Predicting and Reducing Risk for Cardiovascular Disease

Erica Smith
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Abstract

The data used for this analysis is Svetlana Ulianova's "Cardiovascular Disease" dataset found on Kaggle which contains 11 features and 1 target for 70k patients. A classification model was constructed to determine if cardiovascular disease status can be predicted from select clinical and lifestyle data. A cluster analysis was performed to identify commonalities within groups of patients with cardiovascular disease in order to design risk reduction programs targeted to their specific risk factors. The classification model accurately predicted 72% of patients with cardiovascular disease. The cluster analysis found 5 clusters of patients with differentiated needs including smoking cessation, weight loss, and stress reduction.

Motivation

Each year, 1 in every 4 Americans dies from cardiovascular events including heart attack and stroke; millions more will experience a significant decrease in quality of life due to the effects of coronary artery disease and hypertension (CDC, 2019a). Risk for cardiovascular disease includes a combination of clinical factors as well as lifestyle factors such as high cholesterol, sedentary lifestyle, stress, and smoking. When designing outreach and risk reduction programs, it is important to consider that the most successful programs address the *specific risks* of a particular population. For example, one program may address lifestyle factors like smoking and inactivity while another may address genetic high cholesterol.

The purpose of this analysis is to develop a model that can aid in identification of those at risk for cardiovascular disease and classify them into smaller groups with common risk factors. The model output can be used to channel patients to programs to address their specific health promotion needs.

Dataset(s)

The dataset used for this analysis is titled "Cardiovascular Disease" and may be obtained from Kaggle. It is comprised of 70k records containing

- 11 features (age, gender, height, weight, systolic blood pressure, diastolic blood pressure, cholesterol, glucose, smoking, alcohol use, and physical activity
- 1 target (cardiovascular disease)

No information is provided about the source or timeframe of the data.

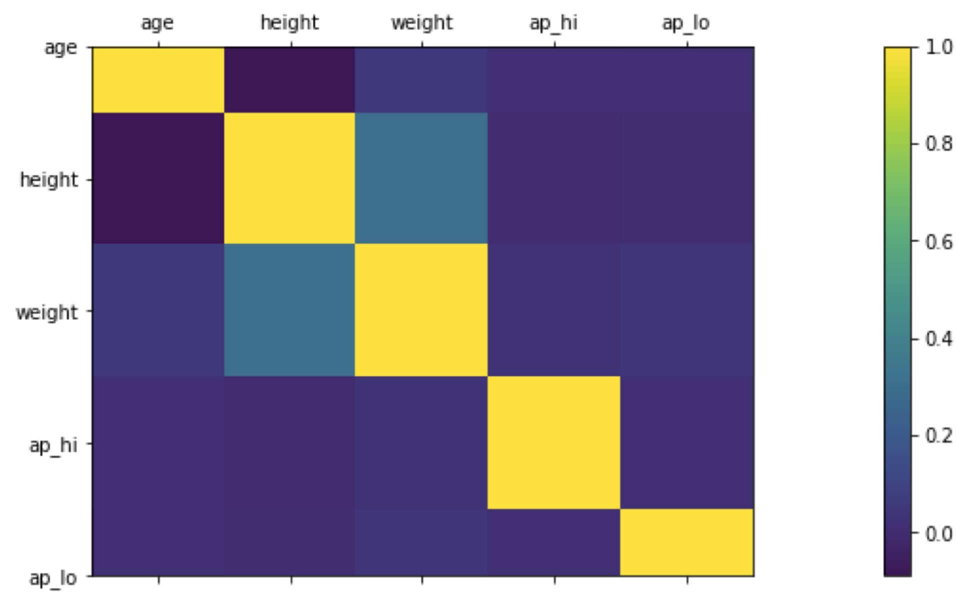
Data Preparation and Cleaning

After reading in the data, it was analyzed for missing and illogical values. No missing data was detected. The dataset did contain 412 records that were filtered out due to one of the following issues (since they are considered illogical given that the minimum age of a patient in the dataset is 29 years):

- Height less than 48 inches (4 feet)
- Weight less than 90 pounds
- Systolic blood pressure less than 50mmHg
- Diastolic blood pressure less than 30mmHg

Data Preparation and Cleaning

A correlation matrix was created to look for and address highly-correlated features. It appears that height and weight are strongly related, which makes sense logically. Therefore, a new variable for BMI was created to normalize the body mass (Weight in pounds x 703 ÷ (Height in Inches^2)) (CDC, 2019b)



Data Preparation and Cleaning

Blood pressure features were separated in the dataset. Although the correlation matrix does not show them being highly correlated, systolic (ap_hi) and diastolic (ap_lo) blood pressure readings are usually interpreted together in the clinical setting. To normalize this, the mean arterial pressure (MAP) was calculated for each patient. MAP reflects the blood pressure during a full cardiac cycle and is calculated as ((2 * diastolic reading) + systolic reading) / 3. (Bonsall, 2011)

After cleaning and normalizing the data, the remaining features were age, gender, cholesterol, glucose, smoking status, alcohol use, activity level, BMI, and MAP.

Research Question(s)

This analysis focuses on two research questions:

- Can we use clinical and behavioral data predict cardiovascular disease?
- How can we cluster patients with cardiovascular disease into small groups with common features in order to design programs to address their specific risk factors?

Research Question 1: Methods

The first research question requires a classification analysis. This is because we are using data to predict whether a patient has cardiovascular disease and we have a known response which allows us to assess the model's accuracy.

In this analysis, the features age, gender, cholesterol, glucose, smoking, alcohol use, activity level, BMI, and MAP were used to try to predict cardiovascular disease.   Two thirds of the data were used to train the model and the last third was held out for testing. A random seed was used for establishing the test data tuples.

Research Question 1: Findings

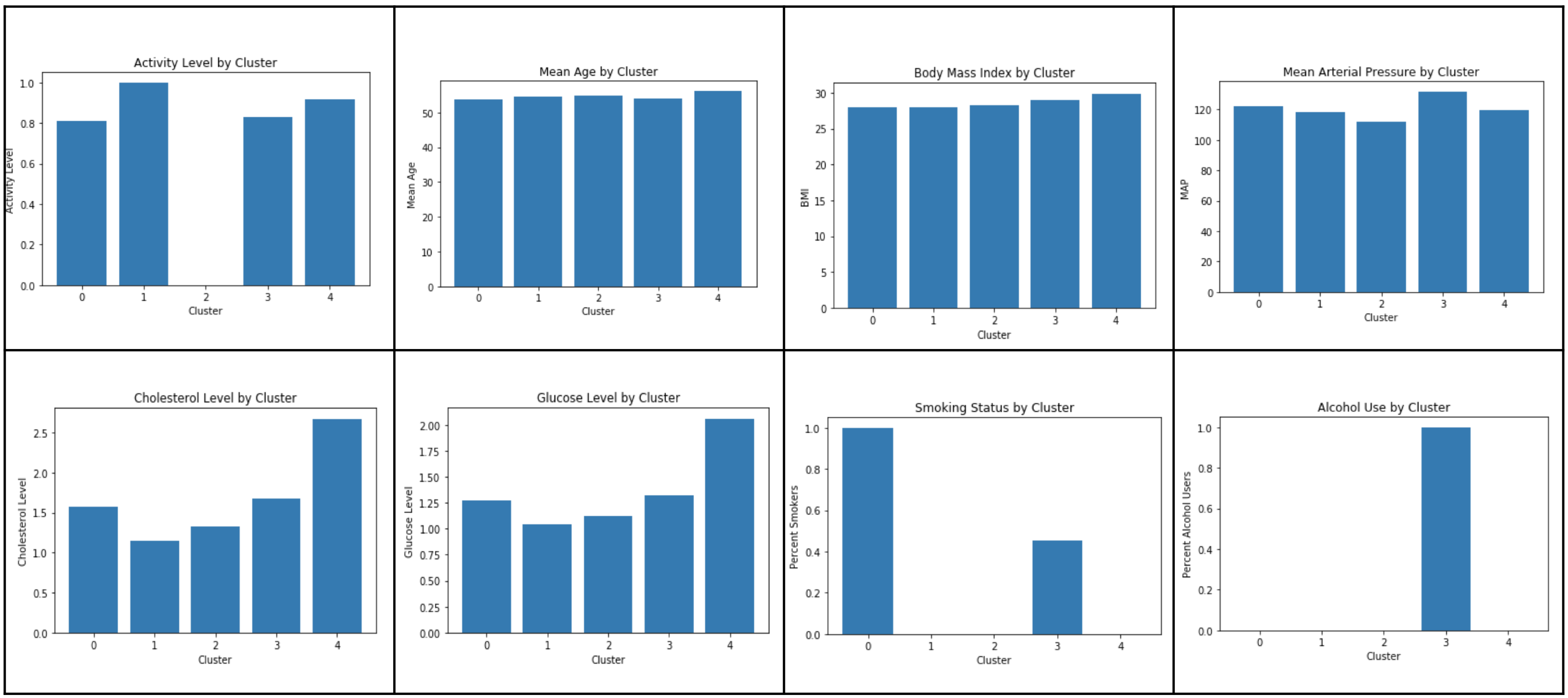
The model accurately predicted 72% of patients with cardiovascular disease. The stability of the model was tested by resetting the random seed several times; each time the prediction remained between 72.0% and 72.9%.

Research Question 2: Methods

The second research question is a cluster analysis because we are using data to partition patients into smaller groups based on commonalities in their risk factors. Since we do not have data to compare to the model's output, this unsupervised learning must be evaluated to ensure it is clinically logical.

For this analysis, the prepped data was filtered to only include patients with known cardiovascular disease (n = 34795). The features age, gender, cholesterol, glucose, smoking, alcohol use, activity level, BMI, and MAP were used in the analysis. Because the features were of mixed types (binary, scaled, continuous), they were normalized using the StandardScaler method. Initially, the analysis was set up to create 10 clusters (k = 10). However, the results were too diverse and the cluster size was reduced to 5.

Research Question 2: Findings



Research Question 2: Findings

Cluster 0	100% of patients in this cluster are smokers. They could benefit from a risk reduction program aimed at smoking cessation
Cluster 1	The majority (52%) of patients fall into this cluster. On average, they have normal blood pressure, BMI, cholesterol, glucose levels and activity levels, and they don't drink or smoke.
Cluster 2	100% of patients in this cluster have very low activity levels. Their other clinical and lifestyle variables are within normal limits. They could benefit from a risk reduction program aimed at increasing physical activity.
Cluster 3	Patients in this cluster have high blood pressure, tend to be smokers and drink alcohol. Since tobacco and alcohol are often used by people under stress, these patients could benefit from a stress reduction program.
Cluster 4	Patients in this cluster have an elevated body mass index and high cholesterol and glucose levels. Clinically, the combination of these factors is known as metabolic syndrome. These patients could benefit from a program aimed at weight reduction through healthy eating.

Limitations

There are several limitations associated with this analysis:

- While the features used in this analysis are common to many cardiovascular diseases, some diseases have different clinical manifestations. For example, arrhythmias can cause low blood pressure while coronary artery disease can cause high blood pressure. The type of cardiovascular disease is not given in the dataset, which may introduce bias when interpreting results.
- The lab value features are scaled, not continuous. A continuous value could help better differentiate patients.
- The lifestyle variables are binary. The model could potentially be improved by providing continuous data instead of binary; for example number of minutes of exercise or packs of cigarettes smoked per day.

Conclusions

This analysis demonstrated that a simple model consisting of a few clinical and lifestyle variables can do a fairly good job of predicting cardiovascular disease. A screening tool could be developed to check for these features and quickly detect and manage risk in a doctor's office.

The analysis also produced some key insights into how to reduce risk in a few clusters of patients with cardiovascular disease. Although the majority of patients fell into a poorly differentiated cluster (cluster 1), the remaining clusters are very well differentiated and lend themselves to programs to address very specific risk factors.

Acknowledgements

Thank you to Svetlana Ulianova for posting the Cardiovascular Disease dataset on Kaggle.

The statistics on heart disease mortality and morbidity in the US were obtained from the Centers for Disease Control and Prevention's Heart Disease Facts Web page at https://www.cdc.gov/heartdisease/facts.htm.

References

Bonsall, L. (2011). Calculating the mean arterial pressure (MAP). Retrieved December 10, 2019 from https://www.nursingcenter.com/ncblog/december-2011/calculating-the-map

Centers for Disease Control and Prevention. (2019a). Heart disease facts. Retrieved December 11, 2019 from https://www.cdc.gov/heartdisease/facts.htm

Centers for Disease Control and Prevention. (2019.b). Retrieved December 10, 2019 from https://www.cdc.gov/healthyweight/assessing/bmi/childrens_bmi/childrens_bmi_formula.html

Ulianova, S. (2018). Cardiovascular disease dataset. Retrieved December 8, 2019 from https://www.kaggle.com/sulianova/cardiovascular-disease-dataset

Smith Final Project

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0.1 Data source

https://www.kaggle.com/sulianova/cardiovascular-disease-dataset#cardio_train.csv

0.2 Import packages

[40]:
```
import numpy as np
import pandas as pd
from sklearn.metrics import accuracy_score
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans
from itertools import cycle, islice
import matplotlib.pyplot as plt
import matplotlib as mpl
from pandas.plotting import parallel_coordinates

%matplotlib inline
```

0.3 Data acquisition and prep

[3]:
```
data = pd.read_table('/Users/ericabadger/Downloads/cardio_train.csv', sep = ';')
```

[4]:
```
data.head()
```

[4]:
```
   id    age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
0   0  18393       2     168    62.0    110     80            1     1      0
1   1  20228       1     156    85.0    140     90            3     1      0
2   2  18857       1     165    64.0    130     70            3     1      0
3   3  17623       2     169    82.0    150    100            1     1      0
4   4  17474       1     156    56.0    100     60            1     1      0

   alco  active  cardio
0     0       1       0
```

1	0	1	1
2	0	0	1
3	0	1	1
4	0	0	0

Columns

- id ID number
- age in days
- gender 1 - women, 2 - men
- height cm
- weight kg
- ap_hi Systolic blood pressure
- ap_lo Diastolic blood pressure
- cholesterol 1: normal, 2: above normal, 3: well above normal
- gluc 1: normal, 2: above normal, 3: well above normal
- smoke whether patient smokes or not
- alco Binary feature
- active Binary feature
- cardio Target variable

0.3.1 Check for nulls

[5]:
```
# check for nulls
data[data.isnull().any(axis=1)]
```

[5]:
```
Empty DataFrame
Columns: [id, age, gender, height, weight, ap_hi, ap_lo, cholesterol, gluc,
smoke, alco, active, cardio]
Index: []
```

0.3.2 Convert from metric to imperial

[58]:
```
# add variable to make age in years
data['age_yrs'] = data['age']/365

# add variable to make height in inches
data['height_in'] = data['height'] / 2.54

# add variable to convert weight to pounds
data['weight_lb'] = data['weight'] * 2.2
```

[59]:
```
# summary stats
data.describe()
```

```
[59]:                 id           age        gender        height        weight  \
count  69588.000000  69588.000000  69588.000000  69588.000000  69588.000000
mean   49969.893243  19470.150026      1.349845    164.452463     74.253697
std    28854.199371   2466.191542      0.476924      7.858600     14.314437
min        0.000000  10798.000000      1.000000    122.000000     41.000000
25%    24996.750000  17666.750000      1.000000    159.000000     65.000000
50%    49997.500000  19703.000000      1.000000    165.000000     72.000000
75%    74889.250000  21327.000000      2.000000    170.000000     82.000000
max    99999.000000  23713.000000      2.000000    250.000000    200.000000

              ap_hi         ap_lo   cholesterol          gluc         smoke  \
count  69588.000000  69588.000000  69588.000000  69588.000000  69588.000000
mean     129.101727     96.680635      1.367492      1.226821      0.088334
std      154.164119    188.678257      0.680783      0.572679      0.283782
min       60.000000     30.000000      1.000000      1.000000      0.000000
25%      120.000000     80.000000      1.000000      1.000000      0.000000
50%      120.000000     80.000000      1.000000      1.000000      0.000000
75%      140.000000     90.000000      2.000000      1.000000      0.000000
max    16020.000000  11000.000000      3.000000      3.000000      1.000000

               alco        active        cardio       age_yrs     height_in  \
count  69588.000000  69588.000000  69588.000000  69588.000000  69588.000000
mean       0.053860      0.803817      0.500014     53.342877     64.745064
std        0.225743      0.397112      0.500004      6.756689      3.093937
min        0.000000      0.000000      0.000000     29.583562     48.031496
25%        0.000000      1.000000      0.000000     48.402055     62.598425
50%        0.000000      1.000000      1.000000     53.980822     64.960630
75%        0.000000      1.000000      1.000000     58.430137     66.929134
max        1.000000      1.000000      1.000000     64.967123     98.425197

          weight_lb
count  69588.000000
mean     163.358133
std       31.491761
min       90.200000
25%      143.000000
50%      158.400000
75%      180.400000
max      440.000000
```

0.3.3 Filtering

```
[60]: # filter data for illogical values
height_filter = data['height_in'] >= 48

weight_filter = data['weight_lb'] >= 90
```

```
ap_hi_filter = data['ap_hi'] >= 50

ap_lo_filter = data['ap_lo'] >= 30

before_filter = data.shape[0]

data = data[height_filter & weight_filter & ap_hi_filter & ap_lo_filter]

after_filter = data.shape[0]

print(before_filter)
print(after_filter)
print(before_filter - after_filter)
```

```
69588
69588
0
```

[61]:
```
data.describe()
```

[61]:

	id	age	gender	height	weight
count	69588.000000	69588.000000	69588.000000	69588.000000	69588.000000
mean	49969.893243	19470.150026	1.349845	164.452463	74.253697
std	28854.199371	2466.191542	0.476924	7.858600	14.314437
min	0.000000	10798.000000	1.000000	122.000000	41.000000
25%	24996.750000	17666.750000	1.000000	159.000000	65.000000
50%	49997.500000	19703.000000	1.000000	165.000000	72.000000
75%	74889.250000	21327.000000	2.000000	170.000000	82.000000
max	99999.000000	23713.000000	2.000000	250.000000	200.000000

	ap_hi	ap_lo	cholesterol	gluc	smoke
count	69588.000000	69588.000000	69588.000000	69588.000000	69588.000000
mean	129.101727	96.680635	1.367492	1.226821	0.088334
std	154.164119	188.678257	0.680783	0.572679	0.283782
min	60.000000	30.000000	1.000000	1.000000	0.000000
25%	120.000000	80.000000	1.000000	1.000000	0.000000
50%	120.000000	80.000000	1.000000	1.000000	0.000000
75%	140.000000	90.000000	2.000000	1.000000	0.000000
max	16020.000000	11000.000000	3.000000	3.000000	1.000000

	alco	active	cardio	age_yrs	height_in
count	69588.000000	69588.000000	69588.000000	69588.000000	69588.000000
mean	0.053860	0.803817	0.500014	53.342877	64.745064
std	0.225743	0.397112	0.500004	6.756689	3.093937
min	0.000000	0.000000	0.000000	29.583562	48.031496
25%	0.000000	1.000000	0.000000	48.402055	62.598425

```
50%         0.000000       1.000000       1.000000      53.980822      64.960630
75%         0.000000       1.000000       1.000000      58.430137      66.929134
max         1.000000       1.000000       1.000000      64.967123      98.425197

           weight_lb
count   69588.000000
mean      163.358133
std        31.491761
min        90.200000
25%       143.000000
50%       158.400000
75%       180.400000
max       440.000000
```

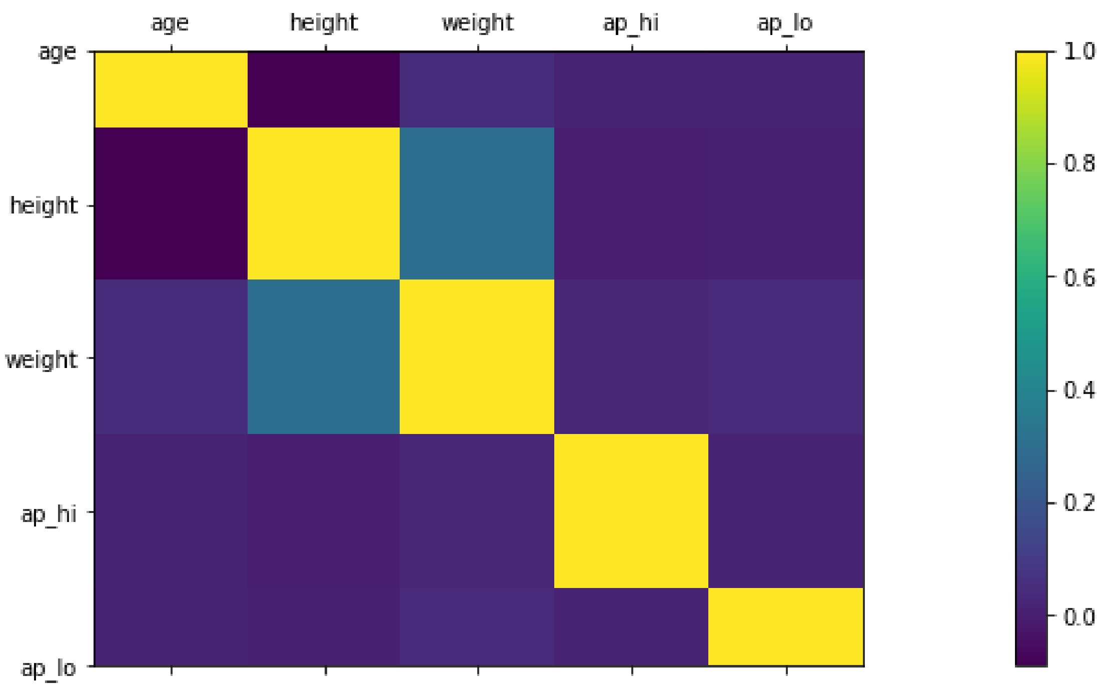
0.3.4 Look for and address highly correlated features

[62]:
```python
# Look at correlations between continuous variables
data_cont = data[['age','height','weight','ap_hi','ap_lo']].copy()
```

[63]:
```python
data_cont.corr()

plt.matshow(data_cont.corr())
plt.xticks(range(len(data_cont.columns)), data_cont.columns)
plt.yticks(range(len(data_cont.columns)), data_cont.columns)
plt.colorbar()
plt.gcf().set_size_inches(25, 5)

plt.show()
```



[64]:
```
# add clinical variables for highly correlated measures

# BMI : Weight (LBS) x 703 ÷ Height (Inches²)
data['bmi'] = (data['weight_lb'] * 703) / (data['height_in']**2)

# Mean Arterial Pressure (MAP): ((2 * DP) + SP) / 3
data['map'] = ((2 * data['ap_lo']) + data['ap_hi']) / 3

data.head()
```

[64]:
```
   id    age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
0   0  18393       2     168    62.0    110     80            1     1      0
1   1  20228       1     156    85.0    140     90            3     1      0
2   2  18857       1     165    64.0    130     70            3     1      0
3   3  17623       2     169    82.0    150    100            1     1      0
4   4  17474       1     156    56.0    100     60            1     1      0

   alco  active  cardio    age_yrs  height_in  weight_lb        bmi  \
0     0       1       0  50.391781  66.141732      136.4  21.918890
1     0       1       1  55.419178  61.417323      187.0  34.850994
2     0       0       1  51.663014  64.960630      140.8  23.456193
3     0       1       1  48.282192  66.535433      180.4  28.647444
4     0       0       0  47.873973  61.417323      123.2  22.960655

         map
```

```
0     90.000000
1    106.666667
2     90.000000
3    116.666667
4     73.333333
```

0.3.5 Final data set

[146]:
```
data2 =␣
↪data[['age','gender','cholesterol','gluc','smoke','alco','active','cardio','bmi','map']].
↪copy()
#data2.head()
```

0.4 Classification

[147]:
```
# make the heart disease label
y = data2[['cardio']].copy()
```

[67]:
```
# specify the features to use
cardio_features = ['age','gender','cholesterol','gluc','smoke',
        'alco','active','bmi','map']
```

[68]:
```
x = data[cardio_features].copy()
```

[69]:
```
# Check the column names
y.columns
```

[69]:
```
Index(['cardio'], dtype='object')
```

[70]:
```
x.columns
```

[70]:
```
Index(['age', 'gender', 'cholesterol', 'gluc', 'smoke', 'alco', 'active',
       'bmi', 'map'],
      dtype='object')
```

[80]:
```
# create the test and train datasets
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.33,␣
↪random_state=777)
```

[81]:
```
# fit the model on the train set
cardio_classifier = DecisionTreeClassifier(max_leaf_nodes=10, random_state=0)
cardio_classifier.fit(x_train, y_train)
```

[81]:
```
DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=None,
                       max_features=None, max_leaf_nodes=10,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, presort=False,
                       random_state=0, splitter='best')
```

[82]:
```
# predict on the test set
predictions = cardio_classifier.predict(x_test)
```

[83]:
```
# check predicted vs. actual for 100 values
predictions[:100]
```

[83]:
```
array([1, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 0,
       0, 0, 1, 1, 0, 1, 0, 0, 1, 1, 1, 1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 0,
       1, 1, 1, 0, 1, 1, 1, 1, 0, 0, 0, 0, 1, 0, 1, 1, 0, 1, 1, 0, 1, 1,
       1, 1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 0, 0, 0, 1, 0, 1, 0, 0, 1, 0,
       0, 0, 1, 1, 1, 0, 1, 1, 0, 1, 1, 0])
```

[84]:
```
y_test['cardio'][:100]
```

[84]:
```
2046     0
15141    1
14535    0
55832    1
61032    1
        ..
16625    1
30421    0
6411     1
27639    1
38023    0
Name: cardio, Length: 100, dtype: int64
```

[85]:
```
# Check the accuracy of the model
accuracy_score(y_true = y_test, y_pred = predictions)
```

[85]:
```
0.7250163291966035
```

0.5 Clustering

For the people with heart disease, try to cluster them into groups to see how they are related. This could help with designing programs to target each cluster's specific needs when it comes to health promotion.

[89]:
```
# First, limit data to only people with heart disease.
patients = data2.copy()

before_filter = patients.shape[0]

heart_disease = patients['cardio'] == 1

patients = patients[heart_disease]

after_filter = patients.shape[0]

print(before_filter)
print(after_filter)
print(before_filter - after_filter)
```

```
69588
34795
34793
```

For features, use cardio_features already established above. Create a new dataframe containing only these features.

[90]:
```
select_df = patients[cardio_features]
select_df.head()
```

[90]:
```
      age  gender  cholesterol  gluc  smoke  alco  active        bmi  \
1   20228       1            3     1      0     0       1  34.850994
2   18857       1            3     1      0     0       0  23.456193
3   17623       2            1     1      0     0       1  28.647444
7   22584       2            3     3      0     0       1  29.917758
15  16782       2            1     1      0     0       0  37.775182

           map
1   106.666667
2    90.000000
3   116.666667
7   103.333333
15   93.333333
```

[91]:
```
# scale the features so they are on normalized scales
X = StandardScaler().fit_transform(select_df)
X
```

[91]:
```
array([[ 0.07390164, -0.73931179,  1.90789673, …,  0.51607348,
         1.16919562, -0.07450624],
       [-0.51810583, -0.73931179,  1.90789673, …, -1.93770854,
        -0.90910928, -0.17895935],
       [-1.05095573,  1.3526093 , -0.66692211, …,  0.51607348,
```

```
        0.0377263 , -0.01183438],
       …,
       [ 1.09857977, -0.73931179,  0.62048731, …,  0.51607348,
         3.99823325, -0.07450624],
       [-0.42785815,  1.3526093 ,  1.90789673, …, -1.93770854,
         0.51874445,  0.00905625],
       [ 1.02517257, -0.73931179, -0.66692211, …, -1.93770854,
        -0.25550143, -0.1267328 ]])
```

[92]:
```
# Set up the K means clustering
kmeans = KMeans(n_clusters= 5) # create a k means object with 5 clusters
model = kmeans.fit(X) # scaled dataframe we are fitting
print("model\n", model) # will be a k means object
```

```
model
 KMeans(algorithm='auto', copy_x=True, init='k-means++', max_iter=300,
       n_clusters=5, n_init=10, n_jobs=None, precompute_distances='auto',
       random_state=None, tol=0.0001, verbose=0)
```

[93]:
```
# Centers of the clusters
centers = model.cluster_centers_
```

[94]:
```
# Plot different pairs of dimensions
labels = kmeans.labels_
```

[102]:
```
select_df2 = select_df.copy()
# select_df2.head()
```

[103]:
```
select_df2['clusters'] = labels
# select_df2.head()
```

[103]:

	age	gender	cholesterol	gluc	smoke	alco	active	bmi	\
1	20228	1	3	1	0	0	1	34.850994	
2	18857	1	3	1	0	0	0	23.456193	
3	17623	2	1	1	0	0	1	28.647444	
7	22584	2	3	3	0	0	1	29.917758	
15	16782	2	1	1	0	0	0	37.775182	

	map	clusters
1	106.666667	4
2	90.000000	2
3	116.666667	1
7	103.333333	4
15	93.333333	2

[104]:
```
# add the cluster column to the feature list
# cardio_features.extend(['clusters'])
```

```
# cardio_features
```

[104]:
```
['age',
 'gender',
 'cholesterol',
 'gluc',
 'smoke',
 'alco',
 'active',
 'bmi',
 'map',
 'clusters']
```

[131]:
```
print(select_df2[cardio_features].groupby(['clusters']).mean())
```

```
                   age    gender  cholesterol      gluc     smoke  alco  \
clusters
0         20564.242993  1.235307     2.449141  2.706826  0.047468  0.00
1         19873.791891  1.999601     1.344717  1.077392  0.164270  0.00
2         19735.732084  1.683021     1.675303  1.326351  0.452591  1.00
3         20066.934352  1.000000     1.374021  1.040382  0.013119  0.00
4         19273.100000  1.350000     1.450000  1.400000  0.050000  0.15

            active        bmi          map
clusters
0         0.789557  30.056903   116.413954
1         0.779708  27.262022   117.424373
2         0.828556  28.995670   122.444322
3         0.791179  28.638399   113.648041
4         0.900000  27.493610  5350.033333
```

[117]:
```
output_n = select_df2[['age','clusters']].groupby(['clusters'], as_index =
 False).count()

output_n
```

[117]:

	clusters	age
0	0	2092
1	1	18247
2	2	6063
3	3	1817
4	4	6576

[138]:
```
# percent in cluster 1
18247/ 34795
```

[138]: 0.5244144273602529

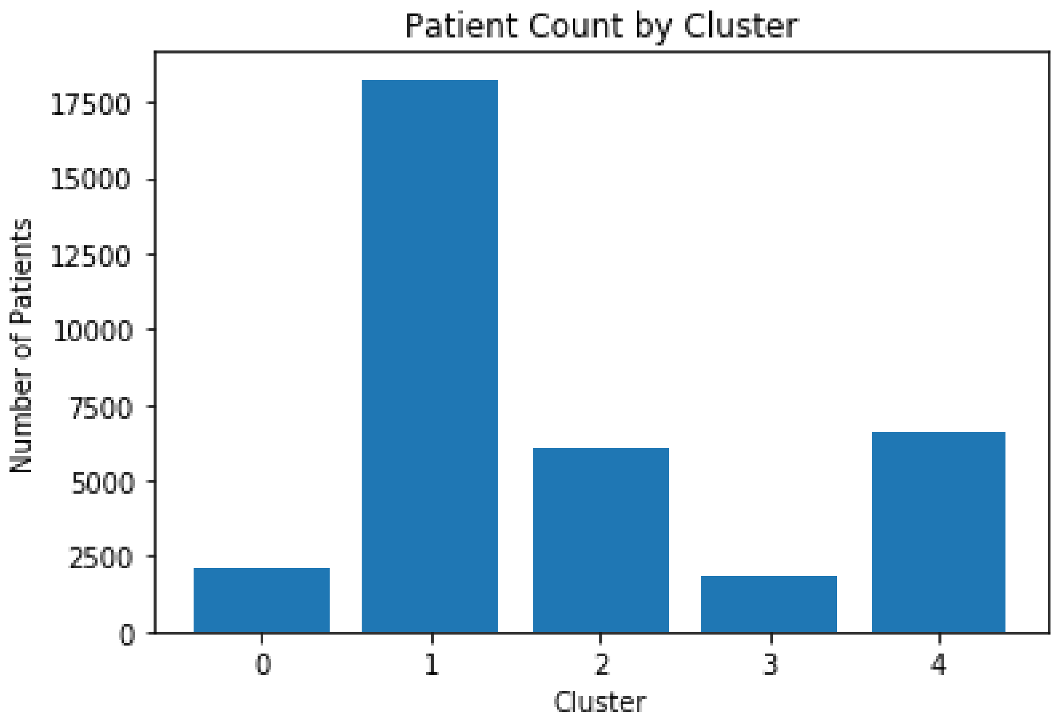
0.5.1 Plots

[118]:
```
# Get the plot variables
clusters = output_n['clusters'].values
# get the values
n = output_n['age'].values

# Label the axes
plt.xlabel('Cluster')
plt.ylabel('Number of Patients')

#label the figure
plt.title('Patient Count by Cluster')


# create
plt.bar(clusters,n)
plt.show()
```



[109]:
```
output = select_df2[cardio_features].groupby(['clusters'], as_index = False).
 ↪mean()
output['age_yrs'] = output['age']/365
output
```

[109]:

	clusters	age	gender	cholesterol	gluc	smoke	alco
0	0	19649.539197	1.851338	1.567400	1.269120	1.000000	0.0
1	1	19957.920480	1.308599	1.147038	1.042308	0.000000	0.0
2	2	20060.004783	1.320798	1.319809	1.126505	0.000000	0.0
3	3	19735.039626	1.682994	1.674739	1.326362	0.452394	1.0
4	4	20546.970955	1.258364	2.671229	2.061283	0.000912	0.0

	active	bmi	map	age_yrs
0	0.808317	27.978445	122.277725	53.834354
1	1.000000	27.967330	118.555945	54.679234
2	0.000000	28.289592	111.908296	54.958917
3	0.828839	28.994345	131.903137	54.068602
4	0.917427	29.887076	119.807938	56.293071

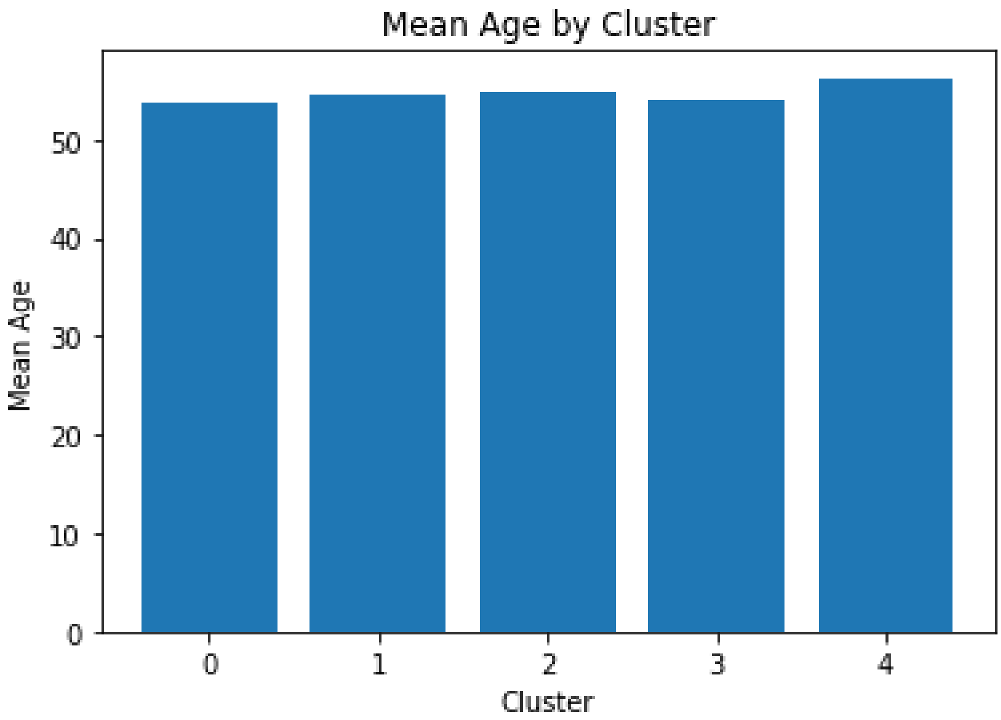
[111]:

```
# Get the plot variables
clusters = output['clusters'].values
# get the values
age = output['age_yrs'].values

# Label the axes
plt.xlabel('Cluster')
plt.ylabel('Mean Age')

#label the figure
plt.title('Mean Age by Cluster')


# create
plt.bar(clusters,age)
plt.show()
```

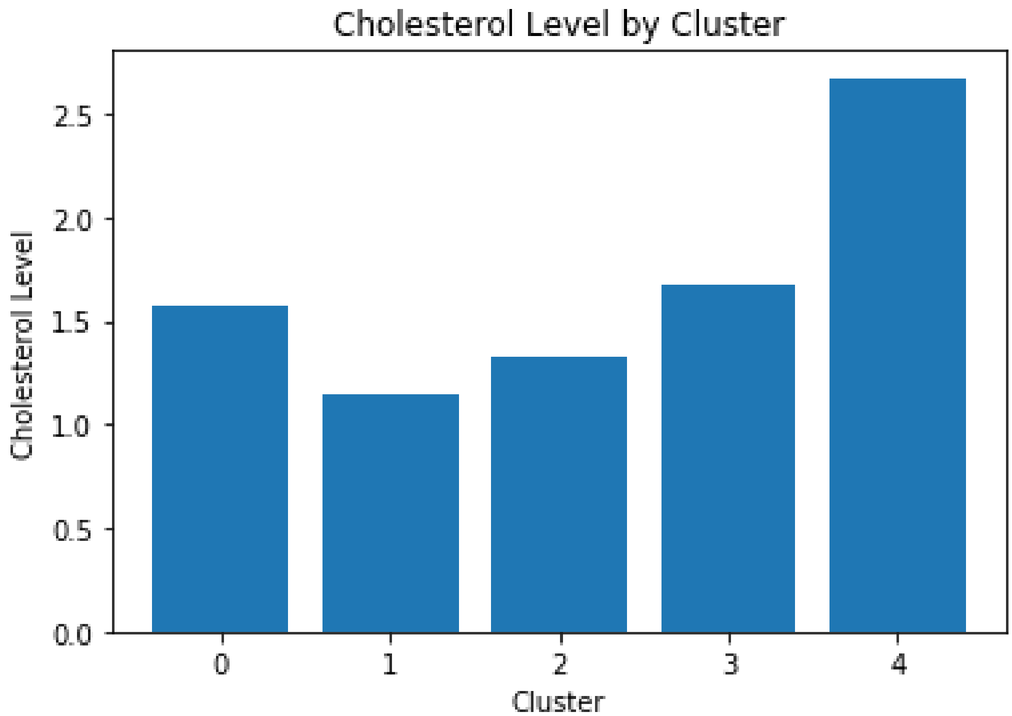


[112]:
```
# Get the plot variables
clusters = output['clusters'].values
# get the values
chol = output['cholesterol'].values

# Label the axes
plt.xlabel('Cluster')
plt.ylabel('Cholesterol Level')

#label the figure
plt.title('Cholesterol Level by Cluster')


# create
plt.bar(clusters,chol)
plt.show()
```

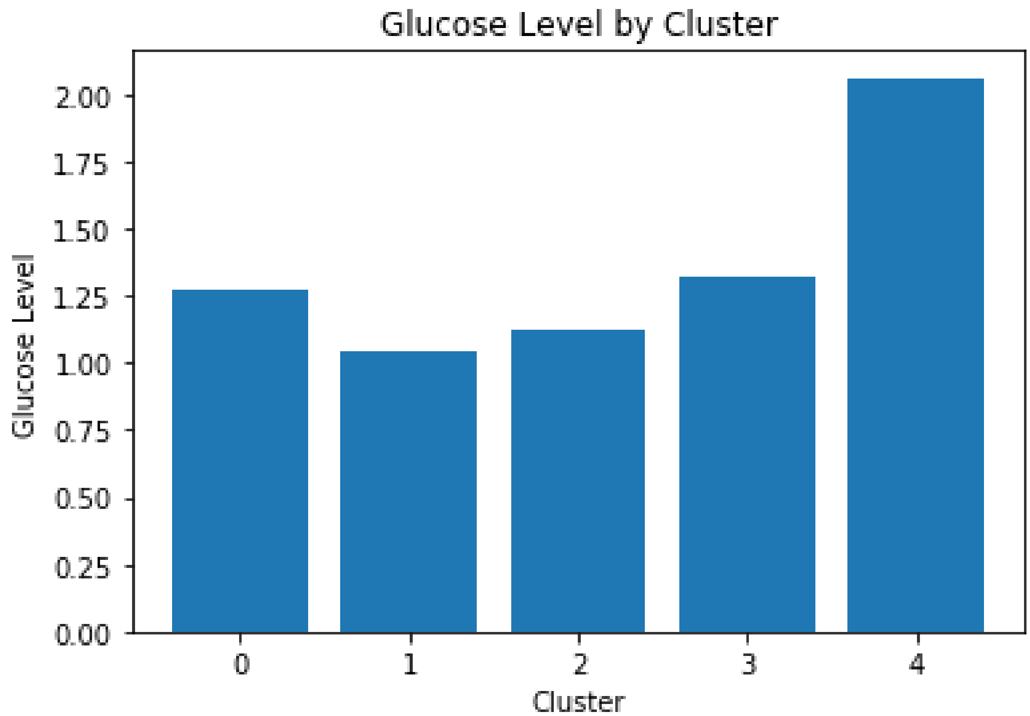


[113]:
```
# Get the plot variables
clusters = output['clusters'].values
# get the values
gluc = output['gluc'].values

# Label the axes
plt.xlabel('Cluster')
plt.ylabel('Glucose Level')

#label the figure
plt.title('Glucose Level by Cluster')


# create
plt.bar(clusters,gluc)
plt.show()
```

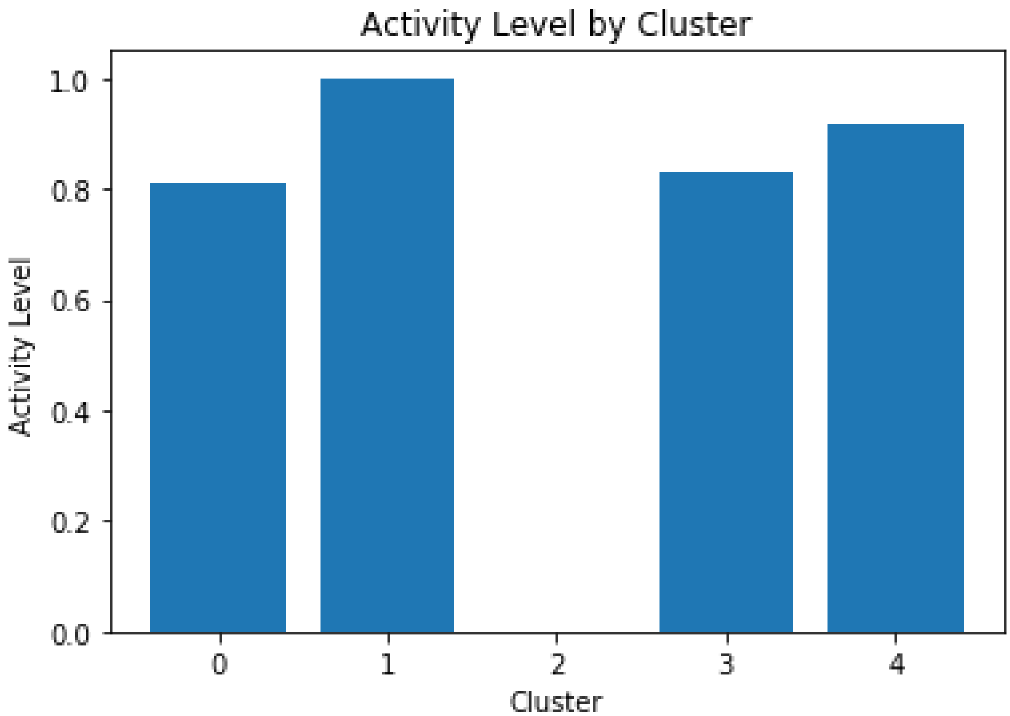


[119]:
```
# Get the plot variables
clusters = output['clusters'].values
# get the values
act = output['active'].values

# Label the axes
plt.xlabel('Cluster')
plt.ylabel('Activity Level')

#label the figure
plt.title('Activity Level by Cluster')


# create
plt.bar(clusters,act)
plt.show()
```

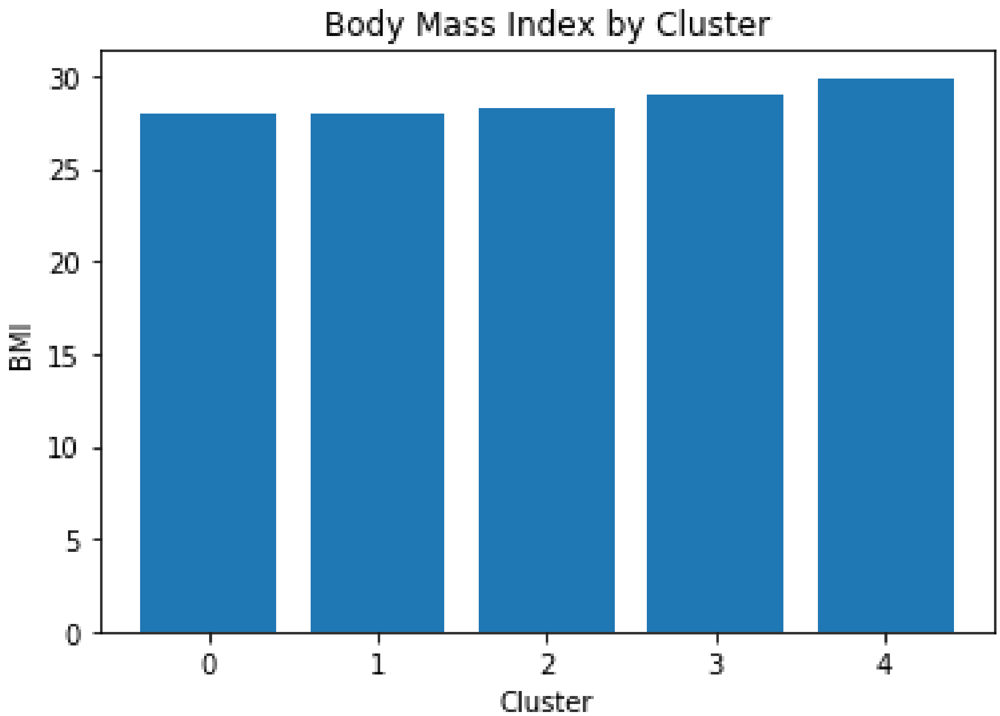


[121]:
```
# Get the plot variables
clusters = output['clusters'].values
# get the values
bmi = output['bmi'].values

# Label the axes
plt.xlabel('Cluster')
plt.ylabel('BMI')

#label the figure
plt.title('Body Mass Index by Cluster')


# create
plt.bar(clusters,bmi)
plt.show()
```

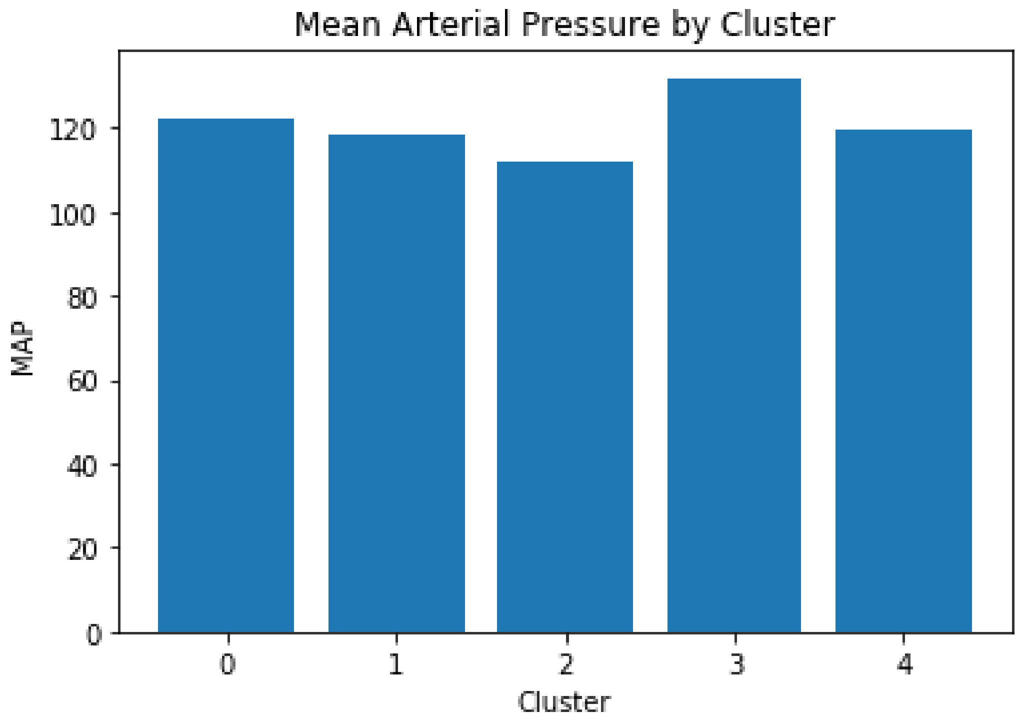


[122]:
```
# Get the plot variables
clusters = output['clusters'].values
# get the values
map = output['map'].values

# Label the axes
plt.xlabel('Cluster')
plt.ylabel('MAP')

#label the figure
plt.title('Mean Arterial Pressure by Cluster')


# create
plt.bar(clusters,map)
plt.show()
```



[135]:
```
output_bin = select_df2[['clusters','smoke','alco']].groupby(['clusters'],␣
↪as_index = False).agg({'smoke': ['sum','count'],
                                                                              ␣
↪                    'alco': ['sum','count']})

output_bin_cols = ['clusters','smoke','smoke_count','alco','total_count']

output_bin.columns = output_bin_cols

del output_bin['smoke_count']

output_bin['percent_smoke'] = output_bin['smoke'] / output_bin['total_count']

output_bin['percent_alco'] = output_bin['alco'] / output_bin['total_count']

output_bin
```

[135]:

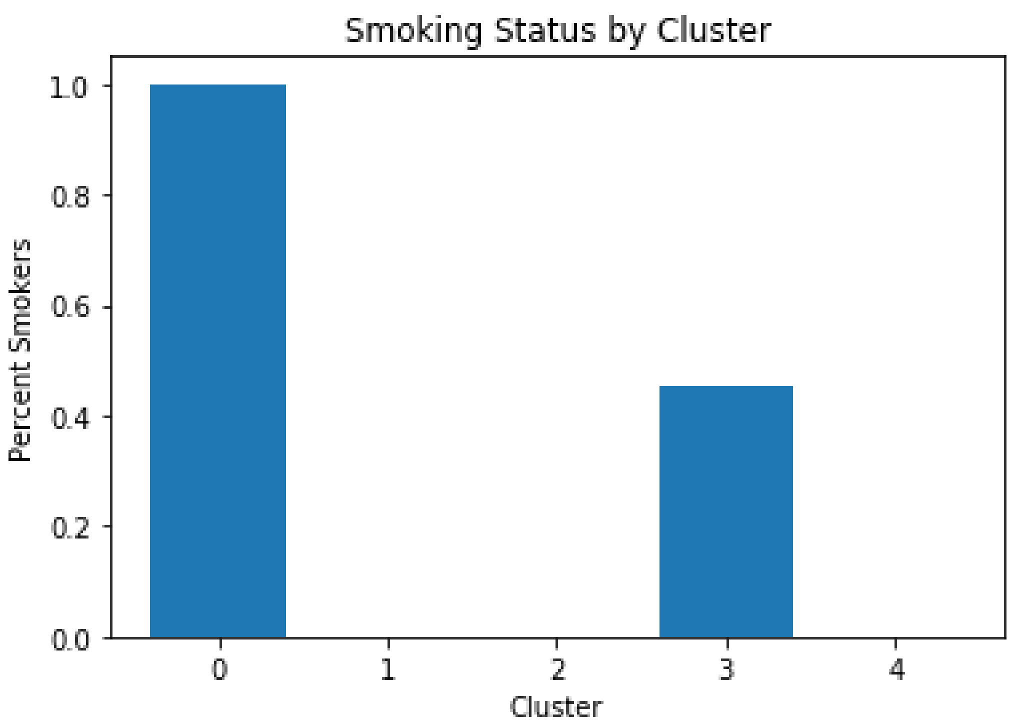
	clusters	smoke	alco	total_count	percent_smoke	percent_alco
0	0	2092	0	2092	1.000000	0.0
1	1	0	0	18247	0.000000	0.0
2	2	0	0	6063	0.000000	0.0
3	3	822	1817	1817	0.452394	1.0
4	4	6	0	6576	0.000912	0.0

[136]:
```
# Get the plot variables
clusters = output_bin['clusters'].values
# get the values
smk = output_bin['percent_smoke'].values

# Label the axes
plt.xlabel('Cluster')
plt.ylabel('Percent Smokers')

#label the figure
plt.title('Smoking Status by Cluster')


# create
plt.bar(clusters,smk)
plt.show()
```



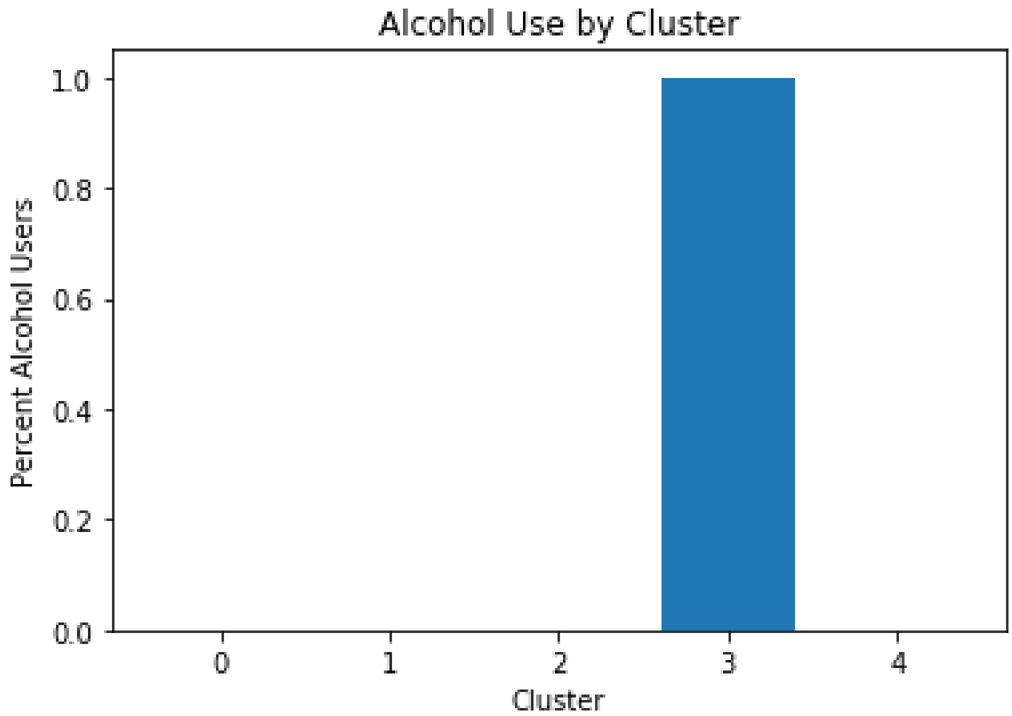
[139]:
```
# Get the plot variables
clusters = output_bin['clusters'].values
# get the values
alc = output_bin['percent_alco'].values

# Label the axes
```

```
plt.xlabel('Cluster')
plt.ylabel('Percent Alcohol Users')

#label the figure
plt.title('Alcohol Use by Cluster')


# create
plt.bar(clusters,alc)
plt.show()
```

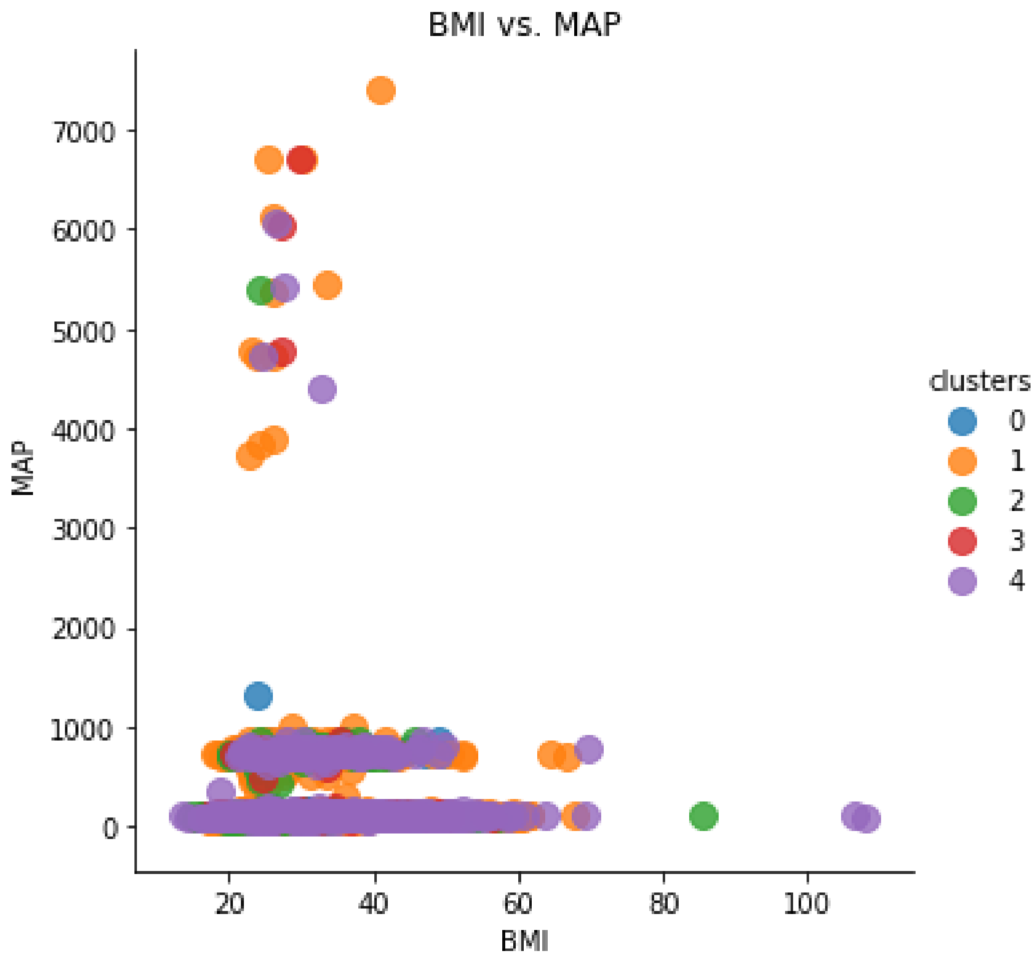


[140]:
```
#Scatter plot
from scipy import stats
import seaborn as sns


sns.lmplot('bmi', 'map',
           data=select_df2,
           fit_reg=False,
           hue="clusters",
           scatter_kws={"marker": "D",
                        "s": 100})
plt.title('BMI vs. MAP')
```

```
plt.xlabel('BMI')
plt.ylabel('MAP')
```

[140]: Text(28.29117187499999, 0.5, 'MAP')

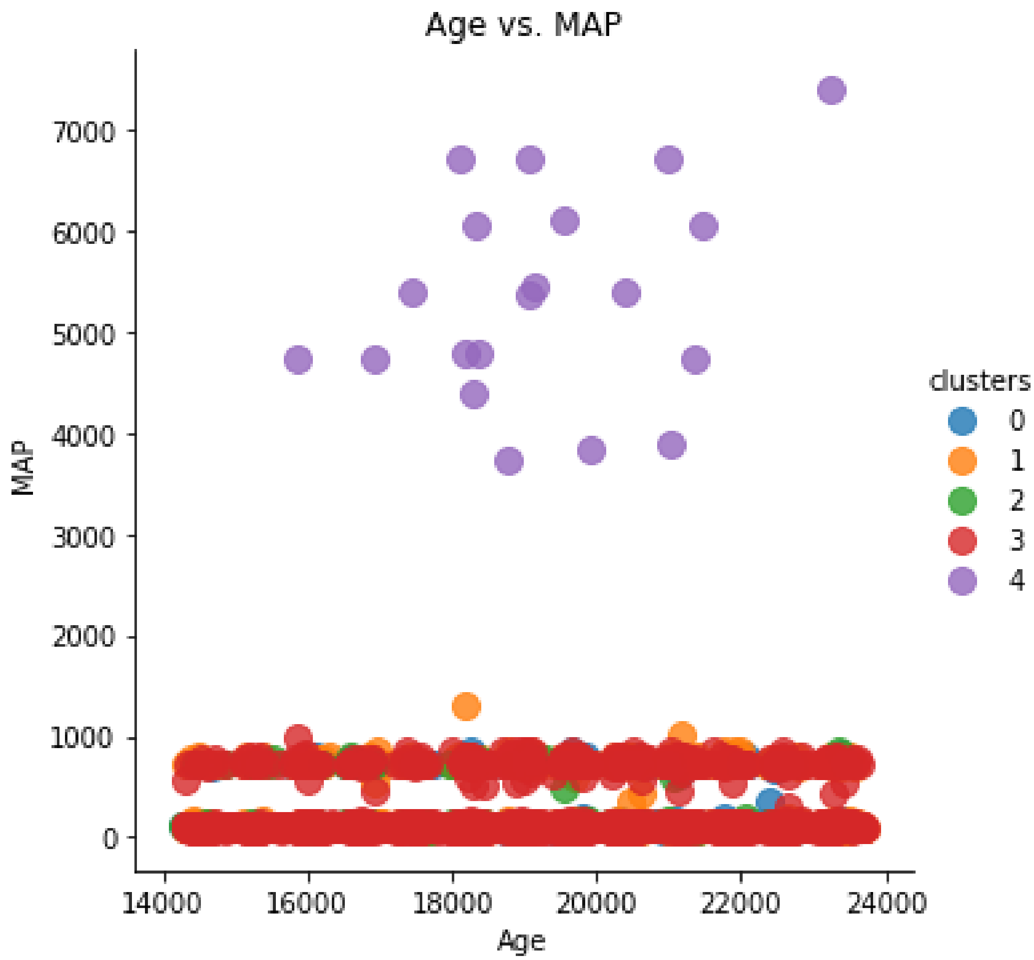


[134]:
```
#Scatter plot
from scipy import stats
import seaborn as sns


sns.lmplot('age', 'map',
           data=select_df2,
           fit_reg=False,
           hue="clusters",
           scatter_kws={"marker": "D",
                        "s": 100})
plt.title('Age vs. MAP')
```

```
plt.xlabel('Age')
plt.ylabel('MAP')
```

[134]: Text(28.29117187499999, 0.5, 'MAP')



[ ]:

[135]:
```
#Scatter plot
from scipy import stats
import seaborn as sns


sns.lmplot('age', 'bmi',
           data=select_df2,
           fit_reg=False,
           hue="clusters",
           scatter_kws={"marker": "D",
```

```
                                    "s": 100})
plt.title('Age vs. BMI')
plt.xlabel('Age')
plt.ylabel('BMI')
```

[135]: Text(27.468689236111118, 0.5, 'BMI')

[137]:
```
select_df2['clusters'].describe()
```

[137]:
```
count    34795.000000
mean         1.991407
std          1.153685
min          0.000000
25%          1.000000
50%          3.000000
75%          3.000000
max          4.000000
```

```
Name: clusters, dtype: float64
```

[146]:
```python
select_df2['pt_count'] = 1

select_df2[['clusters','pt_count']].groupby(['clusters']).sum()
```

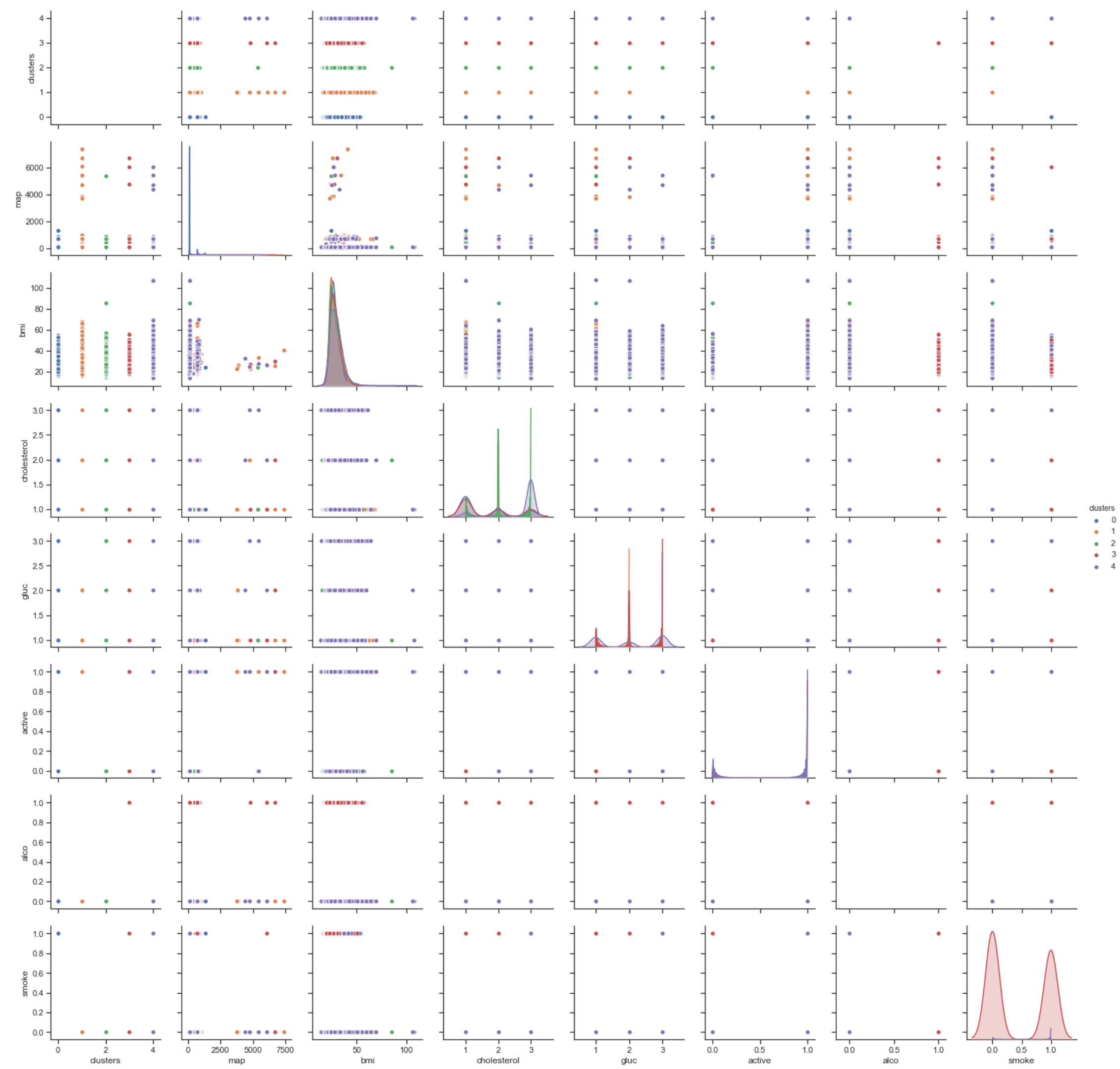
[146]:
```
          pt_count
clusters
0             4424
1            10014
2             1814
3            18523
4               20
```

[145]:
```python
matrix = select_df2[['clusters','map','bmi','cholesterol','gluc','active','alco','smoke']].copy()

sns.set(style="ticks")

sns.pairplot(matrix, hue="clusters")
```

[145]:
```
<seaborn.axisgrid.PairGrid at 0x1a45662f90>
```


clusters
map
bmi
cholesterol
gluc
active
alco
smoke
clusters
0
1
2
3
4