k-mean-clustering

December 12, 2023

[88]:
```
import numpy as np
import pandas as pd
import warnings
import os
import seaborn as sns
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D

from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans
from sklearn.metrics import confusion_matrix,classification_report
```

[89]:
```
df = pd.read_csv("/kaggle/input/winequalityred/winequality-red.csv")
df.head()
```

[89]:
```
   fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0            7.4              0.70         0.00             1.9      0.076
1            7.8              0.88         0.00             2.6      0.098
2            7.8              0.76         0.04             2.3      0.092
3           11.2              0.28         0.56             1.9      0.075
4            7.4              0.70         0.00             1.9      0.076

   free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0                 11.0                  34.0   0.9978  3.51       0.56
1                 25.0                  67.0   0.9968  3.20       0.68
2                 15.0                  54.0   0.9970  3.26       0.65
3                 17.0                  60.0   0.9980  3.16       0.58
4                 11.0                  34.0   0.9978  3.51       0.56

   alcohol  quality
0      9.4        5
1      9.8        5
2      9.8        5
3      9.8        6
4      9.4        5
```

[90]:
```
columns = ['fixed acidity', 'volatile acidity', 'citric acid', 'residual␣
 ↪sugar', 'chlorides', 'free sulfur dioxide',
           'total sulfur dioxide', 'density', 'pH', 'sulphates', 'alcohol',␣
 ↪'quality']
```

[91]:
```
df.columns
```

[91]:
```
Index(['fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar',
       'chlorides', 'free sulfur dioxide', 'total sulfur dioxide', 'density',
       'pH', 'sulphates', 'alcohol', 'quality'],
      dtype='object')
```

[92]:
```
df.shape
```

[92]:
```
(1596, 12)
```

[93]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1596 entries, 0 to 1595
Data columns (total 12 columns):
 #   Column                Non-Null Count  Dtype
---  ------                --------------  -----
 0   fixed acidity         1596 non-null   float64
 1   volatile acidity      1596 non-null   float64
 2   citric acid           1596 non-null   float64
 3   residual sugar        1596 non-null   float64
 4   chlorides             1596 non-null   float64
 5   free sulfur dioxide   1596 non-null   float64
 6   total sulfur dioxide  1596 non-null   float64
 7   density               1596 non-null   float64
 8   pH                    1596 non-null   float64
 9   sulphates             1596 non-null   float64
 10  alcohol               1596 non-null   float64
 11  quality               1596 non-null   int64
dtypes: float64(11), int64(1)
memory usage: 149.8 KB
```

[94]:
```
df.describe()
```

[94]:
```
       fixed acidity  volatile acidity  citric acid  residual sugar  \
count    1596.000000       1596.000000  1596.000000     1596.000000
mean        8.314160          0.527954     0.270276        2.535558
std         1.732203          0.179176     0.193894        1.405515
min         4.600000          0.120000     0.000000        0.900000
25%         7.100000          0.390000     0.090000        1.900000
50%         7.900000          0.520000     0.260000        2.200000
```

```
75%         9.200000          0.640000     0.420000        2.600000
max        15.600000          1.580000     0.790000       15.500000

         chlorides  free sulfur dioxide  total sulfur dioxide      density  \
count  1596.000000          1596.000000           1596.000000  1596.000000
mean      0.087120            15.858396             46.382206     0.996744
std       0.045251            10.460554             32.839138     0.001888
min       0.012000             1.000000              6.000000     0.990070
25%       0.070000             7.000000             22.000000     0.995600
50%       0.079000            14.000000             38.000000     0.996745
75%       0.090000            21.000000             62.000000     0.997833
max       0.611000            72.000000            289.000000     1.003690

                pH    sulphates      alcohol      quality
count  1596.000000  1596.000000  1596.000000  1596.000000
mean      3.311917     0.656385    10.421147     5.637218
std       0.153346     0.163057     1.060371     0.807080
min       2.860000     0.330000     8.400000     3.000000
25%       3.210000     0.550000     9.500000     5.000000
50%       3.310000     0.620000    10.200000     6.000000
75%       3.400000     0.730000    11.100000     6.000000
max       4.010000     1.980000    14.000000     8.000000
```

[95]:
```
df.isnull().sum()
```

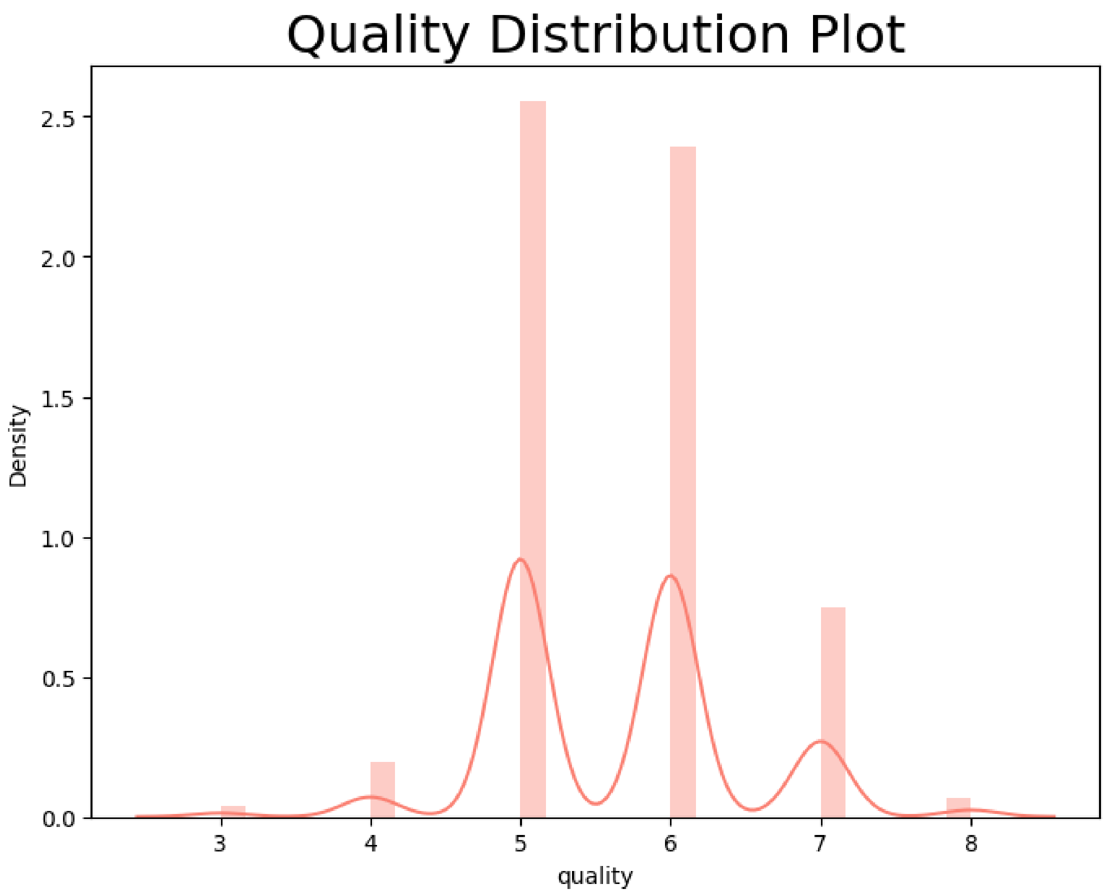
[95]:
```
fixed acidity           0
volatile acidity        0
citric acid             0
residual sugar          0
chlorides               0
free sulfur dioxide     0
total sulfur dioxide    0
density                 0
pH                      0
sulphates               0
alcohol                 0
quality                 0
dtype: int64
```

[96]:
```
# Create a distribution plot
f0, ax = plt.subplots(figsize=(8, 6))
plt.title('Quality Distribution Plot', fontsize=23)
sns.distplot(df['quality'], color='salmon')
```

```
/tmp/ipykernel_43/3282330620.py:4: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.
```

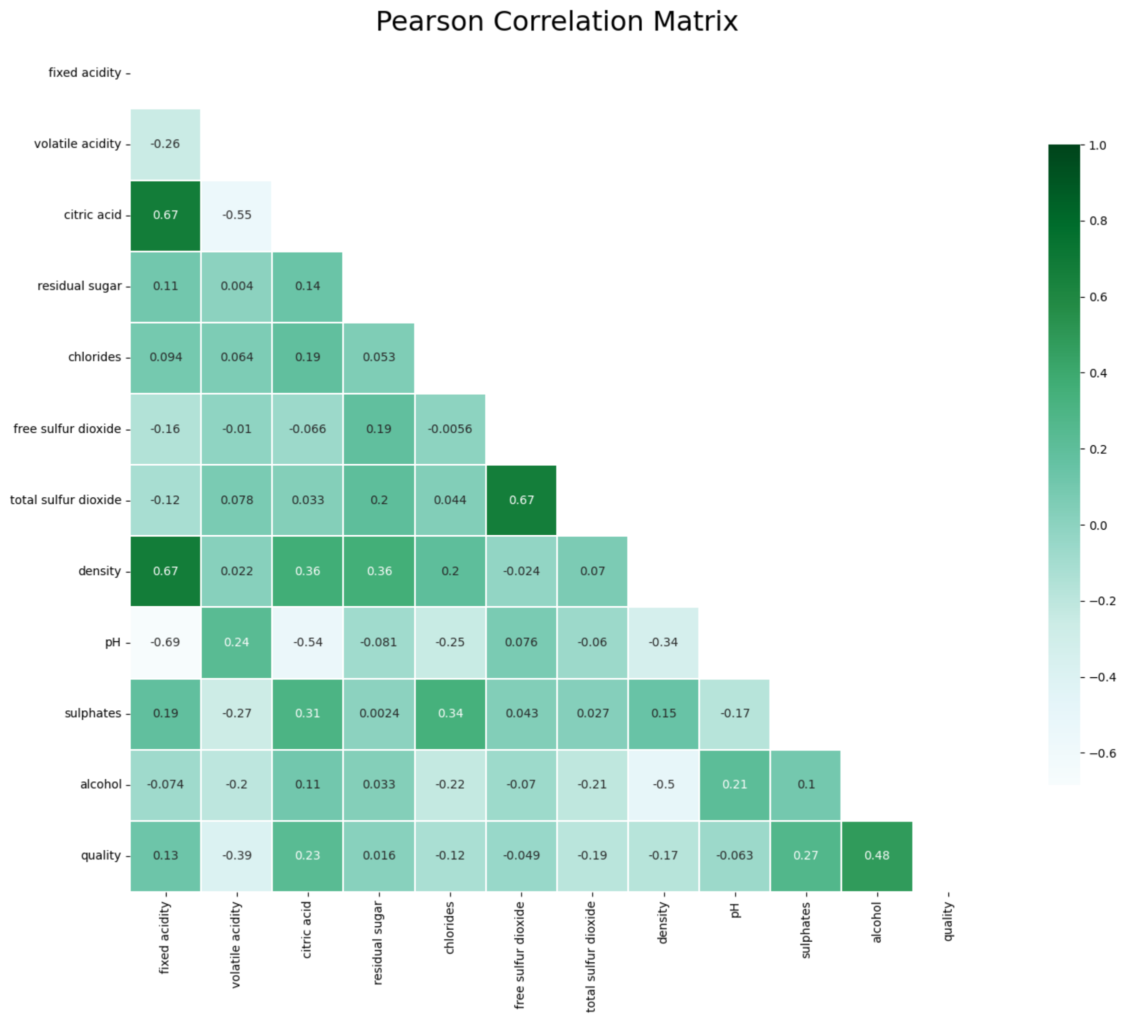
```
Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

  sns.distplot(df['quality'], color='salmon')
```

[96]:
```
<Axes: title={'center': 'Quality Distribution Plot'}, xlabel='quality',
ylabel='Density'>
```



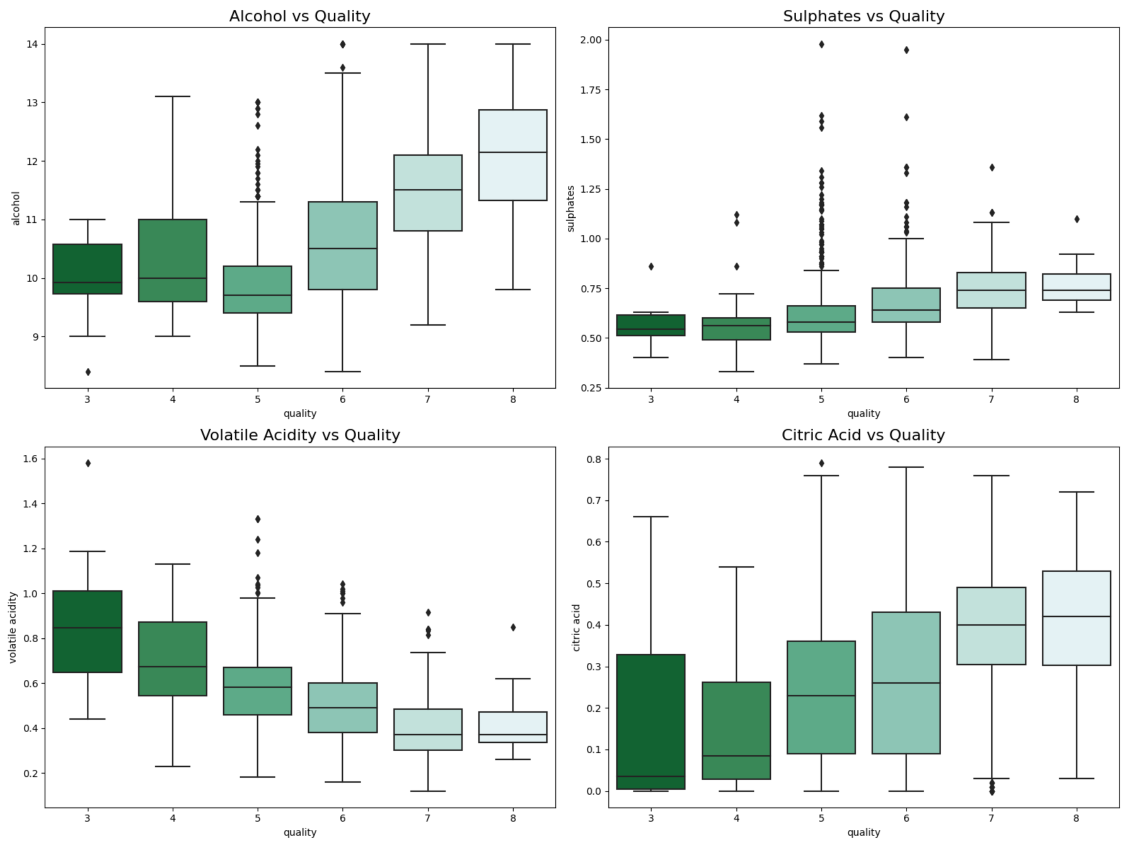
[97]:
```
# create correlation matrix
mask = np.zeros_like(df[columns].corr(), dtype=bool)
mask[np.triu_indices_from(mask)] = True

f, ax = plt.subplots(figsize=(16, 12))
plt.title('Pearson Correlation Matrix',fontsize=23)
```

```
sns.heatmap(df[columns].corr(),linewidths=0.25, vmax=1.0, square=True,␣
↪cmap="BuGn",
            linecolor='w', annot=True, mask=mask, cbar_kws={"shrink": .75})
f.tight_layout()

# most correlating columns
features = ['alcohol', 'sulphates', 'volatile acidity', 'citric acid']
```



```
[98]: # Create box plots for features
f2, ax = plt.subplots(2, 2, figsize=(16, 12))
sns.boxplot(x='quality', y='alcohol', data=df, ax=ax[0, 0], palette='BuGn_r')
sns.boxplot(x='quality', y='sulphates', data=df, ax=ax[0, 1], palette='BuGn_r')
sns.boxplot(x='quality', y='volatile acidity', data=df, ax=ax[1, 0],␣
↪palette='BuGn_r')
```

```
sns.boxplot(x='quality', y='citric acid', data=df, ax=ax[1, 1],␣
 ↪palette='BuGn_r')

# Add plot titles
ax[0, 0].set_title('Alcohol vs Quality', fontsize=16)
ax[0, 1].set_title('Sulphates vs Quality', fontsize=16)
ax[1, 0].set_title('Volatile Acidity vs Quality', fontsize=16)
ax[1, 1].set_title('Citric Acid vs Quality', fontsize=16)

# Adjust layout for better visualization
f2.tight_layout()

# Show the plot
plt.show()
```



[99]:
```
# Normalizing over the standard deviation
df_dropped = df.drop('quality', axis=1)
X =df_dropped.values[:, 1:]
Clus_dataset = StandardScaler().fit_transform(X)
```

[104]:
```python
wcss = []
for i in range(1,11):
    kmeans = KMeans(n_clusters=i, init='k-means++', random_state=42)
    kmeans.fit(X)
    wcss.append(kmeans.inertia_)

# Plot the elbow curve with a marker
f3, ax = plt.subplots(figsize=(8, 6))
plt.plot(range(1,11), wcss, marker='*', linestyle='--',␣
 ↪color='b',markerfacecolor='r',mec = 'r',ms = 20)
plt.title('The Elbow Method')
plt.xlabel('Number of clusters')
plt.ylabel('WCSS')
plt.show()
```

```
/opt/conda/lib/python3.10/site-packages/sklearn/cluster/_kmeans.py:870:
FutureWarning: The default value of `n_init` will change from 10 to 'auto' in
1.4. Set the value of `n_init` explicitly to suppress the warning
  warnings.warn(
/opt/conda/lib/python3.10/site-packages/sklearn/cluster/_kmeans.py:870:
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  warnings.warn(
```
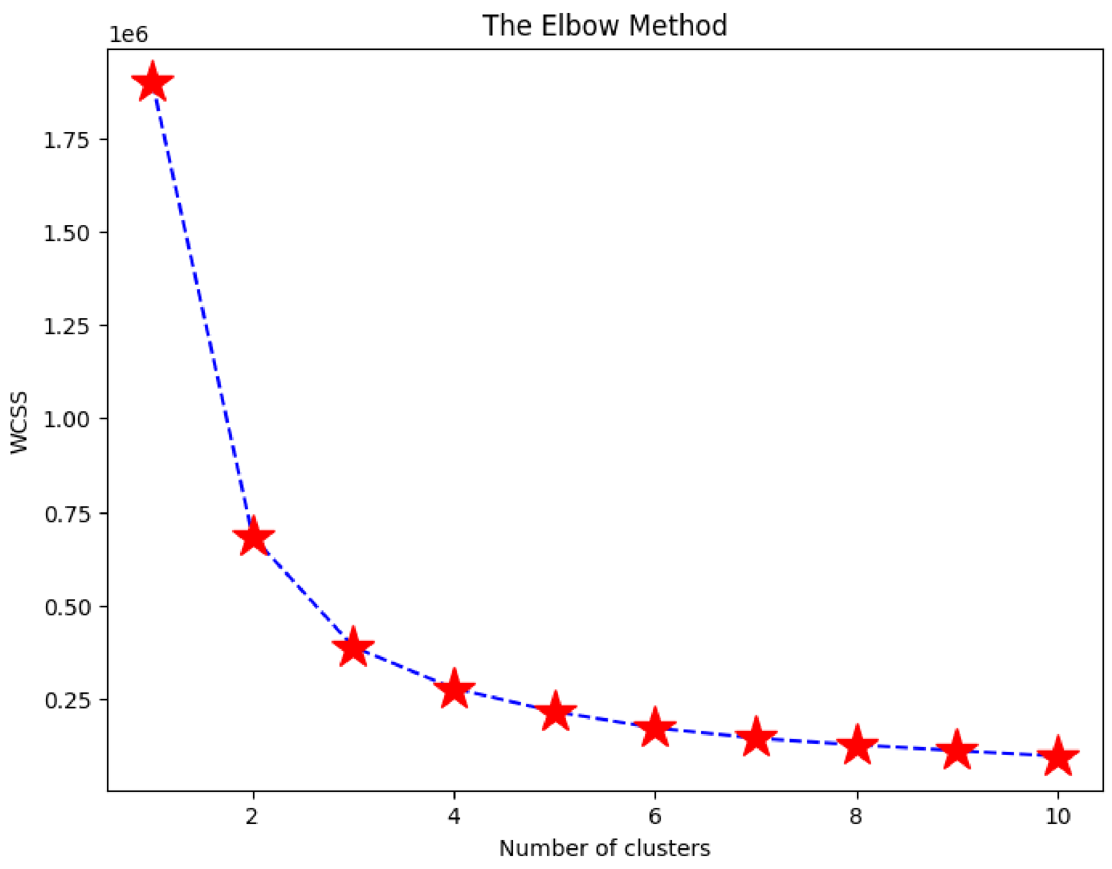



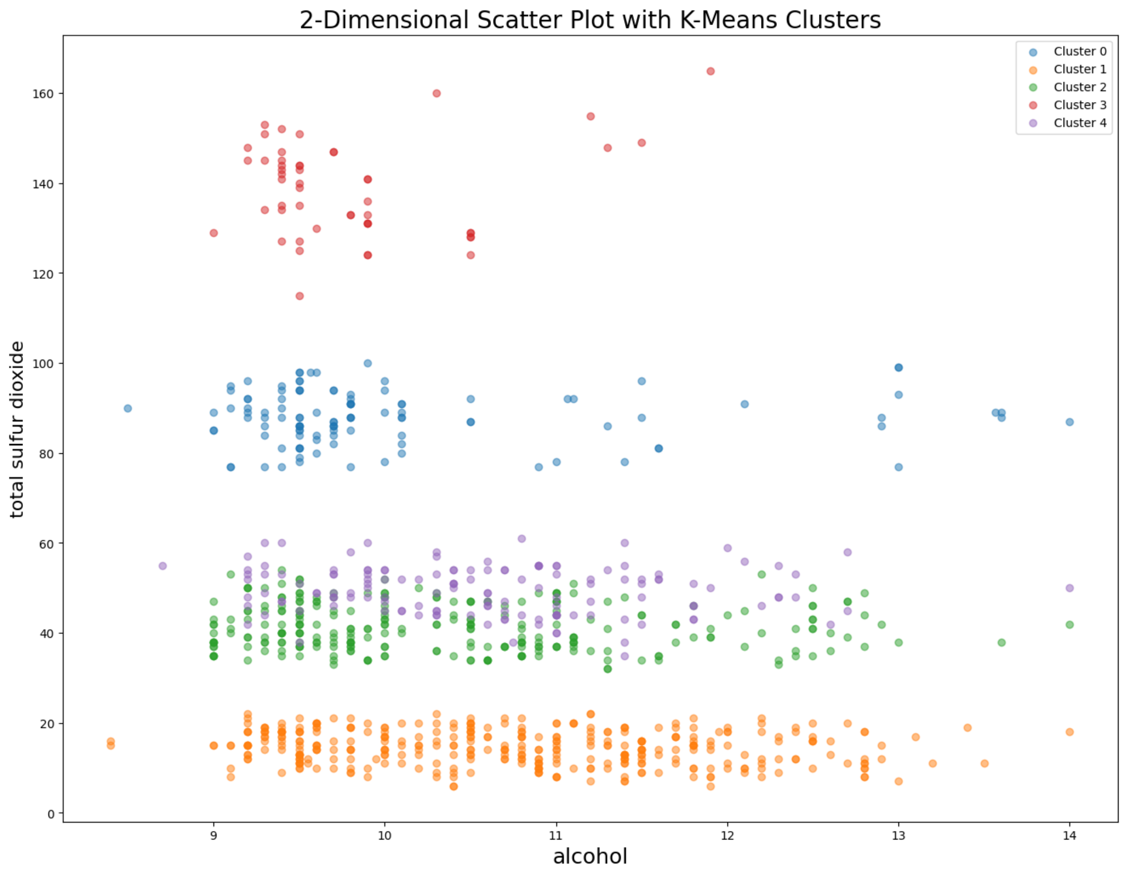
[110]:
```
Kmeans = KMeans(n_clusters=10, init='k-means++',random_state=42)
kmeans.fit(X)
```

```
/opt/conda/lib/python3.10/site-packages/sklearn/cluster/_kmeans.py:870:
FutureWarning: The default value of `n_init` will change from 10 to 'auto' in
1.4. Set the value of `n_init` explicitly to suppress the warning
  warnings.warn(
```

[110]:
```
KMeans(n_clusters=10, random_state=42)
```

[107]:
```
labels = kmeans.labels_
```

[113]:
```python
plt.figure(figsize=(16, 12))

for cluster_label in range(5):
    plt.scatter(
        X[labels == cluster_label, 9],  # alcohol
        X[labels == cluster_label, 5],  # total sulfur dioxide
        alpha=0.5,
        label=f'Cluster {cluster_label}',
    )

plt.xlabel('alcohol', fontsize=18)
plt.ylabel('total sulfur dioxide', fontsize=16)
plt.title('2-Dimensional Scatter Plot with K-Means Clusters', fontsize=20)
plt.legend()
plt.show()
```


2-Dimensional Scatter Plot with K-Means Clusters
Cluster 0
Cluster 1
Cluster 2
Cluster 3
Cluster 4
total sulfur dioxide
alcohol