```
In [33]: import pandas as pd
         import numpy as np
         from sklearn.preprocessing import LabelEncoder, StandardScaler
         from imblearn.over_sampling import RandomOverSampler
         from sklearn.feature_selection import SelectKBest, chi2
In [34]:
         # Load the data into a pandas dataframe
         data = pd.read_csv('kidneyydata.csv')
         # Check the distribution of the target variable
         counts = data['target'].value counts()
         print(counts)
         0.0
                79
         Name: target, dtype: int64
In [35]: import pandas as pd
         import numpy as np
         from sklearn.model selection import train test split
         from sklearn.preprocessing import LabelEncoder, StandardScaler
         from imblearn.over sampling import SMOTE
         from sklearn.feature selection import SelectKBest, chi2
         # Load the dataset
         df = pd.read csv('kidneyydata.csv')
         # Check for class imbalance
         print(df['target'].value counts())
         0.0
                79
```

Name: target, dtype: int64

```
In [36]: import pandas as pd
         from imblearn.over_sampling import SMOTE
         # Load the dataset
         df = pd.read_csv('kidneyydata.csv')
         # Check the class distribution of the dataset
         print(df['target'].value_counts())
         # Separate the features and target
         X = df.drop('target', axis=1)
         y = df['target']
         # Check if the data is imbalanced
         if y.value_counts().min() / y.value_counts().max() < 0.5:</pre>
             # Balance the dataset using SMOTE
             oversampler = SMOTE(random_state=42)
             X, y = oversampler.fit_resample(X, y)
             # Check the class distribution after balancing
             print(y.value_counts())
         else:
             print("The dataset is balanced.")
```

0.0

79

Name: target, dtype: int64 The dataset is balanced.

```
In [37]: # Importing necessary libraries
         import pandas as pd
         from sklearn.preprocessing import LabelEncoder
         # Reading in the dataset
         data = pd.read_csv('kidneyydata.csv')
         # Creating a LabelEncoder object
         le = LabelEncoder()
         # Encoding the 'gravity' feature
         data['gravity_encoded'] = le.fit_transform(data['gravity'])
         # Encoding the 'ph' feature
         data['ph encoded'] = le.fit transform(data['ph'])
         # Encoding the 'osmo' feature
         data['osmo_encoded'] = le.fit_transform(data['osmo'])
         # Encoding the 'cond' feature
         data['cond encoded'] = le.fit transform(data['cond'])
         # Encoding the 'urea' feature
         data['urea encoded'] = le.fit transform(data['urea'])
         # Encoding the 'calc' feature
         data['calc encoded'] = le.fit transform(data['calc'])
         # Encoding the 'target' feature
         data['target_encoded'] = le.fit_transform(data['target'])
         # Printing the first 5 rows of the dataset after encoding
         print(data.head())
```

```
Unnamed: 0 gravity ph osmo cond urea calc target gravity_encoded \
0
          0
               1.021 4.91
                          725 14.0
                                      443 2.45
                                                   0.0
                                                                   16
1
               1.017 5.74 577 20.0
                                      296 4.49
                                                   0.0
                                                                   12
          1
2
               1.008 7.20 321 14.9
                                      101 2.36
                                                   0.0
                                                                    3
          2
3
           3
               1.011 5.51
                            408 12.6
                                      224 2.15
                                                   0.0
                                                                    6
4
           4
               1.005 6.52
                           187 7.5
                                      91 1.16
                                                   0.0
                                                                    0
  ph_encoded osmo_encoded cond_encoded urea_encoded calc_encoded \
          3
                      50
                                   17
                                               65
                                                            30
1
          29
                      36
                                   31
                                               41
                                                            46
2
          64
                       9
                                   21
                                                8
                                                            29
3
         17
                      18
                                   13
                                               32
                                                            24
4
          52
                                   1
                                                            11
                       0
                                                5
  target_encoded
              0
0
0
1
```

```
In [38]: # Importing necessary libraries
         import pandas as pd
         from sklearn.preprocessing import MinMaxScaler
         # Reading the dataset
         data = pd.read_csv('kidneyydata.csv')
         # Creating the MinMaxScaler object
         scaler = MinMaxScaler()
         # Scaling the features
         data[[ 'gravity', 'ph', 'osmo', 'cond', 'urea', 'calc',]] = scaler.fit_transform(data[[ 'gravity', 'ph', 'os
         # Printing the first 5 rows of the dataset after scaling
         print(data.head())
            Unnamed: 0
                        gravity
                                                        cond
                                                                           calc \
                                      ph
                                               osmo
                                                                  urea
         0
                    0 0.457143 0.047170 0.512869 0.270517 0.709836 0.160903
         1
                    1 0.342857 0.308176 0.371783 0.452888 0.468852 0.304869
         2
                    2 0.085714 0.767296 0.127741 0.297872 0.149180 0.154552
         3
                    3 0.171429 0.235849 0.210677 0.227964 0.350820 0.139732
                    4 0.000000 0.553459 0.000000 0.072948 0.132787 0.069866
            target
         0
               0.0
         1
               0.0
         2
              0.0
```

3

0.0

```
In [39]: import pandas as pd
         # Load CSV file
         data = pd.read_csv('kidneyydata.csv')
         # Convert 'target' column to float
         data['target'] = data['target'].astype(float)
         # ... and so on for other columns
         # Save preprocessed data to a new CSV file
         data.to_csv('kidneyydata.csv', index=False)
In [40]: from sklearn.tree import DecisionTreeClassifier
         from sklearn.datasets import load_iris
         iris = load_iris()
         X = iris.data
         y = iris.target
         clf = DecisionTreeClassifier()
         clf.fit(X, y)
```

Out[40]: DecisionTreeClassifier()

```
In [41]: from sklearn.feature_selection import SelectKBest, chi2
         import pandas as pd
         # Load data
         data = pd.read_csv('kidneyydata.csv')
         # Split data into X (features) and y (target)
         X = data.drop('target', axis=1)
         y = data['target']
         # Feature selection
         selector = SelectKBest(chi2, k=5)
         selector.fit(X, y)
         X_new = selector.transform(X)
         # Print selected features
         mask = selector.get_support() # list of booleans
         selected features = [] # The list of your K best features
         for bool, feature in zip(mask, X.columns):
             if bool:
                 selected_features.append(feature)
         print(selected_features)
         ['ph', 'osmo', 'cond', 'urea', 'calc']
In [42]: # Read selected features from file
         with open('kidneydata.csv', 'r') as f:
             selected_features = [line.strip() for line in f]
```

In [43]: print(selected_features)

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In []: