Heart Disease UCI - Unsupervised Learning

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1 IBM Unsupervised Learning Capstone Project

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1.1 Introduction

The heart is an amazing organ. It continuously pumps oxygen and nutrient-rich blood throughout your body to sustain life. This fist-sized powerhouse beats (expands and contracts) 100,000 times per day pumping 23,000 liters (5,000 gallons) of blood every day. To work properly, the heart (just like any other muscle) needs a good blood supply.

A heart attack (also known as myocardial infarction; MI) is defined as the sudden blockage of blood flow to a portion of the heart. Some of the heart muscle begins to die during a heart attack, and without early medical treatment, the loss of the muscle could be permanent.

Conditions such as high blood pressure, high blood cholesterol, obesity, and diabetes can raise the risk of a heart attack. Behaviors such as an unhealthy diet, low levels of physical activity, smoking, and excessive alcohol consumption can contribute to the conditions that can cause heart attacks. Some factors, such as age and family history of heart disease, cannot be modified but are associated with a higher risk of a heart attack.

1.2 Dataset

For the exploration of the risk a person has to develop a heart attack, the Heart Attack Analysis & Prediction Dataset from *kaggle.com* was utilized. It consists of:

- Age of the patient (age in years)
- Sex of the patient (sex; 1 = male, 0 = female)
- Exercise induced angina (exng; 1 = yes, 0 = no)
- Number of major vessels (ca; 0-3)
- Chest pain type (cp; Value 1: typical angina, Value 2: atypical angina, Value 3: non-anginal pain, Value 4: asymptomatic)
- Resting blood pressure (trestpbs; in mm/Hg on admission to the hospital)
- Cholesterol levels (chol; in mg/dl)
- Fasting blood sugar (fbs; if > 120 mg/dl, 1 = true; 0 = false)
- Resting electrocardiographic results (rest_ecg; 0 = normal, 1 = having ST-T wave abnormality, 2 = showing probable or definite left ventricular hypertrophy by Estes' criteria)
- Maximum heart rate achieved (thalach)
- Chance of heart attack (target: Heart disease)

- A blood disorder called thalassemia (thall; 1 = normal; 2 = fixed defect; 3 = reversable defect)
- Previous peak (oldpeak; ST depression induced by exercise relative to rest - 'ST' relates to positions on the ECG plot)
- Slope (slp; the slope of the peak exercise ST segment, Value 1: upsloping, Value 2: flat, Value 3: downsloping)

1.2.1 Acknowledgements

Creators:

```
Hungarian Institute of Cardiology. Budapest: Andras Janosi, M.D.
University Hospital, Zurich, Switzerland: William Steinbrunn, M.D.
University Hospital, Basel, Switzerland: Matthias Pfisterer, M.D.
V.A. Medical Center, Long Beach and Cleveland Clinic Foundation: Robert Detrano, M.D., Ph.D.
```


1.2.2 Aim

The aim of this project is to apply unsupervised learning techniques to find whether an individual will develop a heart attack risk or not. More specifically, after some feature engineering and exploratory data analysis, the k-means and agglomerative clusteing algorithms will be explored.

[35]:

```
# Importing libraries

import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.neighbors import KNeighborsClassifier
from sklearn.preprocessing import MinMaxScaler, StandardScaler, RobustScaler

from sklearn.metrics import confusion_matrix, accuracy_score
from sklearn.metrics import precision_recall_curve
from sklearn.metrics import average_precision_score
from sklearn.metrics import roc_curve
from sklearn.metrics import auc
from sklearn.model_selection import cross_val_score
from sklearn.metrics import f1_score
from sklearn.metrics import classification_report
from sklearn.metrics import accuracy_score
from sklearn.metrics import silhouette_score

from sklearn.decomposition import PCA
from sklearn.cluster import KMeans, DBSCAN, AgglomerativeClustering
from scipy.cluster import hierarchy
```

```
from sklearn.pipeline import Pipeline
from sklearn.model_selection import StratifiedShuffleSplit

%matplotlib inline
```

[2]:
```
import warnings
warnings.filterwarnings('ignore')
```

[3]:
```
sns.set()
```

[4]:
```
heart = pd.read_csv('heart.csv')
```

[5]:
```
heart.head()
```

[5]:
```
   age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak  slope  \
0   63    1   3       145   233    1        0      150      0      2.3      0
1   37    1   2       130   250    0        1      187      0      3.5      0
2   41    0   1       130   204    0        0      172      0      1.4      2
3   56    1   1       120   236    0        1      178      0      0.8      2
4   57    0   0       120   354    0        1      163      1      0.6      2

   ca  thal  target
0   0     1       1
1   0     2       1
2   0     2       1
3   0     2       1
4   0     2       1
```

1.3 Feature Engineering

[6]:
```
heart.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype
---  ------    --------------  -----
 0   age       303 non-null    int64
 1   sex       303 non-null    int64
 2   cp        303 non-null    int64
 3   trestbps  303 non-null    int64
 4   chol      303 non-null    int64
 5   fbs       303 non-null    int64
 6   restecg   303 non-null    int64
 7   thalach   303 non-null    int64
 8   exang     303 non-null    int64
 9   oldpeak   303 non-null    float64
 10  slope     303 non-null    int64
```

```
 11   ca         303 non-null    int64
 12   thal       303 non-null    int64
 13   target     303 non-null    int64
dtypes: float64(1), int64(13)
memory usage: 33.3 KB
```

[7]:
```
heart.describe()
```

[7]:
```
              age         sex          cp    trestbps        chol         fbs  \
count  303.000000  303.000000  303.000000  303.000000  303.000000  303.000000
mean    54.366337    0.683168    0.966997  131.623762  246.264026    0.148515
std      9.082101    0.466011    1.032052   17.538143   51.830751    0.356198
min     29.000000    0.000000    0.000000   94.000000  126.000000    0.000000
25%     47.500000    0.000000    0.000000  120.000000  211.000000    0.000000
50%     55.000000    1.000000    1.000000  130.000000  240.000000    0.000000
75%     61.000000    1.000000    2.000000  140.000000  274.500000    0.000000
max     77.000000    1.000000    3.000000  200.000000  564.000000    1.000000

          restecg     thalach       exang     oldpeak       slope          ca  \
count  303.000000  303.000000  303.000000  303.000000  303.000000  303.000000
mean     0.528053  149.646865    0.326733    1.039604    1.399340    0.729373
std      0.525860   22.905161    0.469794    1.161075    0.616226    1.022606
min      0.000000   71.000000    0.000000    0.000000    0.000000    0.000000
25%      0.000000  133.500000    0.000000    0.000000    1.000000    0.000000
50%      1.000000  153.000000    0.000000    0.800000    1.000000    0.000000
75%      1.000000  166.000000    1.000000    1.600000    2.000000    1.000000
max      2.000000  202.000000    1.000000    6.200000    2.000000    4.000000

             thal      target
count  303.000000  303.000000
mean     2.313531    0.544554
std      0.612277    0.498835
min      0.000000    0.000000
25%      2.000000    0.000000
50%      2.000000    1.000000
75%      3.000000    1.000000
max      3.000000    1.000000
```

[8]:
```
duplicate=heart[heart.duplicated()]
print("Duplicate Rows :")
duplicate
```

```
Duplicate Rows :
```

[8]:
```
     age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak  \
164   38    1   2       138   175    0        1      173      0      0.0

     slope  ca  thal  target
```

```
164       2   4     2       1
```

[9]:
```python
heart_attack = heart.drop_duplicates()
```

[10]:
```python
categorical = ['sex', 'exang', 'ca', 'cp', 'thal', 'fbs', 'restecg', 'slope',␣
 ↪'target']

for cat in categorical:
    heart_attack[cat] = heart_attack[cat].astype('category')
```

[11]:
```python
heart_attack.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 302 entries, 0 to 302
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype
---  ------    --------------  -----
 0   age       302 non-null    int64
 1   sex       302 non-null    category
 2   cp        302 non-null    category
 3   trestbps  302 non-null    int64
 4   chol      302 non-null    int64
 5   fbs       302 non-null    category
 6   restecg   302 non-null    category
 7   thalach   302 non-null    int64
 8   exang     302 non-null    category
 9   oldpeak   302 non-null    float64
 10  slope     302 non-null    category
 11  ca        302 non-null    category
 12  thal      302 non-null    category
 13  target    302 non-null    category
dtypes: category(9), float64(1), int64(4)
memory usage: 18.2 KB
```

[12]:
```python
heart_attack['target'].value_counts(normalize=True)
```

[12]:
```
1    0.543046
0    0.456954
Name: target, dtype: float64
```

[13]:
```python
heart_attack.describe()
```

[13]:

	age	trestbps	chol	thalach	oldpeak
count	302.00000	302.000000	302.000000	302.000000	302.000000
mean	54.42053	131.602649	246.500000	149.569536	1.043046
std	9.04797	17.563394	51.753489	22.903527	1.161452
min	29.00000	94.000000	126.000000	71.000000	0.000000
25%	48.00000	120.000000	211.000000	133.250000	0.000000

50%	55.50000	130.000000	240.500000	152.500000	0.800000
75%	61.00000	140.000000	274.750000	166.000000	1.600000
max	77.00000	200.000000	564.000000	202.000000	6.200000

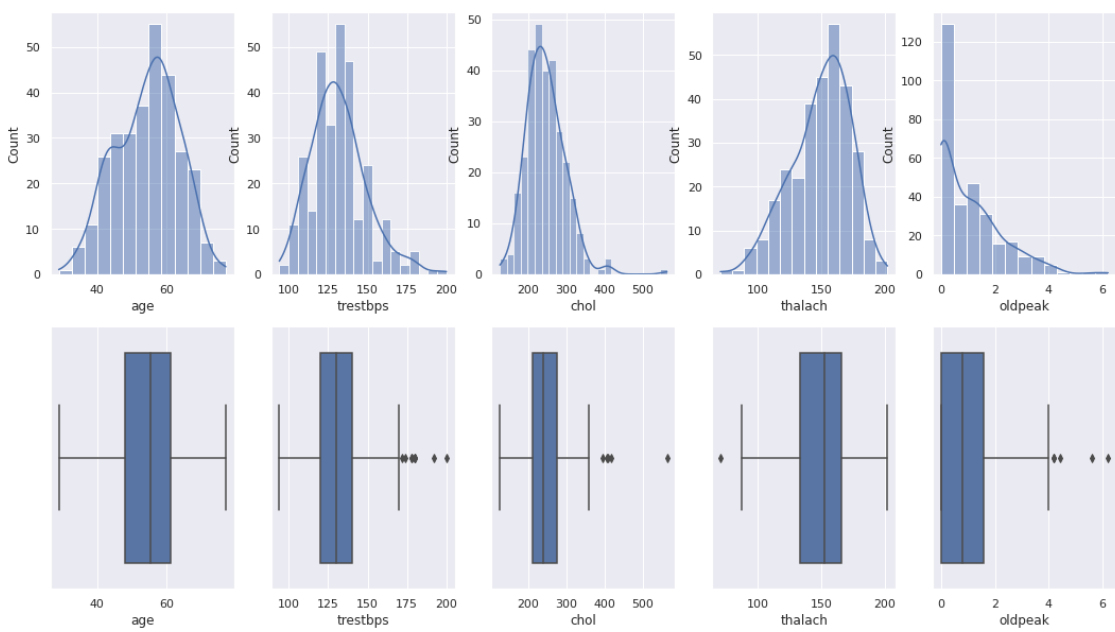
[14]:
```
heart_attack = heart_attack.reset_index(drop=True)
```

[15]:
```
plt.figure(figsize=(9,7))
plt.title('Missing values', fontweight='bold')

ax = sns.heatmap(heart.isnull(),yticklabels=False,cbar='viridis',cmap='viridis')

plt.show()
```

Numerical: Age, trestbps, chol, thalach, oldpeak

[16]:

```python
# Finding outliers and plotting histograms for all numerical features

plt.figure(figsize=(18,10))
plt.subplot(2,5,1)
sns.histplot(heart_attack['age'],kde=True)
plt.subplot(2,5,6)
sns.boxplot(heart_attack['age'])
plt.subplot(2,5,2)
sns.histplot(heart_attack['trestbps'],kde=True)
plt.subplot(2,5,7)
sns.boxplot(heart_attack['trestbps'])
plt.subplot(2,5,3)
sns.histplot(heart_attack['chol'],kde=True)
plt.subplot(2,5,8)
sns.boxplot(heart_attack['chol'])
plt.subplot(2,5,4)
sns.histplot(heart_attack['thalach'],kde=True)
plt.subplot(2,5,9)
sns.boxplot(heart_attack['thalach'])
plt.subplot(2,5,5)
sns.histplot(heart_attack['oldpeak'],kde=True)
plt.subplot(2,5,10)
sns.boxplot(heart_attack['oldpeak']);
```

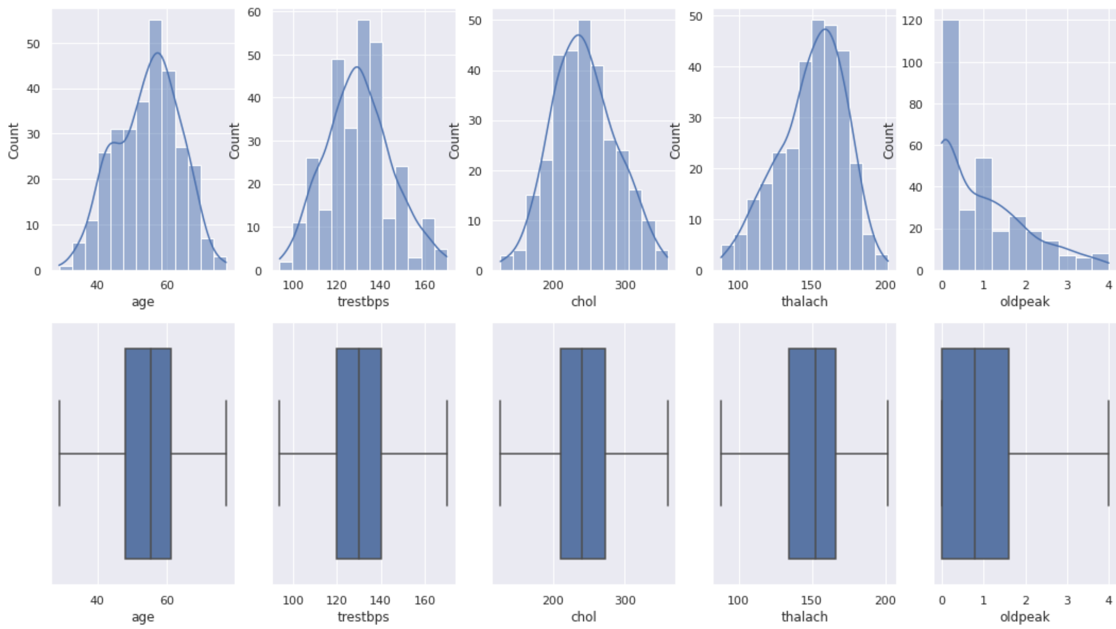


1.3.1 Removing the outliers

[17]:
```
for col in ['trestbps', 'chol', 'oldpeak']:

    Q1 = heart_attack[col].quantile(0.25)
    Q3 = heart_attack[col].quantile(0.75)
    IQR = Q3 - Q1

    heart_attack.loc[heart_attack[col] > Q3 + 1.5 * IQR, col] = heart_attack.
 ↪describe().loc['50%'][col]
```

[18]:
```
Q1 = heart_attack['thalach'].quantile(0.25)
Q3 = heart_attack['thalach'].quantile(0.75)
IQR = Q3 - Q1
min_thalach = Q1 - 1.5 * IQR

median_thalach = heart_attack.describe().loc['50%']['thalach']
heart_attack.loc[heart_attack['thalach'] < min_thalach, 'thalach'] =␣
 ↪median_thalach
```

[19]:
```
plt.figure(figsize=(18,10))
plt.subplot(2,5,1)
sns.histplot(heart_attack['age'],kde=True)
plt.subplot(2,5,6)
sns.boxplot(heart_attack['age'])
plt.subplot(2,5,2)
sns.histplot(heart_attack['trestbps'],kde=True)
plt.subplot(2,5,7)
sns.boxplot(heart_attack['trestbps'])
plt.subplot(2,5,3)
sns.histplot(heart_attack['chol'],kde=True)
plt.subplot(2,5,8)
sns.boxplot(heart_attack['chol'])
plt.subplot(2,5,4)
sns.histplot(heart_attack['thalach'],kde=True)
plt.subplot(2,5,9)
sns.boxplot(heart_attack['thalach'])
plt.subplot(2,5,5)
sns.histplot(heart_attack['oldpeak'],kde=True)
plt.subplot(2,5,10)
sns.boxplot(heart_attack['oldpeak']);
```




```
[20]: for col in heart_attack.columns:
          print(col,":",heart_attack[col].unique().size)
```

```
age : 41
sex : 2
cp : 4
trestbps : 43
chol : 148
fbs : 2
restecg : 3
thalach : 91
exang : 2
oldpeak : 36
slope : 3
ca : 5
thal : 4
target : 2
```

```
[21]: numerical = ['age', 'trestbps', 'chol', 'thalach', 'oldpeak']
```

```
[22]: log_columns = heart_attack[numerical].skew().sort_values(ascending=False)
      log_columns = log_columns.loc[log_columns > 0.75]

      log_columns
```

```
[22]: oldpeak    0.96995
      dtype: float64
```

```
[23]: # The log transformations
for col in log_columns.index:
    heart_attack[col] = np.log1p(heart_attack[col])
```

```
[24]: sc = StandardScaler()
feature_columns = [x for x in heart_attack.columns if x not in categorical]
for col in feature_columns:
    heart_attack[col] = sc.fit_transform(heart_attack[[col]])

heart_attack.head(4)
```

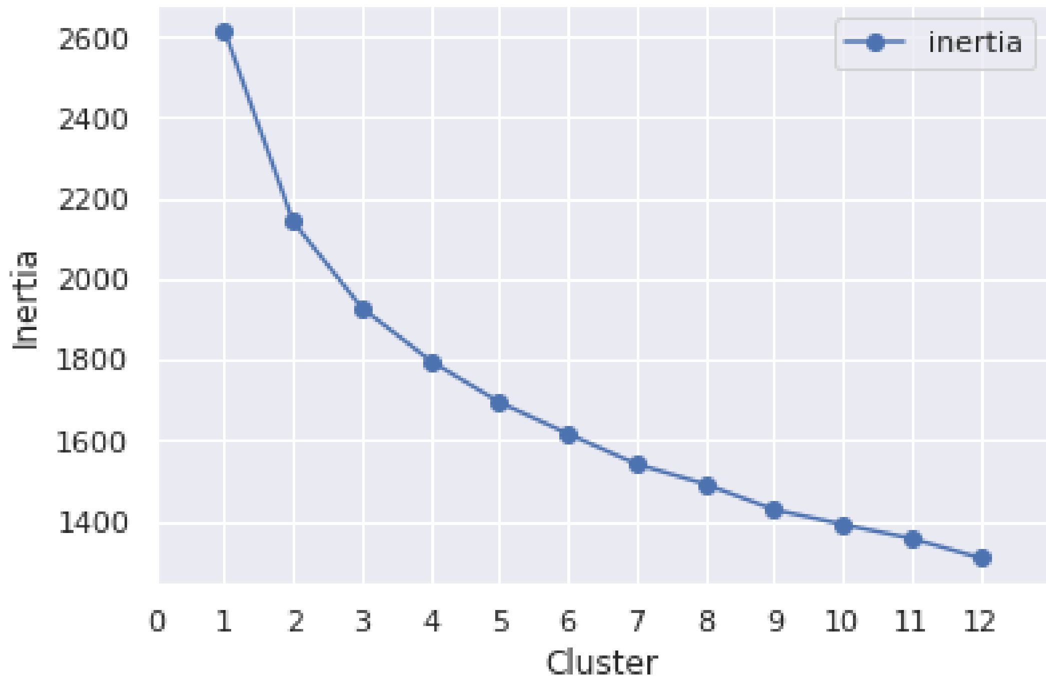
```
[24]:         age  sex  cp  trestbps      chol  fbs  restecg   thalach  exang   oldpeak  \
0  0.949794    1   3  0.987461 -0.229564    1        0  0.007165      0  1.284737
1 -1.928548    1   2 -0.004379  0.152039    0        1  1.657982      0  1.905745
2 -1.485726    0   1 -0.004379 -0.880534    0        0  0.988732      0  0.647114
3  0.174856    1   1 -0.665606 -0.162222    0        1  1.256432      0  0.071103

  slope  ca  thal  target
0     0   0     1       1
1     0   0     2       1
2     2   0     2       1
3     2   0     2       1
```

1.3.2 K-Means Clustering

The scaled data was fitted to a k-means clustering model to determine the optimal number of clusters over a range of 1 to 13 clusters. The diagram below shows a plot of inertia versus clusters.

```
[25]: km_list = list()

for clust in range(1,13):
    km = KMeans(n_clusters=clust, random_state=42)
    km = km.fit(heart_attack.drop('target', axis=1))

    km_list.append(pd.Series({'clusters': clust,
                              'inertia': km.inertia_,
                              'model': km}))
```

```
[26]: plot_data = (pd.concat(km_list, axis=1)
             .T
             [['clusters','inertia']]
             .set_index('clusters'))

ax = plot_data.plot(marker='o',ls='-')
ax.set_xticks(range(0,13))
ax.set_xlim(0,13)
ax.set(xlabel='Cluster', ylabel='Inertia');
```



The plot of inertia versus number of clusters shows an elbow at number of clusters equal to 2, that is k =2.

[27]:
```
km = KMeans(n_clusters=2, random_state=42)
km = km.fit(heart_attack.drop('target', axis=1))

heart_attack['kmeans'] = km.predict(heart_attack.drop('target', axis=1))
(heart_attack[['target','kmeans']]
 .groupby(['kmeans','target'])
 .size()
 .to_frame()
 .rename(columns={0:'number'}))
```

[27]:
```
               number
kmeans target
0      0           40
       1          142
1      0           98
       1           22
```

1.3.3 Agglomerative Clustering

[28]:
```
for linkage in ['complete', 'ward']:
    ag = AgglomerativeClustering(n_clusters=2, linkage=linkage,␣
 ↪compute_full_tree=True)
    ag = ag.fit(heart_attack.drop('target', axis=1))
    heart_attack[str('agglom_'+linkage)] = ag.fit_predict(heart_attack.
 ↪drop('target', axis=1))
```

[29]:
```
(heart_attack[['target','agglom_ward']]
 .groupby(['target','agglom_ward'])
 .size()
 .to_frame()
 .rename(columns={0:'number'}))
```

[29]:
```
                     number
target agglom_ward
0      0                 37
       1                101
1      0                131
       1                 33
```

[30]:
```
(heart_attack[['target','agglom_complete']]
     .groupby(['target','agglom_complete'])
     .size()
     .to_frame()
     .rename(columns={0:'number'}))
```

[30]:
```
                         number
target agglom_complete
0      0                     93
       1                     45
1      0                     18
       1                    146
```

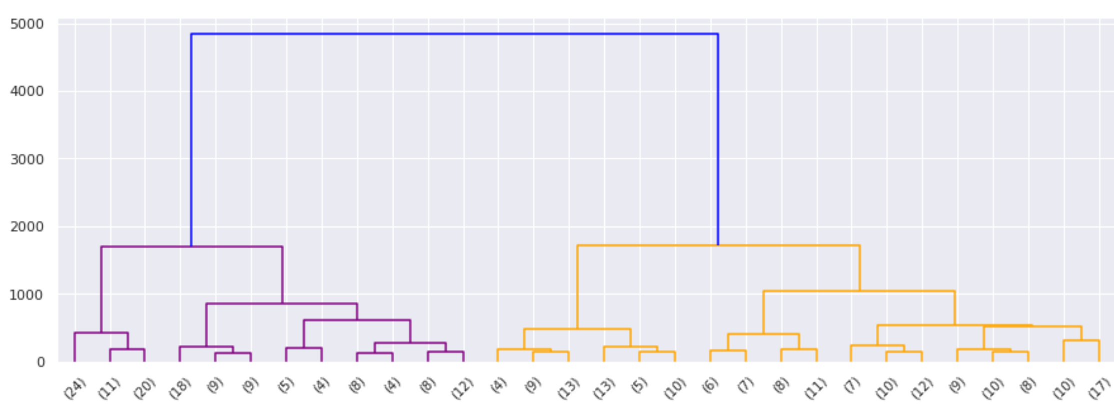
[31]:
```
# Comparison
(heart_attack[['target','agglom_complete', 'agglom_ward','kmeans']]
 .groupby(['target', 'agglom_complete', 'agglom_ward', 'kmeans'])
 .size()
 .to_frame()
 .rename(columns={0:'number'}))
```

[31]:
```
                                                 number
target agglom_complete agglom_ward kmeans
0      0               0           0                  2
                                   1                  0
                       1           0                  3
                                   1                 88
```

	1	0	0	33
			1	2
		1	0	2
			1	8
1	0	0	0	0
			1	0
		1	0	2
			1	16
	1	0	0	131
			1	0
		1	0	9
			1	6

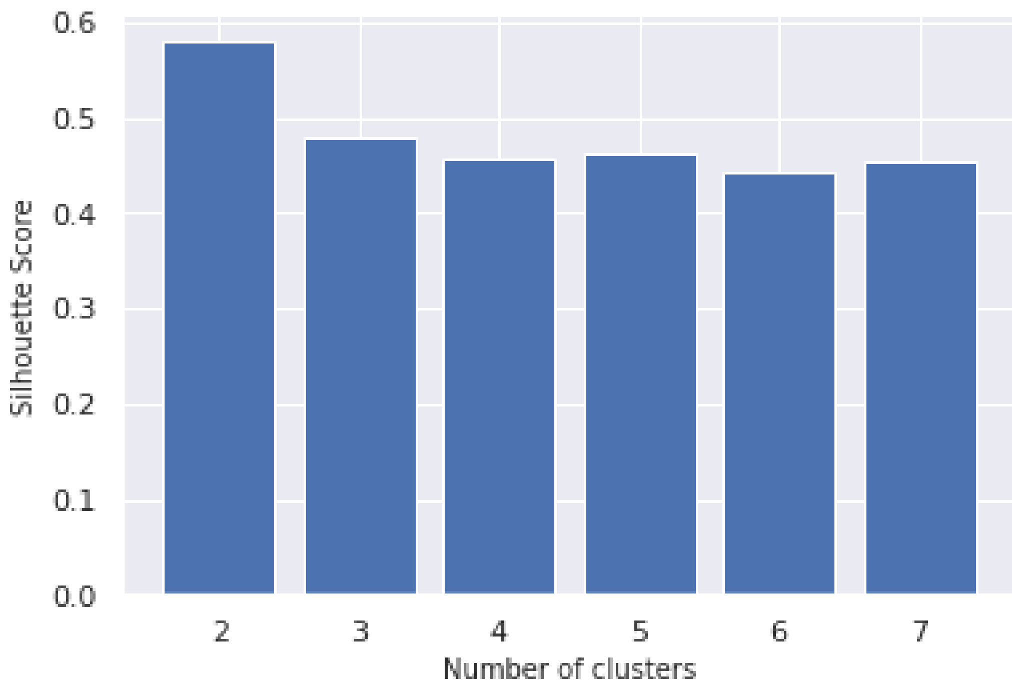
The diagram below shows the dendrogram for the Hierarchical Agglomerative Clustering model.

[32]:
```
Z = hierarchy.linkage(ag.children_, method='ward')

fig, ax = plt.subplots(figsize=(15,5))


hierarchy.set_link_color_palette(['purple', 'orange'])

den = hierarchy.dendrogram(Z, orientation='top',
                           p=30, truncate_mode='lastp',
                           show_leaf_counts=True, ax=ax,
                           above_threshold_color='blue')
```



[37]:
```
silhouette_scores = []

for n_cluster in range(2, 8):
    silhouette_scores.append(
        silhouette_score(ag.children_, AgglomerativeClustering(n_clusters =
 ↪n_cluster).fit_predict(ag.children_)))
```

```
# Plotting a bar graph to compare the results
k = [2, 3, 4, 5, 6,7]
plt.bar(k, silhouette_scores)
plt.xlabel('Number of clusters', fontsize = 10)
plt.ylabel('Silhouette Score', fontsize = 10)
plt.show()
```



1.4 Conclusion

1.4.1 Findings

From the abovementioned analysis, a few important findings can be outlined. Performing both K-means and agglomerative clustering algorithms, one could observe that the best model for the prediction of a potential myocardial infarction is the **Complete-link agglomerative technique**. On the contrary, for predicting those cases that there won't be any implications, the most suitable is the **Ward-link agglomerative clustering**. From both the dendrogram and the silhoute score plots, it is evident that the optimal number of the clusters is **two**.

1.4.2 Next steps

As a further suggestion, a DBSCAN could be implemented, following a Principal Component Analysis.

```
[ ]:
```