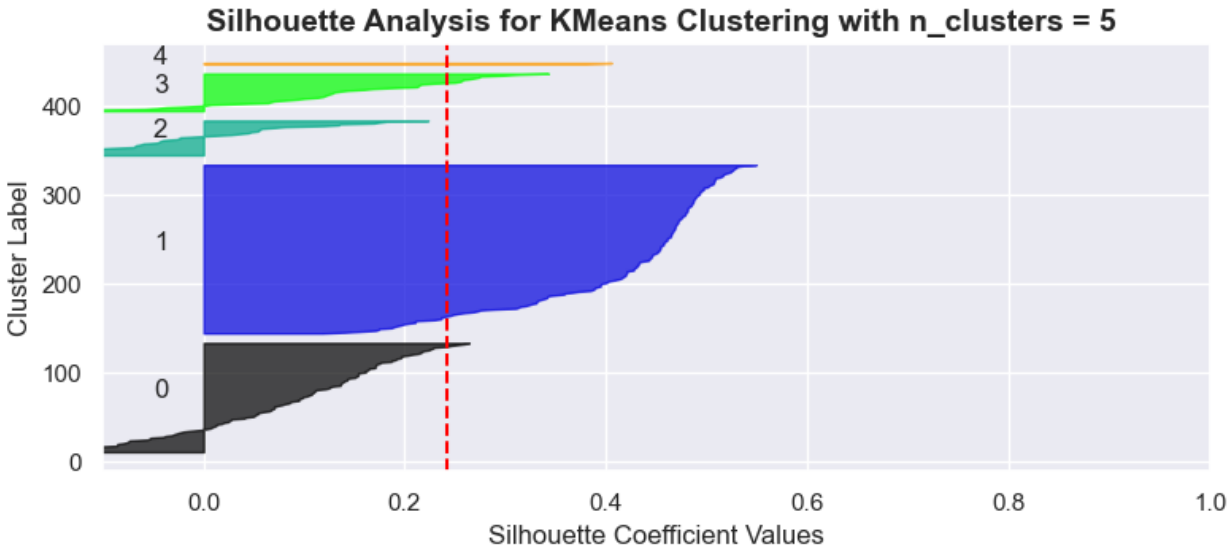
```python
        # Compute the new y_lower for next plot
        y_lower = y_upper + 10

    ax1.set_title("The silhouette plot for various cluster")
    ax1.set_xlabel("Silhouette Coefficient Values")
    ax1.set_ylabel("Cluster Label")

    # The vertical line for average silhouette score of all the values
    ax1.axvline(x=silhouette_avg_km, color="red", linestyle="--")
    plt.title(
        f" Silhouette Analysis for KMeans Clustering with n_clusters = {k}",
        fontsize=14,
        fontweight="bold",
    )
```

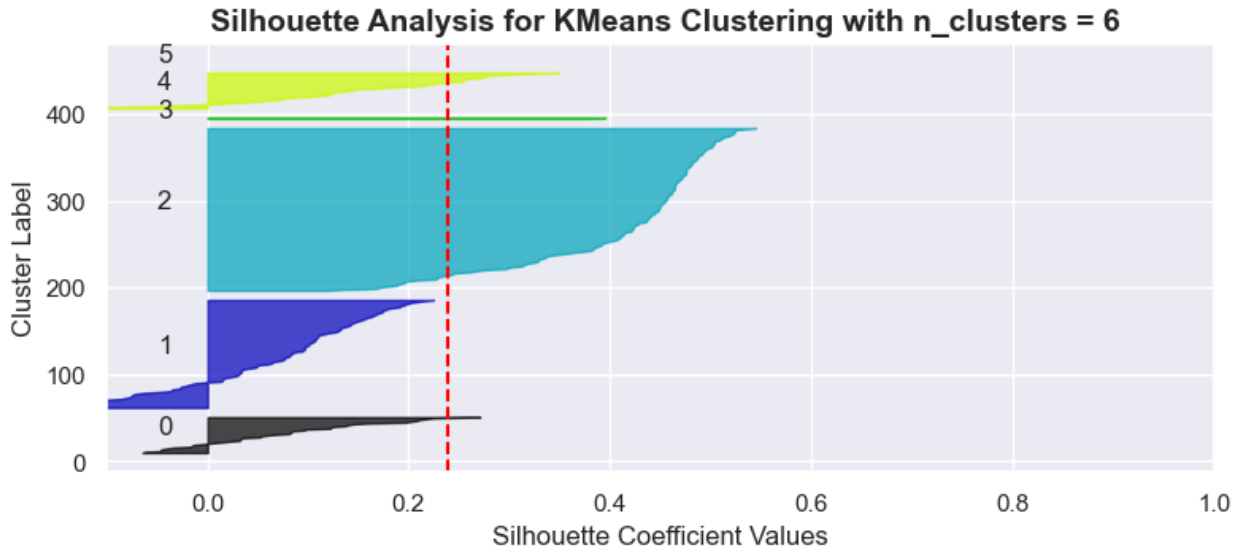
```
c:\Users\chris\anaconda3\Lib\site-packages\sklearn\cluster\_kmeans.py:1382: UserWarning: KMeans
  warnings.warn(
c:\Users\chris\anaconda3\Lib\site-packages\sklearn\cluster\_kmeans.py:1382: UserWarning: KMeans
  warnings.warn(
c:\Users\chris\anaconda3\Lib\site-packages\sklearn\cluster\_kmeans.py:1382: UserWarning: KMeans
  warnings.warn(
c:\Users\chris\anaconda3\Lib\site-packages\sklearn\cluster\_kmeans.py:1382: UserWarning: KMeans
  warnings.warn(
c:\Users\chris\anaconda3\Lib\site-packages\sklearn\cluster\_kmeans.py:1382: UserWarning: KMeans
  warnings.warn(
c:\Users\chris\anaconda3\Lib\site-packages\sklearn\cluster\_kmeans.py:1382: UserWarning: KMeans
  warnings.warn(
```

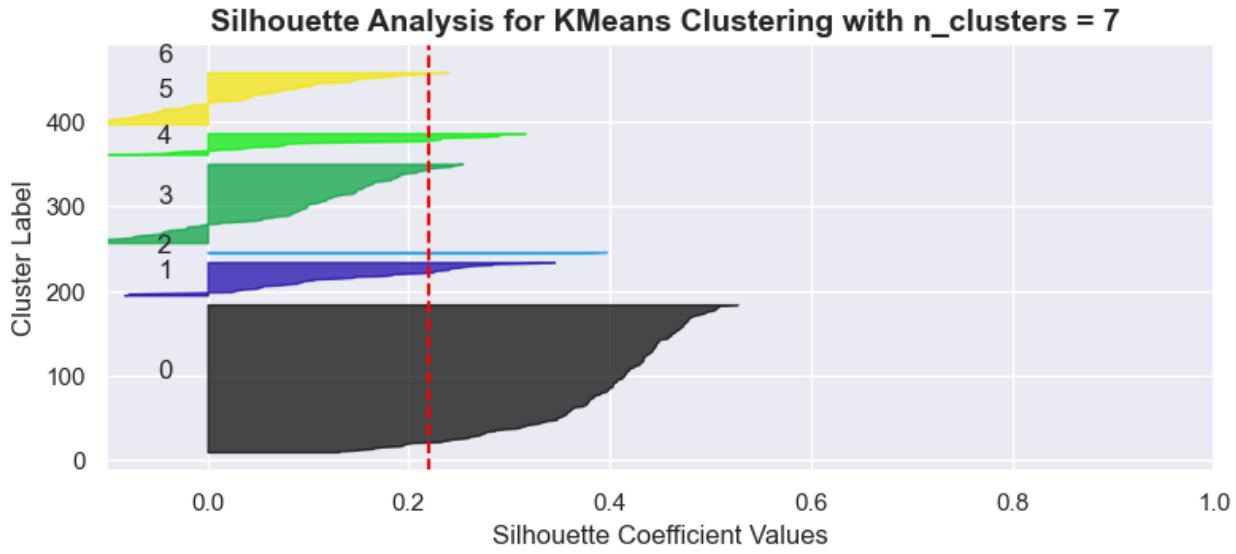

Silhouette Analysis for KMeans Clustering with n_clusters = 2
Cluster Label
0
100
200
300
400
1
0
0.0
0.2
0.4
0.6
0.8
1.0
Silhouette Coefficient Values


Silhouette Analysis for KMeans Clustering with n_clusters = 3
Cluster Label
0
100
200
300
400
2
1
0
0.0
0.2
0.4
0.6
0.8
1.0
Silhouette Coefficient Values


Silhouette Analysis for KMeans Clustering with n_clusters = 4
Cluster Label
Silhouette Coefficient Values
3
2
1
0
0
100
200
300
400
0.0
0.2
0.4
0.6
0.8
1.0


Silhouette Analysis for KMeans Clustering with n_clusters = 5
Cluster Label
Silhouette Coefficient Values
4
3
2
1
0
0
100
200
300
400
0.0
0.2
0.4
0.6
0.8
1.0

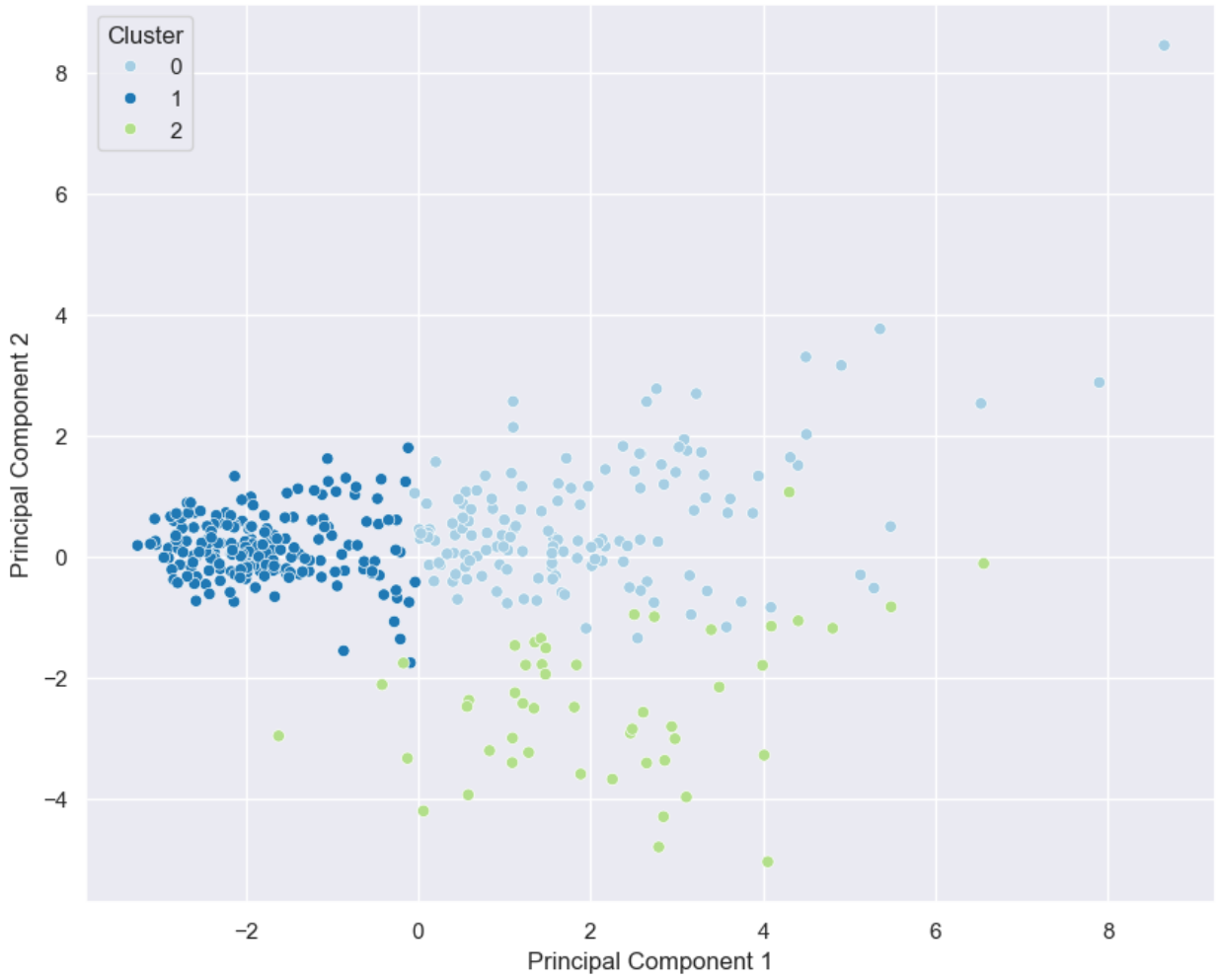





```
scaler = StandardScaler()
all_data_scaled = kidney



k_mean = KMeans(n_clusters=3, random_state=1)
clusters = k_mean.fit_predict(all_data_scaled)



pca = PCA(n_components=2)
```

```
principal_components = pca.fit_transform(all_data_scaled)



plt.figure(figsize=(10, 8))
sns.scatterplot(x=principal_components[:, 0], y=principal_components[:, 1], hue=clusters, palet
plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.legend(title='Cluster')
plt.show()
```

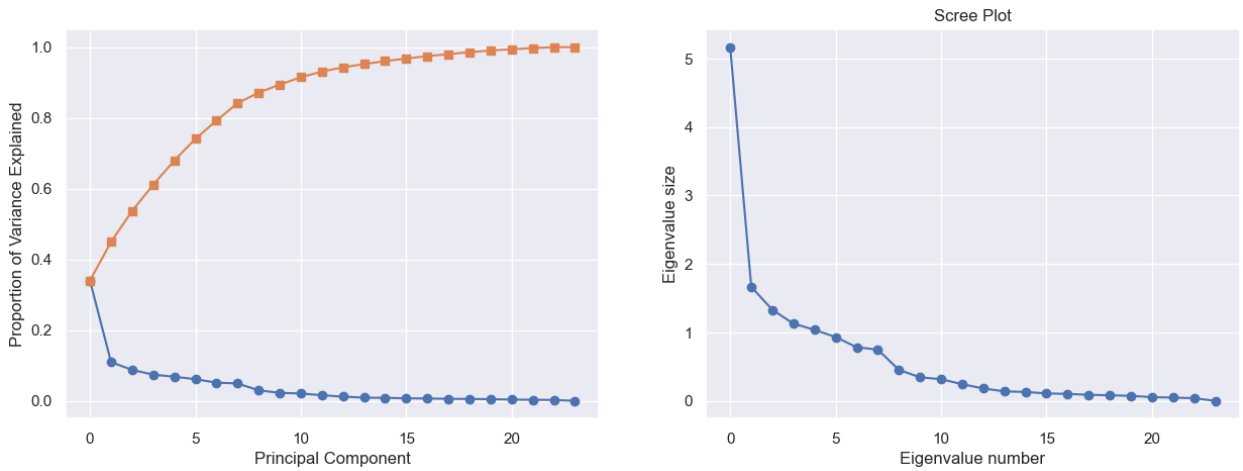
```
c:\Users\chris\anaconda3\Lib\site-packages\sklearn\cluster\_kmeans.py:870: FutureWarning: The d
  warnings.warn(
c:\Users\chris\anaconda3\Lib\site-packages\sklearn\cluster\_kmeans.py:1382: UserWarning: KMeans
  warnings.warn(
```




```
pca_nci = PCA()
fit = pca_nci.fit_transform(kidney)



fig , (ax1,ax2) = plt.subplots(1,2, figsize=(15,5))



#left plot
ax1.plot(pca_nci.explained_variance_ratio_, '-o', label='Individual component')
ax1.plot( np.cumsum(pca_nci.explained_variance_ratio_), '-s', label='Cumulative')
ax1.set_ylabel('Proportion of Variance Explained')
ax1.set_xlabel('Principal Component')
```

```
# ax1.set_xlim(0.75,6.25)
# ax1.set_ylim(0,1.05)
# ax1.set_xticks([1,2,3,4,5,6])
# ax1.legend(loc=2)



#right plot
ax2.plot(pca_nci.explained_variance_,marker='o')
ax2.set_xlabel("Eigenvalue number")
ax2.set_ylabel("Eigenvalue size")
ax2.set_title("Scree Plot")
```

```
Text(0.5, 1.0, 'Scree Plot')
```



question 8

```
X_train, X_test, y_train, y_test = train_test_split(
    kidney,
    y,
    train_size = 0.7,
    test_size = 0.3,
```

```
    random_state = 1,
    stratify = y,
)
```

```
X_train
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	hemo	pcv	wb
103	1.449645	-0.464600	1.015	2.0	0.0	1.0	0.0	1.0	0.0	1.000126	...	-0.863059	-0.356463	1.6
17	-0.248483	0.273446	1.015	1.2	0.4	0.4	0.8	0.0	0.0	-0.461789	...	-0.174424	-0.404342	-0.
254	-0.014258	-1.202647	1.025	0.0	0.0	1.0	1.0	0.0	0.0	-0.657581	...	0.151772	1.199620	-0.
90	0.688415	1.749540	1.010	2.0	2.0	1.0	1.0	0.0	1.0	1.704978	...	0.151772	0.122332	0.5
170	0.864083	-0.464600	1.015	2.0	5.0	0.2	1.0	0.0	0.0	3.884798	...	-0.029448	-0.715559	0.4
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
104	0.219966	1.011493	1.015	0.8	0.8	0.6	0.6	0.0	0.0	-0.083257	...	-0.986288	-0.571920	0.7
398	-2.005166	-1.202647	1.025	0.0	0.0	1.0	1.0	0.0	0.0	-0.461789	...	0.586699	1.439017	-0.
197	0.337078	0.273446	1.016	1.0	0.4	0.2	0.6	0.0	0.0	0.759954	...	-2.095353	-0.883137	-1.
5	0.512747	1.011493	1.015	3.0	0.0	0.6	0.4	0.0	0.0	-0.983902	...	-0.138180	0.002633	-0.
240	0.805527	-0.464600	1.015	1.0	0.0	0.0	1.0	0.0	0.0	0.699911	...	-0.428132	-0.356463	-1.

```
float_col
```

```
['age', 'bp', 'bgr', 'bu', 'sc', 'sod', 'pot', 'hemo', 'pcv', 'wbcc', 'rbcc']
```

question 9

The data frame contains both categorical and numerical data, also the response variable is binary(ckd or notckd). In this case sernario decisions trees are a good choice. Decision Tree can handel mixed data types.Contain selection capability feature as well which can improve the generalizaion of the model. Thus I pick Decision Tree as my model.

Random Forest method average multiple decision trees, reduces the likelihood of overfitting.It also dosen't require any feature scaling . It also can handle missing valued data very well. In this case sernario it is a very good method to try.

question 10

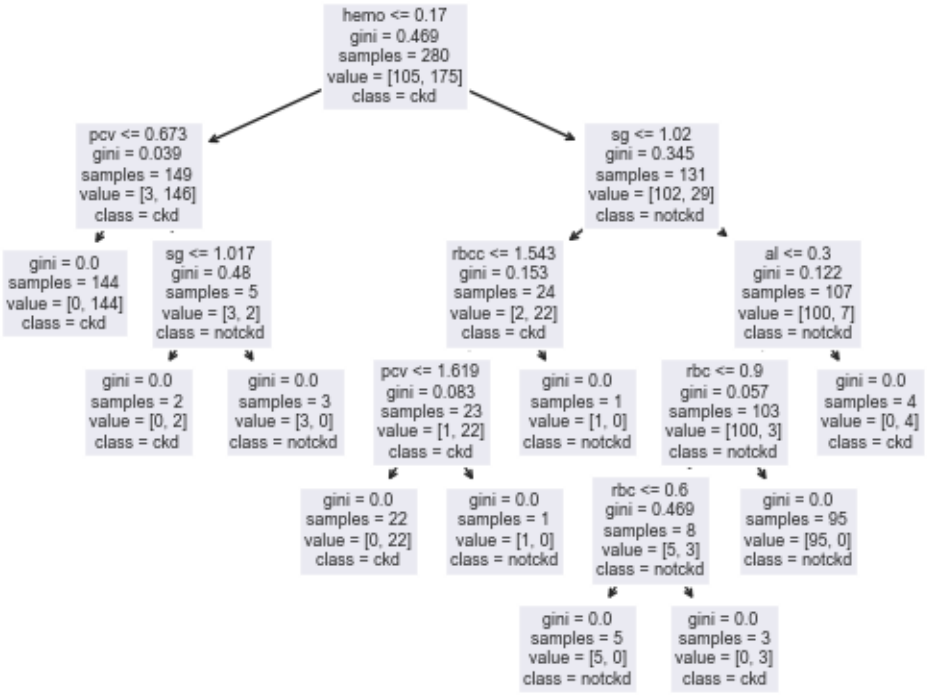
```
#DecisionTree
dt_model = DecisionTreeClassifier(max_depth=1000,random_state=1)
dt_model.fit(X_train, y_train)
```

```
DecisionTreeClassifier(max_depth=1000, random_state=1)
```

```
plot_tree(
    dt_model,
    max_depth= 100,
    feature_names = X_train.columns.tolist(),
    class_names=['notckd', 'ckd']
)
```

```
[Text(0.4230769230769231, 0.9166666666666666, 'hemo <= 0.17\ngini = 0.469\nsamples = 280\nvalue
 Text(0.15384615384615385, 0.75, 'pcv <= 0.673\ngini = 0.039\nsamples = 149\nvalue = [3, 146]\n
 Text(0.07692307692307693, 0.5833333333333334, 'gini = 0.0\nsamples = 144\nvalue = [0, 144]\nc
 Text(0.23076923076923078, 0.5833333333333334, 'sg <= 1.017\ngini = 0.48\nsamples = 5\nvalue =
 Text(0.15384615384615385, 0.4166666666666667, 'gini = 0.0\nsamples = 2\nvalue = [0, 2]\nclass
 Text(0.3076923076923077, 0.4166666666666667, 'gini = 0.0\nsamples = 3\nvalue = [3, 0]\nclass =
 Text(0.6923076923076923, 0.75, 'sg <= 1.02\ngini = 0.345\nsamples = 131\nvalue = [102, 29]\nc
 Text(0.5384615384615384, 0.5833333333333334, 'rbcc <= 1.543\ngini = 0.153\nsamples = 24\nvalue
 Text(0.46153846153846156, 0.4166666666666667, 'pcv <= 1.619\ngini = 0.083\nsamples = 23\nvalue
 Text(0.38461538461538464, 0.25, 'gini = 0.0\nsamples = 22\nvalue = [0, 22]\nclass = ckd'),
 Text(0.5384615384615384, 0.25, 'gini = 0.0\nsamples = 1\nvalue = [1, 0]\nclass = notckd'),
 Text(0.6153846153846154, 0.4166666666666667, 'gini = 0.0\nsamples = 1\nvalue = [1, 0]\nclass =
 Text(0.8461538461538461, 0.5833333333333334, 'al <= 0.3\ngini = 0.122\nsamples = 107\nvalue =
```

```
Text(0.7692307692307693, 0.4166666666666667, 'rbc <= 0.9\ngini = 0.057\nsamples = 103\nvalue =
Text(0.6923076923076923, 0.25, 'rbc <= 0.6\ngini = 0.469\nsamples = 8\nvalue = [5, 3]\nclass =
Text(0.6153846153846154, 0.08333333333333333, 'gini = 0.0\nsamples = 5\nvalue = [5, 0]\nclass
Text(0.7692307692307693, 0.08333333333333333, 'gini = 0.0\nsamples = 3\nvalue = [0, 3]\nclass
Text(0.8461538461538461, 0.25, 'gini = 0.0\nsamples = 95\nvalue = [95, 0]\nclass = notckd'),
Text(0.9230769230769231, 0.4166666666666667, 'gini = 0.0\nsamples = 4\nvalue = [0, 4]\nclass =
```




```
#random forest
forest_model = RandomForestClassifier(max_depth=5)
forest_model.fit(X_train, y_train)
```

```
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\1620030206.py:3: DataConversionWarning: A col
  forest_model.fit(X_train, y_train)
```

```
RandomForestClassifier(max_depth=5)
```

```
print(confusion_matrix(y_test, dt_model.predict(X_test)))
print(f"Accuracy is {round(accuracy_score(y_test, dt_model.predict(X_test))*100, 2)}%")
```

```
[[41  4]
 [ 0 75]]
Accuracy is 96.67%
```

```
print(classification_report(y_test, dt_model.predict(X_test)))
```

```
              precision    recall  f1-score   support

           0       1.00      0.91      0.95        45
           1       0.95      1.00      0.97        75

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

```
print(confusion_matrix(y_test, forest_model.predict(X_test)))
print(f"Accuracy is {round(accuracy_score(y_test, forest_model.predict(X_test))*100, 2)}%")
```

```
[[42  3]
 [ 0 75]]
Accuracy is 97.5%
```

```
print(classification_report(y_test, forest_model.predict(X_test)))
```

```
              precision    recall  f1-score   support

           0       1.00      0.93      0.97        45
           1       0.96      1.00      0.98        75
```

```
    accuracy                           0.97       120
   macro avg       0.98      0.97      0.97       120
weighted avg       0.98      0.97      0.97       120
```

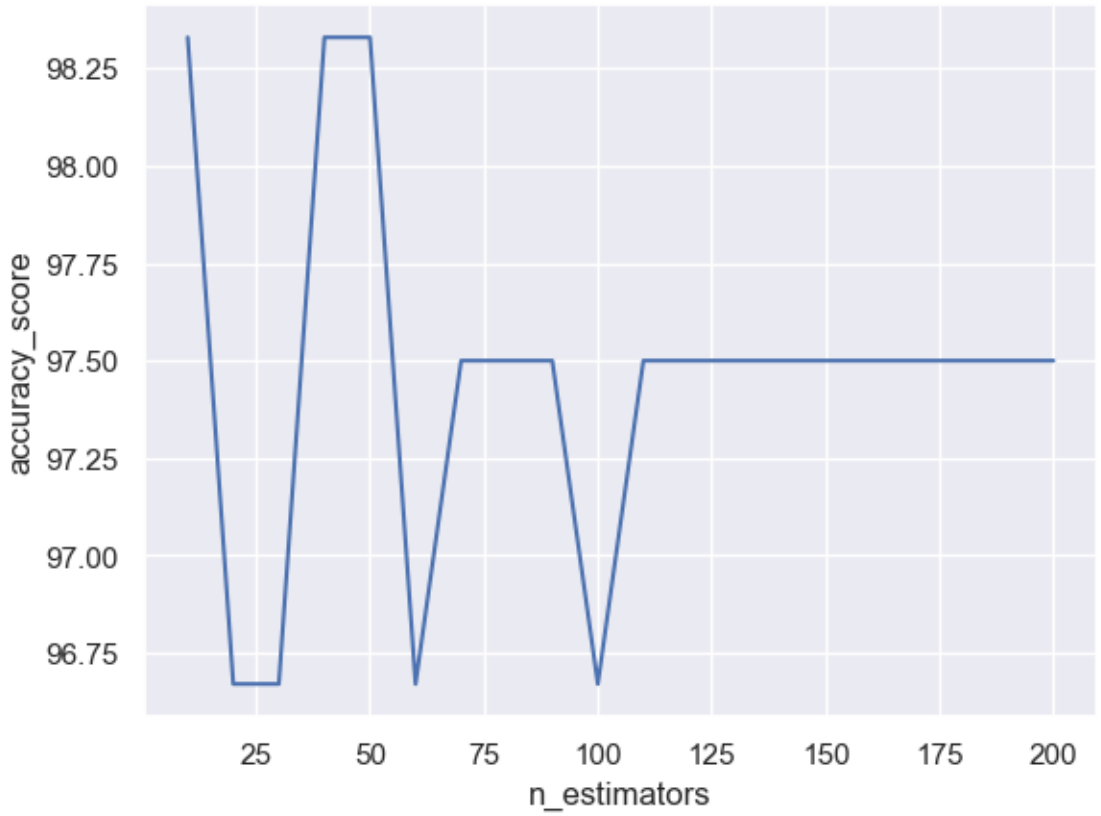
```
n_estimatorss = [i for i in range(10,210,10)]

scores = []
for i in n_estimatorss:
    classifier = RandomForestClassifier(n_estimators=i)
    classifier.fit(X_train, y_train)
    scores.append(round(accuracy_score(y_test, classifier.predict(X_test))*100, 2))

#print(f"best n_estimators:{n_estimatorss[scores.index(max(scores))]} and the accuracy_score is
```

```
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A col
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A col
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A col
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A col
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A col
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A col
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A col
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A col
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A col
  classifier.fit(X_train, y_train)
```

```
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A co
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A co
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A co
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A co
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A co
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A co
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A co
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A co
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A co
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A co
  classifier.fit(X_train, y_train)
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2439767835.py:6: DataConversionWarning: A co
  classifier.fit(X_train, y_train)
```

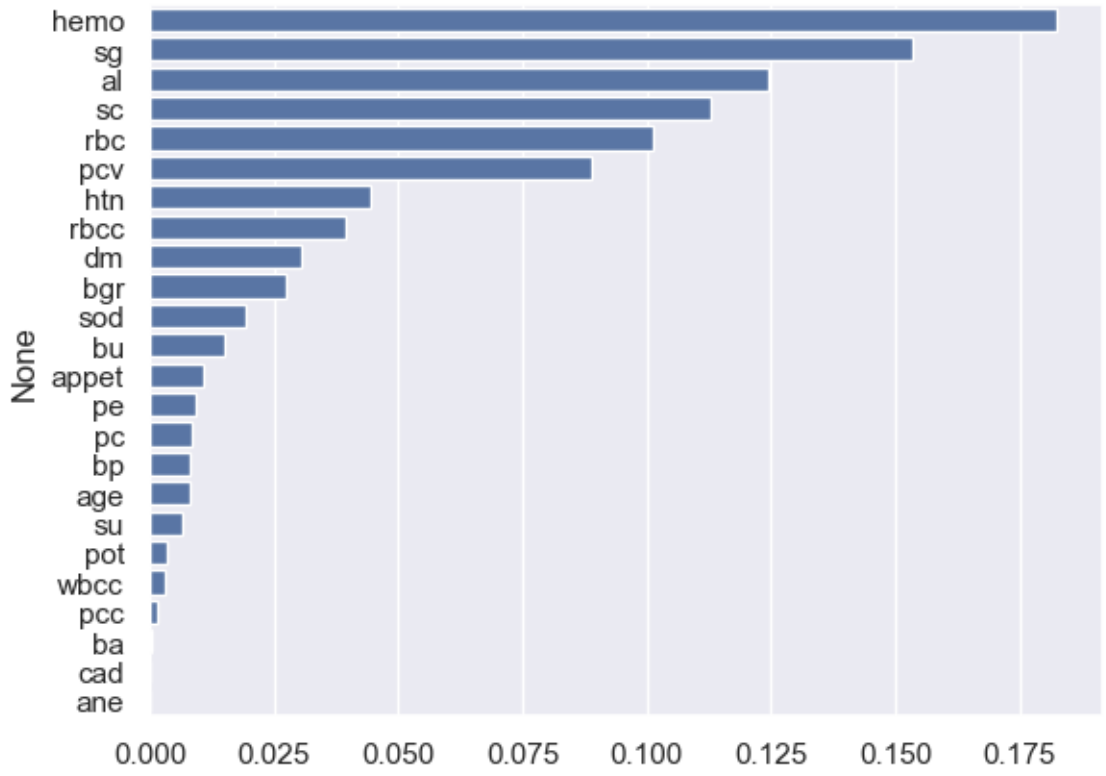
```python
sns.lineplot(
    x= n_estimatorss,
    y=scores
)
plt.ylabel("accuracy_score")
plt.xlabel("n_estimators")
```

```
Text(0.5, 0, 'n_estimators')
```



question 11

```
fea_imp = forest_model.feature_importances_


sorted_indices = fea_imp.argsort()[::-1]# read from the tail of the argsort to get greatest to
sorted_feature_names = X_train.columns[sorted_indices]
sorted_importances = fea_imp[sorted_indices]
sns.barplot(x = sorted_importances, y = sorted_feature_names)
plt.show()
```



we can see the `hemo`, `sg`, `al`, `sc`,`rbc`and `pcv` have obvious influence of random forest model.

question 12

```
dt_model = DecisionTreeClassifier(max_depth=1000,random_state=1)
dt_model.fit(X_train, y_train)
```

```
DecisionTreeClassifier(max_depth=1000, random_state=1)
```

```
#random forest
forest_model = RandomForestClassifier(n_estimators=n_estimatorss[scores.index(max(scores))])
forest_model.fit(X_train, y_train)
```

```
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\3864576791.py:3: DataConversionWarning: A col
  forest_model.fit(X_train, y_train)
```

```
RandomForestClassifier(n_estimators=10)
```

```
print(confusion_matrix(y_test, dt_model.predict(X_test)))
print(f"Accuracy is {round(accuracy_score(y_test, dt_model.predict(X_test))*100, 2)}%")
print(classification_report(y_test, dt_model.predict(X_test)))
```

```
[[41  4]
 [ 0 75]]
Accuracy is 96.67%
              precision    recall  f1-score   support

           0       1.00      0.91      0.95        45
           1       0.95      1.00      0.97        75

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

```
print(confusion_matrix(y_test, forest_model.predict(X_test)))
print(f"Accuracy is {round(accuracy_score(y_test, forest_model.predict(X_test))*100, 2)}%")
print(classification_report(y_test, forest_model.predict(X_test)))
```

```
[[42  3]
 [ 0 75]]
Accuracy is 97.5%
              precision    recall  f1-score   support

           0       1.00      0.93      0.97        45
           1       0.96      1.00      0.98        75

    accuracy                           0.97       120
   macro avg       0.98      0.97      0.97       120
weighted avg       0.98      0.97      0.97       120
```

ramdom forest model have 97.5% accuracy, and desiction tree model have 96.67 accuracy. The ramdom forest model will give a higher accuracy.

question 13

```
new_forest_model = RandomForestClassifier()


new_forest_model.fit(kidney,y)
```

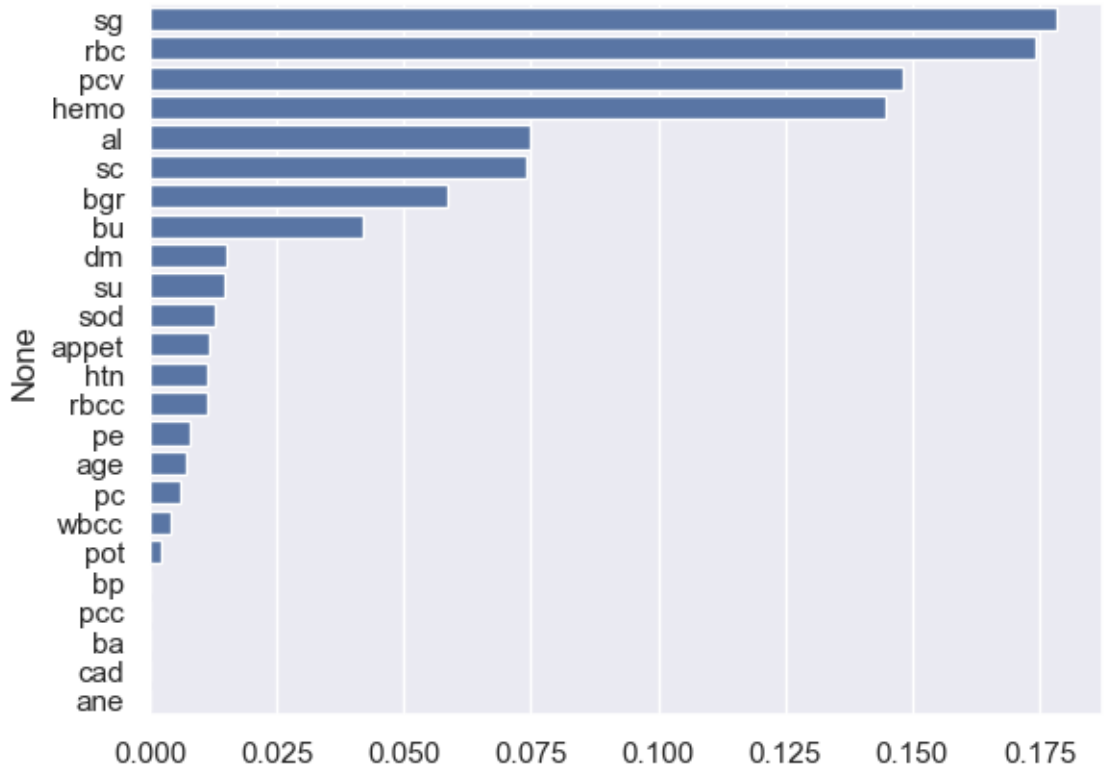
```
C:\Users\chris\AppData\Local\Temp\ipykernel_14464\2498465316.py:3: DataConversionWarning: A co
  new_forest_model.fit(kidney,y)
```

```
RandomForestClassifier()
```

```
print(confusion_matrix(y, forest_model.predict(kidney)))
print(f"Accuracy is {round(accuracy_score(y, forest_model.predict(kidney))*100, 2)}%")
print(classification_report(y, forest_model.predict(kidney)))
```

```
[[147   3]
 [  0 250]]
Accuracy is 99.25%
              precision    recall  f1-score   support

           0       1.00      0.98      0.99       150
           1       0.99      1.00      0.99       250

    accuracy                           0.99       400
   macro avg       0.99      0.99      0.99       400
weighted avg       0.99      0.99      0.99       400
```

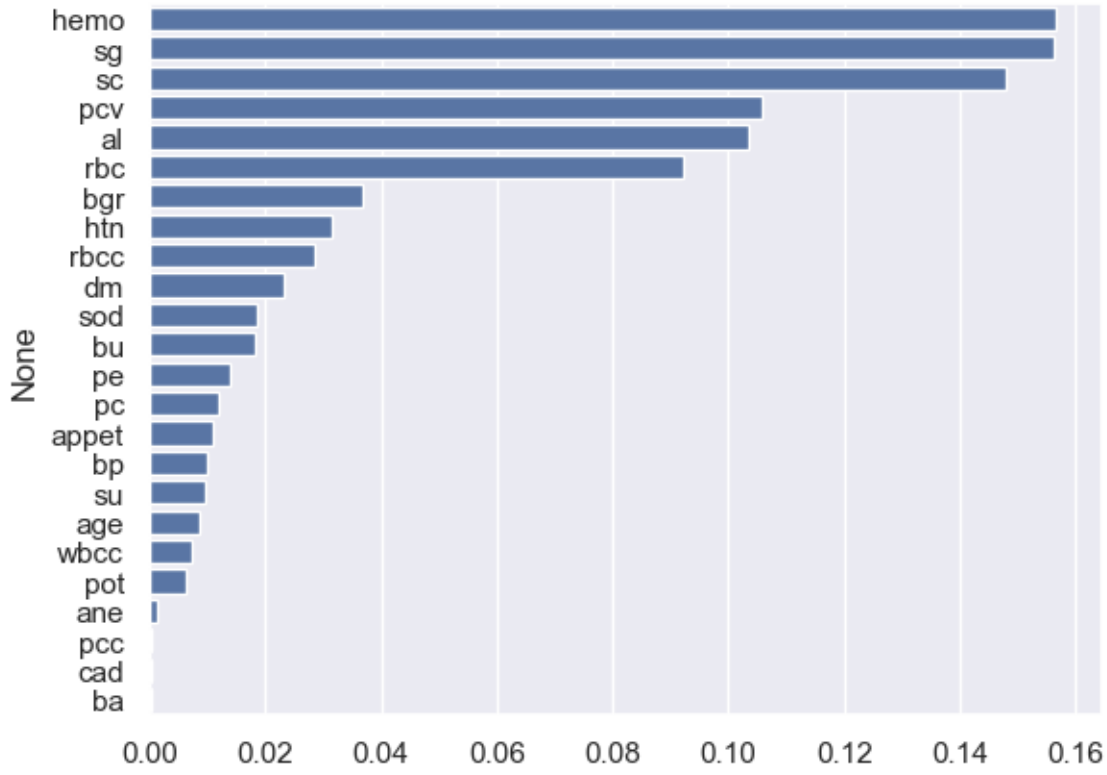
```
fea_imp = forest_model.feature_importances_


sorted_indices = fea_imp.argsort()[::-1]# read from the tail of the argsort to get greatest to
sorted_feature_names = X_train.columns[sorted_indices]
sorted_importances = fea_imp[sorted_indices]
sns.barplot(x = sorted_importances, y = sorted_feature_names)
plt.show()
```



since we have more obveration, because of no test set. So the accuracy score is higher then the model with train, test set.

```
fea_imp = new_forest_model.feature_importances_


sorted_indices = fea_imp.argsort()[::-1]# read from the tail of the argsort to get greatest to
sorted_feature_names = X_train.columns[sorted_indices]
sorted_importances = fea_imp[sorted_indices]
sns.barplot(x = sorted_importances, y = sorted_feature_names)
```

```
plt.show()
```



We can see that the sc variable have more significant impact for the retrain model.

question 15

- yincheng zhu 1 ~ 7 400371892
- Haoyuan Chen 8 ~ 13 400370821

question 16

https://github.com/Christina137/A6

Grading scheme

1.	Answer [1]
2.	Codes [2]
	OR answer [2]
3.	Codes [3] and answer [3]
4.	Codes [2] and answer [3]
5.	Codes [2]
	OR answer [2]
6.	Codes [2]
	OR answer [2]
7.	Codes [3] and Plot [1]
8.	Codes [1]
9.	Answers [2]
10.	Describe the two metrics [2]
11.	Codes [2]
	these codes can be included in (12)
12.	Codes (two classifiers training,
	model selection for each classifier,
	classifiers comparisons) [5] and answer [2]
13.	Codes [1] and answers [2]
14.	Codes and comparison will
	give **bonus 2 points for the final grade**.

The maximum point for this assignment is 39. We will convert this to 100%.

All group members will receive the same grade if they contribute to the same.