House Pricing

```
import pandas as pd
```

```
df=pd.read_csv('/content/Housing_Price (1).csv')
```

```
df.describe()
```

	price	area	bedrooms	bathrooms	stories	parking
count	5.450000e+02	545.000000	545.000000	545.000000	545.000000	545.000000
mean	4.766729e+06	5150.541284	2.965138	1.286239	1.805505	0.693578
std	1.870440e+06	2170.141023	0.738064	0.502470	0.867492	0.861586
min	1.750000e+06	1650.000000	1.000000	1.000000	1.000000	0.000000
25%	3.430000e+06	3600.000000	2.000000	1.000000	1.000000	0.000000
50%	4.340000e+06	4600.000000	3.000000	1.000000	2.000000	0.000000
75%	5.740000e+06	6360.000000	3.000000	2.000000	2.000000	1.000000
max	1.330000e+07	16200.000000	6.000000	4.000000	4.000000	3.000000

```
df.head(5)
```

	price	area	bedrooms	bathrooms	stories	mainroad	guestroom	basement	hotwaterheating	airconditioning	p
0	13300000	7420	4	2	3	yes	no	no	no	yes	
1	12250000	8960	4	4	4	yes	no	no	no	yes	
2	12250000	9960	3	2	2	yes	no	yes	no	no	
3	12215000	7500	4	2	2	yes	no	yes	no	yes	
4	11410000	7420	4	1	2	yes	yes	yes	no	yes	

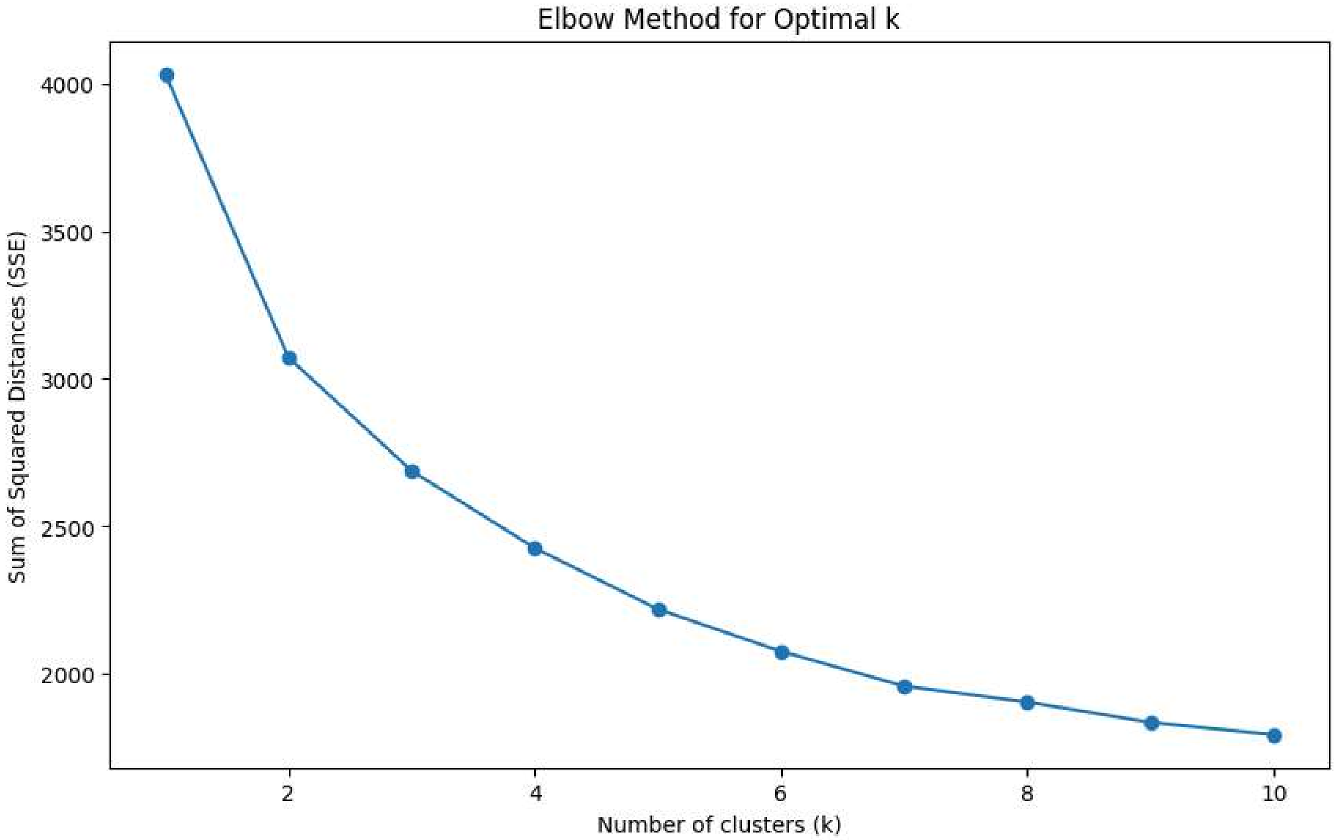
Next steps: Generate code with df | View recommended plots | New interactive sheet

```
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.cluster import KMeans
from sklearn.pipeline import Pipeline
from sklearn.compose import ColumnTransformer
import matplotlib.pyplot as plt

# Identify numerical and categorical columns
numerical_features = ['price', 'area', 'bedrooms', 'bathrooms', 'stories', 'parking']
categorical_features = ['mainroad', 'guestroom', 'basement', 'hotwaterheating', 'airconditioning', 'prefarea', 'furnis

# Preprocessing: Standardizing numerical features and encoding categorical features
preprocessor = ColumnTransformer(
    transformers=[
        ('num', StandardScaler(), numerical_features),
        ('cat', OneHotEncoder(drop='first'), categorical_features)
    ])

# Apply KMeans clustering with a guessed range for clusters (e.g., k=3 for simplicity)
kmeans_pipeline = Pipeline(steps=[('preprocessor', preprocessor),
```

```
                                          ('kmeans', KMeans(n_clusters=3, random_state=0))])

# Fit the model to the data
kmeans_pipeline.fit(df)

# Add cluster labels to the original dataframe
df['Cluster'] = kmeans_pipeline['kmeans'].labels_

# Display the clustered data sample
df[['price', 'area', 'bedrooms', 'Cluster']].head()
```

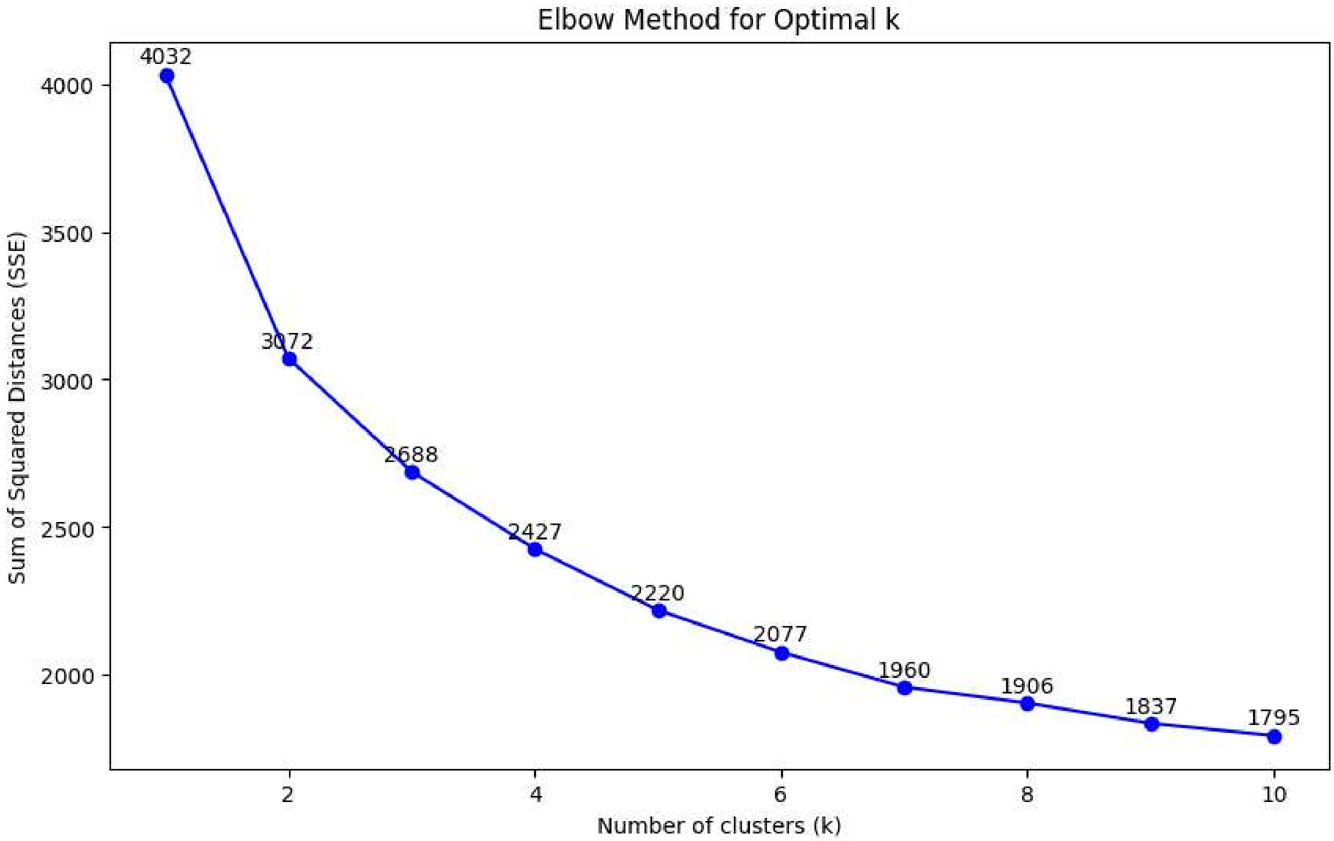
	price	area	bedrooms	Cluster
0	13300000	7420	4	2
1	12250000	8960	4	2
2	12250000	9960	3	2
3	12215000	7500	4	2
4	11410000	7420	4	2

```
# Elbow method to find the optimal number of clusters (k)
sse = []  # Sum of squared distances for each k
k_range = range(1, 11)

# Calculate SSE for each k
for k in k_range:
    kmeans = KMeans(n_clusters=k, random_state=0)
    kmeans.fit(preprocessor.fit_transform(df))
    sse.append(kmeans.inertia_)

# Plotting the elbow graph
plt.figure(figsize=(10, 6))
plt.plot(k_range, sse, marker='o')
plt.xlabel('Number of clusters (k)')
plt.ylabel('Sum of Squared Distances (SSE)')
plt.title('Elbow Method for Optimal k')
plt.show()
```

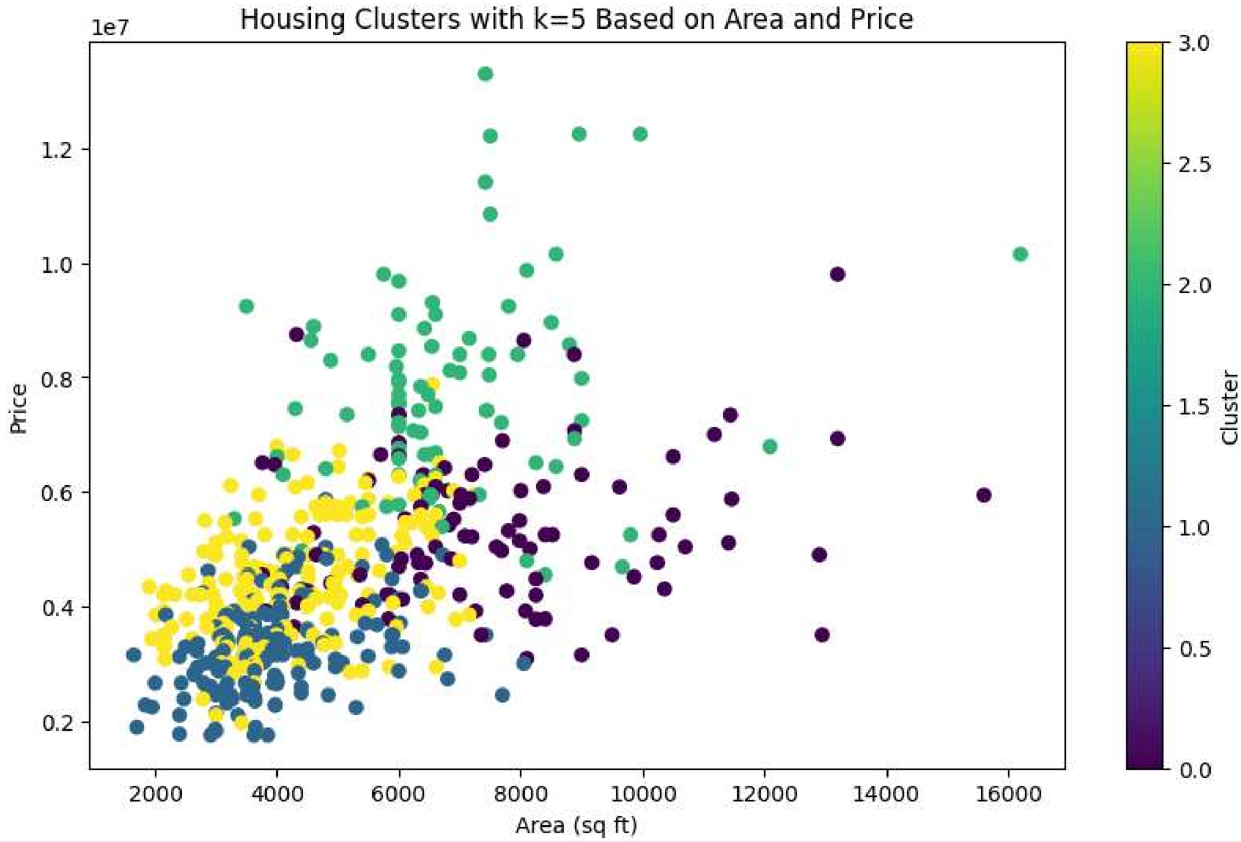



```
from sklearn.cluster import KMeans
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.compose import ColumnTransformer
import matplotlib.pyplot as plt

# Define the relevant features in the dataset
numerical_features = ['price', 'area', 'bedrooms', 'bathrooms', 'stories', 'parking']
categorical_features = ['mainroad', 'guestroom', 'basement', 'hotwaterheating', 'airconditioning', 'prefarea', 'furnishi

# Preprocessing step
preprocessor = ColumnTransformer(
    transformers=[
        ('num', StandardScaler(), numerical_features),
        ('cat', OneHotEncoder(drop='first'), categorical_features)
    ])

# Initialize an empty list to store the sum of squared distances for each k
sse = []
k_values = range(1, 11)

# Calculate SSE for each k value
for k in k_values:
    kmeans = KMeans(n_clusters=k, random_state=0)
    transformed_data = preprocessor.fit_transform(df)  # Preprocess data
    kmeans.fit(transformed_data)
    sse.append(kmeans.inertia_)

# Plot the elbow curve with annotations
plt.figure(figsize=(10, 6))
plt.plot(k_values, sse, marker='o', color='b')
plt.xlabel('Number of clusters (k)')
plt.ylabel('Sum of Squared Distances (SSE)')
plt.title('Elbow Method for Optimal k')

# Annotate each point with its SSE value
```

```
for i, txt in enumerate(sse):
    plt.annotate(f'{txt:.0f}', (k_values[i], sse[i]), textcoords="offset points", xytext=(0,5), ha='center')

plt.show()
```




```
# Fit KMeans with k = 4
kmeans = KMeans(n_clusters=4, random_state=0)
transformed_data = preprocessor.fit_transform(df)
df['Cluster'] = kmeans.fit_predict(transformed_data)

# Plotting clusters based on 'area' and 'price'
plt.figure(figsize=(10, 6))
plt.scatter(df['area'], df['price'], c=df['Cluster'], cmap='viridis', marker='o')
plt.colorbar(label='Cluster')
plt.xlabel('Area (sq ft)')
plt.ylabel('Price')
plt.title('Housing Clusters with k=5 Based on Area and Price')
plt.show()
```

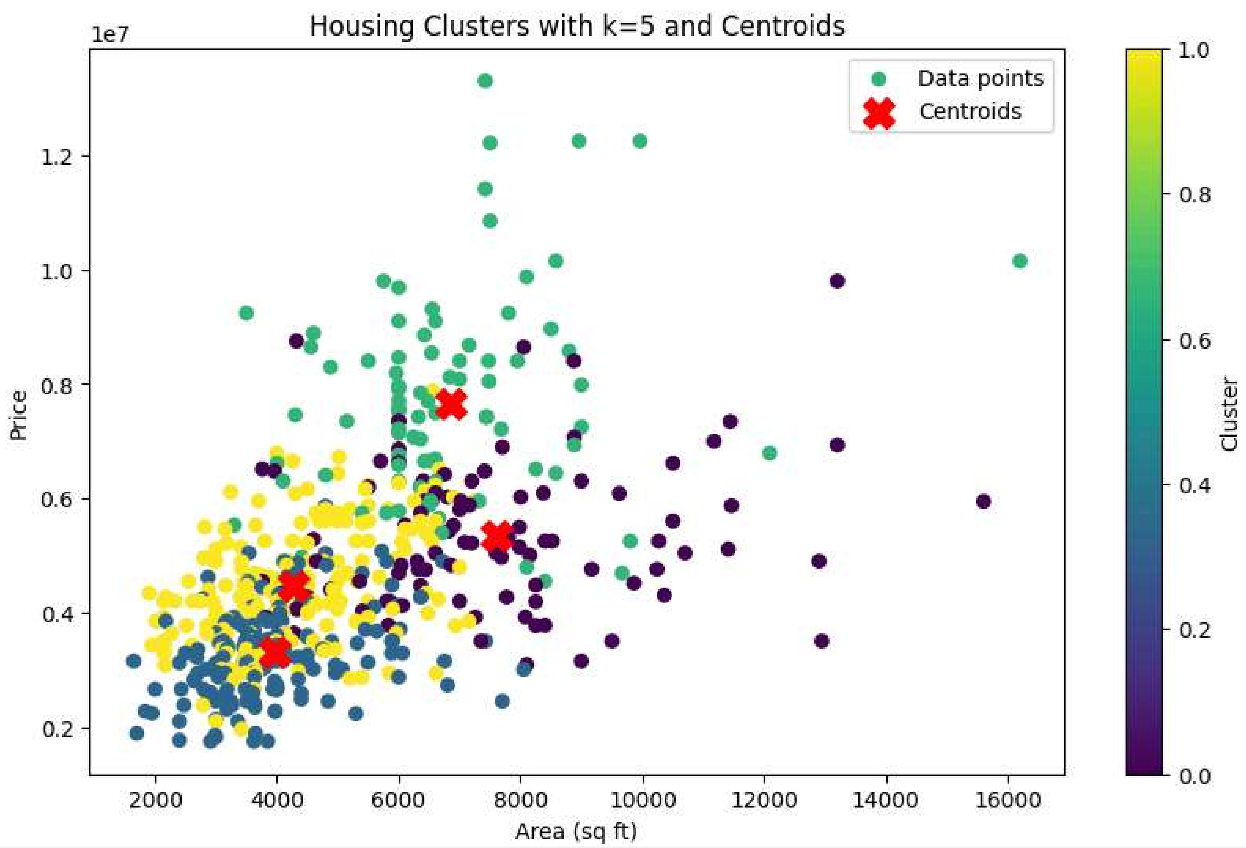



```
# Retrieve the centroids for the 5 clusters
centroids = kmeans.cluster_centers_

# Inverse transform to get the original scale for interpretability
# Only applies to numerical features, as categorical are one-hot encoded
centroids_original_scale = preprocessor.named_transformers_['num'].inverse_transform(centroids[:, :len(numerical_featu

# Convert to a DataFrame for better readability
centroid_df = pd.DataFrame(centroids_original_scale, columns=numerical_features)
print("Centroids of each cluster:\n", centroid_df)
```

```
Centroids of each cluster:
          price         area  bedrooms  bathrooms   stories   parking
0  5.351989e+06  7589.860215  2.774194   1.086022  1.236559  1.569892
1  3.305531e+06  3949.863636  2.340909   1.034091  1.244318  0.267045
2  7.665741e+06  6845.550562  3.483146   2.000000  2.887640  1.202247
3  4.471166e+06  4260.737968  3.401070   1.283422  2.101604  0.417112
```

```
# Fit KMeans with k = 4
kmeans = KMeans(n_clusters=4, random_state=0)
transformed_data = preprocessor.fit_transform(df)
df['Cluster'] = kmeans.fit_predict(transformed_data)

# Retrieve and inverse transform centroids for visualization
centroids = preprocessor.named_transformers_['num'].inverse_transform(kmeans.cluster_centers_[:, :len(numerical_features
centroids_df = pd.DataFrame(centroids, columns=numerical_features)

# Plot clusters and centroids based on 'area' and 'price'
plt.figure(figsize=(10, 6))
plt.scatter(df['area'], df['price'], c=df['Cluster'], cmap='viridis', marker='o', label="Data points")
plt.scatter(centroids_df['area'], centroids_df['price'], c='red', marker='X', s=200, label="Centroids")
plt.colorbar(label='Cluster')
plt.xlabel('Area (sq ft)')
plt.ylabel('Price')
```

```
plt.title('Housing Clusters with k=5 and Centroids')
plt.legend()
plt.show()
```




```
# Retrieve centroid values and inverse transform for better interpretability
centroids_original_scale = preprocessor.named_transformers_['num'].inverse_transform(kmeans.cluster_centers_[:, :len(nur
centroid_df = pd.DataFrame(centroids_original_scale, columns=numerical_features)
print("Centroids of each cluster:\n", centroid_df)
```

```
Centroids of each cluster:
          price         area  bedrooms  bathrooms   stories   parking
0  5.351989e+06  7589.860215  2.774194   1.086022  1.236559  1.569892
1  3.305531e+06  3949.863636  2.340909   1.034091  1.244318  0.267045
2  7.665741e+06  6845.550562  3.483146   2.000000  2.887640  1.202247
3  4.471166e+06  4260.737968  3.401070   1.283422  2.101604  0.417112
```

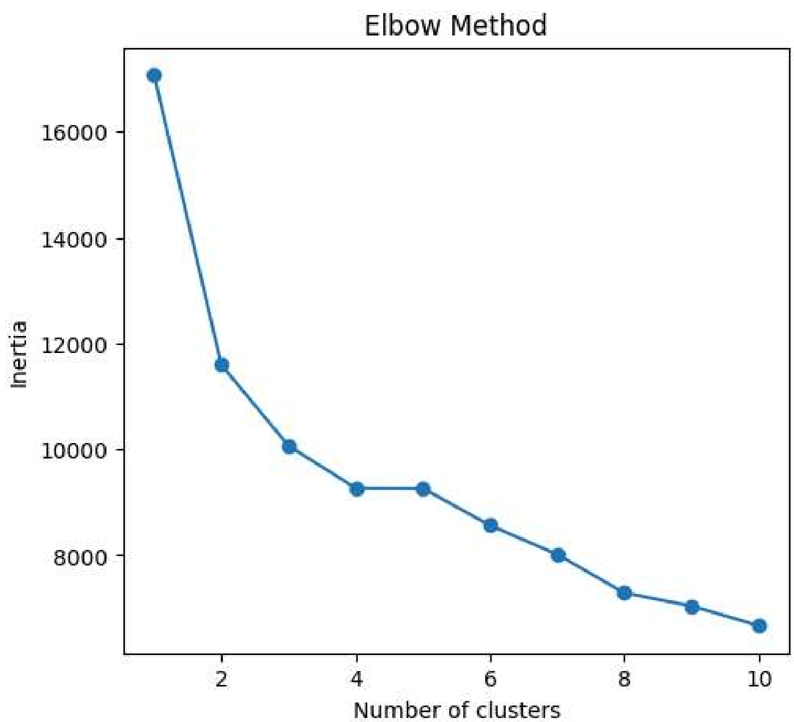
Breast Cancer

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn.datasets import load_breast_cancer
from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans
from sklearn.metrics import silhouette_score
```

```
# Load the breast cancer dataset
data = load_breast_cancer()
df = pd.DataFrame(data.data, columns=data.feature_names)
```

```
df['target'] = data.target  # This includes the labels (malignant/benign)


# Standardize the features
scaler = StandardScaler()
X_scaled = scaler.fit_transform(df.drop('target', axis=1))


# Elbow method to find optimal number of clusters
inertia = []

range_n_clusters = range(1, 11)

for n_clusters in range_n_clusters:
    kmeans = KMeans(n_clusters=n_clusters, random_state=42)
    kmeans.fit(X_scaled)
    inertia.append(kmeans.inertia_)


# Plot inertia
plt.figure(figsize=(12, 5))
plt.subplot(1, 2, 1)
plt.plot(range_n_clusters, inertia, marker='o')
plt.title('Elbow Method')
plt.xlabel('Number of clusters')
plt.ylabel('Inertia')
```

```
Text(0, 0.5, 'Inertia')
```



Wine Quality

```
import pandas as pd
```

```
# Load the dataset
data = pd.read_csv("/content/Wine_Quality.csv")

# Check for missing values
print(data.isnull().sum())
```

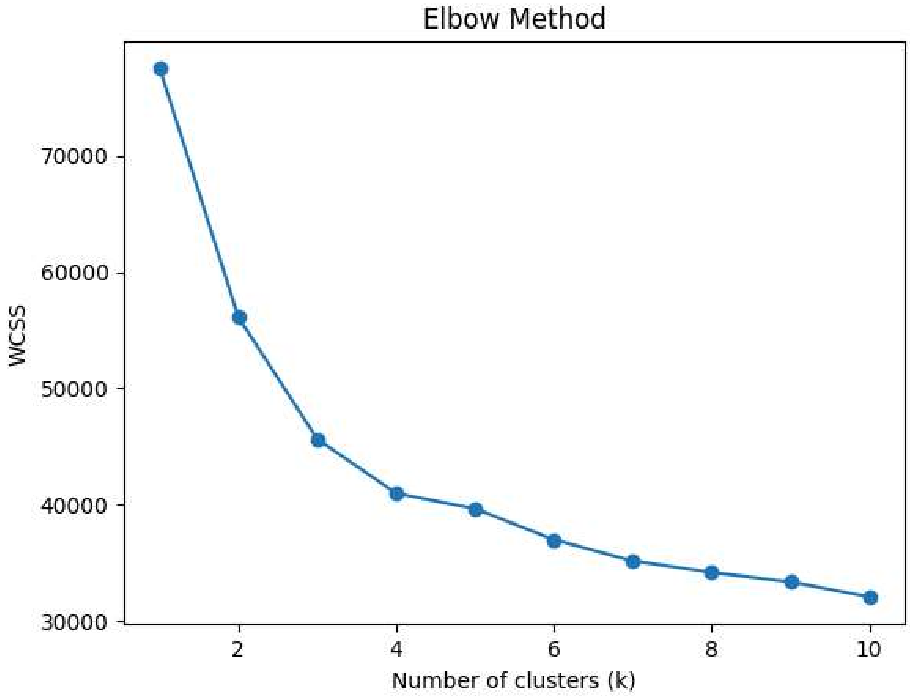
```
type                     0
fixed acidity           10
volatile acidity         8
citric acid              3
residual sugar           2
chlorides                2
free sulfur dioxide      0
total sulfur dioxide     0
density                  0
pH                       9
sulphates                4
alcohol                  0
quality                  0
dtype: int64
```

```
data_clean = data.dropna()
```

```
from sklearn.preprocessing import StandardScaler, LabelEncoder

# Encode 'type' column (if categorical)
data_clean['type'] = LabelEncoder().fit_transform(data_clean['type'])

# Drop 'quality' (if clustering without it) and scale features
features = data_clean.drop('quality', axis=1)
scaler = StandardScaler()
scaled_features = scaler.fit_transform(features)
```

```
<ipython-input-30-1d3208d25c52>:4: 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/indexing.html#return
  data_clean['type'] = LabelEncoder().fit_transform(data_clean['type'])
```

```
import matplotlib.pyplot as plt
from sklearn.cluster import KMeans

wcss = []
for k in range(1, 11):
    kmeans = KMeans(n_clusters=k, random_state=42)
    kmeans.fit(scaled_features)
    wcss.append(kmeans.inertia_)

# Plot the Elbow curve
plt.plot(range(1, 11), wcss, marker='o')
plt.title('Elbow Method')
plt.xlabel('Number of clusters (k)')
plt.ylabel('WCSS')
plt.show()
```

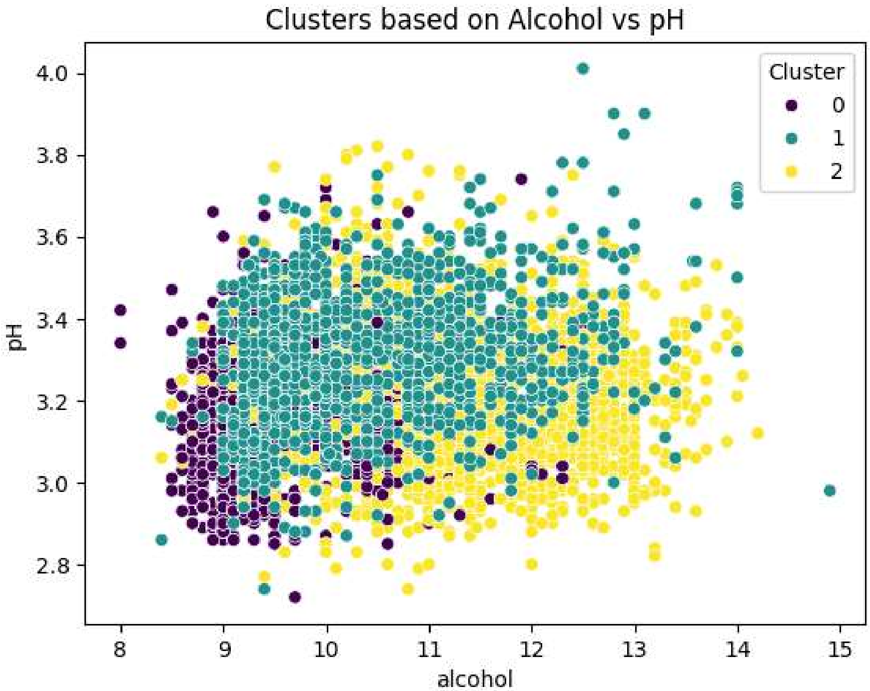



```
# Perform K-Means with the chosen k (e.g., k=3)
kmeans = KMeans(n_clusters=3, random_state=42)
clusters = kmeans.fit_predict(scaled_features)

# Add cluster labels to the original data
data_clean['Cluster'] = clusters
print(data_clean.head())
```

```
   type  fixed acidity  volatile acidity  citric acid  residual sugar  \
0     1            7.0              0.27         0.36            20.7
1     1            6.3              0.30         0.34             1.6
2     1            8.1              0.28         0.40             6.9
3     1            7.2              0.23         0.32             8.5
4     1            7.2              0.23         0.32             8.5

   chlorides  free sulfur dioxide  total sulfur dioxide  density    pH  \
0      0.045                 45.0                 170.0   1.0010  3.00
1      0.049                 14.0                 132.0   0.9940  3.30
2      0.050                 30.0                  97.0   0.9951  3.26
3      0.058                 47.0                 186.0   0.9956  3.19
4      0.058                 47.0                 186.0   0.9956  3.19

   sulphates  alcohol  quality  Cluster
0       0.45      8.8        6        0
1       0.49      9.5        6        2
2       0.44     10.1        6        2
3       0.40      9.9        6        0
4       0.40      9.9        6        0
<ipython-input-55-d39c6c220705>:6: 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/indexing.html#return
  data_clean['Cluster'] = clusters
```

```
import seaborn as sns

# Example visualization (if using 2 features)
sns.scatterplot(data=data_clean, x='alcohol', y='pH', hue='Cluster', palette='viridis')
```

```
plt.title('Clusters based on Alcohol vs pH')
plt.show()
```




```
from sklearn.cluster import KMeans

# Apply K-Means with your optimal k value (e.g., k=3)
kmeans = KMeans(n_clusters=3, random_state=42)
clusters = kmeans.fit_predict(scaled_features)

# Add the cluster labels to the original DataFrame
data_clean['Cluster'] = clusters
```

```
<ipython-input-57-9229bad41349>:8: 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/indexing.html#return
  data_clean['Cluster'] = clusters
```

```
# Calculate the mean of each feature for each cluster
centroids = data_clean.groupby('Cluster').mean()
print("Cluster Centroids:")
print(centroids)
```

```
Cluster Centroids:
             type  fixed acidity  volatile acidity  citric acid  \
Cluster
0        0.997873       6.974322          0.283075     0.358634
1        0.004419       8.343497          0.530780     0.270612
2        0.995997       6.775700          0.274031     0.319176

         residual sugar  chlorides  free sulfur dioxide  total sulfur dioxide  \
Cluster
0             11.189952   0.053310            45.535354            169.863105
1              2.507355   0.087919            15.704861             45.986742
2              3.390377   0.040944            28.919947            118.538359
```

```
          density        pH  sulphates    alcohol   quality
Cluster
0        0.996988  3.156582   0.493530   9.541946  5.619883
1        0.996783  3.310764   0.659230  10.404956  5.627525
2        0.992159  3.208239   0.487081  11.135851  6.044029
```

```
import matplotlib.pyplot as plt
import seaborn as sns

# Plot clusters (example using 'alcohol' vs 'pH')
sns.scatterplot(data=data_clean, x='alcohol', y='pH', hue='Cluster', palette='viridis', legend='full')

# Plot centroids (cluster means)
plt.scatter(centroids['alcohol'], centroids['pH'], s=200, c='red', marker='X', label='Centroids')

# Add title and legend
plt.title('Clusters with Centroids (Alcohol vs pH)')
plt.legend()
plt.show()
```