STATS 3DA3

Homework Assignment 6

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Q1:

```python
from ucimlrepo import fetch_ucirepo

# fetch dataset
chronic_kidney_disease = fetch_ucirepo(id=336)

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

# metadata
print(chronic_kidney_disease.metadata)

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

```
{'uci_id': 336, 'name': 'Chronic Kidney Disease', 'repository_url': 'https://archive.ics.uci.e
     name     role         type demographic              description  \
0     age  Feature      Integer         Age                     None
1      bp  Feature      Integer        None           blood pressure
2      sg  Feature  Categorical        None         specific gravity
3      al  Feature  Categorical        None                  albumin
4      su  Feature  Categorical        None                    sugar
5     rbc  Feature       Binary        None          red blood cells
6      pc  Feature       Binary        None                 pus cell
7     pcc  Feature       Binary        None          pus cell clumps
8      ba  Feature       Binary        None                 bacteria
9     bgr  Feature      Integer        None    blood glucose random
10     bu  Feature      Integer        None               blood urea
11     sc  Feature   Continuous        None         serum creatinine
12    sod  Feature      Integer        None                   sodium
```

```
13    pot  Feature  Continuous        None                potassium
14   hemo  Feature  Continuous        None               hemoglobin
15    pcv  Feature     Integer        None        packed cell volume
16   wbcc  Feature     Integer        None   white blood cell count
17   rbcc  Feature  Continuous        None     red blood cell count
18    htn  Feature      Binary        None             hypertension
19     dm  Feature      Binary        None        diabetes mellitus
20    cad  Feature      Binary        None  coronary artery disease
21  appet  Feature      Binary        None                 appetite
22     pe  Feature      Binary        None              pedal edema
23    ane  Feature      Binary        None                   anemia
24  class   Target      Binary        None           ckd or not ckd

            units missing_values
0            year            yes
1           mm/Hg            yes
2            None            yes
3            None            yes
4            None            yes
5            None            yes
6            None            yes
7            None            yes
8            None            yes
9          mgs/dl            yes
10         mgs/dl            yes
11         mgs/dl            yes
12          mEq/L            yes
13          mEq/L            yes
14            gms            yes
15           None            yes
16      cells/cmm            yes
17   millions/cmm            yes
```

```
18           None             yes
19           None             yes
20           None             yes
21           None             yes
22           None             yes
23           None             yes
24           None              no
```

The classification problem using the dataset is to predict whether a patient has chronic kidney disease (CKD) based on 24 medical attributes including age, blood pressure, blood glucose, and more. The target variable is “class” which indicates if the patient has CKD (“ckd”) or not (“notckd”).

Q2:

```
from ucimlrepo import fetch_ucirepo
from sklearn.model_selection import train_test_split
from sklearn.impute import SimpleImputer
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline
from sklearn.ensemble import RandomForestClassifier

chronic_kidney_disease = fetch_ucirepo(id=336)

X = chronic_kidney_disease.data.features
y = chronic_kidney_disease.data.targets

numeric_features = [col for col, dtype in zip(X.columns, X.dtypes) if dtype in ['int64', 'floa
categorical_features = [col for col in X.columns if col not in numeric_features]

numeric_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='median')),
    ('scaler', StandardScaler())])
```

```
categorical_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='most_frequent')),
    ('onehot', OneHotEncoder(handle_unknown='ignore'))])

preprocessor = ColumnTransformer(
    transformers=[
        ('num', numeric_transformer, numeric_features),
        ('cat', categorical_transformer, categorical_features)])

pipeline = Pipeline(steps=[
    ('preprocessor', preprocessor),
    ('classifier', RandomForestClassifier(random_state=42))])

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

pipeline.fit(X_train, y_train)

accuracy = pipeline.score(X_test, y_test)
print("Model training complete.")
print("Model accuracy on test set: {:.2f}%".format(accuracy * 100))
```

```
Model training complete.
Model accuracy on test set: 100.00%

d:\python\Lib\site-packages\sklearn\base.py:1474: DataConversionWarning: A column-vector y was
  return fit_method(estimator, *args, **kwargs)
```

Q3:

Variables and Data Types:The dataset consists of 24 features and one target variable “class”: Categorical features: Include specific gravity (sg), albumin (al), sugar (su), red blood cells (rbc), pus cell (pc), pus cell clumps (pcc), so on and The target variable, class, categorizes individuals into "ckd" (chronic kidney disease) or "notckd" groups. The set has 400 cases, 250 of which have label 'ckd', and other 150 which are tagged 'notckd', which may require model operators to slightly adjust the algorithms and strategies for training in order to eliminate the bias related to imbalanced class. Dissemination of categorical features likely such "hypertension" and "diabetes mellitus", which have higher prevalence within the "ckd" category, have probably been referenced to show their association with kidney health.

Q4:

Serum creatinine (sCreat) and blood urea (BUN) are not only considered waste products washed out from the blood by the kidneys in the process of clearance. If these variables show high correlation, elimination of one might not be a matter to discuss because the other variable can cover its lack. Diabetes mellitus (dm), which is a known risk factor for chronic kidney disease (ckd), may significantly influence levels of blood glucose random (bmr) and hemoglobine (hemed). Building interaction terms between 'dm' and 'bgr', akala ko, 'dm' and 'hemo' may be a sign of considering the total effect of diabetes on these blood variables. This would likely enhance the model's operations to forecast CKD in those who are already diabetic. Similarly, htn may often accompany CKD and causes elevated bp levels and sometimes could lead to chronic kidney diseases as indicated by the increased serum creatinine levels. The study of links between hypertension, blood pressure and serum creatinine could be helpful and maybe it could be algorightmized as a predictive factor of chronic kidney disease (CKD).

Q5:

```python
from ucimlrepo import fetch_ucirepo





# Check for missing values in the features
missing_values_count = X.isnull().sum()
print("Missing values in each feature:\n", missing_values_count)
```

```
Missing values in each feature:
 age        9
bp         12
sg         47
al         46
su         49
rbc       152
pc         65
pcc         4
ba          4
bgr        44
bu         19
sc         17
sod        87
pot        88
hemo       52
pcv        71
wbcc      106
rbcc      131
htn         2
dm          2
cad         2
appet       1
pe          1
ane         1
dtype: int64
```

```python
from sklearn.impute import SimpleImputer


# Define imputers
# Numeric imputer - using median to avoid influence of outliers
numeric_imputer = SimpleImputer(strategy='median')
# Categorical imputer - using most frequent as it's a common approach for categorical data
```

```python
categorical_imputer = SimpleImputer(strategy='most_frequent')

# Impute numerical columns
numerical_columns = X.select_dtypes(include=['int64', 'float64']).columns
X[numerical_columns] = numeric_imputer.fit_transform(X[numerical_columns])

# Impute categorical columns
categorical_columns = X.select_dtypes(include='object').columns
X[categorical_columns] = categorical_imputer.fit_transform(X[categorical_columns])

# Check if any missing values remain
new_missing_values_count = X.isnull().sum()
print("Missing values after imputation:\n", new_missing_values_count)
```

```
Missing values after imputation:
 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

C:\Users\11831\AppData\Local\Temp\ipykernel_15132\95456835.py:11: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/i
  X[numerical_columns] = numeric_imputer.fit_transform(X[numerical_columns])
C:\Users\11831\AppData\Local\Temp\ipykernel_15132\95456835.py:15: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/i
  X[categorical_columns] = categorical_imputer.fit_transform(X[categorical_columns])
```

Q6:

```python
import pandas as pd



X = X.apply(pd.to_numeric, errors='coerce')

# Now check again for missing values after conversion (these might increase)
missing_after_conversion = X.isnull().sum()
print("Missing values after conversion attempt:\n", missing_after_conversion)
```

```
Missing values after conversion attempt:
 age         0
bp          0
sg          0
al          0
su          0
rbc       400
pc        400
pcc       400
ba        400
bgr         0
bu          0
sc          0
sod         0
pot         0
hemo        0
pcv         0
wbcc        0
rbcc        0
htn       400
dm        400
cad       400
appet     400
pe        400
ane       400
dtype: int64
```

```
# Calculate the IQR (Interquartile Range) to identify outliers
Q1 = X.quantile(0.25)
Q3 = X.quantile(0.75)
IQR = Q3 - Q1
```

```
# Define outliers as those outside of 1.5 * IQR from the Q1 and Q3
outliers = (X < (Q1 - 1.5 * IQR)) | (X > (Q3 + 1.5 * IQR))

# Count outliers in each column
outlier_counts = outliers.sum()
print("Outlier counts in each column:\n", outlier_counts)

# Cap outliers using percentiles
percentiles = X.quantile([0.01, 0.99])
X_capped = X.clip(lower=percentiles.loc[0.01], upper=percentiles.loc[0.99], axis=1)
```

```
Outlier counts in each column:
 age      10
bp       36
sg        7
al        0
su       61
rbc       0
pc        0
pcc       0
ba        0
bgr      53
bu       41
sc       53
sod      18
pot      14
hemo      2
pcv       6
wbcc     17
rbcc     75
htn       0
dm        0
```

```
cad        0
appet      0
pe         0
ane        0
dtype: int64
```

```
print("Data after capping outliers:\n", X_capped.describe())
# Summary statistics before and after capping
```

```
Data after capping outliers:
               age          bp          sg          al          su  rbc   pc  \
count  400.000000  400.000000  400.000000  400.000000  400.000000  0.0  0.0
mean    51.537600   76.300000    1.017712    0.897500    0.387500  NaN  NaN
std     16.864915   12.193511    0.005434    1.306239    1.009898  NaN  NaN
min      5.000000   50.000000    1.005000    0.000000    0.000000  NaN  NaN
25%     42.000000   70.000000    1.015000    0.000000    0.000000  NaN  NaN
50%     55.000000   80.000000    1.020000    0.000000    0.000000  NaN  NaN
75%     64.000000   80.000000    1.020000    2.000000    0.000000  NaN  NaN
max     80.010000  110.000000    1.025000    4.000000    4.000000  NaN  NaN

       pcc   ba         bgr  ...       hemo         pcv          wbcc  \
count  0.0  0.0  400.000000  ...  400.00000  400.000000    400.000000
mean   NaN  NaN  144.709700  ...   12.55124   39.107500   8260.690000
std    NaN  NaN   73.135783  ...    2.68300    8.037079   2273.968995
min    NaN  NaN   70.000000  ...    5.79800   16.990000   4097.000000
25%    NaN  NaN  101.000000  ...   10.87500   34.000000   6975.000000
50%    NaN  NaN  121.000000  ...   12.65000   40.000000   8000.000000
75%    NaN  NaN  150.000000  ...   14.62500   44.000000   9400.000000
max    NaN  NaN  425.220000  ...   17.60100   53.010000  16722.000000

             rbcc  htn   dm  cad  appet   pe  ane
count  400.000000  0.0  0.0  0.0    0.0  0.0  0.0
```

```
mean      4.736740   NaN   NaN   NaN    NaN   NaN   NaN
std       0.822137   NaN   NaN   NaN    NaN   NaN   NaN
min       2.499000   NaN   NaN   NaN    NaN   NaN   NaN
25%       4.500000   NaN   NaN   NaN    NaN   NaN   NaN
50%       4.800000   NaN   NaN   NaN    NaN   NaN   NaN
75%       5.100000   NaN   NaN   NaN    NaN   NaN   NaN
max       6.500000   NaN   NaN   NaN    NaN   NaN   NaN

[8 rows x 24 columns]
```

```
print("Summary statistics before capping:\n", X.describe())
print("Summary statistics after capping:\n", X_capped.describe())
```

```
Summary statistics before capping:
               age          bp          sg         al          su  rbc   pc  \
count  400.000000  400.000000  400.000000  400.00000  400.000000  0.0  0.0
mean    51.562500   76.575000    1.017712    0.90000    0.395000  NaN  NaN
std     16.982996   13.489785    0.005434    1.31313    1.040038  NaN  NaN
min      2.000000   50.000000    1.005000    0.00000    0.000000  NaN  NaN
25%     42.000000   70.000000    1.015000    0.00000    0.000000  NaN  NaN
50%     55.000000   80.000000    1.020000    0.00000    0.000000  NaN  NaN
75%     64.000000   80.000000    1.020000    2.00000    0.000000  NaN  NaN
max     90.000000  180.000000    1.025000    5.00000    5.000000  NaN  NaN

       pcc   ba         bgr  ...       hemo         pcv          wbcc  \
count  0.0  0.0  400.000000  ...  400.00000  400.000000    400.000000
mean   NaN  NaN  145.062500  ...   12.54250   39.082500   8298.500000
std    NaN  NaN   75.260774  ...    2.71649    8.162245   2529.593814
min    NaN  NaN   22.000000  ...    3.10000    9.000000   2200.000000
25%    NaN  NaN  101.000000  ...   10.87500   34.000000   6975.000000
50%    NaN  NaN  121.000000  ...   12.65000   40.000000   8000.000000
75%    NaN  NaN  150.000000  ...   14.62500   44.000000   9400.000000
```

```
max    NaN  NaN  490.000000  ...   17.80000   54.000000  26400.000000

             rbcc  htn   dm  cad  appet   pe  ane
count  400.000000  0.0  0.0  0.0    0.0  0.0  0.0
mean     4.737750  NaN  NaN  NaN    NaN  NaN  NaN
std      0.841439  NaN  NaN  NaN    NaN  NaN  NaN
min      2.100000  NaN  NaN  NaN    NaN  NaN  NaN
25%      4.500000  NaN  NaN  NaN    NaN  NaN  NaN
50%      4.800000  NaN  NaN  NaN    NaN  NaN  NaN
75%      5.100000  NaN  NaN  NaN    NaN  NaN  NaN
max      8.000000  NaN  NaN  NaN    NaN  NaN  NaN

[8 rows x 24 columns]
Summary statistics after capping:
              age          bp          sg          al          su  rbc   pc  \
count  400.000000  400.000000  400.000000  400.000000  400.000000  0.0  0.0
mean    51.537600   76.300000    1.017712    0.897500    0.387500  NaN  NaN
std     16.864915   12.193511    0.005434    1.306239    1.009898  NaN  NaN
min      5.000000   50.000000    1.005000    0.000000    0.000000  NaN  NaN
25%     42.000000   70.000000    1.015000    0.000000    0.000000  NaN  NaN
50%     55.000000   80.000000    1.020000    0.000000    0.000000  NaN  NaN
75%     64.000000   80.000000    1.020000    2.000000    0.000000  NaN  NaN
max     80.010000  110.000000    1.025000    4.000000    4.000000  NaN  NaN

       pcc   ba         bgr  ...       hemo         pcv          wbcc  \
count  0.0  0.0  400.000000  ...  400.00000  400.000000    400.000000
mean   NaN  NaN  144.709700  ...   12.55124   39.107500   8260.690000
std    NaN  NaN   73.135783  ...    2.68300    8.037079   2273.968995
min    NaN  NaN   70.000000  ...    5.79800   16.990000   4097.000000
25%    NaN  NaN  101.000000  ...   10.87500   34.000000   6975.000000
50%    NaN  NaN  121.000000  ...   12.65000   40.000000   8000.000000
75%    NaN  NaN  150.000000  ...   14.62500   44.000000   9400.000000
```

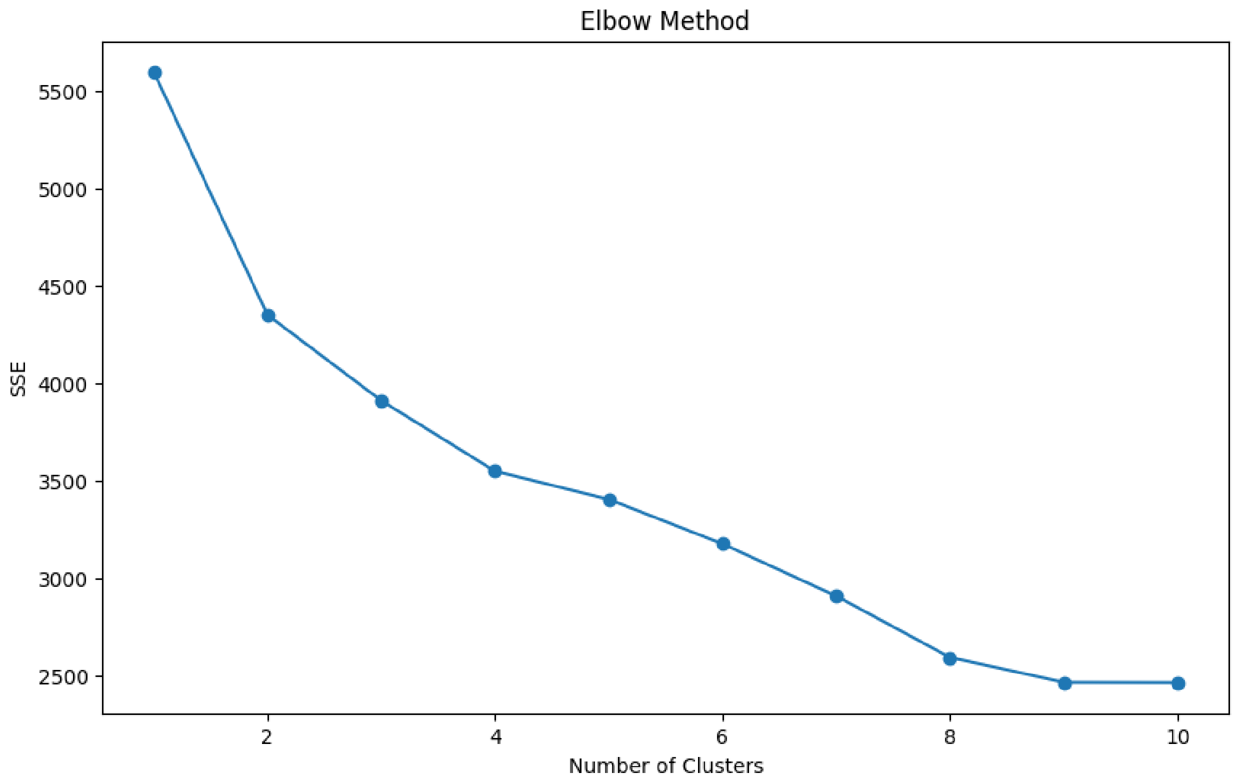
```
max     NaN  NaN  425.220000  ...   17.60100   53.010000  16722.000000

             rbcc  htn   dm  cad  appet   pe  ane
count  400.000000  0.0  0.0  0.0    0.0  0.0  0.0
mean     4.736740  NaN  NaN  NaN    NaN  NaN  NaN
std      0.822137  NaN  NaN  NaN    NaN  NaN  NaN
min      2.499000  NaN  NaN  NaN    NaN  NaN  NaN
25%      4.500000  NaN  NaN  NaN    NaN  NaN  NaN
50%      4.800000  NaN  NaN  NaN    NaN  NaN  NaN
75%      5.100000  NaN  NaN  NaN    NaN  NaN  NaN
max      6.500000  NaN  NaN  NaN    NaN  NaN  NaN

[8 rows x 24 columns]
```

Q7:

```python
from sklearn.impute import SimpleImputer
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import Pipeline
from sklearn.compose import ColumnTransformer
from sklearn.preprocessing import OneHotEncoder

# Identify numerical and categorical columns
numerical_cols = X.select_dtypes(include=['int64', 'float64']).columns
categorical_cols = X.select_dtypes(include=['object', 'category']).columns

# Create pipelines for the different column types
numeric_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='median')),
    ('scaler', StandardScaler())
])

categorical_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='constant', fill_value='missing')),
    ('onehot', OneHotEncoder(handle_unknown='ignore'))
])

# Combine transformers into a single preprocessor object
preprocessor = ColumnTransformer(
    transformers=[
        ('num', numeric_transformer, numerical_cols),
        ('cat', categorical_transformer, categorical_cols)
    ])

# Fit and transform the data
X_preprocessed = preprocessor.fit_transform(X)
```

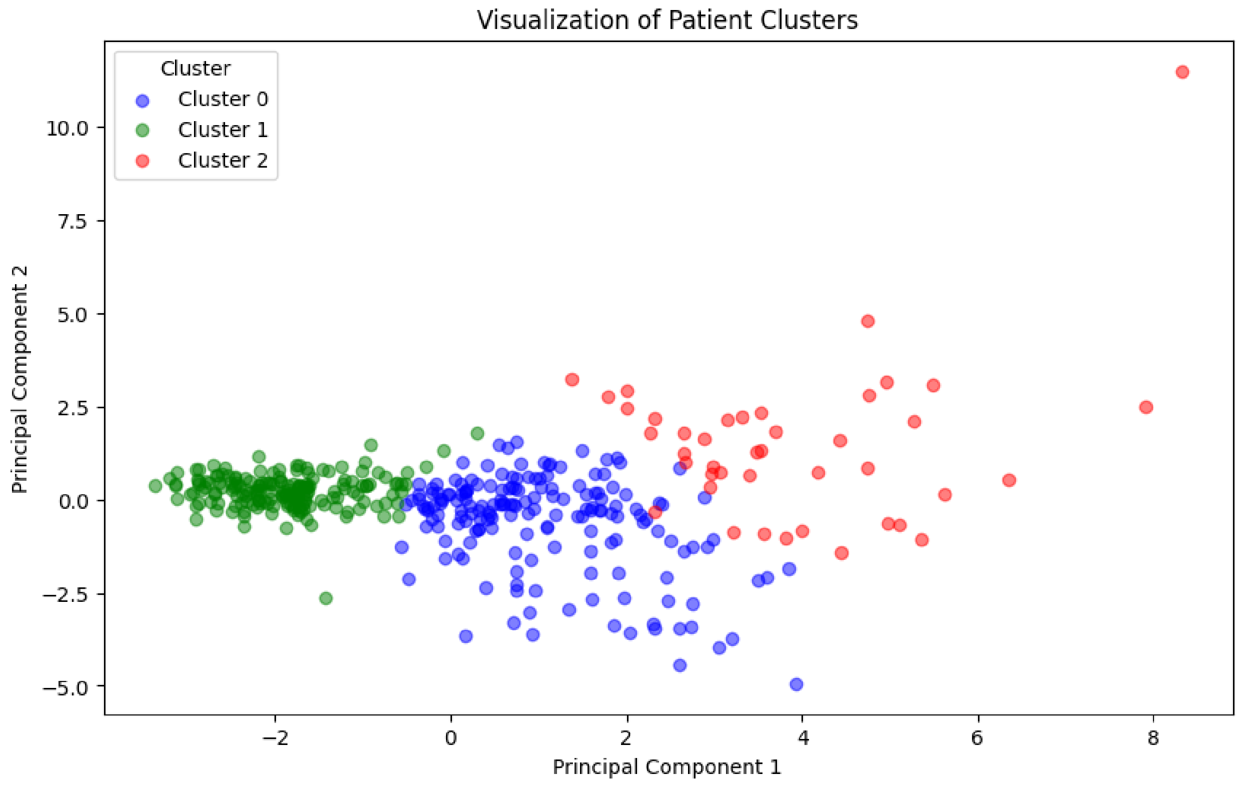
```
d:\python\Lib\site-packages\sklearn\impute\_base.py:577: UserWarning: Skipping features withou
  warnings.warn(
```

```python
from sklearn.cluster import KMeans

# Determine the optimal number of clusters using the Elbow method
sse = []
for k in range(1, 11):
    kmeans = KMeans(n_clusters=k, random_state=42)
    kmeans.fit(X_preprocessed)
    sse.append(kmeans.inertia_)

# Plotting the Elbow curve
import matplotlib.pyplot as plt

plt.figure(figsize=(10, 6))
plt.plot(range(1, 11), sse, marker='o')
plt.title('Elbow Method')
plt.xlabel('Number of Clusters')

plt.ylabel('SSE')

plt.show()


# Assuming the elbow is at k = 3

kmeans = KMeans(n_clusters=3, random_state=42)

clusters = kmeans.fit_predict(X_preprocessed)
```



```
from sklearn.decomposition import PCA

import matplotlib.pyplot as plt

import numpy as np


pca = PCA(n_components=2)

X_pca = pca.fit_transform(X_preprocessed)


# Setting up the plot
```

```python
plt.figure(figsize=(10, 6))
colors = ['blue', 'green', 'red']  # Define a list of colors for the clusters

# Scatter plot
for i in range(np.max(clusters) + 1):  # Loop through the number of clusters
    plt.scatter(X_pca[clusters == i, 0], X_pca[clusters == i, 1],
                color=colors[i], label=f'Cluster {i}', alpha=0.5)

plt.title('Visualization of Patient Clusters')
plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.legend(title='Cluster')  # Add a legend to identify clusters
plt.show()
```



Q8:

```
X_train, X_test = train_test_split(X, test_size=0.30, random_state=1)
print("Training set size:", X_train.shape)
print("Testing set size:", X_test.shape)
```

```
Training set size: (280, 24)
Testing set size: (120, 24)
```

Q9: 1,Logistic Regression Logistic Regression provides clear interpretability, which is crucial in medical settings where understanding the influence of predictors is as important as the prediction itself. 2,Random Forest Random Forest can capture complex interactions between features without requiring feature engineering, making it powerful for medical datasets where interactions between symptoms and biological markers can be non-linear and complex.

Q10: Accuracy:it measures the proportion of true results (both true positives and true negatives) among the total number of cases which examined. It provides a indicator of a model's effectiveness at classifying different cases. Confusion Matrics:It helps in understanding exactly where the classifier is making errors, which is critical for medical applications. Knowing the numbers of false positives and false negatives can be crucial for improving diagnostic procedures and treatments.

Q11

```
from sklearn.model_selection import train_test_split
from sklearn.compose import ColumnTransformer
from sklearn.preprocessing import OneHotEncoder, StandardScaler
from sklearn.impute import SimpleImputer
from sklearn.pipeline import Pipeline
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.30, random_state=1)

# Identify categorical and numerical columns
categorical_cols = X.select_dtypes(include=['object', 'category']).columns
```

```python
numerical_cols = X.select_dtypes(exclude=['object', 'category']).columns

# Preprocessing for numerical data: imputation followed by scaling
numeric_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='median')),
    ('scaler', StandardScaler())])

# Preprocessing for categorical data: imputation followed by one-hot encoding
categorical_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='constant', fill_value='missing')),
    ('onehot', OneHotEncoder(handle_unknown='ignore'))])

preprocessor = ColumnTransformer(
    transformers=[
        ('num', numeric_transformer, numerical_cols),
        ('cat', categorical_transformer, categorical_cols)])

model = RandomForestClassifier(n_estimators=100, random_state=42)

pipeline = Pipeline(steps=[('preprocessor', preprocessor),
                           ('model', model)])

# Train the Random Forest Classifier
pipeline.fit(X_train, y_train)

# Predict using the test set
y_pred = pipeline.predict(X_test)

print(y_pred)
```

```
d:\python\Lib\site-packages\sklearn\impute\_base.py:577: UserWarning: Skipping features withou
```

```
  warnings.warn(
d:\python\Lib\site-packages\sklearn\base.py:1474: DataConversionWarning: A column-vector y was
  return fit_method(estimator, *args, **kwargs)
d:\python\Lib\site-packages\sklearn\impute\_base.py:577: UserWarning: Skipping features withou
  warnings.warn(
```

```
['notckd' 'ckd' 'notckd' 'notckd' 'ckd' 'notckd' 'ckd' 'notckd' 'ckd'
 'notckd' 'ckd' 'notckd' 'ckd' 'notckd' 'notckd' 'ckd' 'notckd' 'ckd'
 'ckd' 'ckd' 'ckd' 'ckd' 'notckd' 'ckd' 'ckd' 'ckd' 'notckd' 'ckd'
 'notckd' 'ckd' 'ckd' 'ckd' 'ckd' 'notckd' 'ckd' 'ckd' 'ckd' 'ckd'
 'notckd' 'ckd' 'notckd' 'ckd' 'ckd' 'ckd' 'notckd' 'ckd' 'notckd'
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 'notckd' 'ckd' 'ckd' 'ckd' 'ckd' 'ckd' 'ckd' 'notckd' 'ckd' 'ckd' 'ckd'
 'notckd' 'ckd' 'notckd' 'ckd' 'ckd' 'notckd' 'notckd' 'notckd' 'ckd'
 'notckd' 'notckd' 'notckd' 'notckd' 'ckd' 'ckd' 'notckd' 'ckd' 'ckd'
 'ckd' 'notckd' 'ckd' 'ckd' 'notckd' 'notckd' 'ckd' 'notckd' 'ckd' 'ckd'
 'ckd' 'ckd' 'notckd' 'ckd' 'ckd' 'notckd']
```

```python
from sklearn.model_selection import train_test_split
from sklearn.compose import ColumnTransformer
from sklearn.preprocessing import OneHotEncoder, StandardScaler
from sklearn.impute import SimpleImputer
from sklearn.pipeline import Pipeline
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report



categorical_cols = X.select_dtypes(include=['object', 'category']).columns
numerical_cols = X.select_dtypes(exclude=['object', 'category']).columns
```

```python
# Preprocessing for numerical data: imputation followed by scaling
numeric_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='median')),
    ('scaler', StandardScaler())])

# Preprocessing for categorical data: imputation followed by one-hot encoding
categorical_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='constant', fill_value='missing')),
    ('onehot', OneHotEncoder(handle_unknown='ignore'))])

# Bundle preprocessing for numerical and categorical data
preprocessor = ColumnTransformer(
    transformers=[
        ('num', numeric_transformer, numerical_cols),
        ('cat', categorical_transformer, categorical_cols)])

# Define the models
forest_model = RandomForestClassifier(n_estimators=100, random_state=42)
logreg_model = LogisticRegression(max_iter=1000, random_state=42)

# Create preprocessing and modelling pipelines
forest_pipeline = Pipeline(steps=[('preprocessor', preprocessor),
                                  ('model', forest_model)])
logreg_pipeline = Pipeline(steps=[('preprocessor', preprocessor),
                                  ('model', logreg_model)])

# Train the Random Forest Classifier
forest_pipeline.fit(X_train, y_train)
# Train the Logistic Regression
logreg_pipeline.fit(X_train, y_train)
```

```python
# Predict using the test set with RandomForest
y_pred_forest = forest_pipeline.predict(X_test)
# Predict using the test set with Logistic Regression
y_pred_logreg = logreg_pipeline.predict(X_test)
```

```
d:\python\Lib\site-packages\sklearn\impute\_base.py:577: UserWarning: Skipping features withou
  warnings.warn(
d:\python\Lib\site-packages\sklearn\base.py:1474: DataConversionWarning: A column-vector y was
  return fit_method(estimator, *args, **kwargs)
d:\python\Lib\site-packages\sklearn\impute\_base.py:577: UserWarning: Skipping features withou
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  warnings.warn(
d:\python\Lib\site-packages\sklearn\impute\_base.py:577: UserWarning: Skipping features withou
  warnings.warn(
```

Q12

```python
from sklearn.metrics import accuracy_score, confusion_matrix

# Accuracy for RandomForest
accuracy_forest = accuracy_score(y_test, y_pred_forest)
conf_matrix_forest = confusion_matrix(y_test, y_pred_forest)

# Accuracy for Logistic Regression
accuracy_logreg = accuracy_score(y_test, y_pred_logreg)
conf_matrix_logreg = confusion_matrix(y_test, y_pred_logreg)
```

```
# Display the results
print("Random Forest Accuracy:", accuracy_forest)
print("Random Forest Confusion Matrix:\n", conf_matrix_forest)
print("Logistic Regression Accuracy:", accuracy_logreg)
print("Logistic Regression Confusion Matrix:\n", conf_matrix_logreg)
```

```
Random Forest Accuracy: 1.0
Random Forest Confusion Matrix:
 [[70  0]
 [ 0 50]]
Logistic Regression Accuracy: 0.975
Logistic Regression Confusion Matrix:
 [[67  3]
 [ 0 50]]
```

Q13

```
from sklearn.compose import ColumnTransformer
from sklearn.preprocessing import OneHotEncoder, StandardScaler
from sklearn.impute import SimpleImputer
from sklearn.pipeline import Pipeline



# Define which columns are categorical and numerical in your dataset
categorical_cols = X.select_dtypes(include=['object', 'bool', 'category']).columns
numerical_cols = X.select_dtypes(include=['int64', 'float64']).columns

# Preprocessing for numerical data: imputation followed by scaling
numeric_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='median')),
    ('scaler', StandardScaler())])
```

```python
# Preprocessing for categorical data: imputation followed by one-hot encoding
categorical_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='constant', fill_value='missing')),
    ('onehot', OneHotEncoder(handle_unknown='ignore'))])

# Bundle preprocessing for numerical and categorical data
preprocessor = ColumnTransformer(
    transformers=[
        ('num', numeric_transformer, numerical_cols),
        ('cat', categorical_transformer, categorical_cols)])

# Apply transformations to the data
X_preprocessed = preprocessor.fit_transform(X)
```

```
d:\python\Lib\site-packages\sklearn\impute\_base.py:577: UserWarning: Skipping features withou
  warnings.warn(
```

```python
from sklearn.linear_model import LogisticRegression

# Initialize the Logistic Regression model
logreg_full = LogisticRegression(random_state=1)

# Fit the model on the preprocessed data
logreg_full.fit(X_preprocessed, y)
```

```
d:\python\Lib\site-packages\sklearn\utils\validation.py:1300: DataConversionWarning: A column-
  y = column_or_1d(y, warn=True)
```

```
LogisticRegression(random_state=1)
```

```python
# Get the coefficients from the trained model
feature_names = preprocessor.get_feature_names_out()  # Get the feature names after preprocessi
coefficients = logreg_full.coef_[0]

# Associate each coefficient with its corresponding feature name
importance = pd.Series(coefficients, index=feature_names)

# Sort features by their coefficient magnitude for interpretation
sorted_importance = importance.abs().sort_values(ascending=False)
print(sorted_importance)
```

```
num__hemo    0.987752
num__al      0.925141
num__sg      0.882522
num__sc      0.714171
num__bu      0.659715
num__su      0.625505
num__pcv     0.519588
num__bgr     0.333517
num__bp      0.270300
num__age     0.244780
num__sod     0.235290
num__pot     0.127910
num__wbcc    0.091388
num__rbcc    0.026597
dtype: float64
```

The features with the highest coefficients are generally those directly related to kidney function tests and blood tests, which are critical in diagnosing and managing CKD. This model effectively highlights the key biomarkers for CKD, which could help in early detection and management strategies.

Q14

As for interaction terms or the polynomial features are concerned they can be employed to ensure the non-linear relationships between them are taken into account. Finally, after the application of learning mechanisms, apply accuracy and confusion matrices to evaluate the upgrade process. Compare these results to the previously used models for the targeted sub-groups to check whether the performance of the model parametrically upgraded or not.

```
from sklearn.model_selection import train_test_split
from sklearn.compose import ColumnTransformer
from sklearn.preprocessing import OneHotEncoder, StandardScaler
from sklearn.impute import SimpleImputer
from sklearn.pipeline import Pipeline
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report, accuracy_score, confusion_matrix



categorical_cols = [col for col in X.columns if X[col].dtype == 'object']
numerical_cols = [col for col in X.columns if X[col].dtype != 'object']  # Numerical columns

# Create transformers for preprocessing
numeric_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='median')),  # Use median for numerical columns
    ('scaler', StandardScaler())
])

categorical_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='constant', fill_value='missing')),  # Use 'missing' fo
    ('onehot', OneHotEncoder(handle_unknown='ignore'))
])

# Bundle preprocessing for numerical and categorical data
preprocessor = ColumnTransformer(
    transformers=[
        ('num', numeric_transformer, numerical_cols),
        ('cat', categorical_transformer, categorical_cols)
    ])

# Define the classifiers
random_forest_classifier = RandomForestClassifier(n_estimators=100, random_state=42)
logistic_regression_classifier = LogisticRegression(max_iter=1000, random_state=42)

# Create preprocessing and modeling pipelines
pipeline_rf = Pipeline(steps=[('preprocessor', preprocessor),
                              ('classifier', random_forest_classifier)])

pipeline_lr = Pipeline(steps=[('preprocessor', preprocessor),
                              ('classifier', logistic_regression_classifier)])



# Fit both classifiers
pipeline_rf.fit(X_train, y_train)
pipeline_lr.fit(X_train, y_train)

# Predict using both classifiers
y_pred_rf = pipeline_rf.predict(X_test)
y_pred_lr = pipeline_lr.predict(X_test)

# Evaluate both classifiers
accuracy_rf = accuracy_score(y_test, y_pred_rf)
conf_matrix_rf = confusion_matrix(y_test, y_pred_rf)

accuracy_lr = accuracy_score(y_test, y_pred_lr)
conf_matrix_lr = confusion_matrix(y_test, y_pred_lr)
```

```python
print(f"Random Forest Accuracy: {accuracy_rf}")
print("Random Forest Confusion Matrix:\n", conf_matrix_rf)

print(f"Logistic Regression Accuracy: {accuracy_lr}")
print("Logistic Regression Confusion Matrix:\n", conf_matrix_lr)
```

```
Random Forest Accuracy: 1.0
Random Forest Confusion Matrix:
 [[70  0]
 [ 0 50]]
Logistic Regression Accuracy: 0.975
Logistic Regression Confusion Matrix:
 [[67  3]
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```
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  return fit_method(estimator, *args, **kwargs)
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d:\python\Lib\site-packages\sklearn\impute\_base.py:577: UserWarning: Skipping features withou
  warnings.warn(
d:\python\Lib\site-packages\sklearn\impute\_base.py:577: UserWarning: Skipping features withou
  warnings.warn(
```

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.