STATS 3DA3

Homework Assignment 6

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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.

1.

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

```
df = pd.read_csv('kidney_disease.csv')
print(df.shape)
df.head()
```

```
(400, 26)
```

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	h
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	...	44	7800	5.2	ye
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	...	38	6000	NaN	n
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31	7500	NaN	n
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32	6700	3.9	ye
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35	7300	4.6	n

```
df.columns
```

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

Our primary objective is to determine if an individual has chronic kidney disease (CKD), leveraging a range of health-related attributes (including 25 features) to predict the likelihood of CKD development.

2.

```
df = df.drop(columns=['id'], axis=1)

df.head()
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wc	rc
0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	...	44	7800	5.2
1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	...	38	6000	NaN
2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	423.0	...	31	7500	NaN
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	117.0	...	32	6700	3.9
4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	106.0	...	35	7300	4.6

```
df.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                 object
wc                  object
rc                  object
htn                 object
```

```
dm                object
cad               object
appet             object
pe                object
ane               object
classification    object
dtype: object
```

```
df.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

```
float64_cols = df.select_dtypes(include=['float64']).columns
object_cols = df.select_dtypes(include=['object']).columns
print(float64_cols)
print(object_cols)
```

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

```python
str_to_bi = {
    '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},
    'classification':{'ckd': 1, 'notckd': 0}
}
for column, mapping in str_to_bi.items():
    df[column] = df[column].replace(mapping)
```

```python
df.head()
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wc	rc	htn	dm	cad	appe
0	48.0	80.0	1.020	1.0	0.0	NaN	1.0	0.0	0.0	121.0	...	44	7800	5.2	1.0	1.0	0.0	1.0
1	7.0	50.0	1.020	4.0	0.0	NaN	1.0	0.0	0.0	NaN	...	38	6000	NaN	0.0	0.0	0.0	1.0
2	62.0	80.0	1.010	2.0	3.0	1.0	1.0	0.0	0.0	423.0	...	31	7500	NaN	0.0	1.0	0.0	0.0
3	48.0	70.0	1.005	4.0	0.0	1.0	0.0	1.0	0.0	117.0	...	32	6700	3.9	1.0	0.0	0.0	0.0
4	51.0	80.0	1.010	2.0	0.0	1.0	1.0	0.0	0.0	106.0	...	35	7300	4.6	0.0	0.0	0.0	1.0

```python
from sklearn.preprocessing import StandardScaler,OneHotEncoder
scaler =  StandardScaler()
df[float64_cols] = scaler.fit_transform(df[float64_cols])
```

```python
df.head()
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wc
0	-0.203139	0.258373	0.454071	-0.012548	-0.410106	NaN	1.0	0.0	0.0	-0.341498	...	44	780
1	-2.594124	-1.936857	0.454071	2.208413	-0.410106	NaN	1.0	0.0	0.0	NaN	...	38	600
2	0.613295	0.258373	-1.297699	0.727772	2.323069	1.0	1.0	0.0	0.0	3.473064	...	31	750
3	-0.203139	-0.473370	-2.173584	2.208413	-0.410106	1.0	0.0	1.0	0.0	-0.392022	...	32	670
4	-0.028189	0.258373	-1.297699	0.727772	-0.410106	1.0	1.0	0.0	0.0	-0.530963	...	35	730

Initially, we opt to exclude the variable id from the dataset, as it lacks pertinent information for our analysis or modeling. Moreover, upon inspection of the output, we note a mixture of numerical and categorical features, with a majority of the categorical features being binary. Hence, for the sake of simplifying data representation and analysis, we propose transforming these binary features into numeric representations, utilizing the values 0 and 1. This transformation is executed with careful consideration of the original significance of each category within the respective binary features. For instance, in the rbc variable, we encode the category ‘normal’ as 1 and ‘abnormal’ as 0. Lastly, to ensure uniformity in feature scales, we apply standardization to all numerical features.

3.

```
print(df.shape)
df.dtypes
```

```
(400, 25)
```

```
age                  float64
bp                   float64
sg                   float64
al                   float64
su                   float64
rbc                  float64
pc                   float64
pcc                  float64
ba                   float64
```

```
bgr                 float64
bu                  float64
sc                  float64
sod                 float64
pot                 float64
hemo                float64
pcv                  object
wc                   object
rc                   object
htn                 float64
dm                  float64
cad                 float64
appet               float64
pe                  float64
ane                 float64
classification        int64
dtype: object
```

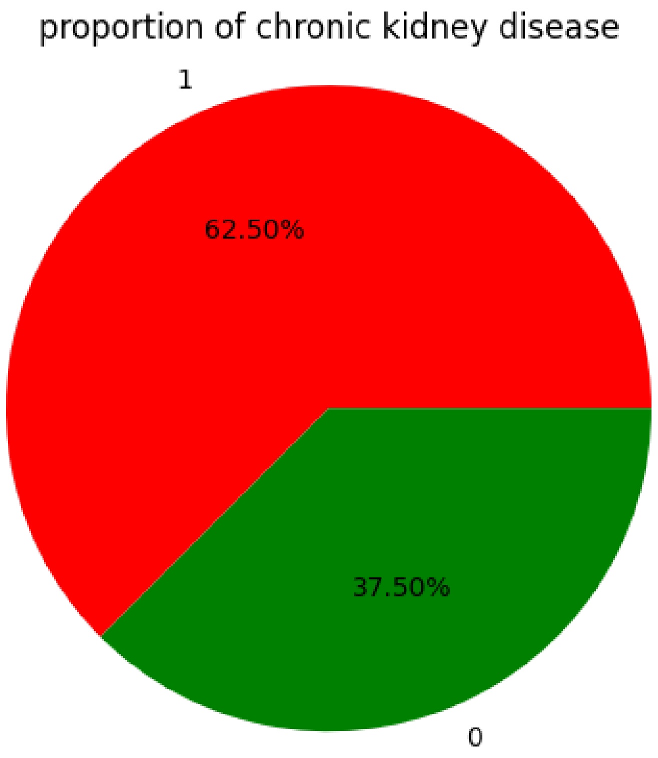
```
df.describe(include='all').transpose()
```

	count	unique	top	freq	mean	std	min	25%	50%	75%
age	391.0	NaN	NaN	NaN	0.0	1.001281	-2.885708	-0.553039	0.205078	0.75908
bp	388.0	NaN	NaN	NaN	-0.0	1.001291	-1.936857	-0.47337	0.258373	0.25837
sg	353.0	NaN	NaN	NaN	0.0	1.001419	-2.173584	-1.297699	0.454071	0.45407
al	354.0	NaN	NaN	NaN	0.0	1.001415	-0.752868	-0.752868	-0.752868	0.72777
su	351.0	NaN	NaN	NaN	0.0	1.001428	-0.410106	-0.410106	-0.410106	-0.41010
rbc	248.0	NaN	NaN	NaN	0.810484	0.392711	0.0	1.0	1.0	1.0
pc	335.0	NaN	NaN	NaN	0.773134	0.419431	0.0	1.0	1.0	1.0
pcc	396.0	NaN	NaN	NaN	0.106061	0.308305	0.0	0.0	0.0	0.0
ba	396.0	NaN	NaN	NaN	0.055556	0.229351	0.0	0.0	0.0	0.0
bgr	356.0	NaN	NaN	NaN	-0.0	1.001407	-1.591967	-0.61938	-0.341498	0.18900
bu	381.0	NaN	NaN	NaN	-0.0	1.001315	-1.10883	-0.603246	-0.305843	0.17000

	count	unique	top	freq	mean	std	min	25%	50%	75%
sc	383.0	NaN	NaN	NaN	0.0	1.001308	-0.466102	-0.378897	-0.309133	-0.0475
sod	313.0	NaN	NaN	NaN	0.0	1.001601	-12.800936	-0.243334	0.045347	0.43025
pot	312.0	NaN	NaN	NaN	-0.0	1.001606	-0.667102	-0.259423	-0.071263	0.08553
hemo	348.0	NaN	NaN	NaN	0.0	1.00144	-3.241109	-0.76552	0.042485	0.85049
pcv	330	44	41	21	NaN	NaN	NaN	NaN	NaN	NaN
wc	295	92	9800	11	NaN	NaN	NaN	NaN	NaN	NaN
rc	270	46	5.2	18	NaN	NaN	NaN	NaN	NaN	NaN
htn	398.0	NaN	NaN	NaN	0.369347	0.483235	0.0	0.0	0.0	1.0
dm	398.0	NaN	NaN	NaN	0.344221	0.475712	0.0	0.0	0.0	1.0
cad	398.0	NaN	NaN	NaN	0.085427	0.279868	0.0	0.0	0.0	0.0
appet	399.0	NaN	NaN	NaN	0.794486	0.404584	0.0	1.0	1.0	1.0
pe	399.0	NaN	NaN	NaN	0.190476	0.39317	0.0	0.0	0.0	0.0
ane	399.0	NaN	NaN	NaN	0.150376	0.357888	0.0	0.0	0.0	0.0
classification	400.0	NaN	NaN	NaN	0.625	0.484729	0.0	0.0	1.0	1.0

```python
class_counts = df['classification'].value_counts()
print(class_counts)
classes = class_counts.index
frequencies = class_counts.values
colors = ['red', 'green']
plt.pie(frequencies, labels=classes, autopct='%1.2f%%', colors=colors)
plt.axis('equal')
plt.title('proportion of chronic kidney disease')
plt.show()
```

```
classification
1    250
0    150
Name: count, dtype: int64
```



First, The dataset comprises 400 observations and 25 columns, featuring 24 distinct attributes and one target variable, class, denoting the presence or absence of chronic kidney disease.
Second, there are two types in the dataset's features: float(float64) and String(object),including Age (age), Blood Pressure (bp), Specific Gravity (sg), Albumin (al), Sugar (su), Red Blood Cells (rbc), Pus Cell (pc), Pus Cell Clumps (pcc), Bacteria (ba), Blood Glucose Random (bgr), Blood Urea (bu), Serum Creatinine (sc), Sodium (sod), Potassium (pot), Hemoglobin (hemo), Packed Cell Volume (pcv), White Blood Cell Count (wc), Red Blood Cell Count (rc), Hypertension (htn), Diabetes Mellitus (dm), Coronary Artery Disease (cad), Appetite (appet), Pedal Edema (pe), and Anemia (ane).
Third, the pie chart above illustrates that roughly 62.50% of the observations indicate the presence of chronic kidney disease.

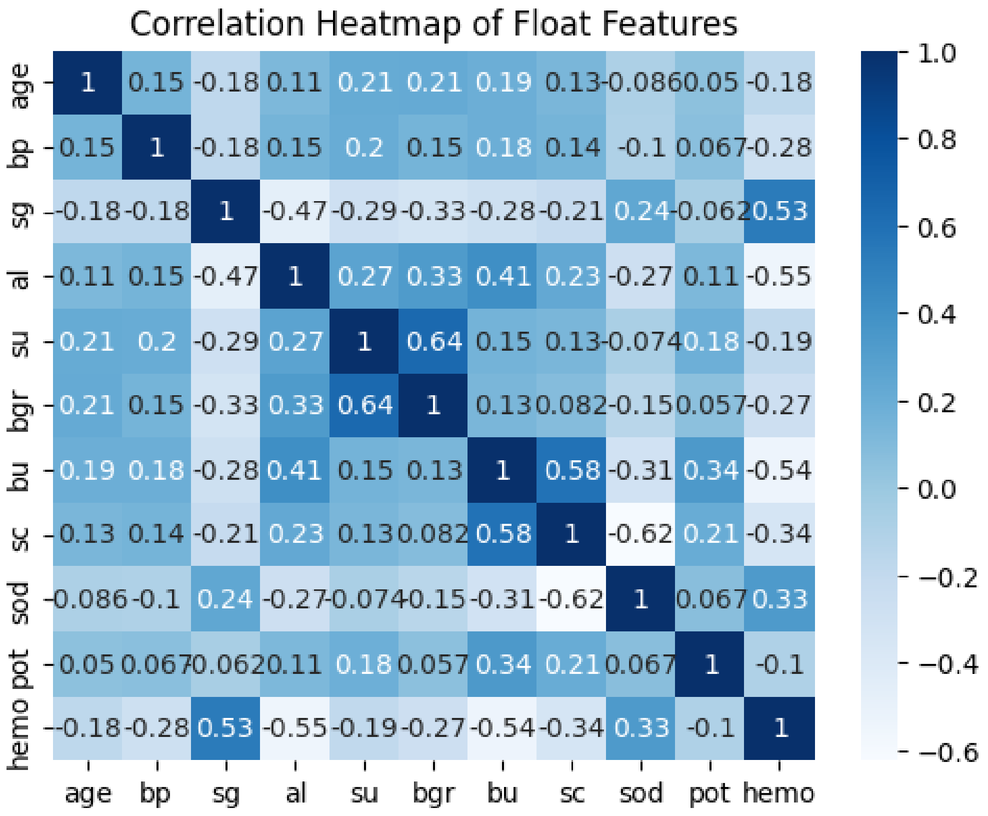
4.

```
float64_df = df[float64_cols].apply(lambda x: x.fillna(x.mean()), axis=0)
print(float64_df.shape)
float64_df.head()
```

```
correlation_matrix = float64_df.corr()
sns.heatmap(correlation_matrix, annot=True, cmap='Blues')
plt.title('Correlation Heatmap of Float Features')
```

```
(400, 11)
```

```
Text(0.5, 1.0, 'Correlation Heatmap of Float Features')
```



	age	bp	sg	al	su	bgr	bu	sc	sod	pot	hemo
age	1	0.15	-0.18	0.11	0.21	0.21	0.19	0.13	-0.086	0.05	-0.18
bp	0.15	1	-0.18	0.15	0.2	0.15	0.18	0.14	-0.1	0.067	-0.28
sg	-0.18	-0.18	1	-0.47	-0.29	-0.33	-0.28	-0.21	0.24	-0.062	0.53
al	0.11	0.15	-0.47	1	0.27	0.33	0.41	0.23	-0.27	0.11	-0.55
su	0.21	0.2	-0.29	0.27	1	0.64	0.15	0.13	-0.074	0.18	-0.19
bgr	0.21	0.15	-0.33	0.33	0.64	1	0.13	0.082	-0.15	0.057	-0.27
bu	0.19	0.18	-0.28	0.41	0.15	0.13	1	0.58	-0.31	0.34	-0.54
sc	0.13	0.14	-0.21	0.23	0.13	0.082	0.58	1	-0.62	0.21	-0.34
sod	-0.086	-0.1	0.24	-0.27	-0.074	-0.15	-0.31	-0.62	1	0.067	0.33
pot	0.05	0.067	-0.062	0.11	0.18	0.057	0.34	0.21	0.067	1	-0.1
hemo	-0.18	-0.28	0.53	-0.55	-0.19	-0.27	-0.54	-0.34	0.33	-0.1	1

Variables bgr and su exhibit a strong positive correlation of 0.64, indicating that as the sugar content increases, there is a corresponding tendency for blood glucose random levels to rise. Additionally, variables sc and bu demonstrate a positive correlation of 0.58, suggesting that patients with higher blood urea levels may also have elevated serum creatinine levels.
Furthermore, variables sod and sc display a significant negative correlation of -0.62. This indicates that as serum creatinine levels decrease, there is a notable tendency for sodium levels to increase.

5.

```
missings = df.isnull().sum()
print(missings)
```

```
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               70
wc               105
rc               130
htn                2
dm                 2
cad                2
appet              1
pe                 1
ane                1
classification     0
dtype: int64
```

```
# drop all missing values
df_withoutNa = df.dropna()
df_withoutNa.shape
```

```
(158, 25)
```

```
# Fill missing values with mean value.
df['pcv'] = pd.to_numeric(df['pcv'], errors='coerce')
df['wc'] = pd.to_numeric(df['wc'], errors='coerce')
df['rc'] = pd.to_numeric(df['rc'], errors='coerce')
mean = df[float64_cols].mean()
df[float64_cols] = df[float64_cols].fillna(mean)
mode = df.mode().iloc[0]
df[object_cols] = df[object_cols].fillna(mode)
print(df.shape)
missings = df.isnull().sum()
print(missings)
```

```
(400, 25)
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
wc                0
rc                0
htn               0
dm                0
cad               0
appet             0
pe                0
ane               0
classification    0
dtype: int64
```

Initially, we opt to exclude the variable id from the dataset, as it lacks pertinent information for our analysis or modeling. Moreover, upon inspection of the output, we note a mixture of numerical and categorical features, with a majority of the categorical features being binary. Hence, for the sake of simplifying data representation and analysis, we propose transforming these binary features into numeric representations, utilizing the values 0 and 1. This transformation is executed with careful consideration of the original significance of each category within the respective binary features. For instance, in the rbc variable, we encode the category ‘normal’ as 1 and ‘abnormal’ as 0. Lastly, to ensure uniformity in feature scales, we apply standardization to all numerical features.

6.

```
from scipy import stats
```

```
float_df = df[float64_cols]
z_scores = np.abs(stats.zscore(float_df))
outliers = np.where(z_scores > 3)
outliers
```

```
(array([  2,   6,   6,   7,   7,  10,  10,  11,  21,  21,  27,  53,  56,
        61,  61,  61,  67,  69,  70,  86,  98,  99,  99, 103, 107, 122,
       128, 130, 140, 143, 145, 145, 148, 153, 158, 168, 170, 170, 180,
       193, 211, 212, 225, 225, 238, 244, 246, 248, 249, 249], dtype=int64),
 array([ 5,  7,  8,  4,  5,  4,  5,  5,  7,  8,  4,  4,  4,  6,  7,  9,  5,
        4,  4,  5,  1,  1,  4,  6,  4,  6,  9,  6,  4,  4,  3,  6,  7,  6,
        5,  4,  4,  5,  4,  6,  1,  4,  4,  5,  6,  5,  6,  5,  6, 10],
      dtype=int64))
```

```python
df_without_outliers = df[(z_scores < 3).all(axis = 1)]
df_without_outliers.shape
```

```
(361, 25)
```

We use z-scores to determine outliers. When z-scores are greater than 3, we consider them outliers and remove them to avoid affecting subsequent models

7.

```python
from sklearn.preprocessing import scale
from sklearn.decomposition import PCA, TruncatedSVD, FactorAnalysis
from sklearn.cluster import KMeans
```

```python
df_without_outliers.head()
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv
0	-0.203139	0.258373	0.454071	-0.012548	-0.410106	1.0	1.0	0.0	0.0	-3.414983e-01	...	44.0
1	-2.594124	-1.936857	0.454071	2.208413	-0.410106	1.0	1.0	0.0	0.0	-1.796316e-16	...	38.0
3	-0.203139	-0.473370	-2.173584	2.208413	-0.410106	1.0	0.0	1.0	0.0	-3.920223e-01	...	32.0
4	-0.028189	0.258373	-1.297699	0.727772	-0.410106	1.0	1.0	0.0	0.0	-5.309633e-01	...	35.0
5	0.496661	0.990117	-0.421814	1.468092	-0.410106	1.0	1.0	0.0	0.0	-9.351554e-01	...	39.0

```
X=df_without_outliers.drop('classification',axis=1)

y = df_without_outliers['classification']
```

```
pca_X=PCA()

pca_loadings=pd.DataFrame(pca_X.fit(X).components_.T, index=X.columns)

pca_loadings
```

	0	1	2	3	4	5	6	7	8
age	0.000039	0.025132	0.604360	-0.670356	0.231947	-0.024345	-0.145562	0.256495	0.120703
bp	0.000019	0.027071	0.299271	-0.011718	-0.905237	0.132439	-0.184218	-0.067330	0.102200
sg	-0.000089	-0.061686	-0.302583	-0.403611	-0.053177	0.709511	0.428842	-0.073294	0.091794
al	0.000101	0.054373	0.298421	0.519152	0.135922	0.371039	0.129107	0.396318	0.416173
su	0.000050	0.013825	0.250088	0.034643	-0.092697	-0.071446	0.447606	-0.080729	-0.125027
rbc	-0.000006	-0.010291	-0.037052	-0.086642	0.015220	-0.055005	0.005314	-0.083746	-0.035956
pc	-0.000017	-0.018161	-0.069924	-0.118638	-0.039131	-0.076110	0.006950	-0.061262	-0.158563
pcc	0.000020	0.008339	0.044608	0.048225	0.025829	-0.003143	-0.002283	0.050542	0.110126
ba	0.000007	0.005043	0.037446	0.055694	0.000924	0.019386	0.010795	0.030036	0.076672
bgr	0.000040	0.023851	0.288770	0.074863	-0.036368	-0.211195	0.627039	-0.157883	-0.215078
bu	0.000027	0.046104	0.177226	0.076737	0.150597	0.450860	-0.276975	-0.115002	-0.541099
sc	0.000017	0.030579	0.114368	0.087768	0.021386	0.204899	-0.147929	-0.091301	-0.266774
sod	-0.000024	-0.029989	-0.113286	-0.162432	-0.120426	-0.010063	-0.003837	-0.001290	0.144283
pot	-0.000003	0.004995	0.010254	-0.018913	-0.008328	0.040184	0.004542	0.003212	0.000943
hemo	-0.000090	-0.093891	-0.137657	-0.166364	-0.022010	-0.090509	0.078045	0.104844	0.237288
pcv	-0.000758	-0.985424	0.125121	0.074243	0.021143	0.021319	-0.034189	-0.047099	-0.014766
wc	1.000000	-0.000778	-0.000066	-0.000042	-0.000014	0.000018	-0.000025	-0.000027	-0.000013
rc	-0.000044	-0.063509	-0.168598	-0.042280	-0.210139	-0.053442	0.124632	0.814275	-0.463462
htn	0.000031	0.033301	0.186337	-0.006086	0.031966	0.082239	0.052397	-0.060909	-0.004367
dm	0.000040	0.023275	0.202090	-0.005499	0.038471	-0.017804	0.125562	-0.087372	-0.143948
cad	0.000004	0.010744	0.057048	-0.017345	0.009566	0.006617	0.094515	-0.034498	-0.006246
appet	-0.000029	-0.015428	-0.083880	-0.040132	-0.025326	-0.044802	-0.023300	0.052373	-0.026736
pe	0.000029	0.016530	0.051229	0.080047	0.083488	0.087138	0.019189	0.072888	0.020400

	0	1	2	3	4	5	6	7	8
ane	0.000009	0.020293	0.007276	0.023540	-0.009743	0.081724	-0.028158	-0.056144	-0.094994

```
pc_scores=pd.DataFrame(pca_X.fit_transform(X),index=X.index)
pc_scores.head()
```

	0	1	2	3	4	5	6	7	8	9
0	-954.573566	-3.409880	0.331950	0.039248	-0.315034	0.189961	0.140593	0.057491	0.239911	-0
1	-2754.568320	3.970022	-1.906385	2.688679	1.210199	0.436795	1.464803	0.798090	0.715874	0
3	-2054.563361	9.912063	1.004531	2.521418	1.365088	-0.437139	-0.724221	0.650579	0.971036	-1
4	-1454.566295	6.092356	-0.097759	0.594017	-0.201928	-0.939786	-0.644195	0.534008	0.802957	0
5	-954.569385	1.819926	1.127304	0.485321	-0.456900	0.321800	-0.588910	0.498738	1.450887	0

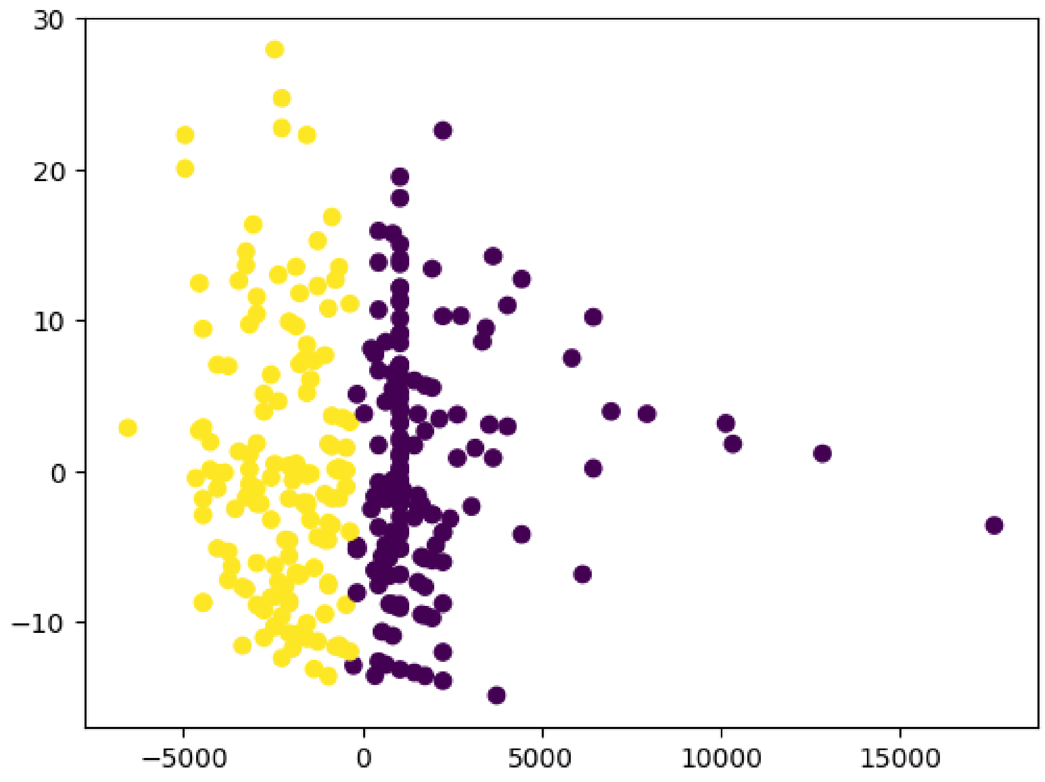
```
kmeans = KMeans(n_clusters=2, n_init=20, random_state=0)
kmeans.fit(X)
kmeans.labels_
```

```
array([1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 0,
       0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0,
       0, 1, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 1, 0,
       0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1, 0,
       1, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0,
       0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1,
       0, 0, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0,
       1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0,
       0, 1, 1, 0, 1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0,
       0, 0, 1, 1, 0, 0, 0, 1, 1, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1,
       1, 0, 1, 1, 0, 1, 0, 1, 0, 0, 1, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 1,
       0, 1, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0, 1, 1, 0, 1, 1, 0, 0, 0, 1, 0,
       1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 0, 0, 0, 1, 1, 0,
       1, 1, 0, 0, 1, 0, 1, 0, 1, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 0, 0, 0, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 0, 1, 0, 0, 0, 1, 0,
       0, 0, 1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1,
       1, 1, 1, 0, 1, 1, 1, 1, 1])
```

```
pd.Series(kmeans.labels_).value_counts()
```

```
0    210
1    151
Name: count, dtype: int64
```

```
plt.scatter(pc_scores[0],pc_scores[1],c=kmeans.labels_)
```



In this step, employing K-means clustering and PCA, it's evident that two subgroups of the data are separated and prominently labeled in yellow and purple on the chart.

8.

```
from sklearn.model_selection import train_test_split


X_train, X_test, y_train, y_test=train_test_split(
    X,  y,  test_size=0.3,
    random_state=1)
```

9.

We decide to choose logistic regression classifier and Random Forest.

Logistic regression classifier: This method furnishes interpretable coefficients that directly convey the impact of each feature in terms of odds ratios, facilitating the understanding of feature effects.

Random Forest: Random forests excel at capturing intricate feature interactions without necessitating extensive feature engineering, owing to their inherent ability to model non-linear relationships.

10.

The evaluation metrics used to assess the model's performance encompass four key measures: Precision, Recall, F1-score, and Accuracy. Precision quantifies the proportion of predicted positive cases that are genuinely positive. Recall gauges the proportion of actual positive cases that are accurately predicted. F1-score, as the harmonic mean of precision and recall, provides a balanced measure between these two metrics.

Accuracy represents the proportion of instances in the dataset that are classified correctly.

For this dataset, we focus on utilizing F1-score and accuracy as our primary evaluation metrics.

11.

12.

```
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, f1_score, roc_auc_score
```

```
#logisticRegression model
log_model = LogisticRegression()
log_model.fit(X_train, y_train)
#make prediction
y_pred_log = log_model.predict(X_test)
#evaluate
print(f'Logistic Regression accuracy score: {accuracy_score(y_test, y_pred_log):.5f}')
print(f'Logistic Regression F1 score: {f1_score(y_test, y_pred_log):.5f}')
```

```
Logistic Regression accuracy score: 0.99083
Logistic Regression F1 score: 0.99225
```

```
#RandomForest model
random_forest_model = RandomForestClassifier(random_state=1)
random_forest_model.fit(X_train, y_train)
#make prediction
y_pred_rf = random_forest_model.predict(X_test)
#evaluate
print(f'Random Forest accuracy score: {accuracy_score(y_test, y_pred_rf):.5f}')
print(f'Random Forest F1 score: {f1_score(y_test, y_pred_rf):.5f}')
```

```
Random Forest accuracy score: 1.00000
Random Forest F1 score: 1.00000
```

```
from mlxtend.feature_selection import SequentialFeatureSelector as SFS
from mlxtend.plotting import plot_sequential_feature_selection as plot_sfs
from sklearn import metrics

np.sqrt(metrics.mean_squared_error(y_test, y_pred_log))
```

```
0.09578262852211514
```

```
sfs = SFS(
    log_model,
    k_features=(1,16),
    forward=True,
    floating=False,
    scoring='neg_mean_squared_error',
    cv=5
    )

sfs = sfs.fit(X_train, y_train)
fig = plot_sfs(sfs.get_metric_dict(), kind='std_err')
plt.title('Sequential Forward Selection')
plt.grid()
plt.show()
```

```
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STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

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```

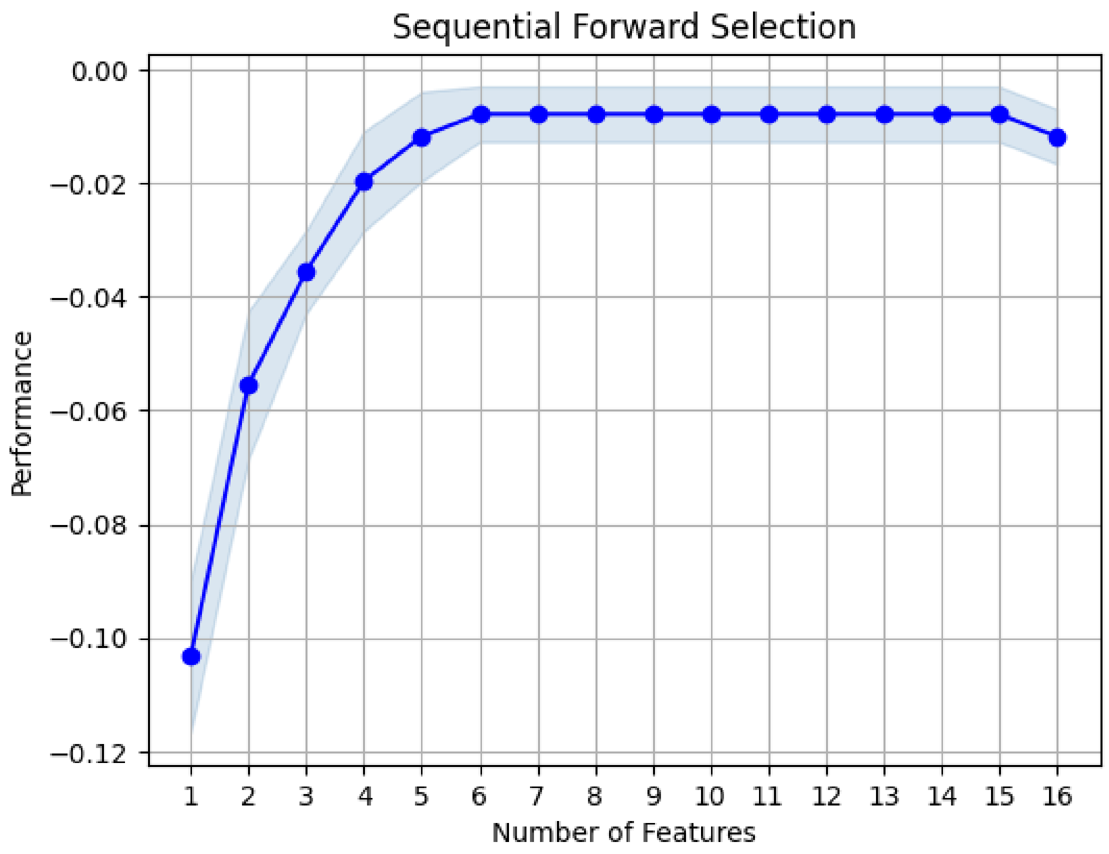

```
print(X_train.columns[list(sfs.k_feature_idx_)])


# Prediction again
sel_col = X_train.columns[list(sfs.k_feature_idx_)]
X_train_sfs = X_train[sel_col]
X_test_sfs = X_test[sel_col]
sfs_m = LogisticRegression()
sfs_m.fit(X_train_sfs, y_train)
sfs_test = sfs_m.predict(X_test_sfs)
np.sqrt(metrics.mean_squared_error(y_test, sfs_test))
```

```
Index(['sg', 'al', 'hemo', 'rc', 'appet', 'pe'], dtype='object')
```

```
0.1659003790827993
```

Upon comparison, it appears that Random Forest outperforms Logistic Regression from Accuracy and F1-score. Accuracy of Logistic Regression model is 0.99083 and F1-score is 0.99225 while Accuracy and F1-score of Random Forest are both 1.00000. However, the 100% accuracy rate suggests that the Random Forest model may be overfitting the training data.

Then we employ the stepwise selection method to enhance the logistic regression classifier. Through verification, we find that this approach reduces the mean squared error (MSE), indicating potential performance improvement for the classifier.

13.

```
feature_effect = pd.DataFrame(log_model.coef_[0], index=X_train.columns, columns=['Coefficient
feature_effect.sort_values(by='Coefficient', ascending=False)
```

	Coefficient
al	1.752082
htn	0.926034
bgr	0.853137
dm	0.799968
bu	0.630571
sc	0.573461
pe	0.540684
bp	0.500789
ane	0.391952
rc	0.326039
su	0.236945
pcc	0.165738
cad	0.149620
ba	0.099905
pot	0.056345
wc	0.000251
pcv	-0.025521
pc	-0.116914

	Coefficient
rbc	-0.142159
age	-0.293829
appet	-0.379363
sod	-0.975375
hemo	-1.932193
sg	-1.938454

It can be seen from the result:
There is indeed a relationship between Albumin(al) and chronic kidney disease (CKD). Albumin is the most important protein in human plasma, which is synthesized by the liver and has the important functions of maintaining the body's nutrition and osmotic pressure, and participating in the body's tissue repair and metabolism. At the same time, albumin is also an important index reflecting liver synthesis function in clinical liver function biochemical tests.

And Blood glucose random levels (bgr) also suggests that elevated glucose levels serve as a predictor of CKD. This finding aligns with the well-established link between diabetes, a leading cause of CKD, and high blood sugar levels, which can progressively damage the kidneys over time.

The negative coefficient associated with sodium levels (sod) suggests that elevated serum sodium concentrations are linked with a reduced likelihood of chronic kidney disease (CKD). This observation implies that lower sodium levels may serve as an indicator of kidney dysfunction, potentially indicating issues with the kidneys' ability to regulate minerals and electrolytes.

15.

Each team member made his or her own contribution to the completion of the assignment, and we consider that contribution equally important:
Zelai Shen (400302233) (Question 1-5)
Shihua Yu (400307953) (Question 6-9)
Tian Xie (400323605) (Question 10-13)

16.

https://github.com/ZelaiShen/Assignment6.git