Q. **Write a program to implement K-means clustering algorithm.**

```
import pandas as pd
from sklearn.preprocessing import StandardScaler, LabelEncoder
from sklearn.cluster import KMeans
import matplotlib.pyplot as plt
import seaborn as sns

df = pd.read_csv('wine-clustering.csv')

df.head()
```

```
   Alcohol  Malic_Acid   Ash  Ash_Alcanity  Magnesium  Total_Phenols  \
0    14.23        1.71  2.43          15.6        127           2.80
1    13.20        1.78  2.14          11.2        100           2.65
2    13.16        2.36  2.67          18.6        101           2.80
3    14.37        1.95  2.50          16.8        113           3.85
4    13.24        2.59  2.87          21.0        118           2.80

   Flavanoids  Nonflavanoid_Phenols  Proanthocyanins  Color_Intensity   Hue  \
0        3.06                  0.28             2.29             5.64  1.04
1        2.76                  0.26             1.28             4.38  1.05
2        3.24                  0.30             2.81             5.68  1.03
3        3.49                  0.24             2.18             7.80  0.86
4        2.69                  0.39             1.82             4.32  1.04

   OD280  Proline
0   3.92     1065
1   3.40     1050
2   3.17     1185
3   3.45     1480
4   2.93      735
```

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 178 entries, 0 to 177
Data columns (total 13 columns):
 #   Column                Non-Null Count  Dtype
---  ------                --------------  -----
 0   Alcohol               178 non-null    float64
 1   Malic_Acid            178 non-null    float64
 2   Ash                   178 non-null    float64
 3   Ash_Alcanity          178 non-null    float64
 4   Magnesium             178 non-null    int64
 5   Total_Phenols         178 non-null    float64
 6   Flavanoids            178 non-null    float64
 7   Nonflavanoid_Phenols  178 non-null    float64
 8   Proanthocyanins       178 non-null    float64
```

```
 9   Color_Intensity       178 non-null    float64
 10  Hue                   178 non-null    float64
 11  OD280                 178 non-null    float64
 12  Proline               178 non-null    int64
dtypes: float64(11), int64(2)
memory usage: 18.2 KB
```

```
df.isnull().sum()
```

```
Alcohol                 0
Malic_Acid              0
Ash                     0
Ash_Alcanity            0
Magnesium               0
Total_Phenols           0
Flavanoids              0
Nonflavanoid_Phenols    0
Proanthocyanins         0
Color_Intensity         0
Hue                     0
OD280                   0
Proline                 0
dtype: int64
```

```
df.corr()
```

	Alcohol	Malic_Acid	Ash	Ash_Alcanity	Magnesium
Alcohol	1.000000	0.094397	0.211545	-0.310235	0.270798
Malic_Acid	0.094397	1.000000	0.164045	0.288500	-0.054575
Ash	0.211545	0.164045	1.000000	0.443367	0.286587
Ash_Alcanity	-0.310235	0.288500	0.443367	1.000000	-0.083333
Magnesium	0.270798	-0.054575	0.286587	-0.083333	1.000000
Total_Phenols	0.289101	-0.335167	0.128980	-0.321113	0.214401
Flavanoids	0.236815	-0.411007	0.115077	-0.351370	0.195784
Nonflavanoid_Phenols	-0.155929	0.292977	0.186230	0.361922	-0.256294
Proanthocyanins	0.136698	-0.220746	0.009652	-0.197327	0.236441
Color_Intensity	0.546364	0.248985	0.258887	0.018732	0.199950
Hue	-0.071747	-0.561296	-0.074667	-0.273955	0.055398
OD280	0.072343	-0.368710	0.003911	-0.276769	0.066004
Proline	0.643720	-0.192011	0.223626	-0.440597	0.393351

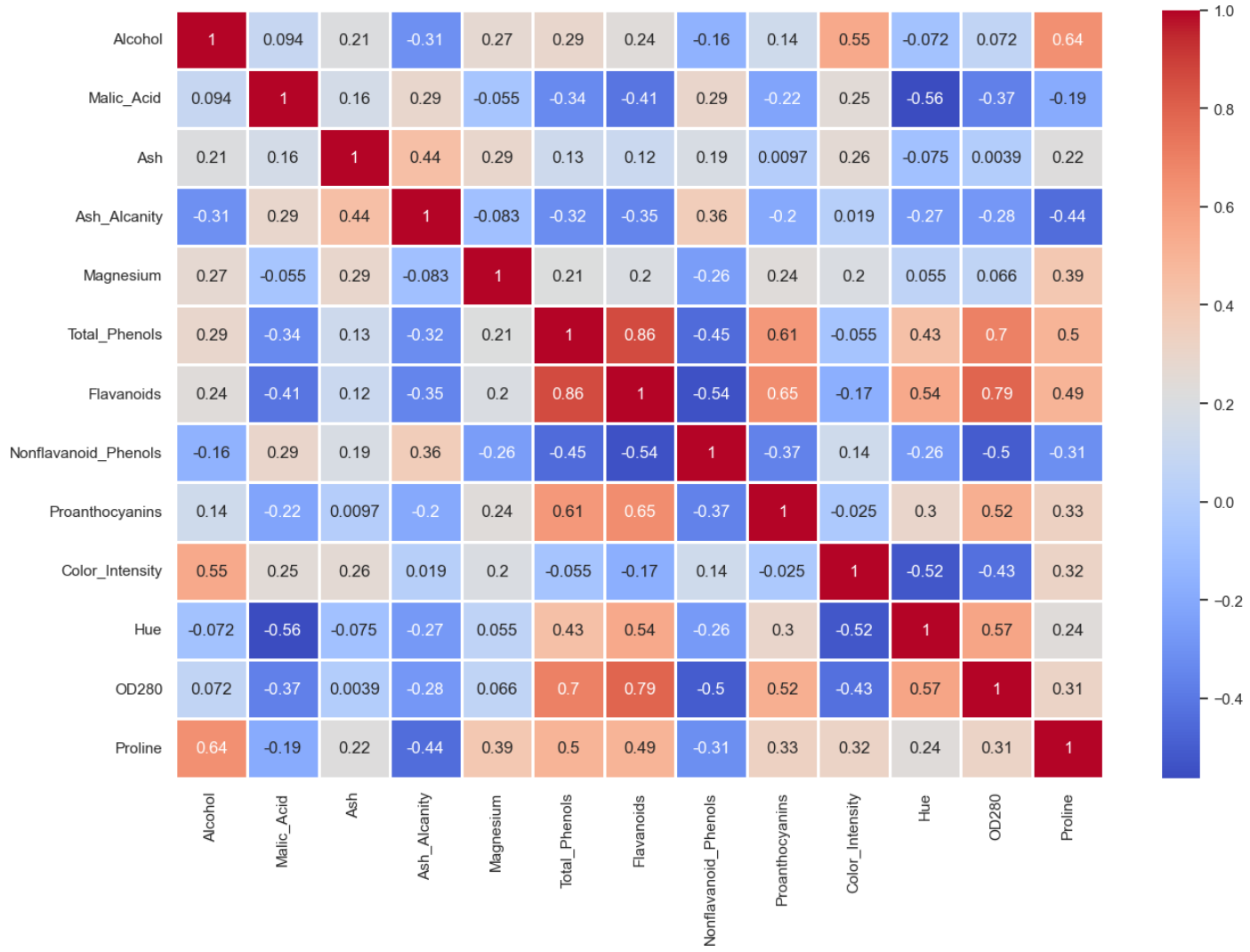
	Total_Phenols	Flavanoids	Nonflavanoid_Phenols
Alcohol	0.289101	0.236815	-0.155929
Malic_Acid	-0.335167	-0.411007	0.292977
Ash	0.128980	0.115077	0.186230
Ash_Alcanity	-0.321113	-0.351370	0.361922
Magnesium	0.214401	0.195784	-0.256294

```
Total_Phenols                 1.000000    0.864564              -0.449935
Flavanoids                    0.864564    1.000000              -0.537900
Nonflavanoid_Phenols         -0.449935   -0.537900               1.000000
Proanthocyanins               0.612413    0.652692              -0.365845
Color_Intensity              -0.055136   -0.172379               0.139057
Hue                           0.433681    0.543479              -0.262640
OD280                         0.699949    0.787194              -0.503270
Proline                       0.498115    0.494193              -0.311385
```

```
                      Proanthocyanins  Color_Intensity       Hue     OD280  \
Alcohol                      0.136698         0.546364 -0.071747  0.072343
Malic_Acid                  -0.220746         0.248985 -0.561296 -0.368710
Ash                          0.009652         0.258887 -0.074667  0.003911
Ash_Alcanity                -0.197327         0.018732 -0.273955 -0.276769
Magnesium                    0.236441         0.199950  0.055398  0.066004
Total_Phenols                0.612413        -0.055136  0.433681  0.699949
Flavanoids                   0.652692        -0.172379  0.543479  0.787194
Nonflavanoid_Phenols        -0.365845         0.139057 -0.262640 -0.503270
Proanthocyanins              1.000000        -0.025250  0.295544  0.519067
Color_Intensity             -0.025250         1.000000 -0.521813 -0.428815
Hue                          0.295544        -0.521813  1.000000  0.565468
OD280                        0.519067        -0.428815  0.565468  1.000000
Proline                      0.330417         0.316100  0.236183  0.312761
```

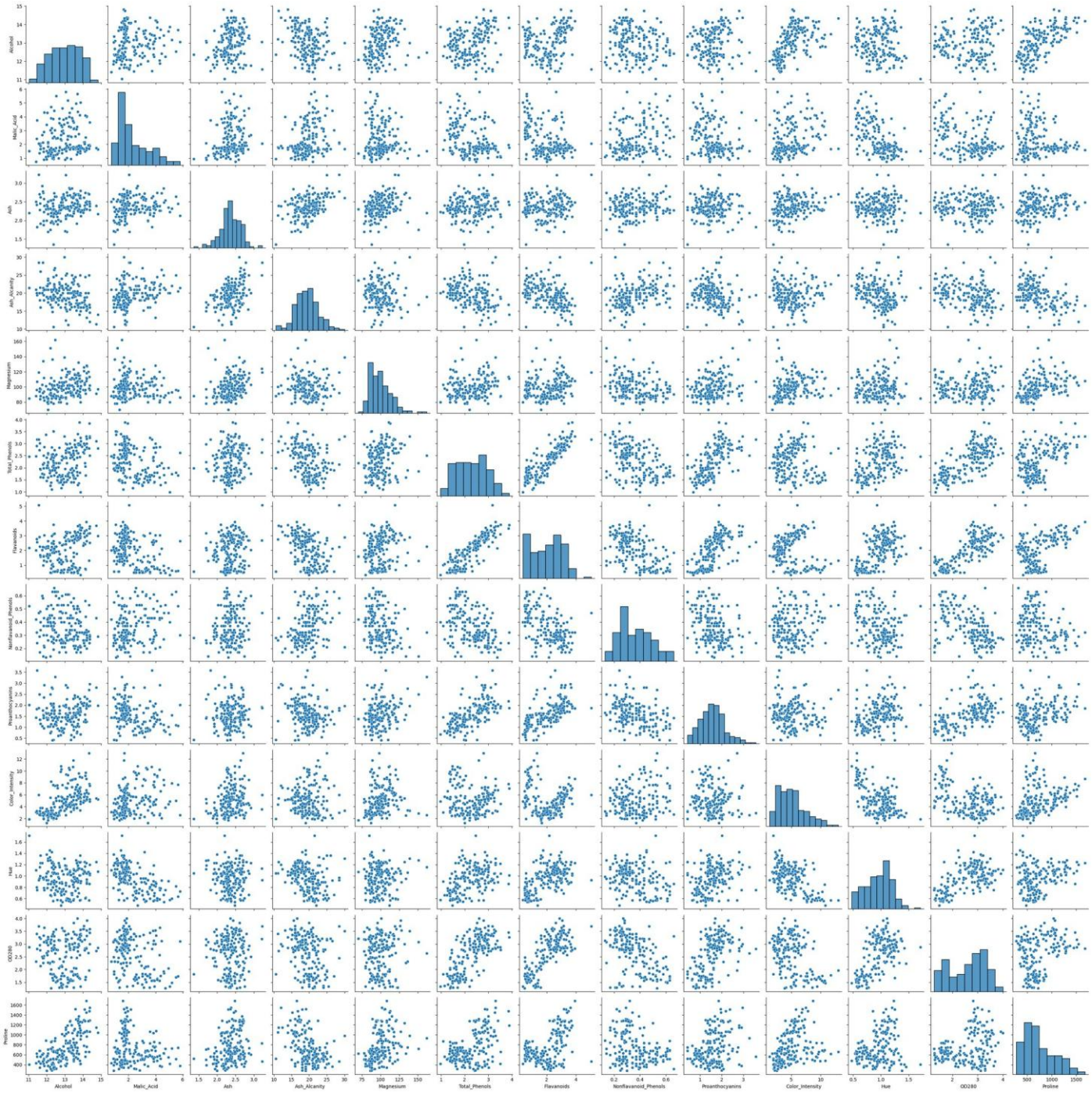
```
                       Proline
Alcohol                0.643720
Malic_Acid            -0.192011
Ash                    0.223626
Ash_Alcanity          -0.440597
Magnesium              0.393351
Total_Phenols          0.498115
Flavanoids             0.494193
Nonflavanoid_Phenols  -0.311385
Proanthocyanins        0.330417
Color_Intensity        0.316100
Hue                    0.236183
OD280                  0.312761
Proline                1.000000
```

```
plt.figure(figsize=(15,10))
sns.heatmap(df.corr(),annot=True, linewidths=1, cmap="coolwarm")
plt.show()
```




```
sns.pairplot(df)
plt.show()
```

```
d:\Anaconda\Lib\site-packages\seaborn\axisgrid.py:118: UserWarning: The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```




```
wcss = []
for i in range(1, 20):
    kmeans = KMeans(n_clusters = i, init = 'k-means++', random_state = 42)
    kmeans.fit(df)
    wcss.append(kmeans.inertia_)
```

```
d:\Anaconda\Lib\site-packages\sklearn\cluster\_kmeans.py:1412: 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
  super()._check_params_vs_input(X, default_n_init=10)
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KMeans is known to have a memory leak on Windows with MKL, when there are less
chunks than available threads. You can avoid it by setting the environment
variable OMP_NUM_THREADS=1.
  warnings.warn(
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  warnings.warn(

sns.set(style="whitegrid")

# Plot the Elbow Method with enhancements
plt.figure(figsize=(12, 8))
plt.plot(range(1, 20), wcss, marker='o', linestyle='-', color='skyblue',
markersize=5, markerfacecolor='orange')

# Adding title and labels with more customization
plt.title('Elbow Method for Optimal Number of Clusters', fontsize=18,
fontweight='bold')
plt.xlabel('Number of Clusters (k)', fontsize=14)
plt.ylabel('Within-Cluster Sum of Squares (WCSS)', fontsize=14)

# Adding gridlines and setting x-axis limits
plt.grid(True, which='both', linestyle='--', linewidth=0.7)
```
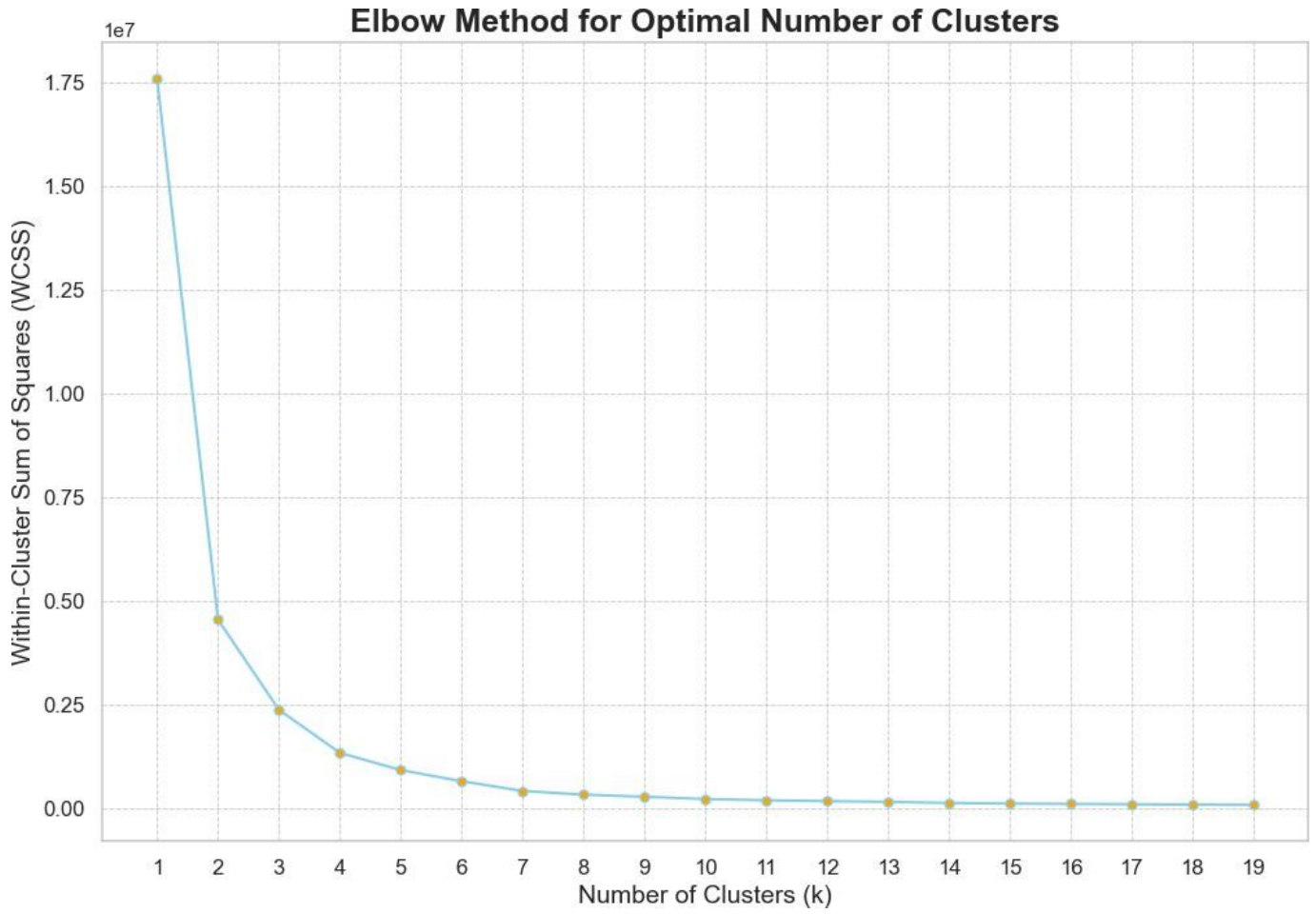

```
plt.xticks(range(1, 20), fontsize=12)
plt.yticks(fontsize=12)
```

```
(array([-2500000.,        0.,  2500000.,  5000000.,  7500000., 10000000.,
        12500000., 15000000., 17500000., 20000000.]),
 [Text(0, -2500000.0, '-0.25'),
  Text(0, 0.0, '0.00'),
  Text(0, 2500000.0, '0.25'),
  Text(0, 5000000.0, '0.50'),
  Text(0, 7500000.0, '0.75'),
  Text(0, 10000000.0, '1.00'),
  Text(0, 12500000.0, '1.25'),
  Text(0, 15000000.0, '1.50'),
  Text(0, 17500000.0, '1.75'),
  Text(0, 20000000.0, '2.00')])
```




```
km2 = KMeans(n_clusters=3)
clusters = km2.fit_predict(df)

data1 = df.copy()

data1["label"] = clusters
```

```
d:\Anaconda\Lib\site-packages\sklearn\cluster\ kmeans.py:1412:  FutureWarning:
The default value of `n_init` will change from 10 to 'auto' in 1.4. Set the
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KMeans is known to have a memory leak on Windows with MKL, when there are less
chunks than available threads. You can avoid it by setting the environment
```

```
variable OMP_NUM_THREADS=1.
  warnings.warn(
```

```
data1['label'].value_counts()
```

```
label
0    69
2    62
1    47
Name: count, dtype: int64
```

```
plt.figure(figsize=(6,6))
sns.barplot(x=[0,1,2], y=[47,69,62])
plt.xlabel('labels')
plt.ylabel('value counts')
plt.title('How many predict each label?')
```

```
Text(0.5, 1.0, 'How many predict each label?')
```