STATS 3DA3

Project Chronic Kidney Disease Classification Challenge

Group 3
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```python
from ucimlrepo import fetch_ucirepo
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
```

1. Classification Problem Identification

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

In this assignment, machine learning (ML) techniques have been deployed to predict, diagnose, and treat chronic kidney disease (CKD).

```python
## Load Dataset
data_url = 'https://archive.ics.uci.edu/static/public/336/data.csv'
df = pd.read_csv(data_url)
df.head(2)
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wbcc	rbcc	ht
0	48.0	80.0	1.02	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	...	44.0	7800.0	5.2	ye
1	7.0	50.0	1.02	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	...	38.0	6000.0	NaN	no

The classification problem is determining whether a patient has early-stage CKD based on various medical measurements included in the dataset. There are two classes here: Early-stage Indian CKD patients and Healthy patients.

2. Variable Transformation

```python
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      float64
wbcc     float64
rbcc     float64
htn       object
dm        object
cad       object
appet     object
pe        object
ane       object
class     object
dtype: object
```

From the dictionary `sg`, `al`, `su` are Categorical variables. `age`, `bp`, `bgr`, `bu`, `sod`, `pcv`, `wbcc` are Integer variable. `rbc`, `pc`, `pcc`, `ba`, `htn`, `dm`, `cad`, `appet`, `pe`, `ane`, `class` are Binary variables. `sc`,`pot`,`hemo`,and `rbcc` are continuous varibles. Then, we need to transform `sg`, `al`, `su` into Categorical variables and convert those binary variables to numerical (0 and 1). Since there are missing values in those cat variables, we will convert them after replacing those missing values.

```
# Binary trans
columns_bin = ['rbc','pc','pcc','ba','htn','dm','cad','appet','pe','ane','class']
mapping = {'normal': 1, 'present': 1, 'abnormal': 0, 'notpresent': 0, 'yes':1,'no':0,'good':1,

for column in columns_bin:
    df[column] = df[column].map(mapping).astype(float)

df.head(3)
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wbcc	rbcc	htn	dm	cad	app
0	48.0	80.0	1.02	1.0	0.0	NaN	1.0	0.0	0.0	121.0	...	44.0	7800.0	5.2	1.0	1.0	0.0	1.0
1	7.0	50.0	1.02	4.0	0.0	NaN	1.0	0.0	0.0	NaN	...	38.0	6000.0	NaN	0.0	0.0	0.0	1.0
2	62.0	80.0	1.01	2.0	3.0	1.0	1.0	0.0	0.0	423.0	...	31.0	7500.0	NaN	0.0	1.0	0.0	0.0

After part 5&6, missing values and outliers are handled, all numerical values will be scaled, while binary/categorical variables will be transformed to categorical type. If variables are scaled too early, it may influence overview and EDA.

3. Dataset Overview

```
# Summary
df.describe()
```

	age	bp	sg	al	su	rbc	pc	pcc
count	391.000000	388.000000	353.000000	354.000000	351.000000	248.000000	335.000000	396.000000
mean	51.483376	76.469072	1.017408	1.016949	0.450142	0.810484	0.773134	0.106061
std	17.169714	13.683637	0.005717	1.352679	1.099191	0.392711	0.419431	0.308305
min	2.000000	50.000000	1.005000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	42.000000	70.000000	1.010000	0.000000	0.000000	1.000000	1.000000	0.000000
50%	55.000000	80.000000	1.020000	0.000000	0.000000	1.000000	1.000000	0.000000

	age	bp	sg	al	su	rbc	pc	pcc
75%	64.500000	80.000000	1.020000	2.000000	0.000000	1.000000	1.000000	0.000000
max	90.000000	180.000000	1.025000	5.000000	5.000000	1.000000	1.000000	1.000000

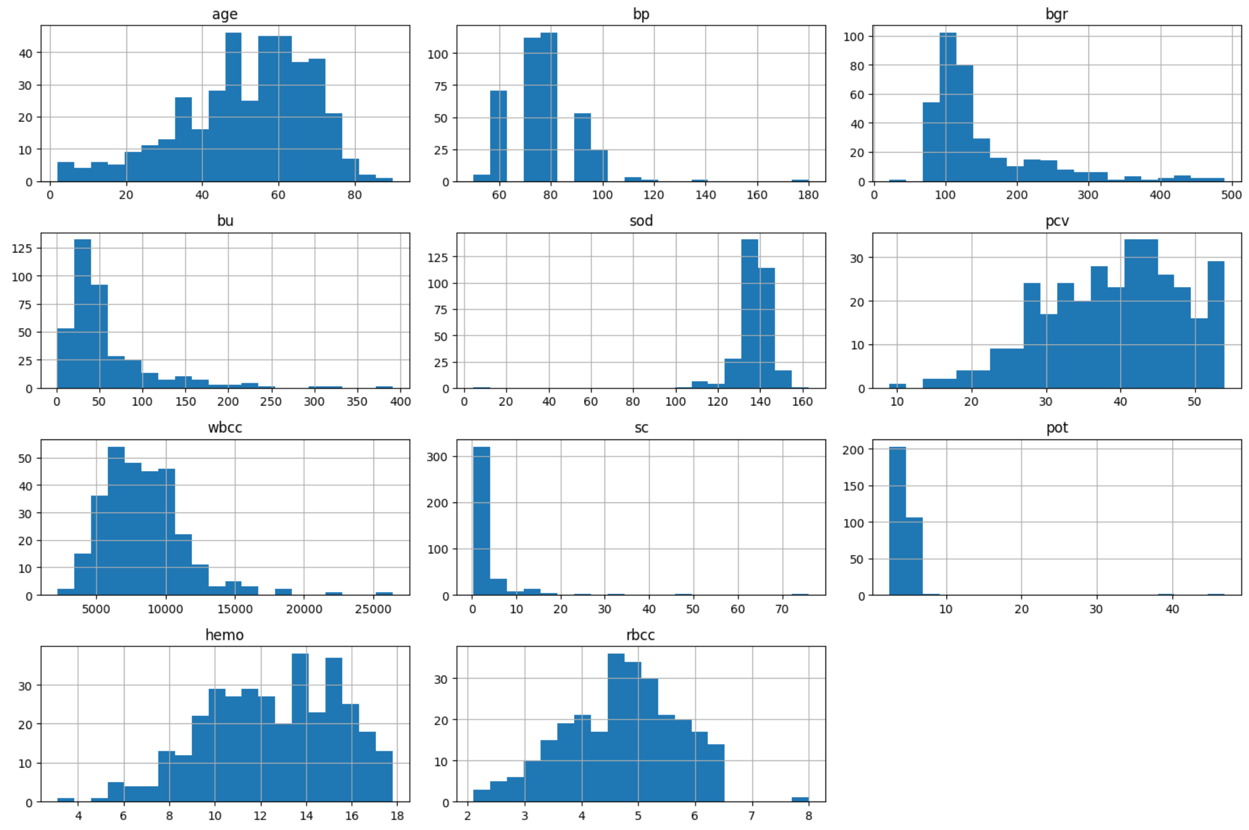
```
# Observations count
print(df.shape)
# type check
df.dtypes
```

```
(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      float64
wbcc     float64
rbcc     float64
htn      float64
dm       float64
```

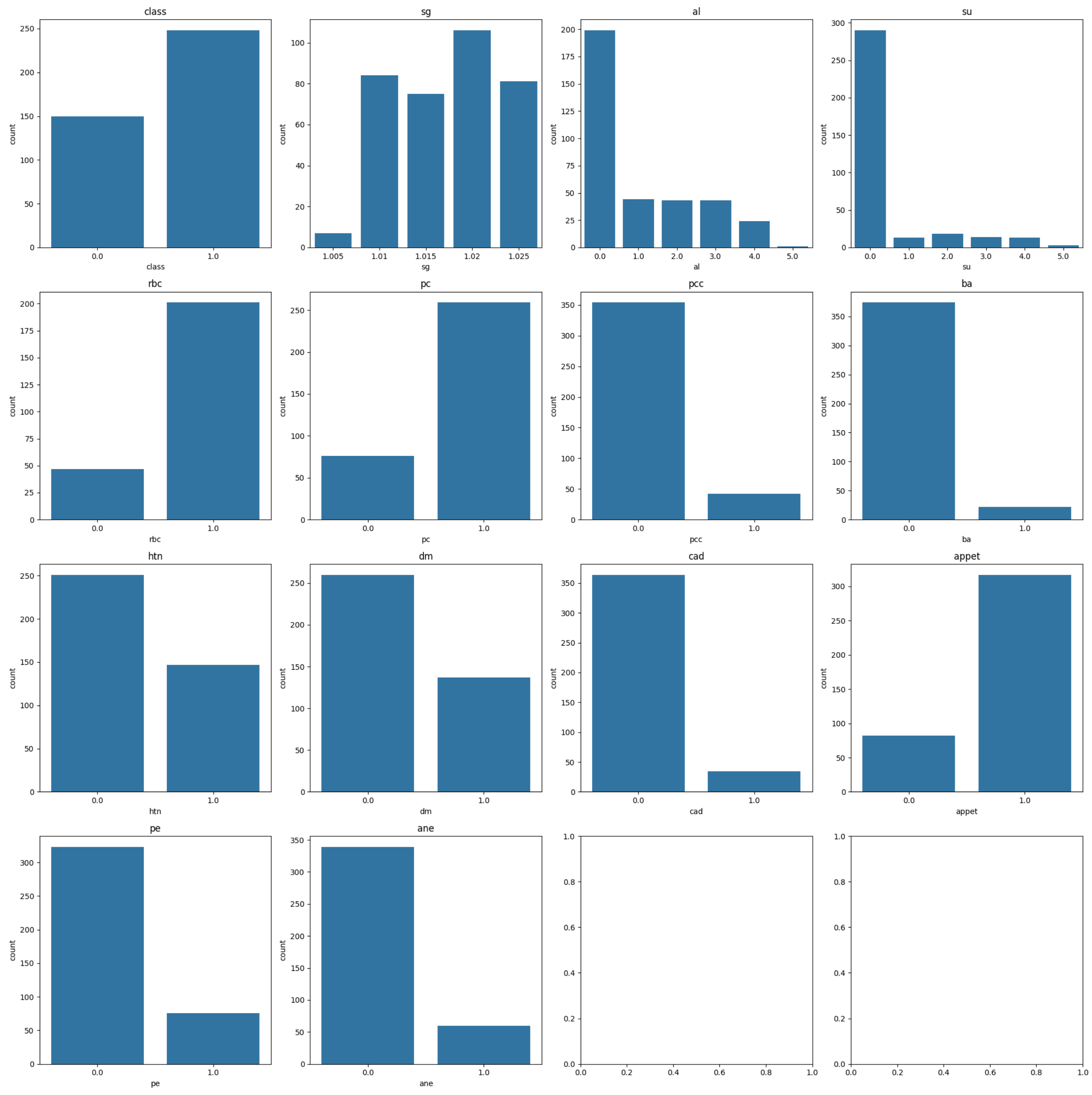
```
cad       float64
appet     float64
pe        float64
ane       float64
class     float64
dtype: object
```

```
num_col = ['age','bp','bgr','bu','sod','pcv','wbcc','sc','pot','hemo','rbcc']
df[num_col].hist(bins=20, figsize=(15,10))
plt.tight_layout()
plt.show()
```



```
columns_cat = ['class', 'sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'htn', 'dm', 'cad', 'appet


rows = 4
cols = 4
```

```
fig, axes = plt.subplots(rows, cols, figsize=(20, 20))

for i, column in enumerate(columns_cat):
    row = i // cols
    col = i % cols
    sns.countplot(x=column, data=df, ax=axes[row, col])
    axes[row, col].set_title(column)

plt.tight_layout()
plt.show()
```



There are 400 observations and 25 variables in the dataset. `sg`, `al`, `su` are Categorical variables now. `age`, `bp`, `bgr`, `bu`, `sod`, `pcv`, `wbcc`,`sc`,`pot`,`hemo`,and `rbcc` variables are all of type float. The rest of the variables are object(in this case Binary).

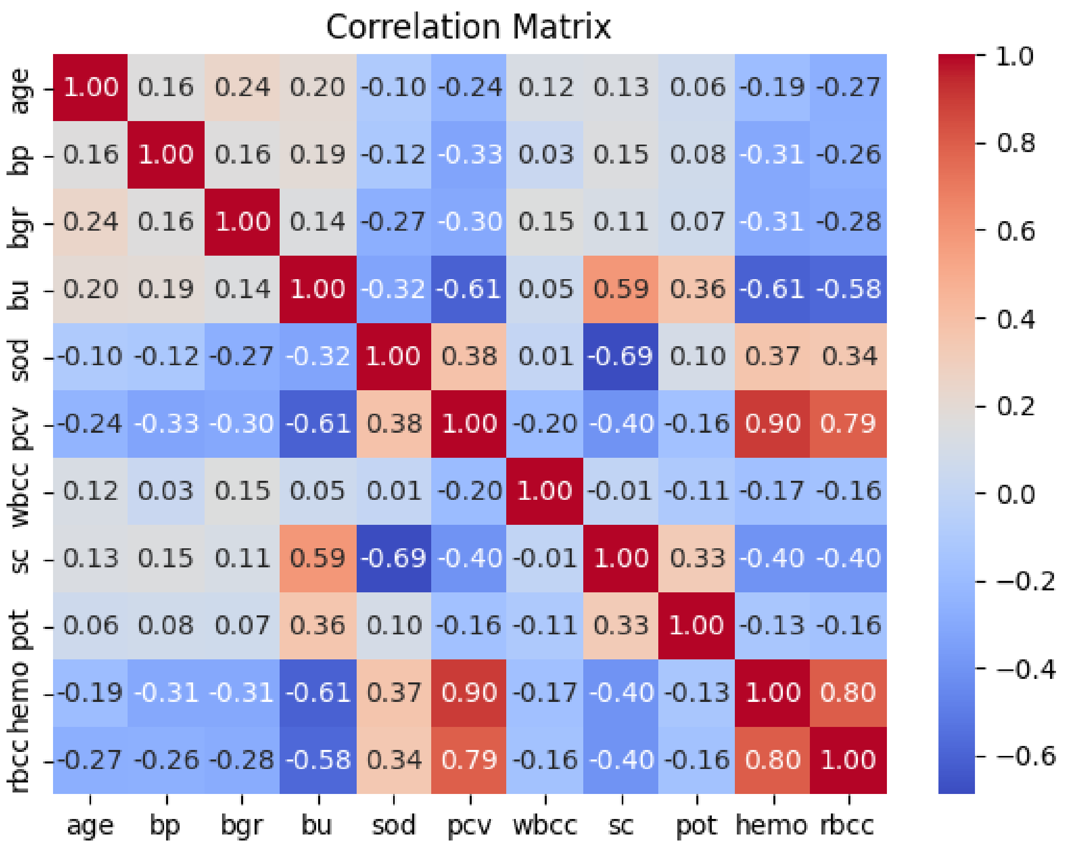
According to the data summary, the mean of observations under the `age` variable was about 51.48. The maximum and minimum age are 90 and 2 respectively, respectively. Also, the mean of `bp` (blood pressure) is about 76.47. But there may be some missing values and outliers in the dataset based on the data summary.

Also, we can find that most of them have the skewness problem by looking at the distribution of observations under each variable. So, this implies that there exist a lot of missing values and outliers in our dataset. And, depending on the distribution, we might consider replacing the missing values with a median.

4. Association Between Variables

Create a heatmap to find potential relationship between variables.

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

# Compute the correlation matrix
correlation_matrix = df[num_col].corr()

# Plot the correlation matrix
plt.figure(figsize=(7, 5))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', fmt=".2f")
plt.title('Correlation Matrix')
plt.show()
```



	age	bp	bgr	bu	sod	pcv	wbcc	sc	pot	hemo	rbcc
age	1.00	0.16	0.24	0.20	-0.10	-0.24	0.12	0.13	0.06	-0.19	-0.27
bp	0.16	1.00	0.16	0.19	-0.12	-0.33	0.03	0.15	0.08	-0.31	-0.26
bgr	0.24	0.16	1.00	0.14	-0.27	-0.30	0.15	0.11	0.07	-0.31	-0.28
bu	0.20	0.19	0.14	1.00	-0.32	-0.61	0.05	0.59	0.36	-0.61	-0.58
sod	-0.10	-0.12	-0.27	-0.32	1.00	0.38	0.01	-0.69	0.10	0.37	0.34
pcv	-0.24	-0.33	-0.30	-0.61	0.38	1.00	-0.20	-0.40	-0.16	0.90	0.79
wbcc	0.12	0.03	0.15	0.05	0.01	-0.20	1.00	-0.01	-0.11	-0.17	-0.16
sc	0.13	0.15	0.11	0.59	-0.69	-0.40	-0.01	1.00	0.33	-0.40	-0.40
pot	0.06	0.08	0.07	0.36	0.10	-0.16	-0.11	0.33	1.00	-0.13	-0.16
hemo	-0.19	-0.31	-0.31	-0.61	0.37	0.90	-0.17	-0.40	-0.13	1.00	0.80
rbcc	-0.27	-0.26	-0.28	-0.58	0.34	0.79	-0.16	-0.40	-0.16	0.80	1.00

Variables `sc` (serum creatinine) and `hemo` (hemoglobin) have a strong negative correlation (-0.61), suggesting that as serum creatinine levels increase, hemoglobin levels tend to decrease.

`pcv` (packed cell volume) and `hemo` (hemoglobin) show a strong positive correlation (0.90). This indicates that when the Packed cell volume rises, the amount of Hemoglbin will also increase. This may be because both are related to the blood's ability to carry oxygen.

`sod` (sodium) appears to have a moderate negative correlation with `bu` (blood urea) and `sc` (serum creatinine), which might suggest that higher levels of urea and creatinine in the blood are associated with lower sodium levels.

```
from statsmodels.stats.outliers_influence import variance_inflation_factor as VIF


df_cleaned = df[num_col].dropna()
vals = [VIF(df_cleaned, i)
        for i in range(1, df_cleaned.shape[1])]
```

```
vif = pd.DataFrame({'vif':vals}, index=df_cleaned.columns[1:])
vif
```

	vif
bp	33.314145
bgr	5.228453
bu	10.308152
sod	154.643905
pcv	106.157383
wbcc	10.830481
sc	7.157653
pot	3.696926
hemo	110.751640
rbcc	63.753595

From variance inflation factor, `sod`, `pcv` and `hemo` have extremely large value, this indicates that they have severe multicollinearity issues. To solve this problem, Ridge Regression/ PCA or LASSO will be applied in the next part.

5. Missing Value Analysis and Handling

```
## Check the missing vlaue
df.isna().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         3
cad        2
appet      1
pe         1
ane        1
class      2
dtype: int64
```

```
print(df.shape)


## Drop the missing values
df_dropna = df.dropna()
print(df_dropna.shape)
```

```
(400, 25)
(158, 25)
```

Based on the distribution of observed values for each variable in the dataset overview, we need to replace in those missing values in different ways. If the distribution is approximately normal, we choose to replace it with mean. If there is a skewness, we need to replace it in with median.

So, for `age`, `pcv`, `rbcc` variables. We choose to replace their missing values with mean. For the missing observations in the remaining variables, we replace them with median

```
median_col = ['age', 'pcv', 'rbcc', 'bp', 'bgr', 'bu', 'sod', 'wbcc', 'sc', 'pot', 'hemo']
columns_bin = ['rbc', 'pc', 'pcc', 'ba', 'htn', 'dm', 'cad', 'appet', 'pe', 'ane', 'class']
columns_cat = ['sg', 'al', 'su']

for column in median_col:
    df[column].fillna(df[column].median(), inplace=True)

for column in columns_bin + columns_cat:
    mode_value = df[column].mode()[0]
    df[column].fillna(mode_value, inplace=True)
```

Now, we can convert those three numerical variables into categorical variables.

```
columns_cat = [ 'class','sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'htn', 'dm', 'cad', 'appet
for col in columns_cat:
    df[col] = pd.Categorical(df[col])



df.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
class      category
dtype: object
```

```
df.head(10)
```

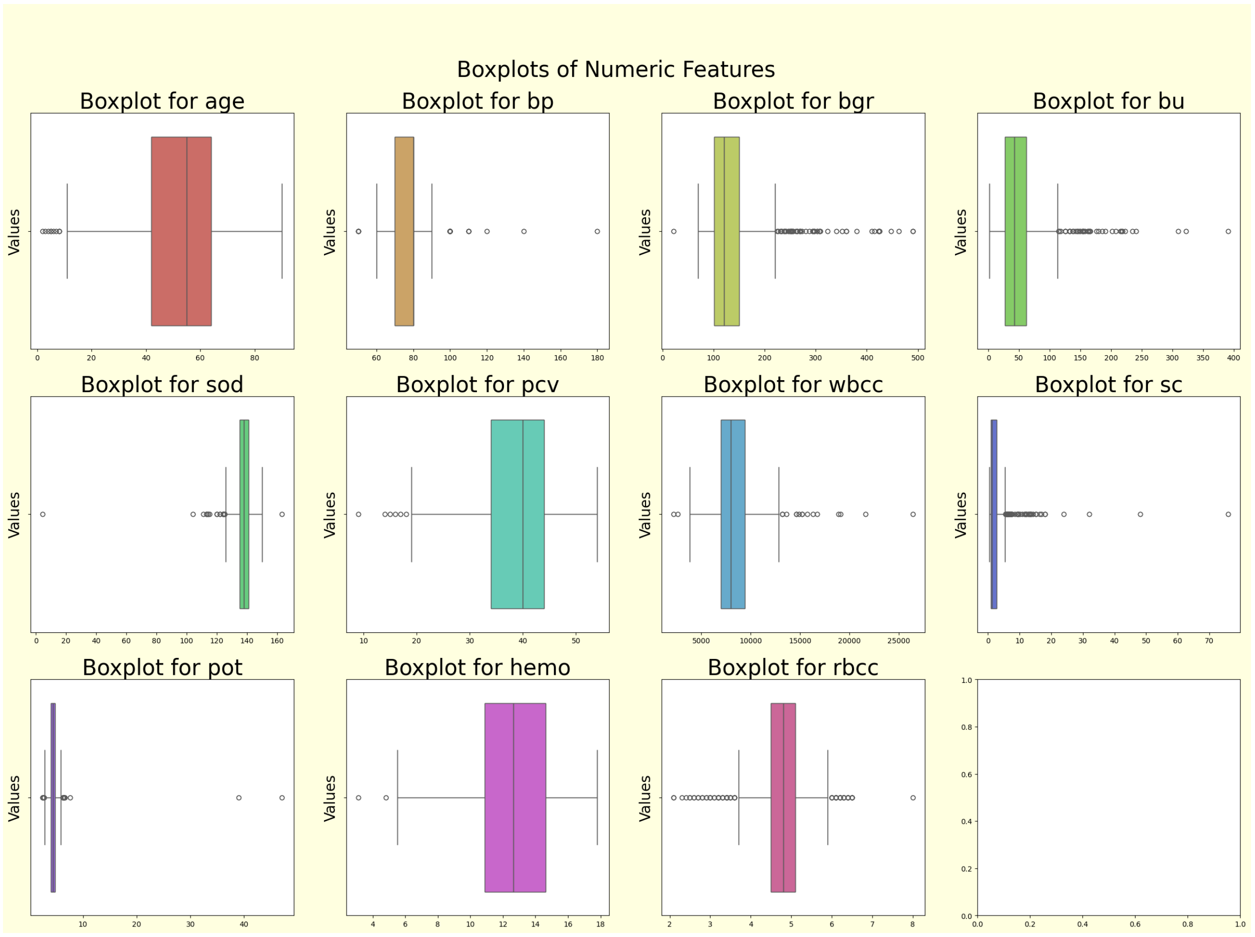
	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wbcc	rbcc	htn	dm	cad	a
0	48.0	80.0	1.020	1.0	0.0	1.0	1.0	0.0	0.0	121.0	...	44.0	7800.0	5.2	1.0	1.0	0.0	1
1	7.0	50.0	1.020	4.0	0.0	1.0	1.0	0.0	0.0	121.0	...	38.0	6000.0	4.8	0.0	0.0	0.0	1
2	62.0	80.0	1.010	2.0	3.0	1.0	1.0	0.0	0.0	423.0	...	31.0	7500.0	4.8	0.0	1.0	0.0	0
3	48.0	70.0	1.005	4.0	0.0	1.0	0.0	1.0	0.0	117.0	...	32.0	6700.0	3.9	1.0	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	...	35.0	7300.0	4.6	0.0	0.0	0.0	1
5	60.0	90.0	1.015	3.0	0.0	1.0	1.0	0.0	0.0	74.0	...	39.0	7800.0	4.4	1.0	1.0	0.0	1
6	68.0	70.0	1.010	0.0	0.0	1.0	1.0	0.0	0.0	100.0	...	36.0	8000.0	4.8	0.0	0.0	0.0	1
7	24.0	80.0	1.015	2.0	4.0	1.0	0.0	0.0	0.0	410.0	...	44.0	6900.0	5.0	0.0	1.0	0.0	1
8	52.0	100.0	1.015	3.0	0.0	1.0	0.0	1.0	0.0	138.0	...	33.0	9600.0	4.0	1.0	1.0	0.0	1
9	53.0	90.0	1.020	2.0	0.0	0.0	0.0	1.0	0.0	70.0	...	29.0	12100.0	3.7	1.0	1.0	0.0	0

```
# Check Missing Values again
df.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
sod      0
pot      0
hemo     0
pcv      0
wbcc     0
rbcc     0
htn      0
dm       0
cad      0
appet    0
pe       0
ane      0
class    0
dtype: int64
```

6. Outlier Analysis

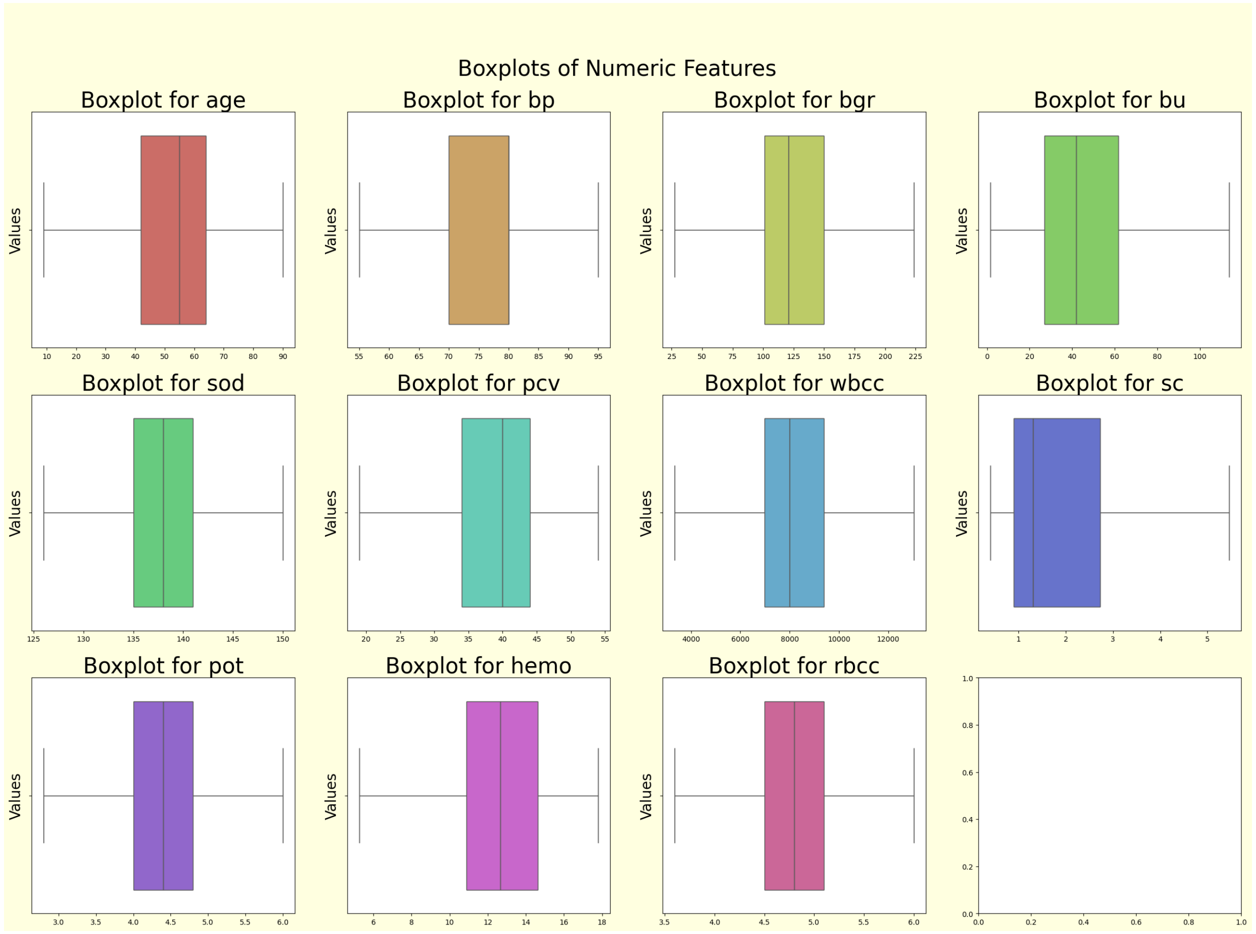
```
n_rows, n_cols = (3, 4)

colors = sns.color_palette("hls", len(df[num_col].columns))

figure, axes = plt.subplots(nrows=n_rows, ncols=n_cols, figsize=(30, 20), facecolor='lightyell
figure.suptitle('\n\nBoxplots of Numeric Features', fontsize=30)

for index, column in enumerate(df[num_col].columns):

    i, j = index // n_cols, index % n_cols

    collabel = column

    sns.boxplot(x=df[column], ax=axes[i, j])

    sns.boxplot(x=df[column], ax=axes[i, j], color=colors[index])

    axes[i, j].set_title(f'Boxplot for {collabel}', fontsize=30)

    axes[i, j].set_xlabel(None)

    axes[i, j].set_ylabel("Values", fontsize=20)

plt.show()
```



```python
from sklearn.preprocessing import scale
```

```python
for column in df[num_col].columns:
    # Q3
    Q3 = df[column].quantile(0.75)
    Q1 = df[column].quantile(0.25)
    # Max val
    max_val = df[column].max()

    # outlier threshold
    threshold_max = Q3 + 1.5 * (Q3 - df[column].quantile(0.25))
    threshold_min = Q1 - 1.5 * (Q3 - df[column].quantile(0.25))
    # replace outlier with Q3 + 1.5IQR or Q1 - 1.5IQR
    df[column] = np.where(
        df[column] > threshold_max,

        threshold_max,

        df[column]

        )


    df[column] = np.where(

        df[column] < threshold_min,

        threshold_min,

        df[column]

        )
```

```
n_rows, n_cols = (3, 4)


colors = sns.color_palette("hls", len(df[num_col].columns))


figure, axes = plt.subplots(nrows=n_rows, ncols=n_cols, figsize=(30, 20), facecolor='lightyello
figure.suptitle('\n\nBoxplots of Numeric Features', fontsize=30)


for index, column in enumerate(df[num_col].columns):


    i, j = index // n_cols, index % n_cols


    collabel = column


    sns.boxplot(x=df[column], ax=axes[i, j])


    sns.boxplot(x=df[column], ax=axes[i, j], color=colors[index])


    axes[i, j].set_title(f'Boxplot for {collabel}', fontsize=30)


    axes[i, j].set_xlabel(None)
    axes[i, j].set_ylabel("Values", fontsize=20)


plt.show()
```



We ended up replacing all the outliers in this step. We let outliers to be transfered to (Q3 + 1.5IQR) or (Q1 - 1.5IQR).

7. Sub-group Analysis

In subgroup analysis, we need the unsupervised clustering technique K-Means to explore potential sub-groups.

```
# Check the mean
df[num_col].mean()
```

```
age        51.647500
bp         75.825000
bgr       134.011250
bu         50.277687
sod       138.217500
pcv        39.145000
wbcc     8169.093750
sc          2.071406
pot         4.382750
hemo       12.549000
rbcc        4.769750
dtype: float64
```

```
# Check the variance
df[num_col].var()
```

```
age     2.807652e+02
bp      1.203703e+02
bgr     2.124512e+03
bu      9.171178e+02
sod     2.780972e+01
pcv     6.371326e+01
wbcc    4.123827e+06
sc      2.659236e+00
pot     4.035864e-01
hemo    7.272142e+00
rbcc    4.553984e-01
dtype: float64
```

Variables with large variance have a greater impact on the algorithm in unsupervised learning. Therefore, we must scale all the variables before performing further algorithms.

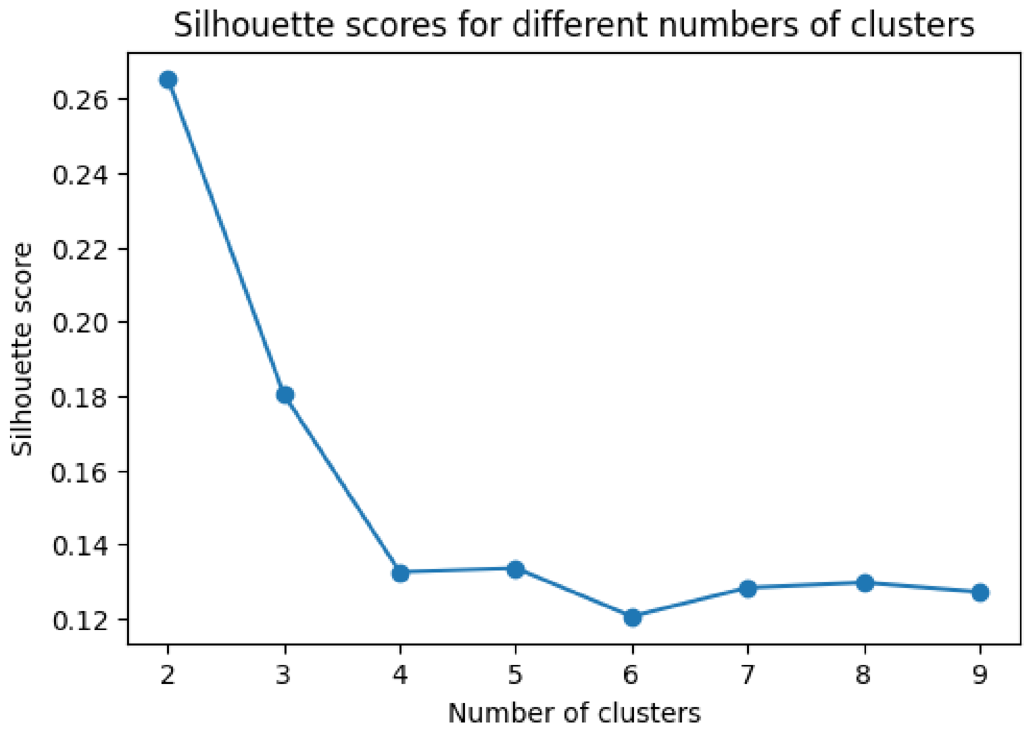
```python
# Scale the numerical data

from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import scale
from sklearn.decomposition import PCA, TruncatedSVD, FactorAnalysis

scaler = StandardScaler()
df[num_col] = scaler.fit_transform(
    df[num_col]
)
print(df[num_col].head(3))
```

```
        age        bp       bgr        bu       sod       pcv      wbcc  \
0 -0.217955  0.381013 -0.282640 -0.472051 -0.041296  0.609001 -0.181983
1 -2.548388 -1.900504 -0.282640 -1.067169 -0.041296 -0.143626 -1.069478
2  0.618610  0.381013  1.943938  0.090005 -0.041296 -1.021691 -0.329898

         sc       pot      hemo      rbcc
0 -0.535039  0.027187  1.058546  0.638364
1 -0.780638  0.027187 -0.463740  0.044882
2 -0.166642  0.027187 -1.094932  0.044882
```

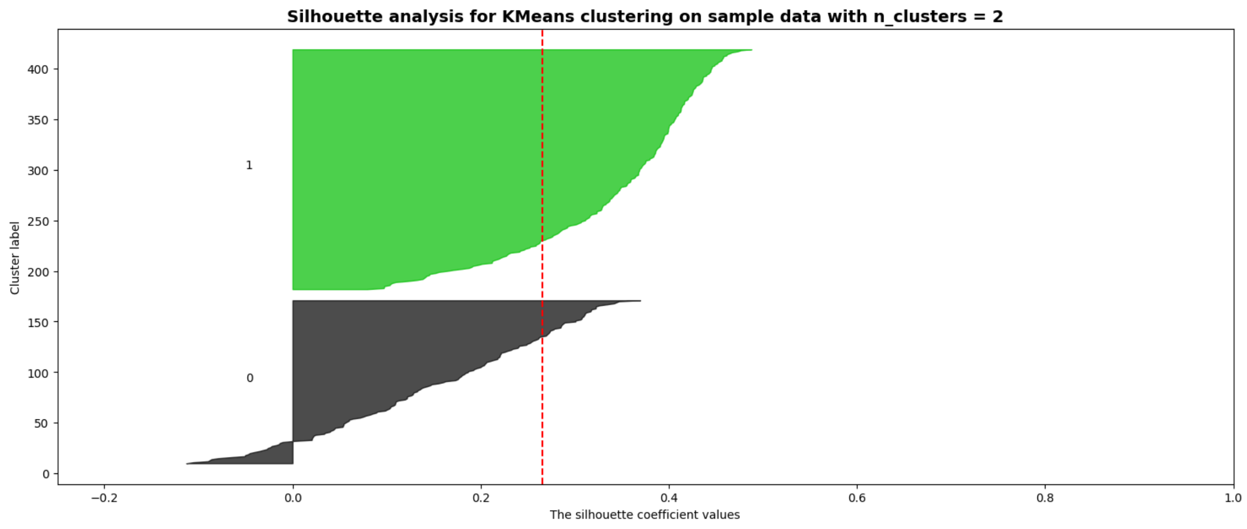
K-mean clustering can be used to perform sub-group analysis.

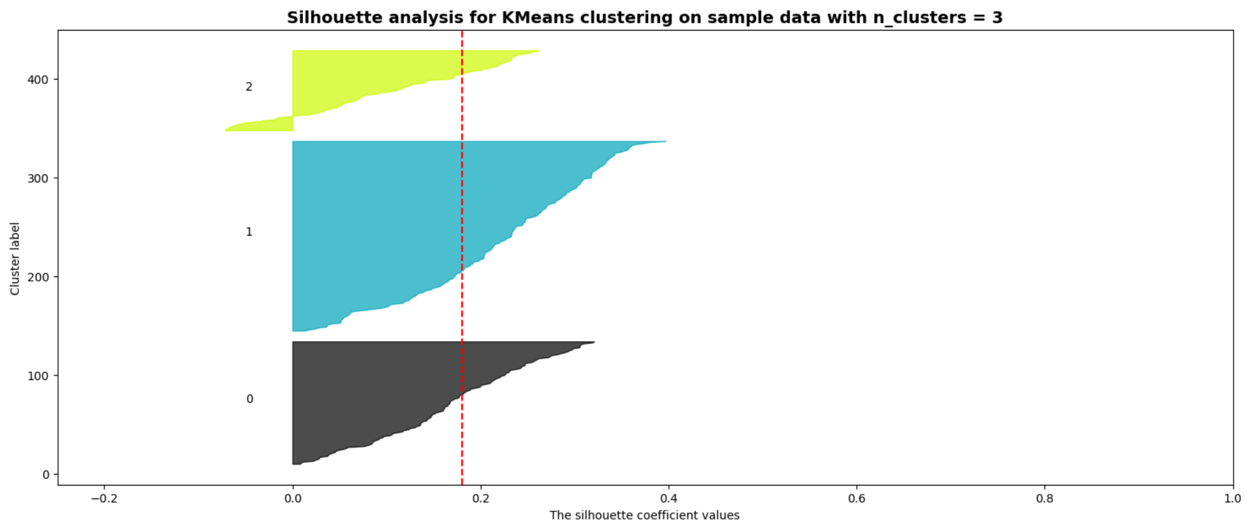
```python
# Perform K-Mean

columns_to_drop = ['class', 'sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'htn', 'dm', 'cad', 'a
df_test = df.drop(columns=columns_to_drop)

from sklearn.cluster import KMeans
from sklearn.metrics import silhouette_samples, silhouette_score
```

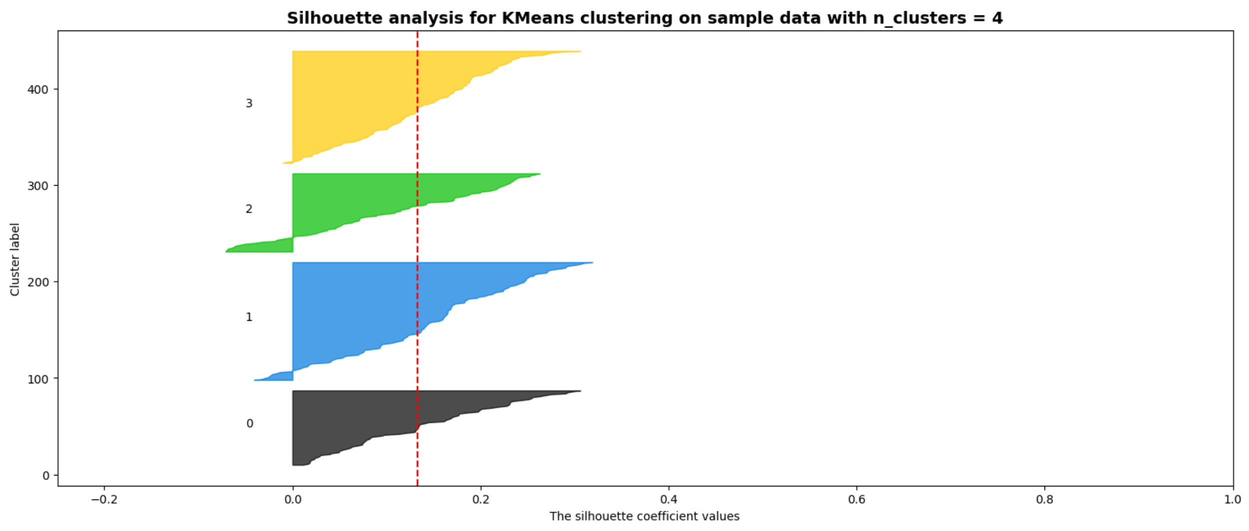
```
silhouette_scores = []


K_range = range(2, 10)
for K in K_range:
    km = KMeans(n_clusters=K, n_init=20,random_state=1)
    clusters = km.fit_predict(df_test)
    silhouette_scores.append(silhouette_score(df_test, clusters))


plt.figure(figsize=(6,4))
plt.plot(K_range, silhouette_scores, marker='o')
plt.title('Silhouette scores for different numbers of clusters')
plt.xlabel('Number of clusters')
plt.ylabel('Silhouette score')
plt.show()
```

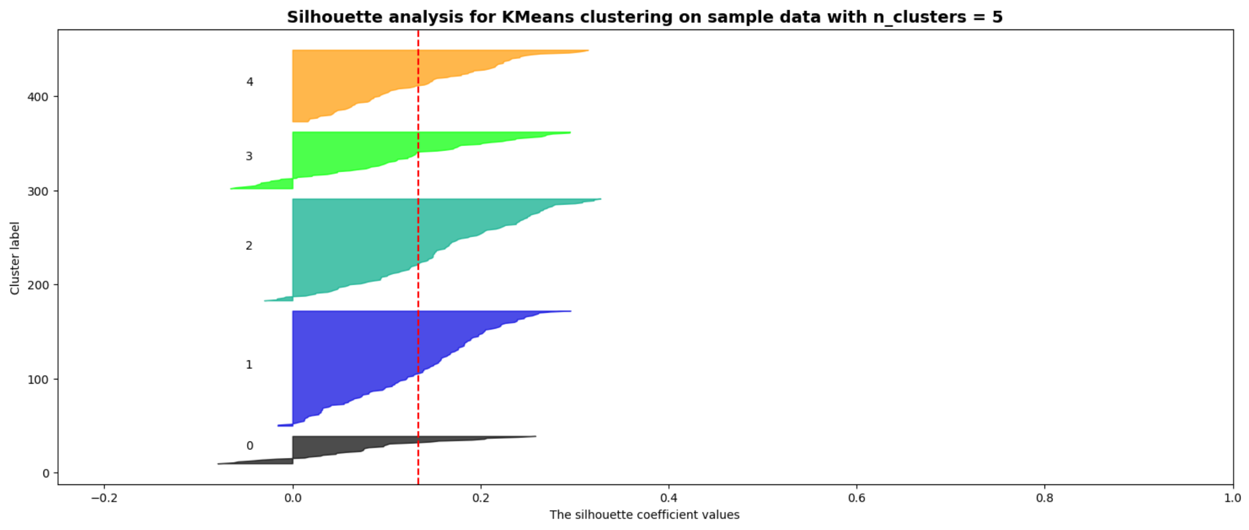


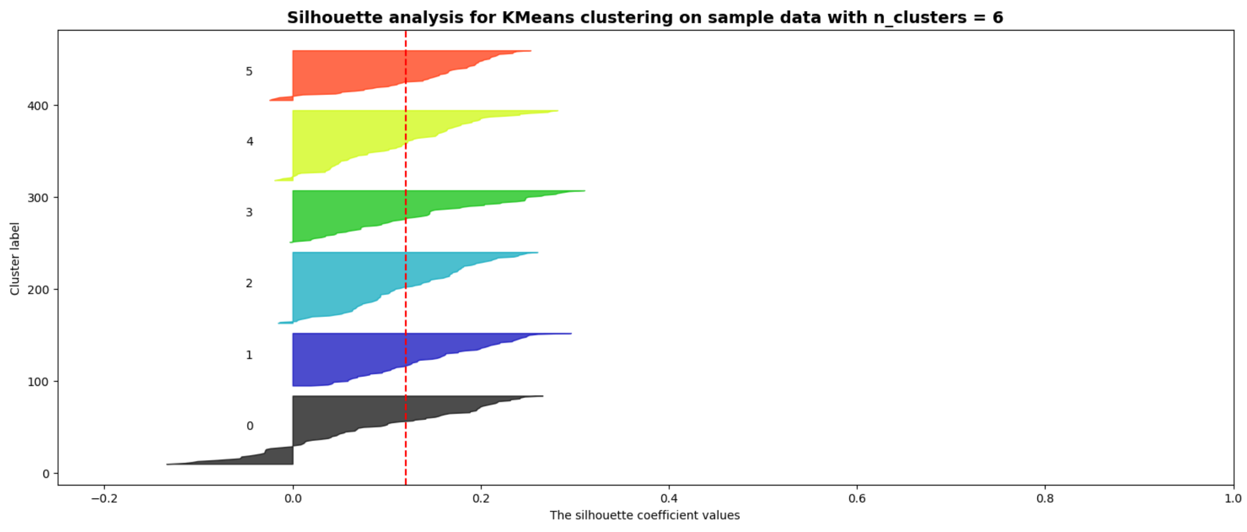
```
import matplotlib.cm as cm


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=1)

    cluster_labels_km = km.fit_predict(df_test)

    silhouette_avg_km = silhouette_score(df_test, cluster_labels_km)

    # Compute the silhouette scores for each sample

    sample_silhouette_values = silhouette_samples(df_test, cluster_labels_km)

    fig, ax1 = plt.subplots(1, 1)

    fig.set_size_inches(18, 7)

    ax1.set_xlim([-0.25, 1])# change this based on the silhouette range


    y_lower = 10


    for i in range(n_clusters):

        # Aggregate the silhouette scores for samples belonging to

        # cluster i, and sort them

        ith_cluster_silhouette_values = sample_silhouette_values[cluster_labels_km == 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) / n_clusters)

        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))

        # 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("The 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(
        "Silhouette analysis for KMeans clustering on sample data with n_clusters = %d"
        % n_clusters,
        fontsize=14,
        fontweight="bold",
    )
```




Silhouette analysis for KMeans clustering on sample data with n_clusters = 3
Cluster label
The silhouette coefficient values
0
1
2
0
100
200
300
400
−0.2
0.0
0.2
0.4
0.6
0.8
1.0


Silhouette analysis for KMeans clustering on sample data with n_clusters = 4
Cluster label
The silhouette coefficient values
0
1
2
3
0
100
200
300
400
−0.2
0.0
0.2
0.4
0.6
0.8
1.0


Silhouette analysis for KMeans clustering on sample data with n_clusters = 5
Cluster label
The silhouette coefficient values
0
1
2
3
4
0
100
200
300
400
−0.2
0.0
0.2
0.4
0.6
0.8
1.0



Negative silhouette scores are observed. This suggests that some samples are in the wrong clusters.

These Silhouette scores are very low, which indicate that the data dimensions are very high, and we can use PCA to reduce the dimensions first. Notice that we cannot include the reponse variable and those categorical variables. So, we have to drop them.

```
# Check the variance after scaling
df[num_col].var()
```

```
age      1.002506
bp       1.002506
bgr      1.002506
bu       1.002506
sod      1.002506
pcv      1.002506
wbcc     1.002506
sc       1.002506
pot      1.002506
hemo     1.002506
rbcc     1.002506
dtype: float64
```

All variables variance almost equal to 1, profomance is good.

We have to do PCA here.

```
columns_to_drop = ['class', 'sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'htn', 'dm', 'cad', 'ap
df_test = df.drop(columns=columns_to_drop)
X = pd.DataFrame(df_test, index=df_test.index, columns=df_test.columns)
X.shape
```

```
(400, 11)
```

```
from sklearn.decomposition import PCA, TruncatedSVD
pca_X = PCA()
```

```
pc_scores = pd.DataFrame(pca_X.fit_transform(X), index=X.index)
pc_scores.head(3)
```

	0	1	2	3	4	5	6	7	8	9
0	-1.349650	0.183226	0.243718	-0.483879	-0.242939	0.128189	-0.349051	0.480114	-0.217832	-0.
1	-1.411052	1.130044	-2.195523	0.472222	0.305535	-2.071453	0.399006	-0.528309	0.366322	0.1
2	1.419362	-0.610541	0.774332	-0.952723	0.336169	-1.066977	0.156837	-0.674355	0.971088	-0.

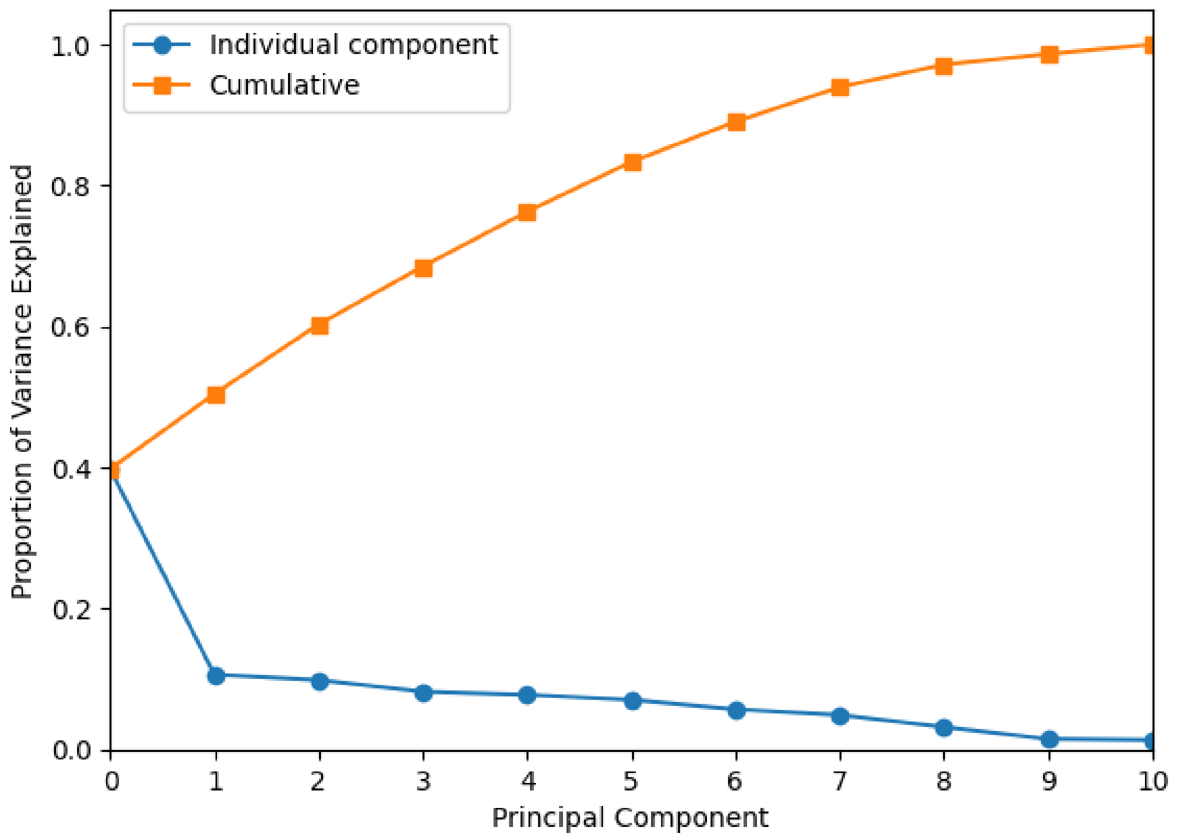
```
pc_scores.var()
```

```
0     4.388083
1     1.173689
2     1.086787
3     0.906036
4     0.856147
5     0.777539
6     0.630324
7     0.540595
8     0.352652
```

```
9     0.166055
10    0.149662
dtype: float64
```

use first 3 PC for their eigenvalue > 1

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


plt.plot(pca_X.explained_variance_ratio_, '-o', label='Individual component')
plt.plot( 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([0,1,2,3,4,5,6,7,8,9,10])
plt.legend(loc=2)
```



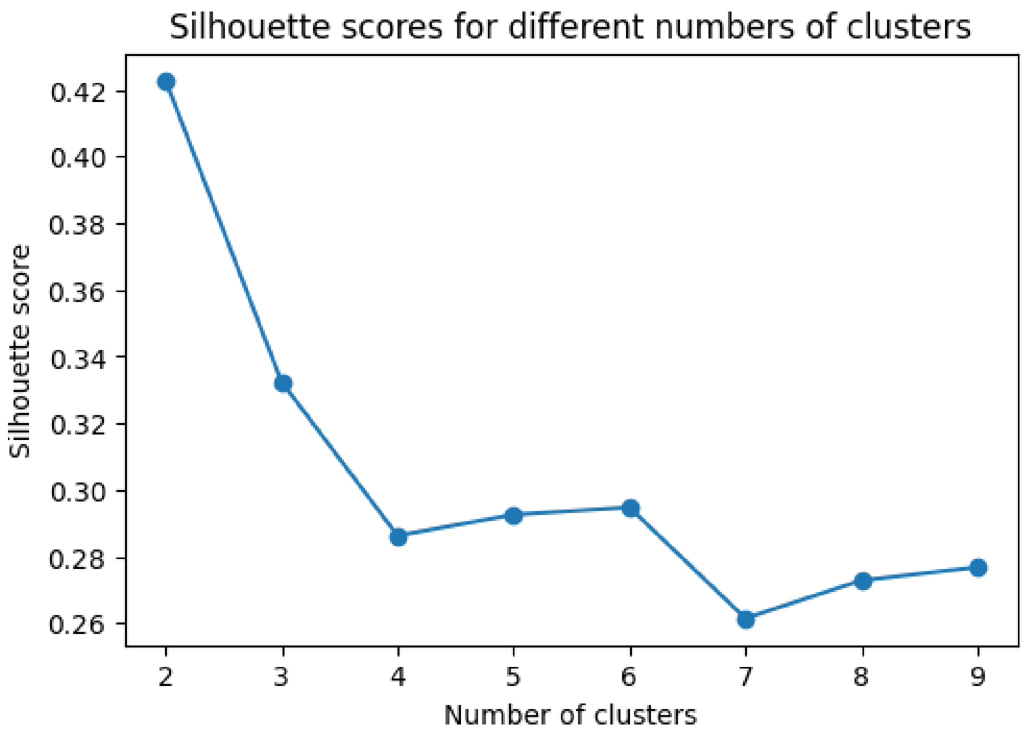
```
pca = PCA().fit(X)
print(pca_X.explained_variance_ratio_)
sum(pca.explained_variance_ratio_[:3])
```

```
[0.3979193  0.10643227 0.09855181 0.08216101 0.07763696 0.07050862
 0.05715895 0.04902216 0.03197913 0.01505815 0.01357164]
```

```
0.6029033851452663
```

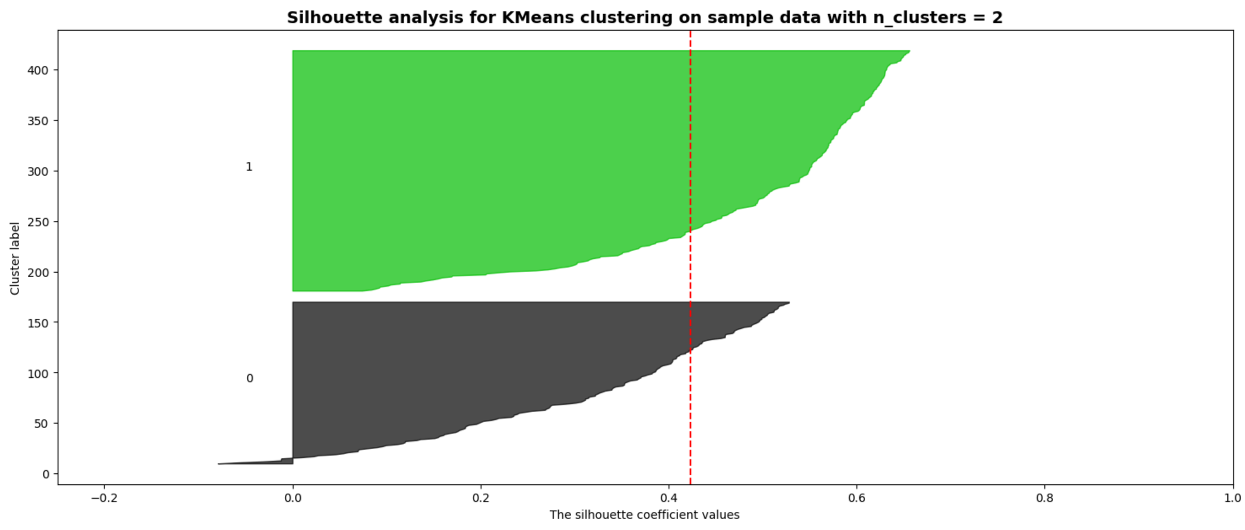
```
# Perform K-Mean

pca = PCA(n_components=3)
df_pca = pca.fit_transform(df_test)

silhouette_scores = []
```

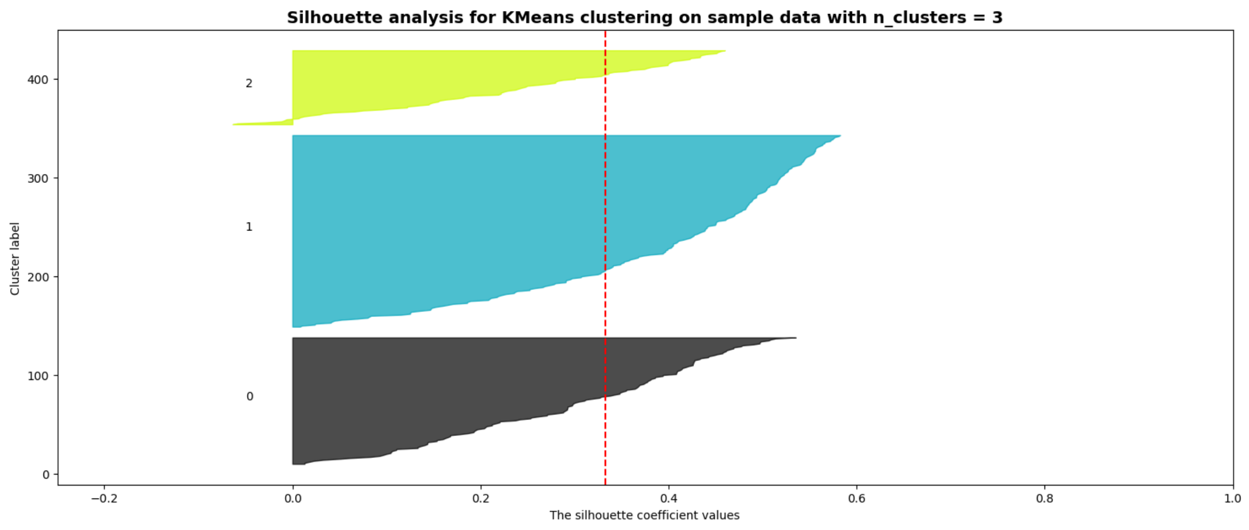
```python
K_range = range(2, 10)
for K in K_range:
    km = KMeans(n_clusters=K, n_init=20,random_state=1)
    clusters = km.fit_predict(df_pca)
    silhouette_scores.append(silhouette_score(df_pca, clusters))

plt.figure(figsize=(6,4))
plt.plot(K_range, silhouette_scores, marker='o')
plt.title('Silhouette scores for different numbers of clusters')
plt.xlabel('Number of clusters')
plt.ylabel('Silhouette score')
plt.show()
```

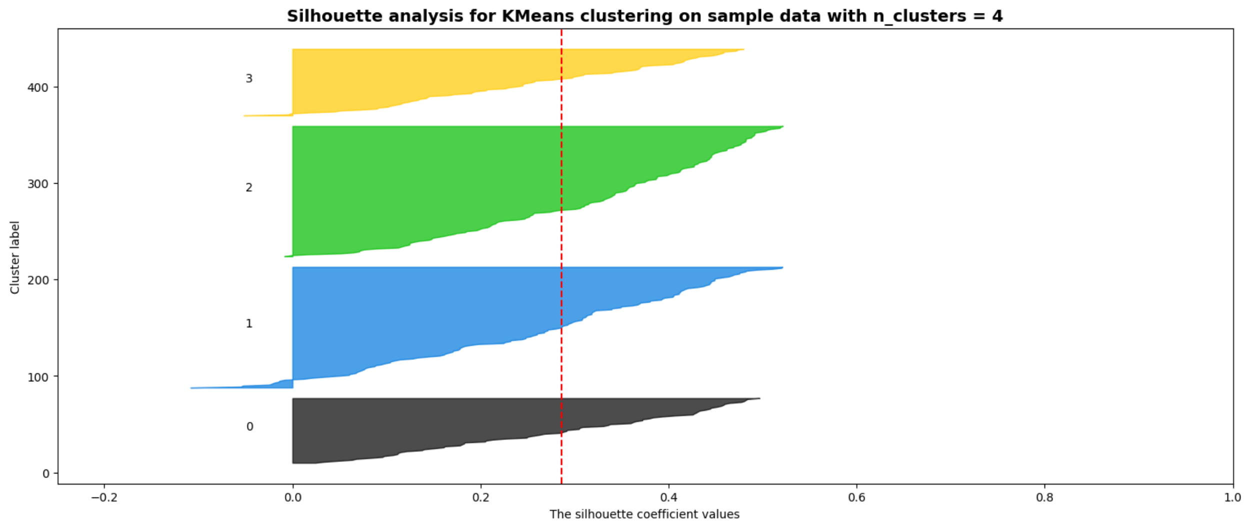


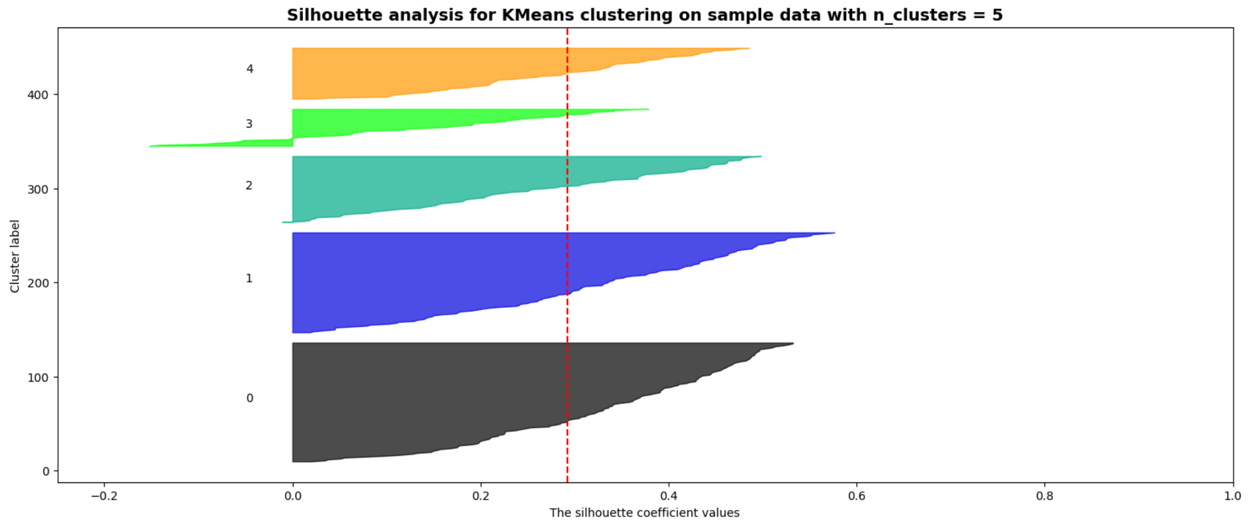
```python
pca = PCA(n_components=3)
df_pca = pca.fit_transform(df_test)


import matplotlib.cm as cm
```

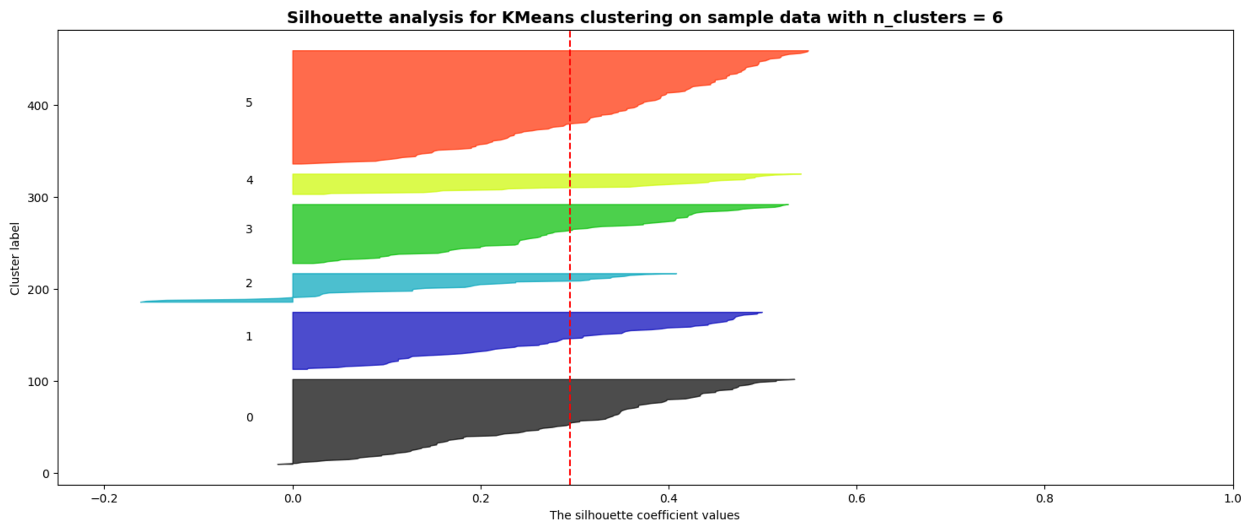
```
range_n_clusters = [2, 3, 4, 5, 6]
for n_clusters in range_n_clusters:
    km = KMeans(n_clusters = n_clusters, n_init = 20, random_state=1)
    cluster_labels_km = km.fit_predict(df_pca)
    silhouette_avg_km = silhouette_score(df_pca, cluster_labels_km)
    # Compute the silhouette scores for each sample
    sample_silhouette_values = silhouette_samples(df_pca, cluster_labels_km)
    fig, ax1 = plt.subplots(1, 1)
    fig.set_size_inches(18, 7)
    ax1.set_xlim([-0.25, 1])# change this based on the silhouette range

    y_lower = 10

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

        # 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("The 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(
        "Silhouette analysis for KMeans clustering on sample data with n_clusters = %d"
        % n_clusters,
        fontsize=14,
        fontweight="bold",
    )
```




Silhouette analysis for KMeans clustering on sample data with n_clusters = 3
Cluster label
The silhouette coefficient values
0
1
2
0
100
200
300
400
−0.2
0.0
0.2
0.4
0.6
0.8
1.0


Silhouette analysis for KMeans clustering on sample data with n_clusters = 4
Cluster label
The silhouette coefficient values
0
1
2
3
0
100
200
300
400
−0.2
0.0
0.2
0.4
0.6
0.8
1.0

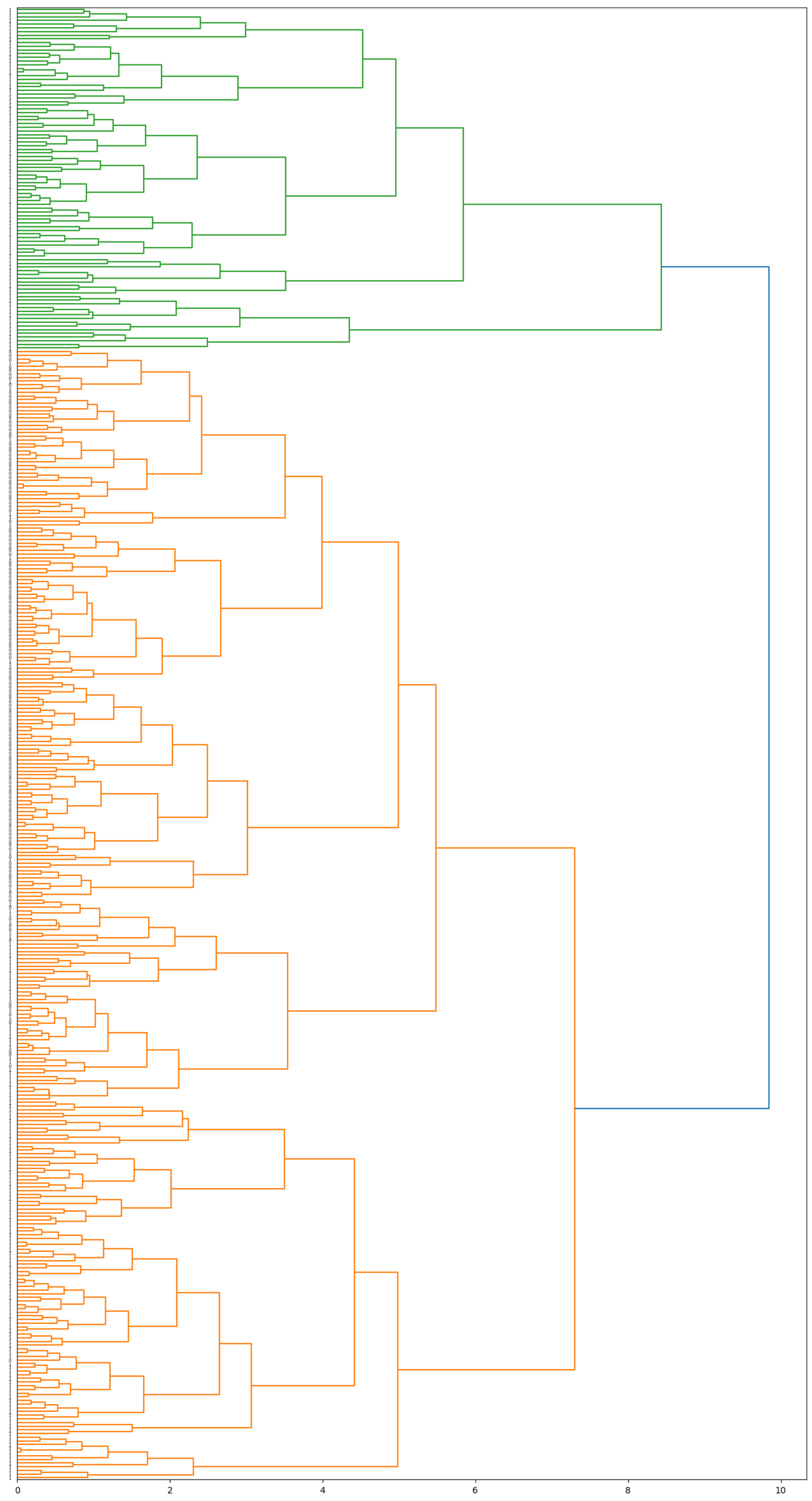

Silhouette analysis for KMeans clustering on sample data with n_clusters = 5
Cluster label
The silhouette coefficient values
0
1
2
3
4
0
100
200
300
400
−0.2
0.0
0.2
0.4
0.6
0.8
1.0



Now K-mean perfroms really good at K=2 after PCA.

Let's use Hierarchical clustering for visualization.

```python
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


plt.figure(figsize=(16,30))


pca_cluster = hierarchy.dendrogram(
    hierarchy.complete(df_pca),
    labels=df['class'].astype(int).astype(str).tolist(),
    orientation='right',
    color_threshold=9
)
```

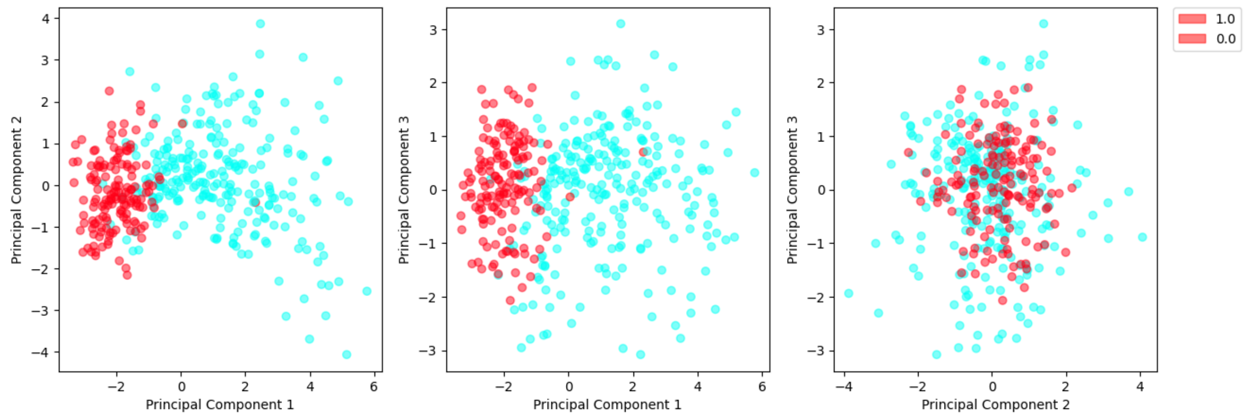

0
2
4
6
8
10

```python
y = df['class']
y
```

```
0      1.0
1      1.0
2      1.0
3      1.0
4      1.0
      ...
395    0.0
396    0.0
397    0.0
398    0.0
399    0.0
Name: class, Length: 400, dtype: category
Categories (2, float64): [0.0, 1.0]
```

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

df1 = pd.read_csv(data_url)

df2_plot = pd.DataFrame(pca_X.fit_transform(X))
y = pd.Series(df1['class'])
y_ts = y.map({'ckd': 1, 'notckd': 0})

df_pca_with_target = pd.DataFrame(df_pca, columns=['PC1', 'PC2', 'PC3'])

color_idx = pd.factorize(y_ts)[0]
```

```
cmap = plt.cm.hsv



fig, axes = plt.subplots(1, 3, figsize=(15, 5))
# PC1 vs PC2
axes[0].scatter(df2_plot.iloc[:,0], -df2_plot.iloc[:,1], c=color_idx, cmap=cmap, alpha=0.5)
axes[0].set_xlabel('Principal Component 1')
axes[0].set_ylabel('Principal Component 2')

# PC1 vs PC3
axes[1].scatter(df2_plot.iloc[:,0], df2_plot.iloc[:,2], c=color_idx, cmap=cmap, alpha=0.5)
axes[1].set_xlabel('Principal Component 1')
axes[1].set_ylabel('Principal Component 3')

# PC2 vs PC3
axes[2].scatter(df2_plot.iloc[:,1], df2_plot.iloc[:,2], c=color_idx, cmap=cmap, alpha=0.5)
axes[2].set_xlabel('Principal Component 2')
axes[2].set_ylabel('Principal Component 3')

handles = []
labels = pd.factorize(y_ts.unique())
norm = mpl.colors.Normalize(vmin=0.0, vmax=14.0)

for i, v in zip(labels[0], labels[1]):
    handles.append(mpl.patches.Patch(color=cmap(norm(i)), label=v, alpha=0.5))

axes[2].legend(handles=handles, bbox_to_anchor=(1.05, 1), loc=2, borderaxespad=0.)
```



This visualization will help illustrate how the clusters are distributed in the reduced-dimensional space.

```python
from sklearn.metrics import adjusted_rand_score


# K = 2

km1 = KMeans(n_clusters=2, n_init=20, random_state=1)

km1.fit(df_pca)


# Status variable saved in (1)

status = df['class'].astype(int).astype(str)


rand_score(km1.labels_, status).round(4)


print('Rand score is ' + str(rand_score(km1.labels_, status).round(4)))
```

```
Rand score is 0.6531
```

Rand score shows that under PCA, k-means has good performance.

8. Data Splitting

```
from sklearn.model_selection import train_test_split
```

```
df_feature = df.drop(columns =['class'])
df_target = df['class']
```

```
# 30% of the data for testing
X_train, X_test, y_train, y_test = train_test_split(
    df_feature, df_target, test_size=0.3, random_state=1)
```

9. Classifier Choices

The dataset is about binary classification, and logistic regression performs well on such problems. Therefore, we first choose logistic regression. Secondly, random forest has consistently shown good performance in the field of machine learning and is very popular. So, our Classifier Choices are logistic regression and random forest.

10. Performance Metrics

We will choose 2-3 metrics to predict the effectiveness and accuracy of these two models. We will use Accuracy, Area Under the ROC curve, AUC is usually. Also,we can check the Kolmogorov-Smirnov statistic.

11&12. Feature Selection/Extraction and Classifier Comparison

In these two parts, we will first build the model using two classifiers. Then, we will evaluate our model using the metrics mentioned in Part 10. After that, we will select the appropriate features and then build the model to analyze whether the performance of the model is improved.

Classifier I: logistic regression

```
from sklearn.linear_model import LogisticRegression
```

```
def_log = LogisticRegression(max_iter = 500)
```

Train the model on the training set and make predictions on the test set.

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

```
LogisticRegression(max_iter=500)
```

```
pred_prob = def_log.predict_proba(X_test)
df_pro = pd.DataFrame(data = {'prob': pred_prob[:,1], 'y_test': y_test})
df_pro.head(5)
```

	prob	y_test
398	0.006833	0.0
125	0.998951	1.0
328	0.040847	0.0
339	0.033545	0.0
172	0.999942	1.0

```
# Create a data frame with predicted probabilities (for default) and the class labels in the te
df_logit = pd.DataFrame(
    data = {'prob0': pred_prob[:,1], 'y_test': y_test}
    )
```

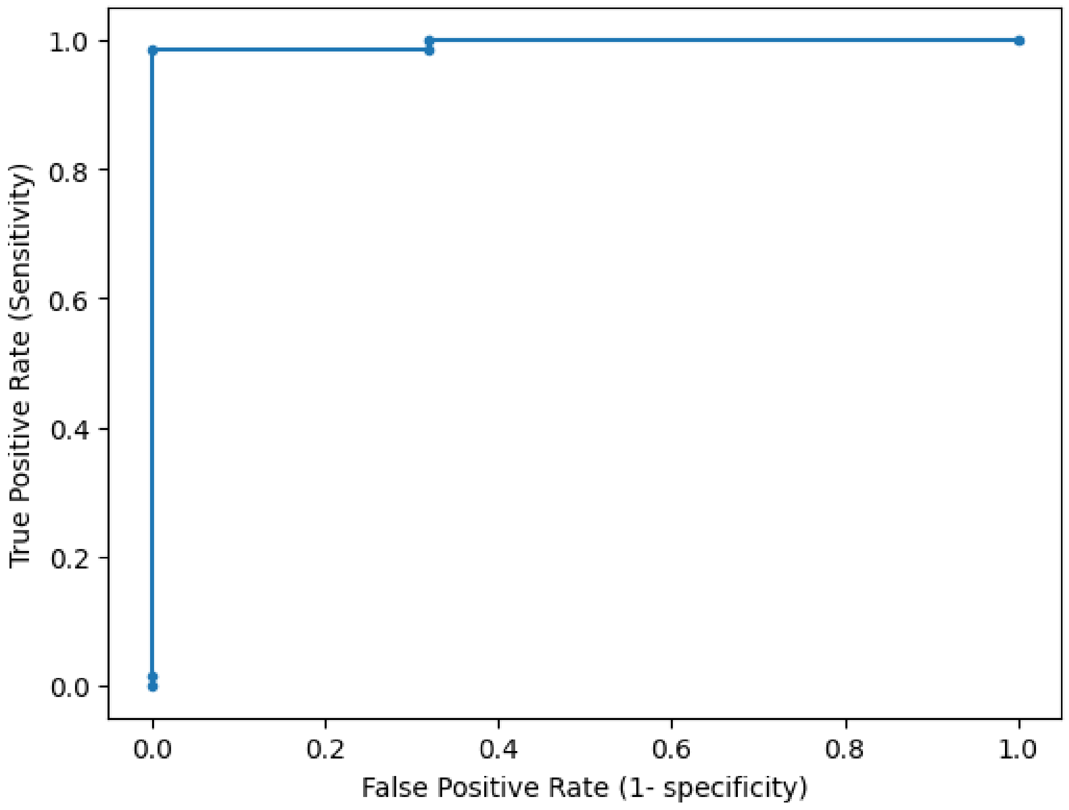
```
from sklearn.metrics import confusion_matrix, classification_report, roc_curve, roc_auc_score
```

```
fpr, tpr, thresholds = roc_curve(df_logit.y_test, df_logit.prob0)
```

```
# AUC
roc_auc_score(df_logit.y_test, df_logit.prob0)
```

```
0.9954285714285713
```

```
# plot the roc curve for the model
plt.plot(fpr, tpr, marker='.', label='Logistic')
plt.xlabel('False Positive Rate (1- specificity)')
plt.ylabel('True Positive Rate (Sensitivity)')

plt.show()
```



ROC Analysis of Binary Classifier (Youden’s J statistic)

```
j_statistic = tpr - fpr
optimal_index = np.argmax(j_statistic)
optimal_threshold = thresholds[optimal_index]
optimal_threshold
```

```
0.2872090139237359
```

```
ind = np.where(np.isclose(thresholds, optimal_threshold, atol=0.001))
print(tpr[ind])
print(1-fpr[ind])
```

```
[0.98571429]
[1.]
```

ROC Analysis of Binary Classifier (Kolmogorov–Smirnov statistic)

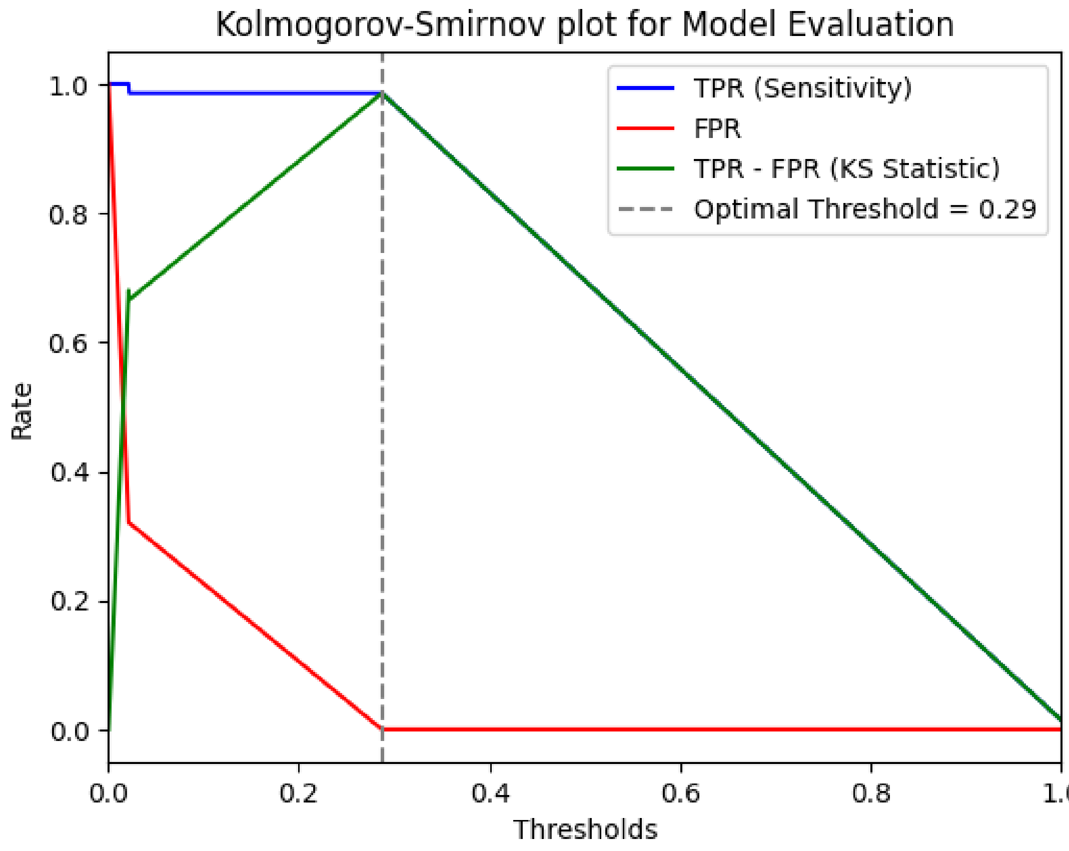
```
ks_statistic = np.max(tpr - fpr)
ks_threshold = thresholds[np.argmax(tpr - fpr)]
ks_threshold
```

```
0.2872090139237359
```

```
ind = np.where(np.isclose(thresholds, ks_threshold, atol=0.001))
print(tpr[ind])
print(1-fpr[ind])
```

```
[0.98571429]
[1.]
```

```
plt.plot(thresholds, tpr, label='TPR (Sensitivity)', color='blue')
plt.plot(thresholds, fpr, label='FPR', color='red')
plt.plot(thresholds, tpr - fpr, label='TPR - FPR (KS Statistic)', color='green')
plt.axvline(x=ks_threshold, color='grey', linestyle='--', label=f'Optimal Threshold = {ks_thres
plt.title('Kolmogorov-Smirnov plot for Model Evaluation')
plt.xlabel('Thresholds')
plt.ylabel('Rate')
plt.legend()
plt.xlim([0.0, 1.0])
#plt.gca().invert_xaxis()
plt.show()
```



The area under the ROC curve (AUC) is around 99.54% indicates that the model has excellent discriminatory power. From the result of Youden's J statistics and Kolmogorov-Smirnov statistics, the optimal probability cut-off point is at around 0.2878.

```
from patsy import dmatrices, dmatrix
import statsmodels.api as sm
from sklearn.linear_model import LinearRegression
from sklearn.metrics import confusion_matrix, classification_report
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score
```

choose optimal threshold

```
# Create a data frame with predicted probabilities (for default) and the class labels in the te
df_logit = pd.DataFrame(
    data = {'prob0': pred_prob[:,1], 'y_test': y_test}
    )

# Use cutoff = threshold and compute misclassification error, sensitivity, and specificity.
df_logit['y_test_pred'] = df_logit.prob0.map(lambda x: 1 if x>ks_threshold else 0)
```

```
cm = confusion_matrix(df_logit.y_test, df_logit.y_test_pred)
print('Confusion Matrix : \n', cm)

total = sum(sum(cm))
accuracy = (cm[0,0]+cm[1,1])/total
print ('Accuracy : ', accuracy)
```

```
Confusion Matrix :
 [[50  0]
 [ 2 68]]
Accuracy :  0.9833333333333333
```

```
sensitivity = cm[1,1]/(cm[1,0]+cm[1,1])
print('Sensitivity : ', sensitivity)

specificity = cm[0,0]/(cm[0,0]+cm[0,1])
print('Specificity : ', specificity )
```

```
Sensitivity :  0.9714285714285714
Specificity :  1.0
```

Using all features from the dataset, the ROC curve illustrates the trade-off between sensitivity (true positive rate) and specificity (true negative rate). The logistic regression model achieves an accuracy of 98.3% at the optimal threshold.

Classifier II: Random forest

For random forests, we use grid search to find the optimal values for the number of estimators, maximum depth, and minimum sample split.

```python
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import GridSearchCV
```

Parameter Selection:

```python
import warnings
warnings.filterwarnings("ignore")

from sklearn.model_selection import GridSearchCV

param_grid = {
    'n_estimators': list(range(0, 200, 20)),
    'max_depth': [None,list(range(1, 20, 5))],
    'min_samples_split': list(range(1, 10, 1))
}

rf = RandomForestClassifier(random_state=1)

grid_search = GridSearchCV(rf, param_grid, cv=5)
grid_search.fit(X_train, y_train)
print(grid_search.best_params_)
```

```
best_rf = grid_search.best_estimator_
y_test_pred = best_rf.predict(X_test)
```

```
{'max_depth': None, 'min_samples_split': 3, 'n_estimators': 120}
```

Model training and prediction:

```
rf = RandomForestClassifier(max_depth=None, min_samples_split=3,n_estimators=120)
```

```
rf.fit(X_train,y_train)
y_test_pred = rf.predict(X_test)
```

Probability of each class predicted by the test set:

```
pred_prob = rf.predict_proba(X_test)
df_rf = pd.DataFrame(data = {'prob0': pred_prob[:,1], 'y_test': y_test})
```

```
fpr, tpr, thresholds = roc_curve(df_rf.y_test, df_rf.prob0)
```

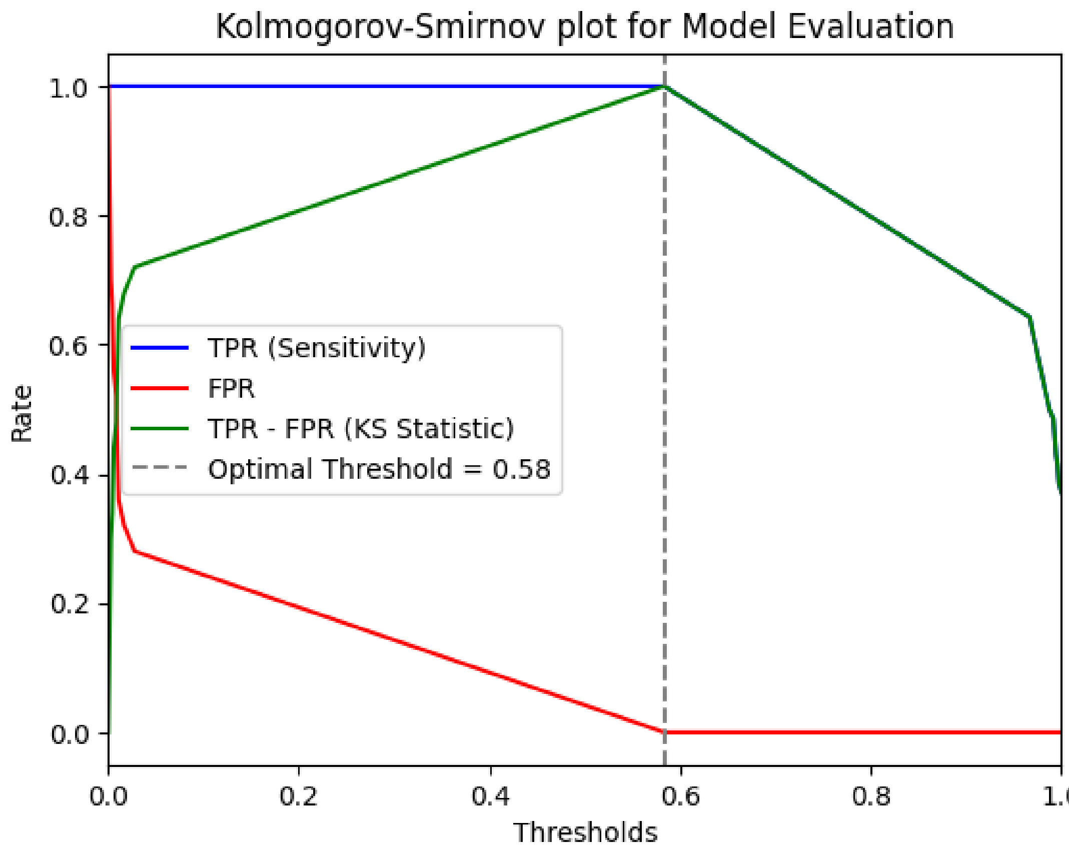
```
ks_statistic = np.max(tpr - fpr)
ks_threshold = thresholds[np.argmax(tpr - fpr)]
ks_threshold
```

```
0.5833333333333334
```

```
ind = np.where(np.isclose(thresholds, ks_threshold, atol=0.001))
print(tpr[ind])
print(1-fpr[ind])
```

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

```
plt.plot(thresholds, tpr, label='TPR (Sensitivity)', color='blue')
plt.plot(thresholds, fpr, label='FPR', color='red')
plt.plot(thresholds, tpr - fpr, label='TPR - FPR (KS Statistic)', color='green')
plt.axvline(x=ks_threshold, color='grey', linestyle='--', label=f'Optimal Threshold = {ks_thres
plt.title('Kolmogorov-Smirnov plot for Model Evaluation')
plt.xlabel('Thresholds')
plt.ylabel('Rate')
plt.legend()
plt.xlim([0.0, 1.0])
#plt.gca().invert_xaxis()
plt.show()
```



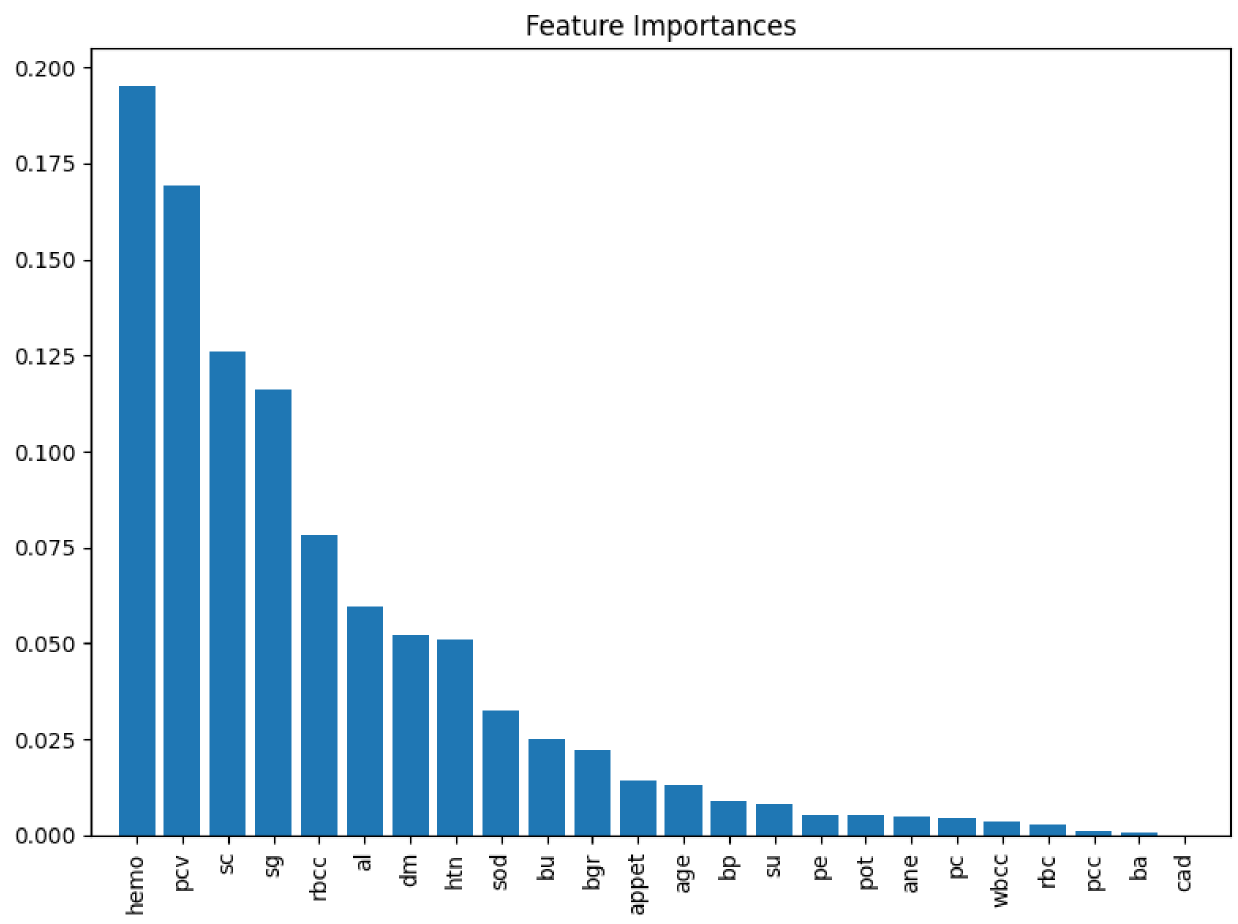
```
# Use cutoff = threshold and compute misclassification error, sensitivity, and specificity.
df_rf['y_test_pred'] = df_rf.prob0.map(lambda x: 1 if x>ks_threshold else 0)
```

```
cm = confusion_matrix(df_rf.y_test, df_rf.y_test_pred)
print('Confusion Matrix : \n', cm)

total = sum(sum(cm))
accuracy = np.trace(cm) / np.sum(cm)
print ('Accuracy : ', accuracy)
```

```
Confusion Matrix :
 [[50  0]
 [ 1 69]]
Accuracy :  0.9916666666666667
```

Features Selection:

```
importances = best_rf.feature_importances_

feature_names = X_train.columns

indices = np.argsort(importances)[::-1]

plt.figure(figsize=(8, 6))
plt.title("Feature Importances")
plt.bar(range(X_train.shape[1]), importances[indices], align="center")
plt.xticks(range(X_train.shape[1]), feature_names[indices], rotation=90)
plt.xlim([-1, X_train.shape[1]])
plt.tight_layout()
plt.show()
```



Using all features from the dataset, the ROC curve illustrates the trade-off between sensitivity (true positive rate) and specificity (true negative rate). The random forest model achieves an accuracy of 99.167% at the optimal threshold.

We can try with Elastic Net

```
from sklearn.linear_model import Ridge, Lasso, ElasticNet, RidgeCV, LassoCV, ElasticNetCV
```

```
enet_cv = ElasticNetCV(cv=10, random_state=1)
enet_cv.fit(X_train, y_train)
```

```
ElasticNetCV(cv=10, random_state=1)
```

```
from sklearn.metrics import mean_squared_error
```

```
#test MSE associated with this value of $\lambda$ and $l1_ratio$
m_enet =ElasticNet(alpha=enet_cv.alpha_, l1_ratio=enet_cv.l1_ratio_)
m_enet.fit(X_train, y_train)
m_enet_pre = m_enet.predict(X_test)
np.sqrt(mean_squared_error(y_test, m_enet_pre))
```

```
0.2858361665891256
```

```
pd.DataFrame({'Feature': X_train.columns, 'Coefficient': m_enet.coef_.reshape(len(X_train.colu
```

	Feature	Coefficient
0	age	0.010934
1	bp	0.026887
2	sg	-0.000000
3	al	0.054397
4	su	0.005206
5	rbc	0.000000
6	pc	0.000000
7	pcc	0.000000
8	ba	-0.000000
9	bgr	0.034062
10	bu	-0.069892
11	sc	0.046177
12	sod	-0.052905
13	pot	-0.009485
14	hemo	-0.186465
15	pcv	-0.038239
16	wbcc	0.013581
17	rbcc	-0.036926

	Feature	Coefficient
18	htn	0.039218
19	dm	0.164746
20	cad	-0.030368
21	appet	-0.006058
22	pe	0.000000
23	ane	-0.050048

Based on the analysis above, [`age`, `bp`, `al`, `su`, `bgr`, `bu`, `sc`, `sod`, `pot`, `hemo`, `pcv`, `wbcc`, `rbcc`, `htn`, `dm`, `cad`, `appet`, `ane`] are important features.

```
sel_col = ['age', 'bp', 'al', 'su', 'bgr', 'bu', 'sc', 'sod', 'pot', 'hemo', 'pcv', 'wbcc', 'r
X_train_elastic_net = X_train[sel_col]
```

```
from sklearn import metrics
X_test_elastic_net = X_test[sel_col]
EN_log = LogisticRegression(max_iter = 500)
EN_log.fit(X_train_elastic_net, y_train)
EN_test = EN_log.predict(X_test_elastic_net)
np.sqrt(metrics.mean_squared_error(y_test, EN_test))
```

```
0.18257418583505536
```

use feature selection to do logistic again

```
# use feature selection to do logistic again
EN_log = LogisticRegression(max_iter = 500)
EN_log.fit(X_train_elastic_net, y_train)
pred_prob = EN_log.predict_proba(X_test_elastic_net)
df_pro = pd.DataFrame(data = {'prob': pred_prob[:,1], 'y_test': y_test})
EN_df_logit = pd.DataFrame(
    data = {'prob0': pred_prob[:,1], 'y_test': y_test}
    )
fpr, tpr, thresholds = roc_curve(EN_df_logit.y_test, EN_df_logit.prob0)
```

```
ks_statistic = np.max(tpr - fpr)
ks_threshold = thresholds[np.argmax(tpr - fpr)]
ks_threshold
```

```
0.3054643741096191
```

```
# Use cutoff = 0.3052 and compute misclassification error, sensitivity, and specificity.
EN_df_logit['y_test_pred'] = EN_df_logit.prob0.map(lambda x: 1 if x>0.3052 else 0)
```

```
cm = confusion_matrix(EN_df_logit.y_test, EN_df_logit.y_test_pred)
print('Confusion Matrix : \n', cm)

total = sum(sum(cm))
accuracy = (cm[0,0]+cm[1,1])/total
print ('Accuracy : ', accuracy)
```

```
Confusion Matrix :
 [[50  0]
 [ 1 69]]
Accuracy :  0.9916666666666667
```

Elastic net successfully achieves shrinkage through feature selection and extraction while accuracy also increased from 98.3% to 99.2%.

Let’s try Sequential Forward Selection for logistic regression

```
from mlxtend.feature_selection import ExhaustiveFeatureSelector as EFS
from mlxtend.feature_selection import SequentialFeatureSelector as SFS
from mlxtend.plotting import plot_sequential_feature_selection as plot_sfs
```

```
def_log = LogisticRegression(max_iter = 500)
def_log.fit(X_train, y_train)
d_l_test = def_log.predict(X_test)
```

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

```
0.18257418583505536
```

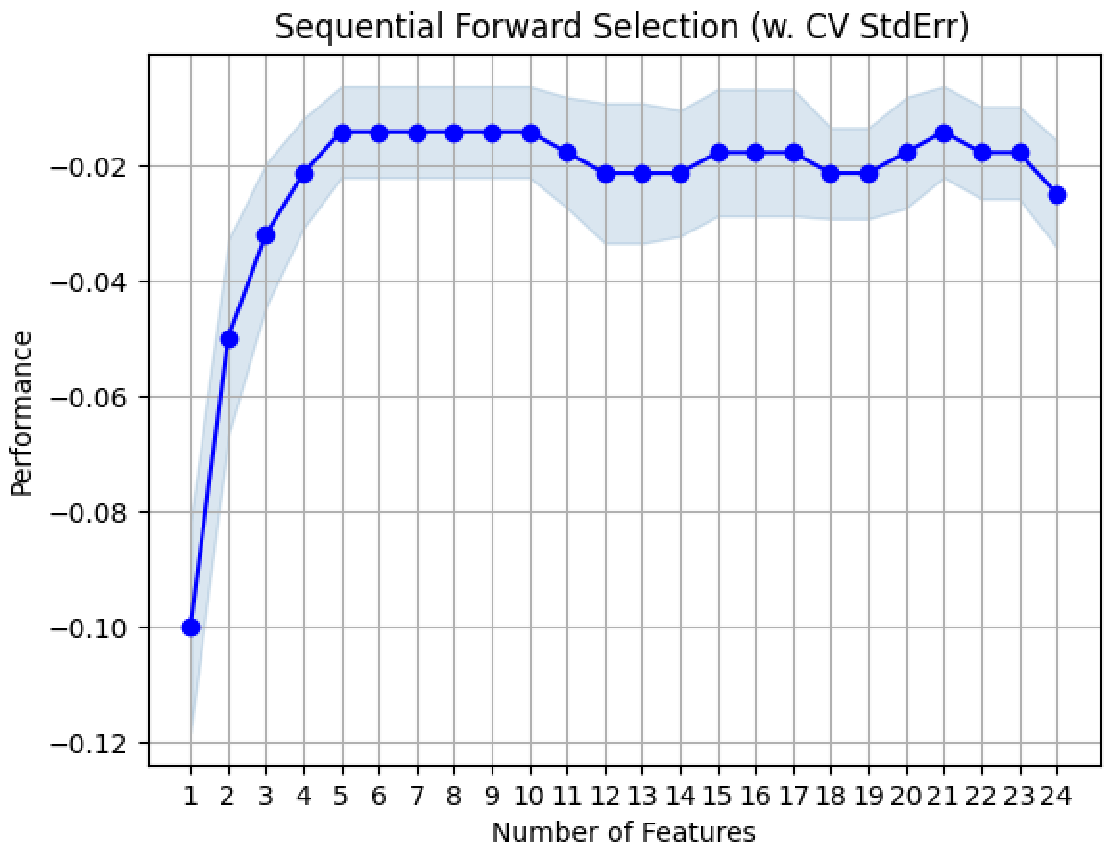
```
df_feature.shape
```

```
(400, 24)
```

```
sfs = SFS(
    def_log,
    k_features=(1,df_feature.shape[1]),
    forward=True,
    floating=False,
    scoring='neg_mean_squared_error',
    cv=10
    )
```

```
sfs = sfs.fit(X_train, y_train)
```

```
fig = plot_sfs(sfs.get_metric_dict(), kind='std_err')


plt.title('Sequential Forward Selection (w. CV StdErr)')
plt.grid()
plt.show()
```



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

```
Index(['al', 'su', 'sc', 'pot', 'hemo'], dtype='object')
```

By feature selection, [‘al’, ‘su’, ‘sc’, ‘pot’, ‘hemo’] are chosen

```
# Prediction on hold-out set
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_log = LogisticRegression(max_iter = 500)
sfs_log.fit(X_train_sfs, y_train)
sfs_test = sfs_log.predict(X_test_sfs)
np.sqrt(metrics.mean_squared_error(y_test, sfs_test))
```

```
0.2041241452319315
```

```
# use feature selection to do logistic again
sfs_log = LogisticRegression(max_iter = 500)
sfs_log.fit(X_train_sfs, y_train)
pred_prob = sfs_log.predict_proba(X_test_sfs)
df_pro = pd.DataFrame(data = {'prob': pred_prob[:,1], 'y_test': y_test})
sfs_df_logit = pd.DataFrame(
    data = {'prob0': pred_prob[:,1], 'y_test': y_test}
    )
fpr, tpr, thresholds = roc_curve(sfs_df_logit.y_test, sfs_df_logit.prob0)
```

```
# AUC
roc_auc_score(sfs_df_logit.y_test, sfs_df_logit.prob0)
```

```
0.9925714285714284
```

```
ks_statistic = np.max(tpr - fpr)
ks_threshold = thresholds[np.argmax(tpr - fpr)]
ks_threshold
```

```
0.42263344889380317
```

```
# Use cutoff = 0.287 and compute misclassification error, sensitivity, and specificity.
sfs_df_logit['y_test_pred'] = sfs_df_logit.prob0.map(lambda x: 1 if x>0.4228 else 0)
```

```
cm = confusion_matrix(sfs_df_logit.y_test, sfs_df_logit.y_test_pred)
print('Confusion Matrix : \n', cm)

total = sum(sum(cm))
accuracy = (cm[0,0]+cm[1,1])/total
print ('Accuracy : ', accuracy)
```

```
Confusion Matrix :
 [[50  0]
 [ 5 65]]
Accuracy :  0.9583333333333334
```

It's evident that the final performance of logistic-based sequential forward selection is not as good as Elastic Net. Therefore, we will choose the results of Elastic Net as Elastic net successfully achieves shrinkage through feature selection and extraction while accuracy also increased from 98.3% to 99.2%.

sel_col = [`age`, `bp`, `al`, `su`, `bgr`, `bu`, `sc`, `sod`, `pot`, `hemo`, `pcv`, `wbcc`, `rbcc`, `htn`, `dm`, `cad`, `appet`, `ane`]

For Random Forest, if we choose features from Elastic Net.

```python
import warnings
warnings.filterwarnings("ignore")

from sklearn.model_selection import GridSearchCV

param_grid = {
    'n_estimators': list(range(0, 200, 20)),
    'max_depth': [None,list(range(0, 20, 5))],
    'min_samples_split': list(range(1, 10, 1))
}

rf = RandomForestClassifier(random_state=1)

grid_search = GridSearchCV(rf, param_grid, cv=5)
grid_search.fit(X_train_elastic_net, y_train)
print(grid_search.best_params_)

best_rf = grid_search.best_estimator_
y_test_pred = best_rf.predict(X_test_elastic_net)
```

```
{'max_depth': None, 'min_samples_split': 3, 'n_estimators': 40}
```

```
rf = RandomForestClassifier(max_depth=None, min_samples_split=3, n_estimators=40)
rf.fit(X_train_elastic_net,y_train)
pred_prob = rf.predict_proba(X_test_elastic_net)
df_rf = pd.DataFrame(data = {'prob0': pred_prob[:,1], 'y_test': y_test})
```

```
fpr, tpr, thresholds = roc_curve(df_rf.y_test, df_rf.prob0)
```

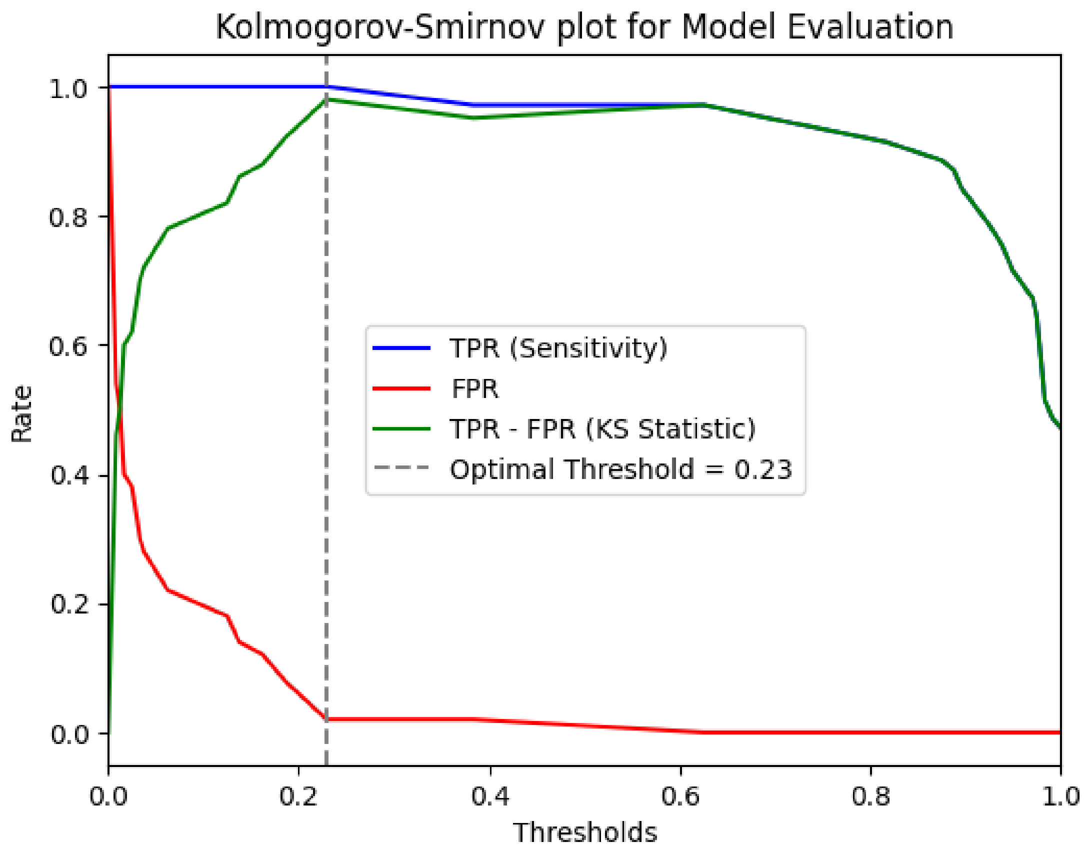
```
ks_statistic = np.max(tpr - fpr)
ks_threshold = thresholds[np.argmax(tpr - fpr)]
ks_threshold
```

```
0.22916666666666666
```

```
ind = np.where(np.isclose(thresholds, ks_threshold, atol=0.001))
print(tpr[ind])
print(1-fpr[ind])
```

```
[1.]
[0.98]
```

```
plt.plot(thresholds, tpr, label='TPR (Sensitivity)', color='blue')
plt.plot(thresholds, fpr, label='FPR', color='red')
plt.plot(thresholds, tpr - fpr, label='TPR - FPR (KS Statistic)', color='green')
plt.axvline(x=ks_threshold, color='grey', linestyle='--', label=f'Optimal Threshold = {ks_thre
plt.title('Kolmogorov-Smirnov plot for Model Evaluation')
plt.xlabel('Thresholds')
plt.ylabel('Rate')
plt.legend()
plt.xlim([0.0, 1.0])
#plt.gca().invert_xaxis()
plt.show()
```



```
# Use cutoff = threshold and compute misclassification error, sensitivity, and specificity.
df_rf['y_test_pred'] = df_rf.prob0.map(lambda x: 1 if x>ks_threshold else 0)
```

```
cm = confusion_matrix(df_rf.y_test, df_rf.y_test_pred)
print('Confusion Matrix : \n', cm)


total = sum(sum(cm))
accuracy = (cm[0,0]+cm[1,1])/total
print ('Accuracy : ', accuracy)
```

```
Confusion Matrix :
 [[49  1]
 [ 1 69]]
Accuracy :  0.9833333333333333
```

By employing Elastic Net feature selection, it appears that random forest does not perform well. Therefore Random forest should use original dataset.

Finding:

Based on ROC-derived optimal thresholds and testing the prediction results of logistic regression and random forest, we found that after elastic net feature selection, logistic regression achieved a superior accuracy of 99.167%.
Confusion Matrix:
[50 0]
[1 69]

The random forest model, utilizing the full feature set, also delivered a similar accuracy with an identical confusion matrix.
Confusion Matrix:
[50 0]
[1 69]

This parallel in performance suggests that both models are performing exceptionally well. However, in keeping with the principle of Occam's razor, the logistic regression model, which maintains high accuracy with a reduced feature set post elastic net regularization, is deemed more efficient and is therefore the preferable model.

We also attempted sequential forward selection based on logistic regression, but the final accuracy was even lower than before selection. This indicates that different feature selection methods are suitable for different datasets, and the appropriate data science method for feature selection should be chosen based on the characteristics of the dataset.

13. Interpretable Classifier Insight

```
# features from elastic net
sel_col = ['al', 'su', 'sc', 'pot', 'hemo']
```

```
# re-training the interpretable classifier with all available data
model = sm.Logit(df_target,df[sel_col]).fit()
```

```
Warning: Maximum number of iterations has been exceeded.
         Current function value: 0.113334
         Iterations: 35
```

```
model.summary()
```

Dep. Variable:	class	**No. Observations:**	400
Model:	Logit	**Df Residuals:**	395
Method:	MLE	**Df Model:**	4
Date:	Thu, 18 Apr 2024	**Pseudo R-squ.:**	0.8287
Time:	14:08:41	**Log-Likelihood:**	-45.334
converged:	False	**LL-Null:**	-264.63
Covariance Type:	nonrobust	**LLR p-value:**	1.276e-93

	coef	**std err**	**z**	**P> |z|**	**[0.025**	**0.975]**
al	23.9086	8131.221	0.003	0.998	-1.59e+04	1.6e+04
su	13.8046	1.76e+05	7.84e-05	1.000	-3.45e+05	3.45e+05
sc	1.0387	0.345	3.011	0.003	0.363	1.715
pot	-0.3635	0.371	-0.979	0.328	-1.091	0.364
hemo	-4.5635	0.844	-5.405	0.000	-6.218	-2.909

Possibly complete quasi-separation: A fraction 0.44 of observations can be
perfectly predicted. This might indicate that there is complete
quasi-separation. In this case some parameters will not be identified.

`al` and `su` have really large coefficients, but their p-values are high, close to 1, indicating unreliable coefficient estimates possibly due to fitting issues.

The coefficient of `sc` is positive and p-value is really small, indicating a significant effect on the classification outcome while controlling for other variables. serum creatinine level could be an important predictor with a high correlation to the classification of kidney disease.

The coefficient of `hemo` is negative p-value is really small, indicating a significant effect on the classification outcome while controlling for other variables. hemoglobin could be an important predictor with a high negative correlation to the classification of kidney disease.

14. [Bonus] Sub-group Improvement Strategy

For sub-group analysis we did in previous part, K=2 proforms well. We want to apply logistic regression, but this solver needs samples of at least 2 classes in the data, but the data contains only one class: 1.0.

Therefore we try random forest here.

```
pca = PCA(n_components = 3)
# K = 2
km1 = KMeans(n_clusters=2, n_init=20, random_state=1)
km1.fit(df_pca)
```

```
KMeans(n_clusters=2, n_init=20, random_state=1)
```

```
# add K=2 cluster labels to df
df['cluster'] = km1.labels_

# seperate cluster
cluster_0 = df[df['cluster'] == 0]
cluster_1 = df[df['cluster'] == 1]
```

```
from sklearn.ensemble import RandomForestClassifier

# rf train each cluster
rf_cluster_0 = RandomForestClassifier()
rf_cluster_1 = RandomForestClassifier()

# split
```

```python
X_cluster_0 = cluster_0.drop(['class', 'cluster'], axis=1)
y_cluster_0 = cluster_0['class']
X_cluster_1 = cluster_1.drop(['class', 'cluster'], axis=1)
y_cluster_1 = cluster_1['class']

# train model
rf_cluster_0.fit(X_cluster_0, y_cluster_0)
rf_cluster_1.fit(X_cluster_1, y_cluster_1)
```

```
RandomForestClassifier()
```

```python
from sklearn.metrics import accuracy_score

# calculate accuracy
y_test_pred_cluster_0 = rf_cluster_0.predict(X_test)
accuracy_cluster_0 = accuracy_score(y_test, y_test_pred_cluster_0)

y_test_pred_cluster_1 = rf_cluster_1.predict(X_test)
accuracy_cluster_1 = accuracy_score(y_test, y_test_pred_cluster_1)

print("Accuracy for Cluster 0:", accuracy_cluster_0)
print("Accuracy for Cluster 1:", accuracy_cluster_1)
```

```
Accuracy for Cluster 0: 0.5833333333333334
Accuracy for Cluster 1: 1.0
```

We found that after performing PCA on the dataset and conducting subgroup analysis using K-means with K=2, cluster 01 exhibited excellent performance in random forest, achieving a prediction accuracy of 100%. This suggests that PCA and clustering techniques may improve the performance of one classifier.

15. Team Contributions

Lingyun Huang: P.1: read dataset from repository_url | P.2: Categorical variables transformation | P.4 heatmap, added VIF | P5: missing value | P.6:outlier, handling outliers and plotting | P.7: PCA, PCA plot, add PCA loading, K-mean plot, Hierarchical clustering for visualization, Rand score | P.8: Data Splitting | P.9: text | P.10: add confusion matrix+sensitivity+specificity, ROC, logistic regression, grid search+RF | P. 11: feature selection+Elastic Net+SFS | P.12 text Classifier Comparison | P.13 interpret the significance of predictor variables | P.14: sub group analysis+P14Sub-group Improvement Strategy

Xiangdong Wang: 1. Identified the classification problem. 2. Conducted Variable transformations. 3. Analyzed data overview (according to distribution). 4. Analyzed correlation matrix. 5. Processed missing values. 6. Discussed potential data science methods for finding subgroups. Examples include Hierarchical clustering and K-Mean. Implemented K-Mean and PCA in Subgroup Analysis and visualized the result of K-mean. 7. Discussed the classifier options 8. Analyzed Random Forest in Classifier Comparison

Jingyang Li: 1. Fix the classification problem, issuing the roc labelling problem and fixed it, 2. Outlier analysis and box plot created and fixed, 3. Analyze matrix fixed and statement made, 4. Random forest in classifier comparison, 5. Random forest revamp and interpretation added, 6. K-means updated, hierarchical clustering updated 7. Help sub group analysis and accuracy comparision. 8. PCA comparison, 9. Model and code check, import and install packages for name error and undefined function.

16. Link to the public GitHub repository

https://github.com/Barkesty/Project-Chronic-Kidney-Disease-Classification-Challenge.git