Cardiovascular Disease Classification

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CHAPTER

ONE

BUSINESS UNDERSTANDING

The provided cardiovascular dataset is available for academic purposes, aimed at classifying whether a patient may have cardiovascular disease. Stated differently, this data was collected and created to build and train models using a variety of predictors to classify a patient as having cardiovascular disease or not having cardiovascular disease. The outcomes of the cardiovascular dataset can be defined as a classification problem of a categorical response variable. For example, to determine whether smoking is a predictor of cardiovascular disease and using accuracy statistics to measure the effectiveness of smoking as a predictor. If the model correctly predicts the presence of cardiovascular disease in a given a patient 70% of the time actions such as early, noninvasive, and safe intervention therapies (such as with diet and exercise), may replace necessary (surgical, and dangerous interventions) as an undiagnosed problem worsens. A low false-negative rate, that is incorrectly diagnosing a patient as not having cardiovascular disease may be a beneficial measure of having mined useful knowledge. Given the categorical response variable and classification of cardiovascular disease, the effectiveness of the prediction algorithm may be measured through accuracy or precision statistics, ROC curves or cross-validation ("CV"), for example a 10-fold CV.

1.1 Library Imports

[1]:
```
import pandas as pd
import numpy as np
from matplotlib import pyplot as plt
from matplotlib.ticker import MaxNLocator
import seaborn as sns
import plotly.express as px
%matplotlib inline
```

1.2 Load the CSV Data

[2]:
```
df = pd.read_csv('../data/cardio_train.csv', delimiter=';')
```

CHAPTER

TWO

DATA MEANING TYPE

The cardiovascular dataset consists of 11 features and 1 target variable. Attribute descriptions can be found on Kaggle. They are provided below.

There are 3 types of input features in the data set. - **Objective**: factual information - **Examination**: results from a medical examination - **Subjective**: response provided by patient

Table 1: Cardiovascular Dataset - Attribute Descriptions

Column Description	Feature Type	Column Name	Data Type
Age	Objective	age	int (days)
Height	Objective	height	int (cm)
Weight	Objective	weight	float (kg)
Gender	Objective	gender	1: female, 2: male
Systolic blood pressure	Examination	ap_hi	int
Diastolic blood pressure	Examination	ap_lo	int
Cholesterol	Examination	cholesterol	1: normal, 2: above normal, 3: well above normal
Glucose	Examination	gluc	1: normal, 2: above normal, 3: well above normal
Smoking	Subjective	smoke	binary
Alcohol intake	Subjective	alco	binary
Physical activity	Subjective	active	binary
Has CVD?	Target	cardio	binary

[3]:
```
df.head()
```

[3]:
```
   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
```

We decided to use the id column as the index as it appears to be a unique identifier for the subject.

[4]:
```
df.set_index("id", inplace=True)
```

[5]:
```
df.index.is_unique
```

[5]:
```
True
```

CHAPTER

THREE

DATA QUALITY

[6]:
```
df.shape
```

[6]:
```
(70000, 12)
```

Our data set has `70 thousand` rows and `12` columns, which should work nicely for many of the machine learning classifiers we may attempt to utilize.

[7]:
```
cols = df.columns
```

Store columns for later use.

[8]:
```
cols
```

[8]:
```
Index(['age', 'gender', 'height', 'weight', 'ap_hi', 'ap_lo', 'cholesterol',
       'gluc', 'smoke', 'alco', 'active', 'cardio'],
      dtype='object')
```

[9]:
```
df.isna().any()
```

[9]:
```
age            False
gender         False
height         False
weight         False
ap_hi          False
ap_lo          False
cholesterol    False
gluc           False
smoke          False
alco           False
active         False
cardio         False
dtype: bool
```

There are no missing values in any of the columns of the default data. But upon furhter inspection we found that zeros or other values may have been used in place of missing entries which should also be addressed.

[10]:
```
df.duplicated().any()
```

[10]:
```
True
```

There do appear to be missing values.

[11]:
```
df.duplicated().sum()
```

[11]:
```
24
```

There were a total of 24 sets where all columns of an observation equal at least one other record in the set. It was important to remove `id` as part of the data frame otherwise these duplicated entries would have been more difficult to detect.

[12]:
```
duplicated = df[df.duplicated(keep=False)].sort_values(by=['age', 'gender', 'height',
↪'weight', 'ap_hi', 'ap_lo', 'cholesterol',
       'gluc', 'smoke', 'alco', 'active', 'cardio'])
```

[13]:
```
duplicated.head(10)
```

[13]:
```
         age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
id
9004   14552       1     158    64.0    120     80            1     1      0
57690  14552       1     158    64.0    120     80            1     1      0
24435  16160       1     168    65.0    120     80            1     1      0
91592  16160       1     168    65.0    120     80            1     1      0
1685   16793       1     165    68.0    120     80            1     1      0
31110  16793       1     165    68.0    120     80            1     1      0
40450  16805       1     157    67.0    120     80            1     1      0
86345  16805       1     157    67.0    120     80            1     1      0
14974  16937       2     170    70.0    120     80            1     1      0
63776  16937       2     170    70.0    120     80            1     1      0

       alco  active  cardio
id
9004      0       1       0
57690     0       1       0
24435     0       1       1
91592     0       1       1
1685      0       1       0
31110     0       1       0
40450     0       1       0
86345     0       1       0
14974     0       0       0
63776     0       0       0
```

[14]:
```
df_clean = df.copy(deep=True)
```

[15]:
```
df_clean.drop_duplicates(inplace=True)
```

We'll remove the duplicates entirely, as this should not affect the ability of our models to make predictions with the amount of observations at our disposal.

[16]:
```
# %%time
# df_clean['age'] = df_clean['age'].apply(lambda x: round(x / 365))
df_clean['age'] = (df_clean['age'] / 365).round().astype('int')
```

`Age` was provided in `days`, and for the sake of interpretability we'll be converting this to years for all observations.

[17]:
```
plt.style.use('ggplot')
```

3.1 Age

[18]:

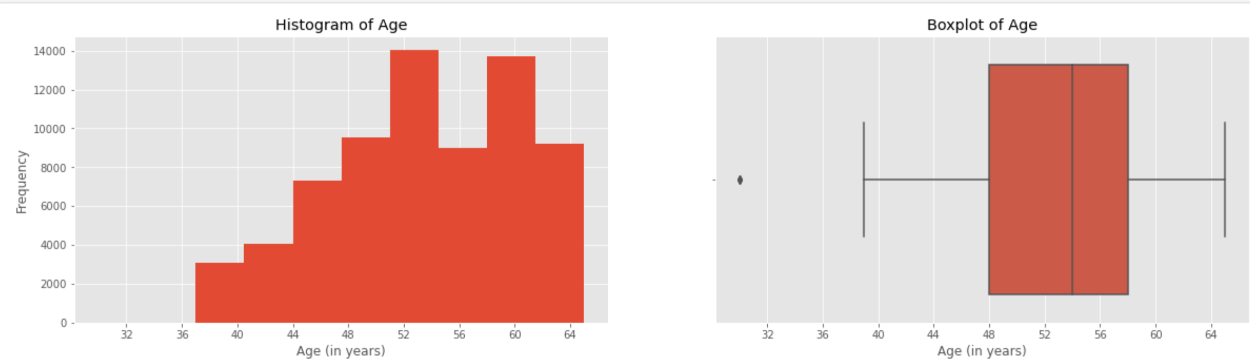
```
fig_1 = plt.figure(1, figsize=(20, 5))

chart_1 = fig_1.add_subplot(121)
chart_2 = fig_1.add_subplot(122)

chart_1.hist(df_clean["age"])
chart_1.xaxis.set_major_locator(MaxNLocator(integer=True))
chart_1.set_title('Histogram of Age')
chart_1.set_xlabel('Age (in years)')
chart_1.set_ylabel('Frequency')

sns.boxplot(x="age", data=df_clean, ax=chart_2)
chart_2.xaxis.set_major_locator(MaxNLocator(integer=True))
chart_2.set_title('Boxplot of Age')
chart_2.set_xlabel('Age (in years)')


plt.show()
```



Age has relatively few outliers but is slightly right-skewed.

3.2 Height

[19]:

```
fig_2 = plt.figure(1, figsize=(20, 5))

chart_1 = fig_2.add_subplot(121)
chart_2 = fig_2.add_subplot(122)

chart_1.hist(df_clean["height"])
chart_1.xaxis.set_major_locator(MaxNLocator(integer=True))
chart_1.set_title('Histogram of Height')
chart_1.set_xlabel('Height (in cm)')
chart_1.set_ylabel('Frequency')

sns.boxplot(x="height", data=df_clean, ax=chart_2)
chart_2.xaxis.set_major_locator(MaxNLocator(integer=True))
chart_2.set_title('Boxplot of Height')
chart_2.set_xlabel('Height (in cm)')
```

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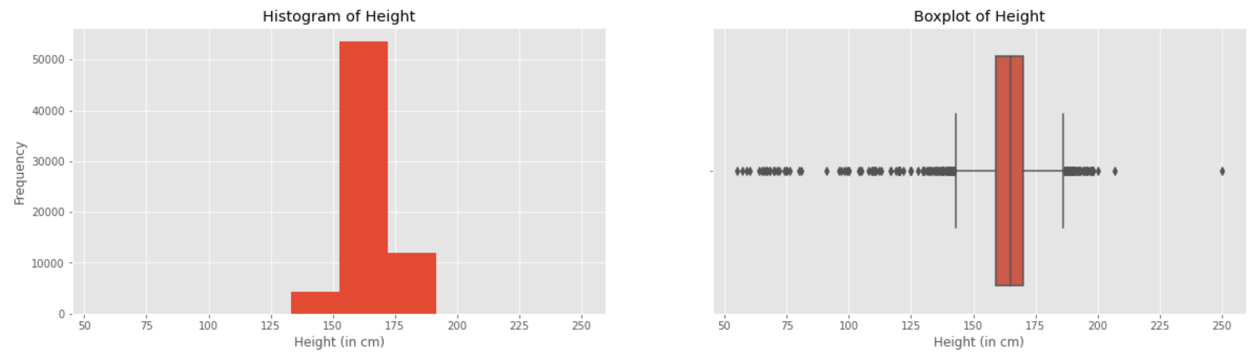
```
plt.show()
```

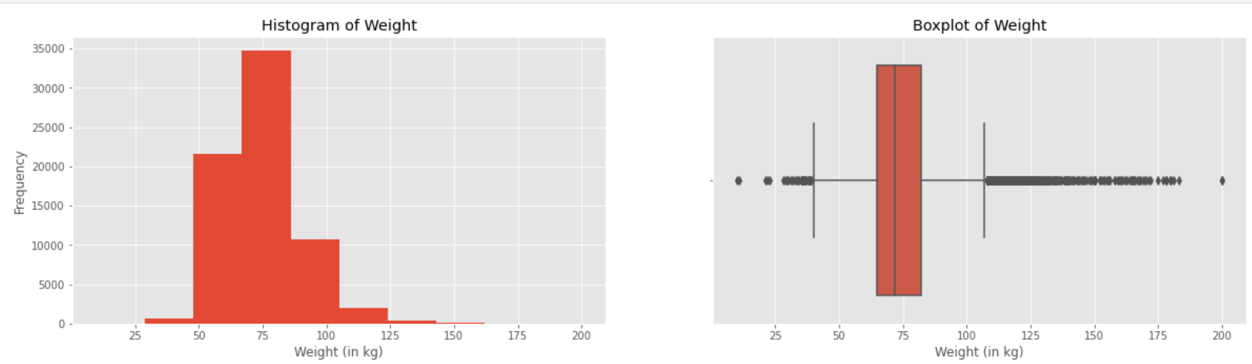


There are quite a few outliers in the height column that should be addressed. The largest of 250cm is over 8 feet tall and appears to be an error.

3.3 Weight

[20]:

```
fig_3 = plt.figure(1, figsize=(20, 5))

chart_1 = fig_3.add_subplot(121)
chart_2 = fig_3.add_subplot(122)

chart_1.hist(df_clean["weight"])
chart_1.xaxis.set_major_locator(MaxNLocator(integer=True))
chart_1.set_title('Histogram of Weight')
chart_1.set_xlabel('Weight (in kg)')
chart_1.set_ylabel('Frequency')

sns.boxplot(x="weight", data=df_clean, ax=chart_2)
chart_2.xaxis.set_major_locator(MaxNLocator(integer=True))
chart_2.set_title('Boxplot of Weight')
chart_2.set_xlabel('Weight (in kg)')


plt.show()
```

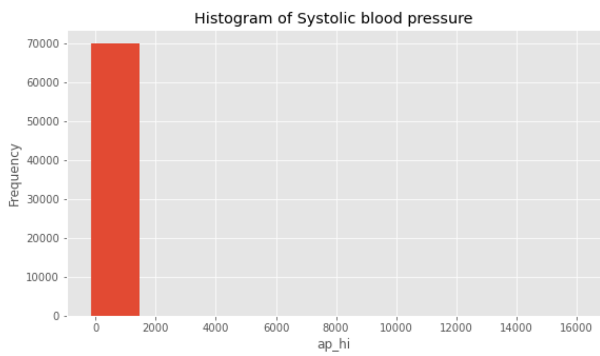


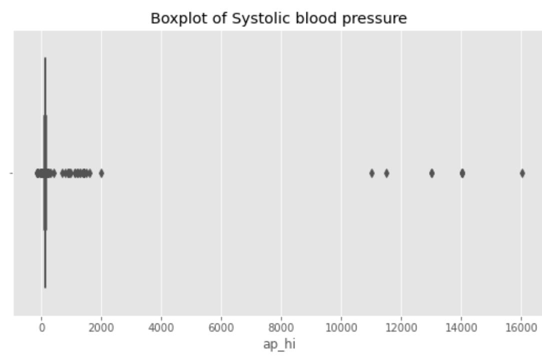
Similarly, there are a lot of outliers in the weight column as well.

3.4 Systolic blood pressure (ap_hi)

[21]:

```
fig_4 = plt.figure(1, figsize=(20, 5))

chart_1 = fig_4.add_subplot(121)
chart_2 = fig_4.add_subplot(122)

chart_1.hist(df_clean["ap_hi"])
chart_1.xaxis.set_major_locator(MaxNLocator(integer=True))
chart_1.set_title('Histogram of Systolic blood pressure')
chart_1.set_xlabel('ap_hi')
chart_1.set_ylabel('Frequency')

sns.boxplot(x="ap_hi", data=df_clean, ax=chart_2)
chart_2.xaxis.set_major_locator(MaxNLocator(integer=True))
chart_2.set_title('Boxplot of Systolic blood pressure')
chart_2.set_xlabel('ap_hi')


plt.show()
```





The distribution of the `Systolic blood pressure` was quite unusual with several readings that were likely erroneous.

[22]:

```
df_clean["ap_hi"].sample(10)
```

[22]:

```
id
13160    130
29293    115
61102    150
90710    120
72912    120
90865    120
63998    140
78175    120
90864    120
96667    110
Name: ap_hi, dtype: int64
```

A random sample show values within the expected range.

[23]:
```
df_clean["ap_hi"].sort_values()
```

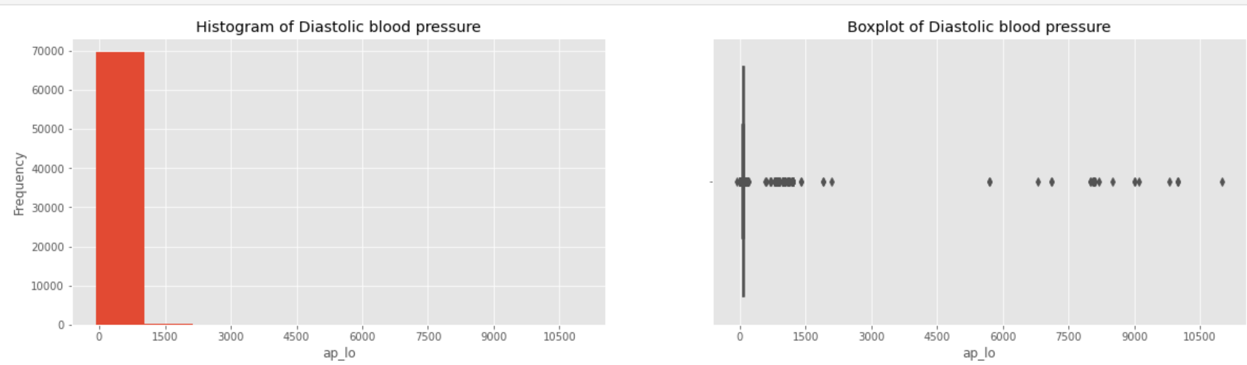
[23]:
```
id
50055     -150
34295     -140
66571     -120
36025     -120
22881     -115
          ...
36339    14020
66998    14020
67502    14020
36414    14020
58374    16020
Name: ap_hi, Length: 69976, dtype: int64
```

But there were negative values and extremely high ones that should be reviewed. We'll address these outliers later within the imputation section.

[24]:
```
# df_clean = df_clean[~(df_clean['ap_hi'] < 40) & (df_clean['ap_hi'] < 300)]
# df_clean.shape[0]
```

3.5 Diastolic blood pressure (ap_lo)

[25]:
```

fig_5 = plt.figure(1, figsize=(20, 5))

chart_1 = fig_5.add_subplot(121)
chart_2 = fig_5.add_subplot(122)

chart_1.hist(df_clean["ap_lo"])
chart_1.xaxis.set_major_locator(MaxNLocator(integer=True))
chart_1.set_title('Histogram of Diastolic blood pressure')
chart_1.set_xlabel('ap_lo')
chart_1.set_ylabel('Frequency')

sns.boxplot(x="ap_lo", data=df_clean, ax=chart_2)
chart_2.xaxis.set_major_locator(MaxNLocator(integer=True))
chart_2.set_title('Boxplot of Diastolic blood pressure')
chart_2.set_xlabel('ap_lo')


plt.show()
```



[26]:
```
df_clean["ap_lo"].sample(10)
```

[26]:
```
id
68416     80
73487     80
72381    100
93163     70
37294     80
89255     70
43796     70
61619     70
90459     80
47189     90
Name: ap_lo, dtype: int64
```

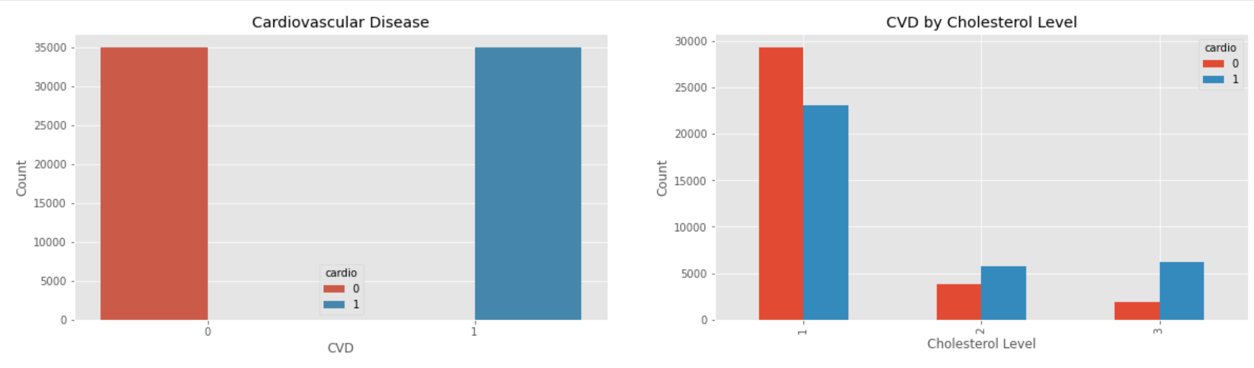
[27]:
```
df_clean["ap_lo"].sort_values()
```

[27]:
```
id
85816      -70
98095        0
45400        0
75007        0
81298        0
         ...
62058     9800
34098    10000
3352     10000
97907    10000
61901    11000
Name: ap_lo, Length: 69976, dtype: int64
```

The same technique should be applied to the `ap_lo` feature.

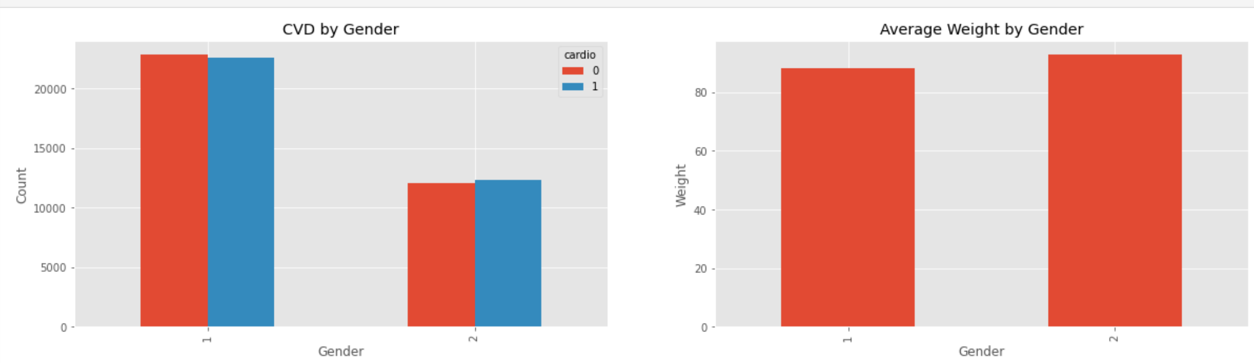
3.5.1 Categorical Variables

[28]:
```
fig_0 = plt.figure(1, figsize=(20, 5))

chart_1 = fig_0.add_subplot(121)
chart_2 = fig_0.add_subplot(122)

sns.countplot(x="cardio", hue="cardio", data=df_clean, ax=chart_1)
# chart_1.legend(bbox_to_anchor=(1,1), title='CVD')
chart_1.set_title('Cardiovascular Disease')
chart_1.set_xlabel('CVD')
chart_1.set_ylabel('Count')

pd.crosstab(df_clean["cholesterol"], df_clean["cardio"]).plot(kind="bar", ax=chart_2)
chart_2.set_title('CVD by Cholesterol Level')
chart_2.set_xlabel('Cholesterol Level')
chart_2.set_ylabel('Count')


plt.show()
```



The Cardiovascular Disease (CVD) response variable is equally distributed. The presence or absence of CVD does seem to change with the cholesterol levels.

[29]:
```
fig_6 = plt.figure(1, figsize=(20, 5))

chart_1 = fig_6.add_subplot(121)
chart_2 = fig_6.add_subplot(122)

pd.crosstab(df_clean["gender"], df_clean["cardio"]).plot(kind="bar", ax=chart_1)
chart_1.set_title('CVD by Gender')
chart_1.set_xlabel('Gender')
chart_1.set_ylabel('Count')

df_clean.groupby(['gender', 'height']).sum().reset_index()

df_clean.groupby(['gender', 'weight']).mean().reset_index().groupby('gender')['weight
↪'].mean().plot(kind='bar', ax=chart_2)
chart_2.set_title('Average Weight by Gender')
chart_2.set_xlabel('Gender')
chart_2.set_ylabel('Weight')


plt.show()
```



There are more subjects with the `label 1` in the study than those with `label 2`.

We're going to assume that label 2 is for male as the mean weight is slightly heigher for that category.

[30]:
```
fig_7 = plt.figure(1, figsize=(20, 5))

chart_1 = fig_7.add_subplot(121)
```

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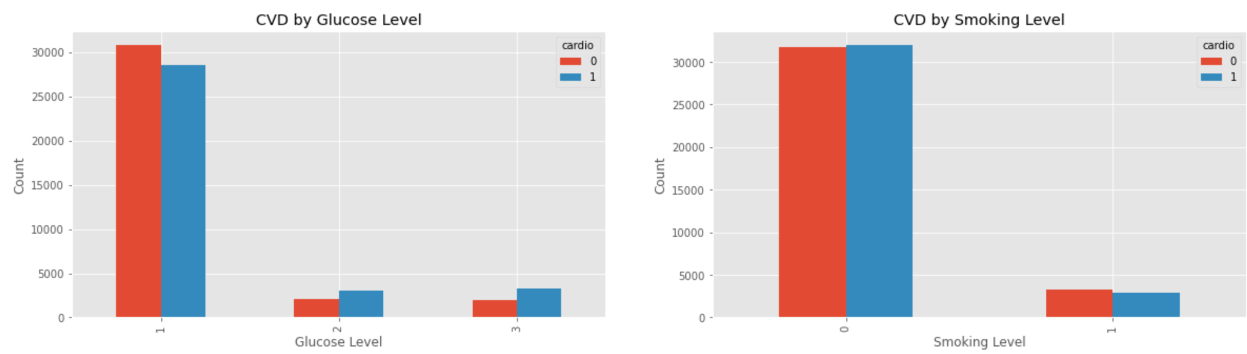
```
chart_2 = fig_7.add_subplot(122)

pd.crosstab(df_clean["gluc"], df_clean["cardio"]).plot(kind="bar", ax=chart_1)
chart_1.set_title('CVD by Glucose Level')
chart_1.set_xlabel('Glucose Level')
chart_1.set_ylabel('Count')


pd.crosstab(df_clean["smoke"], df_clean["cardio"]).plot(kind="bar", ax=chart_2)
chart_2.set_title('CVD by Smoking Level')
chart_2.set_xlabel('Smoking Level')
chart_2.set_ylabel('Count')


plt.show()
```



The presence or absence of CVD also changes with the glucose levels but suprsingly not with smoking.

[31]:
```
df_clean.groupby(['gluc', 'cardio']).size().unstack(fill_value=0)
```

[31]:
```
cardio      0      1
gluc
1       30877  28578
2        2112   3078
3        2015   3316
```

There are only a few thousand entries within levels 2 and 3 of the Choleserol column.

[32]:
```
fig_8 = plt.figure(1, figsize=(20, 5))

chart_1 = fig_8.add_subplot(121)
chart_2 = fig_8.add_subplot(122)

pd.crosstab(df_clean["alco"], df_clean["cardio"]).plot(kind="bar", ax=chart_1)
chart_1.set_title('CVD by Alchohol Level')
chart_1.set_xlabel('Alchohol Level')
chart_1.set_ylabel('Count')


pd.crosstab(df_clean["active"], df_clean["cardio"]).plot(kind="bar", ax=chart_2)
chart_2.set_title('CVD by Activity Level')
chart_2.set_xlabel('Activity Level')
chart_2.set_ylabel('Count')
```

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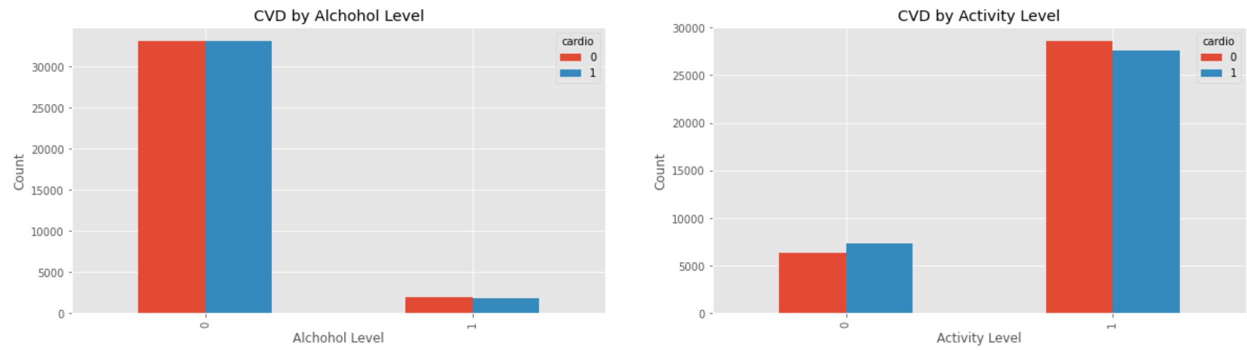
```
plt.show()
```



Also suprising is that the `Alcohol level` didn't seem to have an impact on the response variable. The `Activity Level` did show good seperation.

Imputation

3.6 Age

[33]:
```
median_age = df_clean['age'].median()
```

[34]:
```
age_outlier_ids = df_clean.index[(np.abs(df_clean['age'] - df_clean['age'].mean()) >␣
↪(3 * df_clean['age'].std()))]
```

[35]:
```
df_clean.loc[df_clean.index.isin(age_outlier_ids), "age"] = median_age
```

[36]:
```
df_clean.loc[df_clean.index.isin(age_outlier_ids)].head()
```

[36]:
```
        age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
id
8850   54.0       1     175    59.0    120     80            1     1      0
31922  54.0       2     175    92.0    100     60            1     1      0
43842  54.0       1     159    59.0    120     80            1     1      0
79749  54.0       1     160    59.0    110     70            1     1      0

       alco  active  cardio
id
8850      0       1       0
31922     0       1       0
43842     0       1       0
79749     0       1       0
```

We've imputed observations with an `age` of more than `three standard deviations` from the mean with the median value. (~4 observations in total) These may well have been valid observations but we wanted our model to extend well to other new and unseen data sets.

3.7 Height

[37]:
```
median_height = df_clean['height'].median()
```

[38]:
```
height_outlier_ids = df_clean.index[(np.abs(df_clean['height'] - df_clean['height'].
↪mean()) > (3 * df_clean['height'].std()))]
```

[39]:
```
df_clean.loc[df_clean.index.isin(height_outlier_ids), "height"] = median_height
```

[40]:
```
df_clean.loc[df_clean.index.isin(height_outlier_ids)].head()
```

[40]:
```
       age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
id
309   60.0       2   165.0    55.0    120     80            1     1      0
1432  42.0       2   165.0   111.0    148     86            1     1      0
1554  61.0       2   165.0    68.0    120     80            1     1      0
3049  44.0       2   165.0    74.0    140     90            1     1      1
3399  62.0       2   165.0    52.0    140    100            1     1      0

      alco  active  cardio
id
309      0       1       0
1432     0       1       1
1554     0       1       1
3049     1       1       1
3399     0       1       1
```

We've imputed observations with a `height` more than three standard deviations from the mean with the median value. (~287 observations in total)

3.8 Weight

[41]:
```
median_weight = df_clean['weight'].median()
```

[42]:
```
weight_outlier_ids = df_clean.index[(np.abs(df_clean['weight'] - df_clean['weight'].
↪mean()) > (3 * df_clean['weight'].std()))]
```

[43]:
```
df_clean.loc[df_clean.index.isin(weight_outlier_ids), "weight"] = median_weight
```

[44]:
```
df_clean.loc[df_clean.index.isin(weight_outlier_ids)].head()
```

[44]:
```
      age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
id
474  58.0       1   157.0    72.0    120     80            1     1      0
552  46.0       2   165.0    72.0    120     80            1     1      0
618  46.0       1   186.0    72.0    130     70            1     1      0
634  58.0       2   178.0    72.0    160     90            1     3      0
846  40.0       1   164.0    72.0    130     90            1     1      0

     alco  active  cardio
```

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```
id
474      0        1        1
552      0        1        0
618      0        0        0
634      0        1        1
846      0        0        0
```

The same method was applied to the 702 `weight` outliers.

3.9 Systolic blood pressure (ap_hi)

```
[45]: median_ap_hi = df_clean['ap_hi'].median()
```

```
[46]: ap_hi_outlier_ids = df_clean.index[(np.abs(df_clean['ap_hi'] - df_clean['ap_hi'].
       ↪mean()) > (3 * df_clean['ap_hi'].std()))]
```

```
[47]: df_clean.loc[df_clean.index.isin(ap_hi_outlier_ids), "ap_hi"] = median_ap_hi
```

```
[48]: df_clean.loc[df_clean.index.isin(ap_hi_outlier_ids)].head()
```

```
[48]:        age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
id
2654   41.0       1   160.0    60.0  120.0     60            1     1      0
2845   62.0       2   167.0    59.0  120.0      0            1     1      0
6822   40.0       1   168.0    63.0  120.0     60            2     1      0
11089  58.0       1   175.0    80.0  120.0     90            1     1      0
12710  52.0       1   164.0    75.0  120.0     80            2     1      0

       alco  active  cardio
id
2654      0       1       0
2845      0       1       0
6822      0       1       0
11089     0       1       1
12710     0       1       1
```

```
[49]: ap_hi_outlier_ids2 = df_clean.index[(df_clean['ap_hi'] < 40) | (df_clean['ap_hi'] >␣
       ↪300)]
```

```
[50]: df_clean.loc[df_clean.index.isin(ap_hi_outlier_ids2), "ap_hi"] = median_ap_hi
```

Even after handling the `ap_hi` outliers through the standard deviation method, there were still some unusual entries that were manually addressed. (readings less that 40 or greater than 300)

3.10 Diastolic blood pressure (ap_lo)

```
[51]: median_ap_lo = df_clean['ap_lo'].median()
```

```
[52]: ap_lo_outlier_ids = df_clean.index[(np.abs(df_clean['ap_lo'] - df_clean['ap_lo'].
      ↪mean()) > (3 * df_clean['ap_lo'].std()))]
```

```
[53]: df_clean.loc[df_clean.index.isin(ap_lo_outlier_ids), "ap_lo"] = median_ap_lo
```

```
[54]: df_clean.loc[df_clean.index.isin(ap_lo_outlier_ids)].head()
```

```
[54]:       age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
      id
      314  48.0       2   183.0    98.0  160.0   80.0            1     2      1
      334  60.0       2   157.0    60.0  160.0   80.0            2     1      0
      357  50.0       1   150.0    83.0  140.0   80.0            1     1      0
      458  64.0       1   176.0    63.0  160.0   80.0            2     2      0
      482  51.0       1   154.0    81.0  140.0   80.0            2     1      0

           alco  active  cardio
      id
      314     0       1       1
      334     0       0       1
      357     0       1       1
      458     0       0       1
      482     0       1       1
```

```
[55]: ap_lo_outlier_ids2 = df_clean.index[(df_clean['ap_lo'] < 40) | (df_clean['ap_lo'] >␣
      ↪300)]
```

```
[56]: df_clean.loc[df_clean.index.isin(ap_lo_outlier_ids2), "ap_lo"] = median_ap_lo
```

The `ap_lo` feature needed similar processing.

CHAPTER

FOUR

SIMPLE STATISTICS

[57]:
```
df_clean.describe()
```

[57]:
```
                age        gender        height        weight         ap_hi  \
count  69976.000000  69976.000000  69976.000000  69976.000000  69976.000000
mean      53.340317      1.349648    164.411884     73.643909    126.981551
std        6.763333      0.476862      7.708061     13.193980     17.075701
min       39.000000      1.000000    140.000000     32.000000     60.000000
25%       48.000000      1.000000    159.000000     65.000000    120.000000
50%       54.000000      1.000000    165.000000     72.000000    120.000000
75%       58.000000      2.000000    170.000000     81.000000    140.000000
max       65.000000      2.000000    188.000000    117.000000    240.000000

              ap_lo   cholesterol          gluc         smoke          alco  \
count  69976.000000  69976.000000  69976.000000  69976.000000  69976.000000
mean      81.365125      1.366997      1.226535      0.088159      0.053790
std        9.624691      0.680333      0.572353      0.283528      0.225604
min       40.000000      1.000000      1.000000      0.000000      0.000000
25%       80.000000      1.000000      1.000000      0.000000      0.000000
50%       80.000000      1.000000      1.000000      0.000000      0.000000
75%       90.000000      2.000000      1.000000      0.000000      0.000000
max      190.000000      3.000000      3.000000      1.000000      1.000000

             active        cardio
count  69976.000000  69976.000000
mean       0.803718      0.499771
std        0.397187      0.500004
min        0.000000      0.000000
25%        1.000000      0.000000
50%        1.000000      0.000000
75%        1.000000      1.000000
max        1.000000      1.000000
```

In the table above we have an overview of all of our attributes included in the dataset. This gives an idea of our counts after the cleaning of our data and provides us with data we can hope to draw inferences from. Below we will look at the simplest level of some ofour attributes to review if some general assumptions are true or false within our given data.

[58]:
```
df_clean.agg({'age':['min','max','median','skew','std'],'gender':['min','max','median
↪','skew','std'],'height':['min','max','median','skew','std'],'weight':['min','max',
↪'median','skew','std'],'ap_hi':['min','max','median','skew','std'],'ap_lo':['min',
↪'max','median','skew','std']})
```

[58]:

```
            age    gender      height      weight       ap_hi       ap_lo
min     39.000000  1.000000  140.000000   32.000000   60.000000   40.000000
max     65.000000  2.000000  188.000000  117.000000  240.000000  190.000000
median  54.000000  1.000000  165.000000   72.000000  120.000000   80.000000
skew    -0.305042  0.630605    0.088790    0.550598    0.918609    0.680160
std      6.763333  0.476862    7.708061   13.193980   17.075701    9.624691
```

This table narrows down our quantitative variables, giving us a quick look at the balanceof the dataset. The variable "skew" helps us see in which way our observations lean, none of which were too far out of preferred parameters. We noticed that age of our population is slightly younger (leaning towards our min of 39), gender favors men slightly (as it is a higher value and 2 represents male), height is almost indiscernible, weight favors our max slightly, and blood pressure is slightly higher in our dataset. As stated previously, with the clean data we feel comfortable making assumptions from this data and have decided to move forward.

[59]:

```
df_clean.groupby("cholesterol").mean()
```

[59]:

```
                   age    gender      height     weight       ap_hi  \
cholesterol
1            52.831879  1.359275  164.653272  72.626377  125.074903
2            53.712326  1.329459  163.912452  75.766443  131.291444
3            56.200471  1.311059  163.436152  77.736511  134.256385

                 ap_lo      gluc     smoke      alco    active    cardio
cholesterol
1            80.524875  1.099139  0.085235  0.048089  0.802353  0.440175
2            83.085140  1.335218  0.105666  0.076134  0.799037  0.602157
3            84.783412  1.924870  0.086412  0.064344  0.818125  0.765435
```

Cholesterol has been a topic of debate for years given advancements in technology. We felt that this would possibly give us some insight into the weight that it would have in regards to classifying cardiovascular disease. This attribute classifies 1 as normal levels of cholesterol, 2 as being above normal, and 3 being well above normal

[60]:

```
df_clean.groupby("smoke").mean()
```

[60]:

```
             age    gender      height     weight       ap_hi      ap_lo  \
smoke
0      53.441221  1.299513  163.941166  73.374581  126.832824  81.293510
1      52.296645  1.868212  169.280597  76.429616  128.519857  82.105852

       cholesterol      gluc      alco    active    cardio
smoke
0         1.364819  1.227389  0.029934  0.800523  0.502186
1         1.389528  1.217701  0.300535  0.836764  0.474793
```

As made clear from numerous medical studies, smoking can greatly affect health. In thisattribute we hold that 0 is a non-smoker and 1 is a smoker. We observed here that height was higher in the smoking population (which could be attributed to more male smokers than females). Weight was slightly higher which could also correspond with the skewed height, but it is also known that smokers do generally weigh more than non-smokers from previous medical studies. What was most expected is that the overall blood pressure (both diastolic and systolic) were both higher than non-smokers.

[61]:

```
df_clean.groupby("active").mean()
```

[61]:

```
              age    gender      height     weight       ap_hi      ap_lo  \
active
0       53.473244  1.343939  164.542774  74.082461  126.954277  81.372552
1       53.307854  1.351043  164.379919  73.536808  126.988211  81.363311
```

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```
        cholesterol      gluc     smoke      alco    cardio
active
0          1.353331  1.234365  0.073316  0.042155  0.535857
1          1.370335  1.224623  0.091784  0.056631  0.490959
```

Lastly, we wanted to evaluate the physical activity of our population. This attribute's levels are 0 for non-active and 1 for active. What was curious about this attribute is thatthe age is not skewed towards either older nor younger. Only ever so slightly is the age skewed towards younger persons, but generally physical activity is not determined by age through this dataset, where normally we'd expect as a population ages, they become less active.Weight was another variable we felt we'd expect to see a difference between active andnon-active. Here we did find this to be true as those who are active were approximately a half kilogram lighter than non-active. This wasn't as great as we would have expected,but it does prove our general assumption. Additionally, we'd really expect the systolic and diastolic blood pressures to be affected by this variable, however there was notable nearly no change here as well. From this table, we'd draw a conclusion that physical activity does not necessarily help prevent or predict cardiovascular disease, but much more investigation is required to prove or disprove this entirely as well.

CHAPTER

FIVE

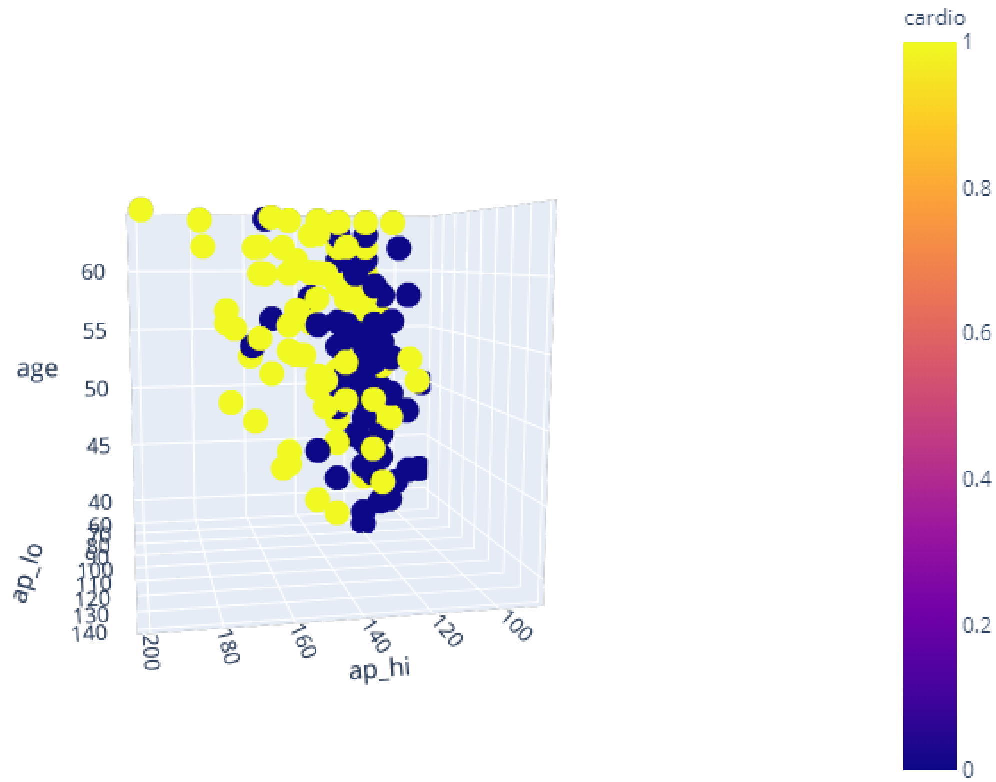
VISUALIZE ATTRIBUTES

[62]:
```
fig = px.scatter_3d(df_clean.sample(200), x='ap_hi', y='ap_lo', z='age',
              color='cardio')

fig.update_layout(margin=dict(l=0, r=0, b=0, t=0))

fig.show()
```

Data type cannot be displayed: application/vnd.plotly.v1+json

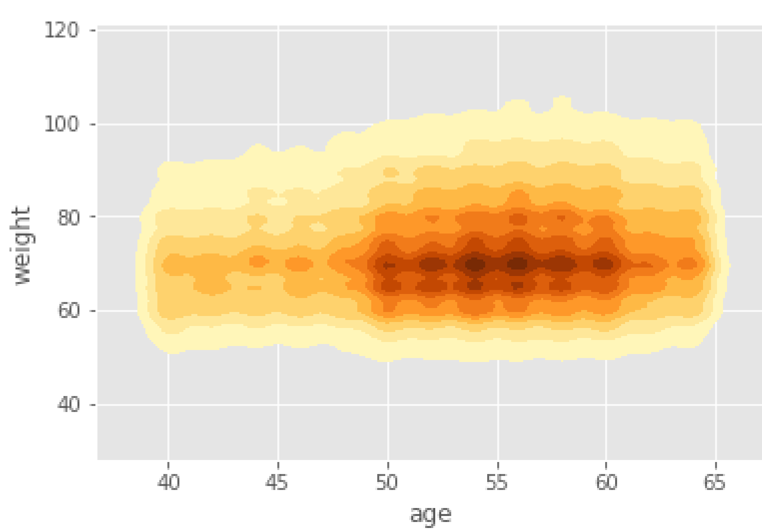
[63]:
```
import base64, io, IPython
from PIL import Image as PILImage

image = PILImage.open("../img/3d_scatterplot.png")

output = io.BytesIO()
image.save(output, format='PNG')
encoded_string = base64.b64encode(output.getvalue()).decode()

html = '<img src="data:image/png;base64,{}"/>'.format(encoded_string)
IPython.display.HTML(html)
```

[63]:
```
<IPython.core.display.HTML object>
```



The 3D scatterplot shows higher CVD response rates from `ap_hi` and `ap_lo` but not for `age`.

```
[65]: df_sub3 = df_clean[['age', 'weight', 'cholesterol', 'ap_hi', 'cardio', 'ap_lo', 'smoke
      ↪', 'active']]
      df_sub3.cardio = df_sub3.cardio=='1'
      #Adapted from https://towardsdatascience.com/the-art-of-effective-visualization-of-
      ↪multi-dimensional-data-6c7202990c57
      ax = sns.kdeplot(df_sub3['age'], df_sub3['weight'],
                        cmap="YlOrBr", shade=True, shade_lowest=False)
```



The above Kernal Density plot depicts the density of those with cardiovascular disease by age and weight. As can be seen, the most dense areas are shown with an age value of 54-56 and a weight value of about 70. This may be indicative of ages and weights that may be predictive of cardiovascular disease.

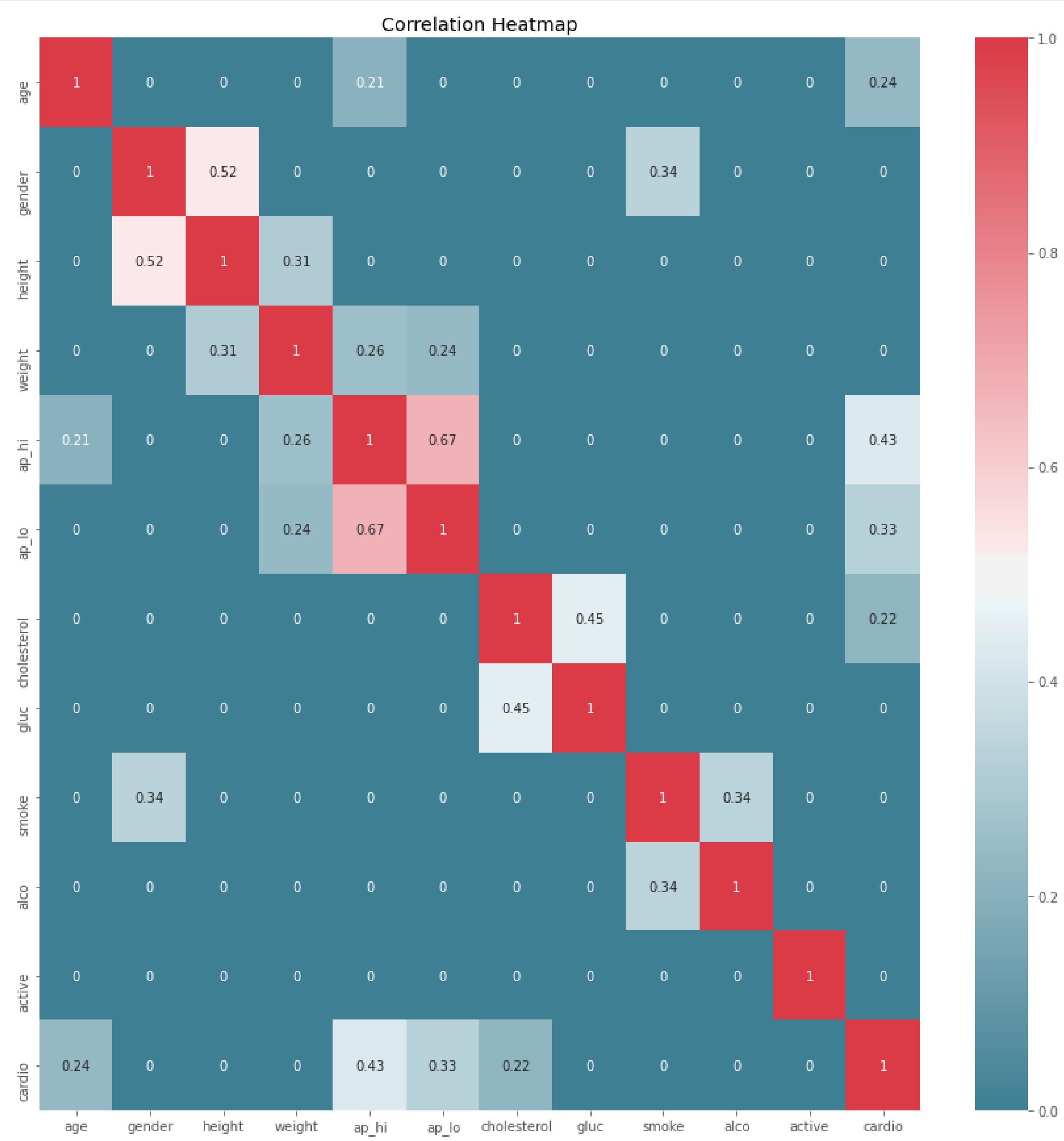
CHAPTER

SIX

EXPLORE JOINT ATTRIBUTES

We can create a feature correlation heatmap using Seaborn.

```
[66]: features = ['age', 'gender', 'height', 'weight', 'ap_hi', 'ap_lo', 'cholesterol',
     ↪'gluc', 'smoke', 'alco', 'active', 'cardio']

plt.figure(figsize=(15,15))

# Use an easier to see colormap
cmap = sns.diverging_palette(220, 10, as_cmap=True)

# Mask
correlation = df_clean[features].corr()
correlation[np.abs(correlation)<.2] = 0

sns.heatmap(correlation, annot = True, cmap=cmap).set(title = 'Correlation Heatmap')
plt.show()
```



The above heatmap shows some interesting correlations, namely between

- Height and Gender
- Gender and Smoking
- Alcohol and Smoking
- Glucose and Cholesterol

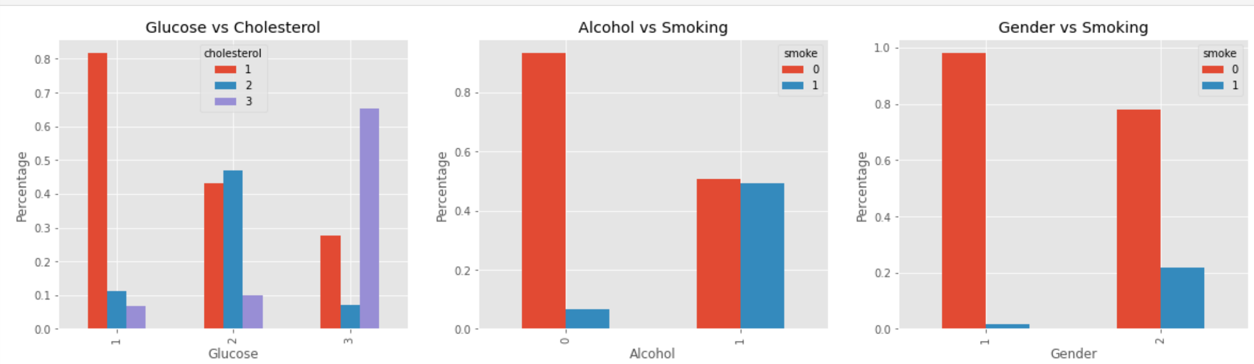
Additionally, we see the following are correlated with out target variable, 'cardio'.

- Age

- Blood Pressure (High/Low)
- Cholesterol

Let's cross tabulate a few of these and inspect further.

[67]:
```
fig = plt.figure(1, figsize=(20, 5))

chart_1 = fig.add_subplot(131)
chart_2 = fig.add_subplot(132)
chart_3 = fig.add_subplot(133)

pd.crosstab(df_clean["gluc"], df_clean["cholesterol"]).apply(lambda r: r/r.sum(),␣
↪axis=1).plot(kind="bar", ax=chart_1)
chart_1.set_title('Glucose vs Cholesterol')
chart_1.set_xlabel('Glucose')
chart_1.set_ylabel('Percentage')


pd.crosstab(df_clean["alco"], df_clean["smoke"]).apply(lambda r: r/r.sum(), axis=1).
↪plot(kind="bar", ax=chart_2)
chart_2.set_title('Alcohol vs Smoking')
chart_2.set_xlabel('Alcohol')
chart_2.set_ylabel('Percentage')

pd.crosstab(df_clean["gender"], df_clean["smoke"]).apply(lambda r: r/r.sum(), axis=1).
↪plot(kind="bar", ax=chart_3)
chart_3.set_title('Gender vs Smoking')
chart_3.set_xlabel('Gender')
chart_3.set_ylabel('Percentage')

plt.show()
```



Some observations based on the above charts:

- We see above that glucose and cholesterol trend nicely. That is, if you are a x in one group, you are likely to be the same value in the other group.
- If you are a drinker, you are more than likely a smoker too.
- If you are a male, you are more likely a smoker in this group.

CHAPTER

SEVEN

EXPLORE ATTRIBUTES AND CLASS

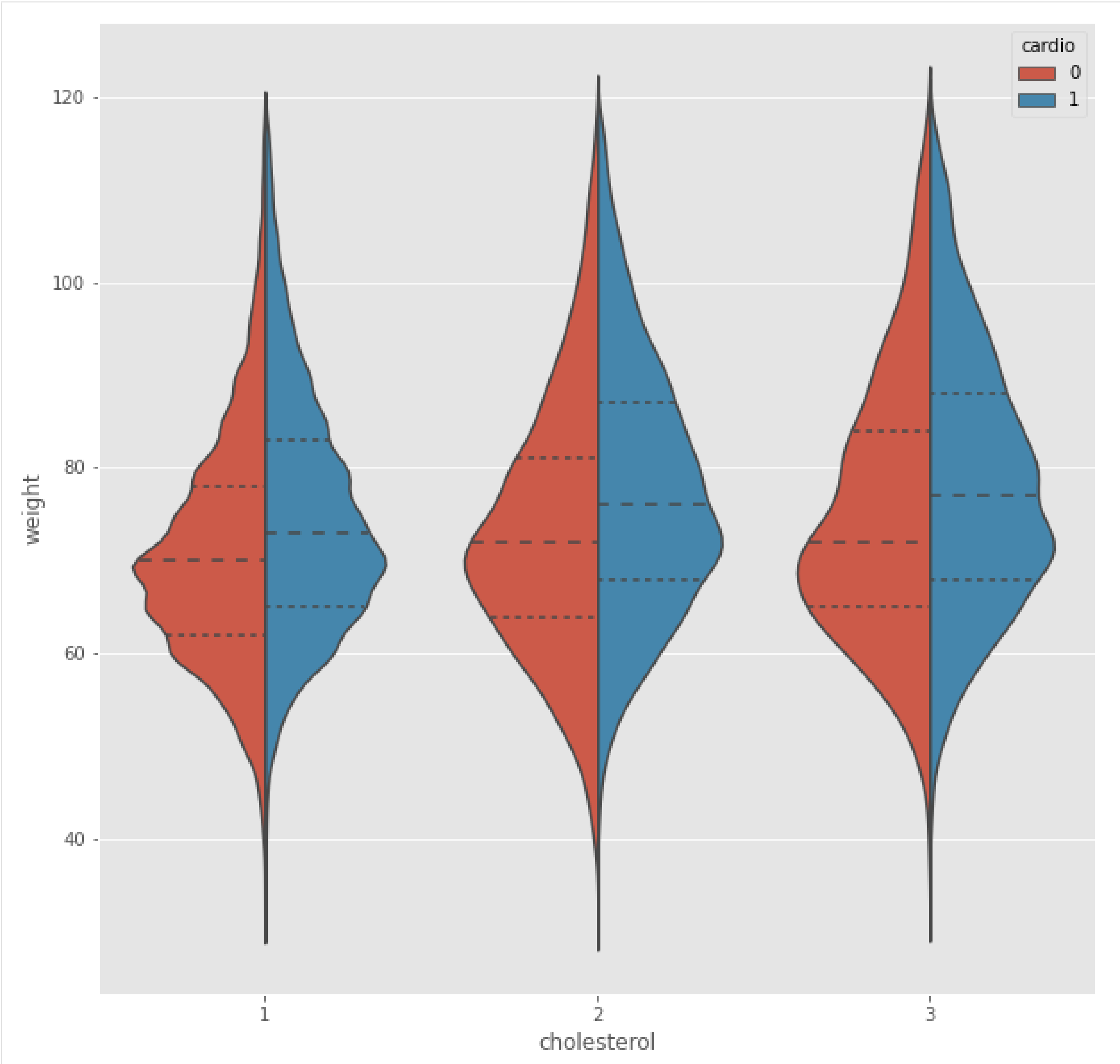
[68]:
```
#Scatterplot Matrix
cmap = sns.diverging_palette(220, 10, as_cmap=True)

df_clean_jitter = df_clean[['cardio', 'ap_hi', 'ap_lo', 'cholesterol', 'weight', 'age
↪']]
df_clean_jitter[['cholesterol', 'age', 'weight']] = df_clean_jitter[['cholesterol',
↪'age', 'weight']].values + np.random.rand(len(df_clean_jitter),3)/2
sns.pairplot(df_clean_jitter, hue="cardio", height=2)
```

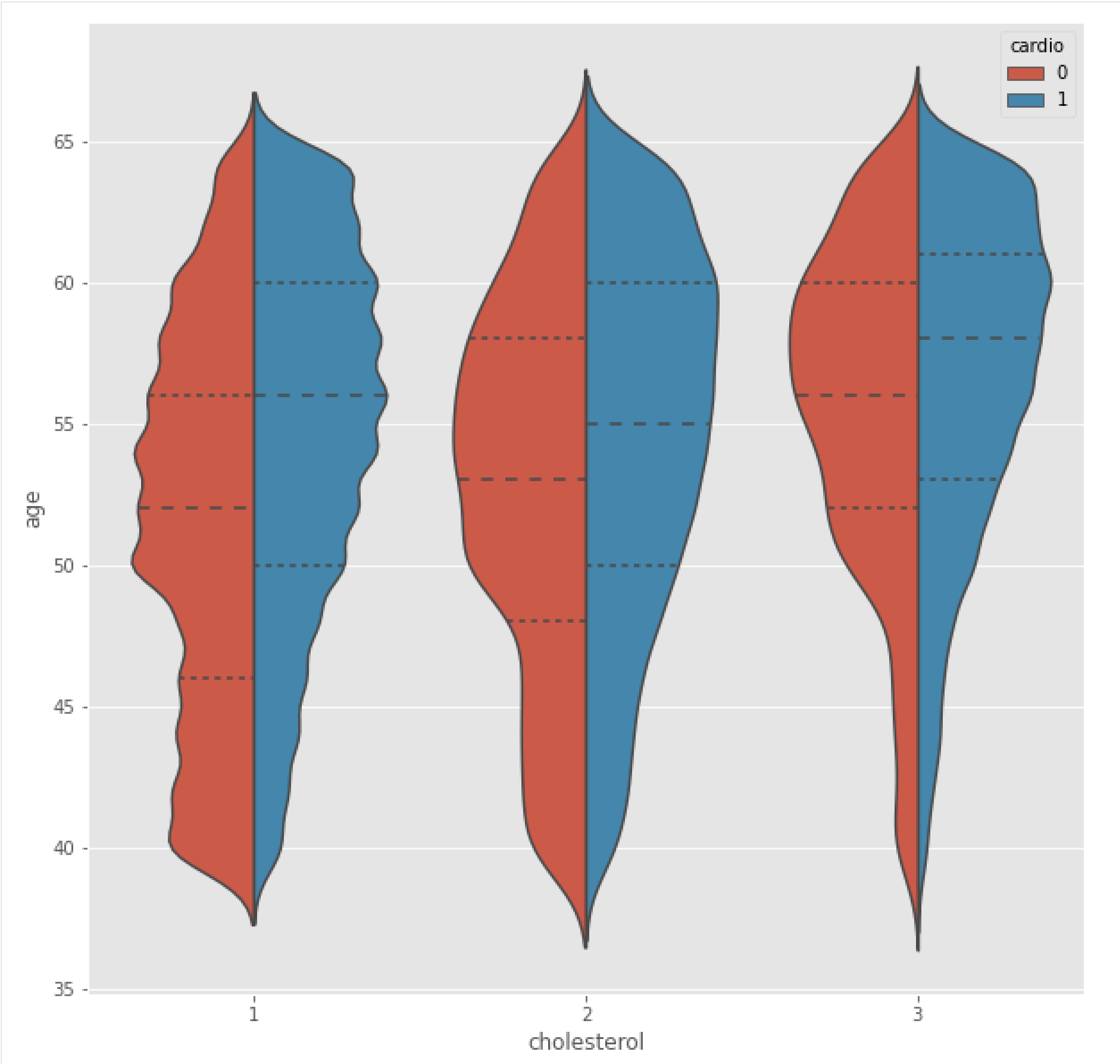
[68]:
```
<seaborn.axisgrid.PairGrid at 0x20f0f11c438>
```

The above pairwise scatter plot depicts the distribtuions of each of those that had cardiovascular disease and those that did not for each attribute across the center diagonal. As show in those distributions, there are apparent differences in those that had cardiovascular disease and those that did not. For example, as will be discussed in more, below details, the distrbutions show that as blood pressure, cholesterol, weight and age increase, the number of those that had cardiovascular disease also increases. In addition, the pairwise scatter plot shows scatterplot distrbutions between each of the attributes. Some seperation between those that had cardiovasular disease and those that did not can be seen in the plots between weight and age, cholesterol and weight, and age and blood pressure, despite the presence of some values seemingly ranndomly distributed. Therefore, these attributes may be indicative of cardiovascular disease.

[69]:
```
f, ax = plt.subplots(figsize=(10, 10))

sns.violinplot(x="cholesterol", y="weight", hue="cardio", data=df_clean,
               split=True, inner="quart")

f, ax = plt.subplots(figsize=(10, 10))

sns.violinplot(x="cholesterol", y="age", hue="cardio", data=df_clean,
               split=True, inner="quart")
```

[69]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x20f0ebe45f8>
```


cardio
0
1
120
100
80
60
40
weight
1
2
3
cholesterol

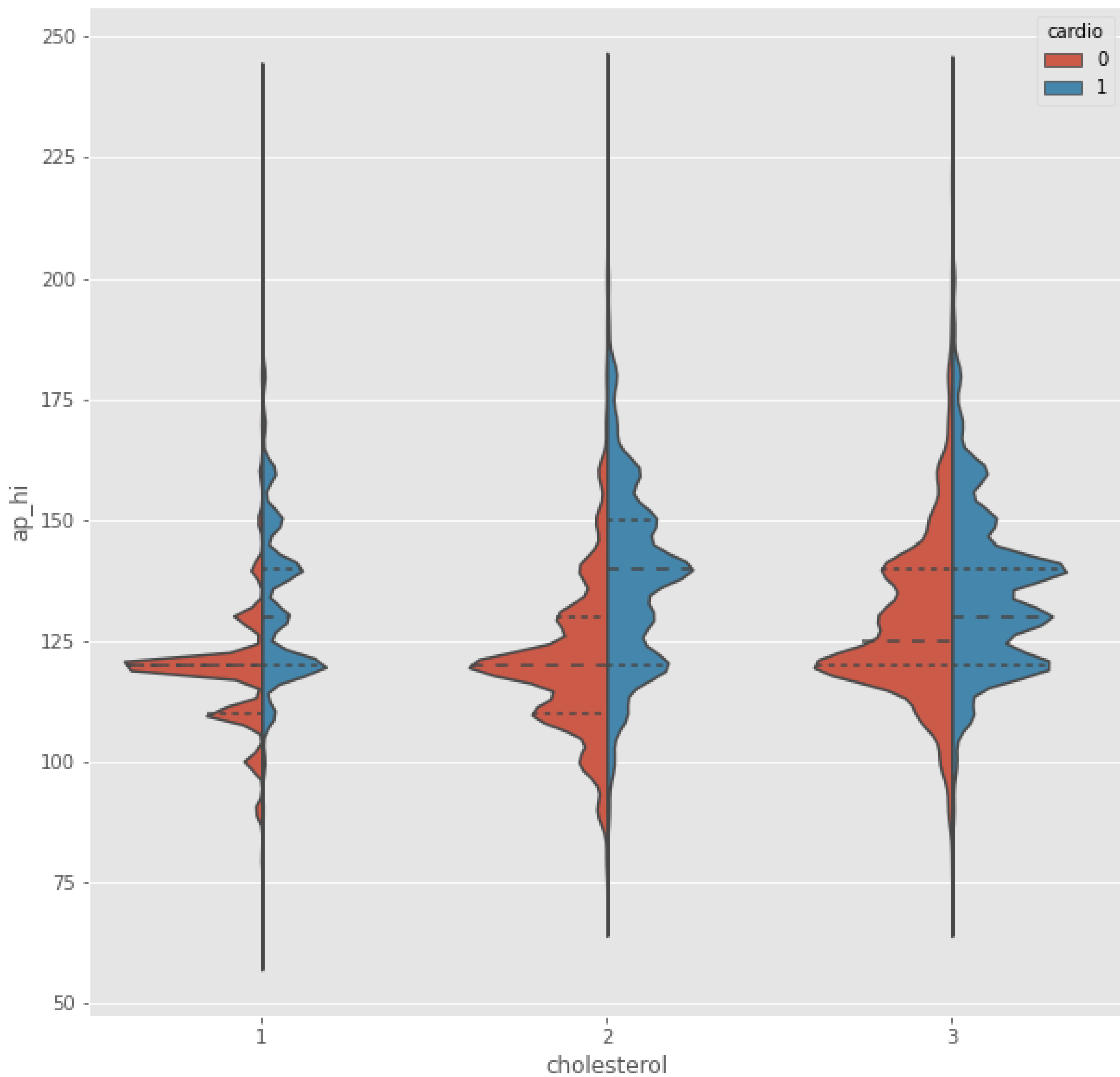


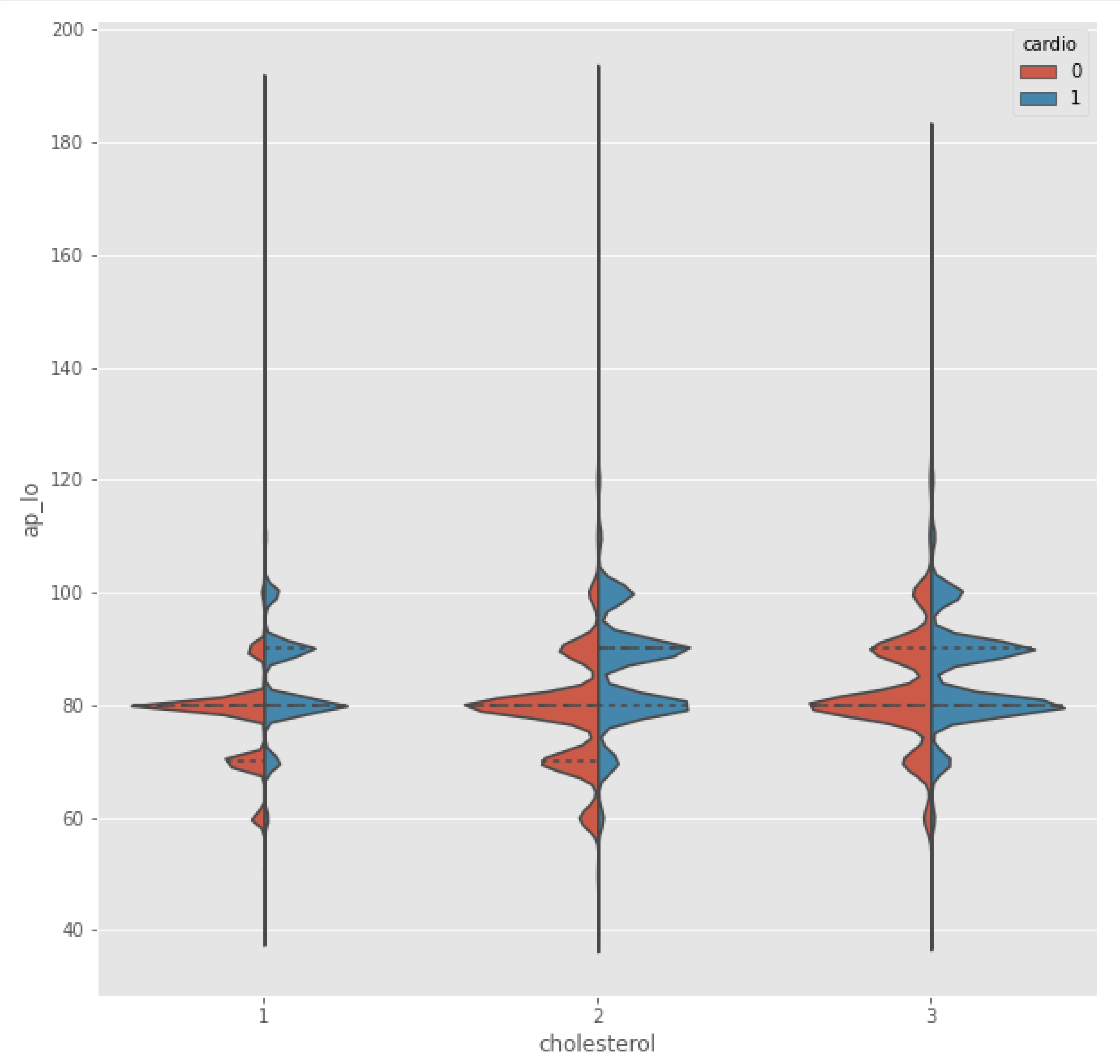
The above violin plots show the relationship between cholesterol and weight between groups having cardiovascular disease (1), and not having cardiovascular disease. The violin plots show that as the level of cholesterol increases from 1-3, the median difference in weight between the cardiovascular and non-cardiovascular disease groups also increases. It is also apparent that the median weight for cholesterol levels 2-3 for each group represents an increase from cholesterol level 1. This is consistent with the understanding that as cholesterol levels increase, weight also increases.

The violin plots depicting cholesterol and age shows that the distribution between those that had cardiovascular disease and those that did not is consistent across cholesterol levels 2 and 3. For example, the difference between the median ages of those that had cardiovasular disease and those that did not for cholesterol levels 2-3 is approximately equal. This is consistent with that people typically increase cholesterol levels with age as activites such as exercise decrease. However, in the distributions between those that had cardiovascular disease and those that did not for cholesterol level 1 shows that age is a potential indicator of cardiovascular disease. The distrbution that had cardiovascular disease at cholesterol level 1 is approximately 56, which is potentially, significantly greater than the median age of those that did not have cardiovascular disease at 52.

[70]:
```
f, ax = plt.subplots(figsize=(10, 10))

sns.violinplot(x="cholesterol", y="ap_hi", hue="cardio", data=df_clean,
               split=True, inner="quart")

f, ax = plt.subplots(figsize=(10, 10))

sns.violinplot(x="cholesterol", y="ap_lo", hue="cardio", data=df_clean,
               split=True, inner="quart")
```

[70]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x20f0f5200b8>
```





Violin plots of blood pressure and cholesterol between those that had and did not have cardiovascular disease appears to include multiple peaks. Otherwise, it appears that those with lower overall blood pressure, between low and high pressure values, suffered less cardiovascular disease. As can be seen, as both low and high blood pressure values increase, the distrbution of those with cardiovascular disease also increases. Therefore, it appears as if blood pressure is an indicator of cardiovascular disease.

[71]:
```
import plotly.express as px

df_sub2 = df_clean[['age', 'weight', 'cholesterol', 'ap_hi', 'cardio', 'ap_lo']]
#Normalizing the data
df_normalized2 = (df_sub2-df_sub2.mean())/(df_sub2.std())
df_normalized2.cardio = df_sub2.cardio
df_normalized2.cholesterol = df_normalized2.cholesterol+np.random.rand(*df_
↪normalized2.cholesterol.shape)/2
df_normalized2.ap_hi = df_normalized2.ap_hi+np.random.rand(*df_normalized2.ap_hi.
↪shape)/2
```

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```
fig = px.parallel_coordinates(df_sub2, color='cardio', labels={"age": "Age", "weight":
↪ "Weight", "cholesterol": "Cholesterol", "ap_hi": "High Blood Pressure Value",
               "cardio": "Cardiovascular Disease", "ap_lo": "Low Blood Pressure Value
↪"},
                             color_continuous_scale=px.colors.diverging.Tealrose,
                             color_continuous_midpoint=1)
fig.show()
```

Data type cannot be displayed: application/vnd.plotly.v1+json

The above parallel coordinates plot shows interconnections between those that had cardiovascular disease and those that did not, and the attributes that appear to be indicators of cardiovascular disease. Here, those with cardiovascular disease are shown in beige, and those without cardiovascular disease is shown in teal. In the above plot, separation can be seen between age and weight around 43, suggesting that age and weight may interact in predicting cardiovascular disease. Some separation between weight, cholesterol and high blood pressure indicating that as weight, cholesterol and high blood pressure values increase, cardiovascular disease also increases. Lastly, as shown, there is more influence of cardiovascular disease as all of the attributes increase.

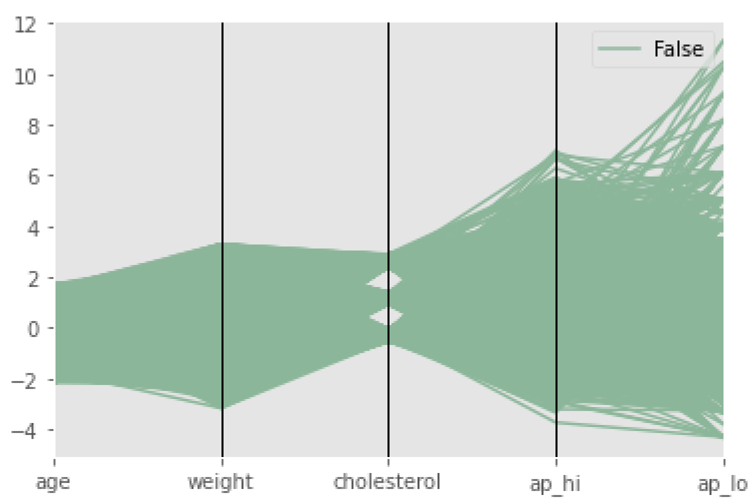
[72]:
```
from pandas.plotting import parallel_coordinates


#df_sub2 = df_clean[['age', 'weight', 'cholesterol', 'ap_hi', 'cardio', 'ap_lo']]

df_sub = df_clean[['age', 'weight', 'cholesterol', 'ap_hi', 'cardio', 'ap_lo']]
df_sub.cardio = df_sub.cardio=='1'
#normalizing values
df_normalized = (df_sub-df_sub.mean())/(df_sub.std())
df_normalized.cardio = df_sub.cardio
df_normalized.cholesterol = df_normalized.cholesterol+np.random.rand(*df_normalized.
↪cholesterol.shape)/2
df_normalized.ap_hi = df_normalized.ap_hi+np.random.rand(*df_normalized.ap_hi.shape)/2


parallel_coordinates(df_normalized,'cardio')

plt.show()
```



The above parallel coordinates plot shows the axes of the attrivutes for the group that includes cardiovascular disease. Eliminating the group that does not have cardiovascular disease shows more detail after normalization. For example, there appears to be age and weight bands that may be indicative of cardiovascular disease such that outside of this band is indicative of not having cardiovascular disease. Lastly, while most of the axes are clustered 2 and -2, more axes extend from the high values of high and low blood pressure. This is indicative of an increase in cardiovascular disease as the values for high and low blood pressure increase, which also fits the domain knowledge of the problem.

CHAPTER

EIGHT

NEW FEATURES

We can combine the height and weight features into a single feature, Body Mass Index. BMI can be calculated using the formula below. In general, we can see a higher instance of cardiovascular disease in patients with a higher BMI.

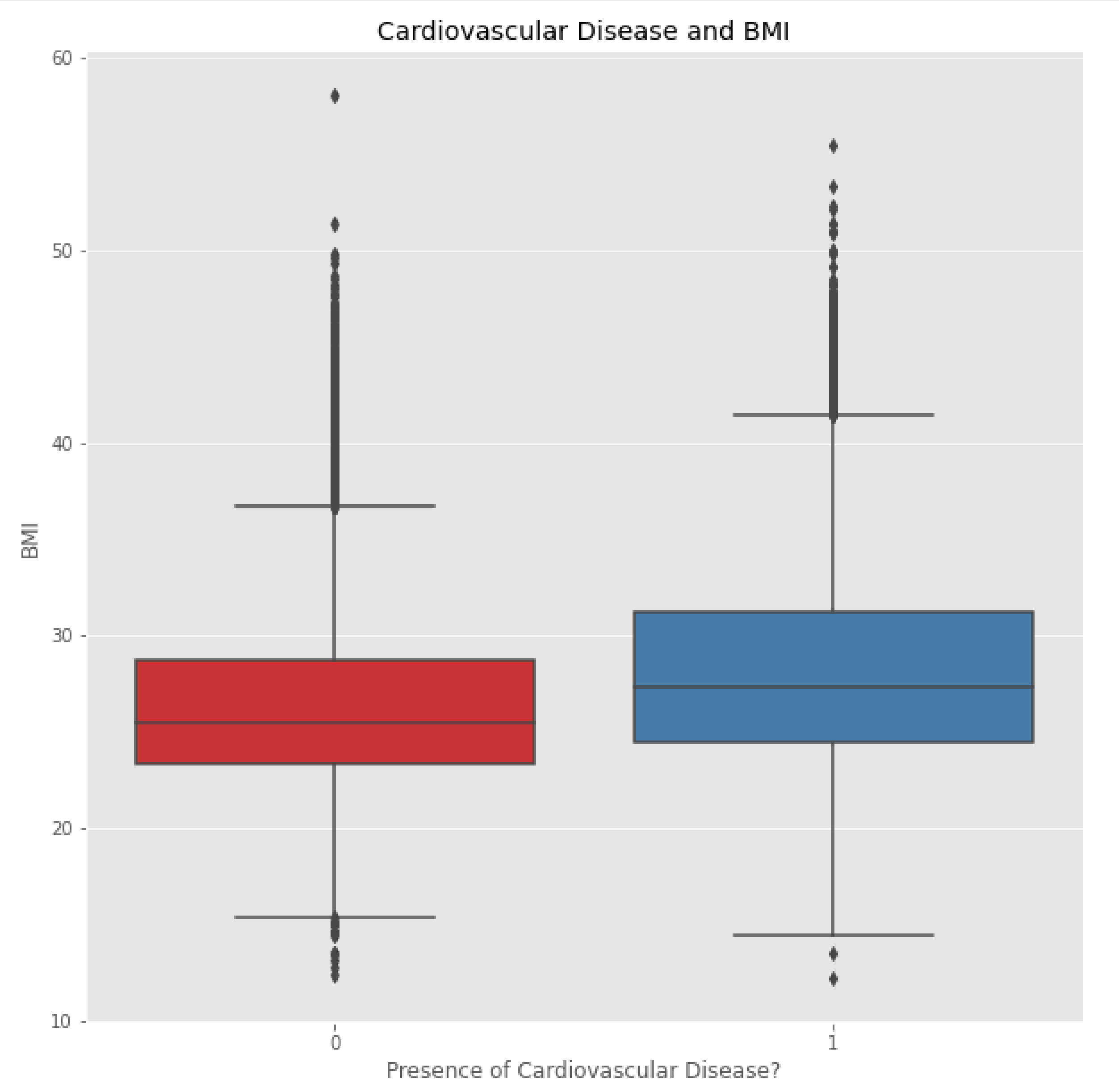
$BMI = Weight\ (kg)\ /\ Height\ (m^2)$

[73]:
```
plt.figure(figsize=(10,10))

df_clean['bmi'] = df_clean['weight'] / (df_clean['height']/100)**2

sns.boxplot(x='cardio',
            y='bmi',
            data=df_clean,
            palette="Set1").set(title = 'Cardiovascular Disease and BMI',
                                xlabel = 'Presence of Cardiovascular Disease?',
                                ylabel = 'BMI')

plt.show()
```



For entertainment, we can use some of what we learned in stats so that we don't forget, and do a ttest between the diseased and healthy group. It shows what would expect, that there is some statistical signficance in the mean difference of BMI between the two groups (healthy vs diseased).

[74]:
```
from scipy import stats
import researchpy as rp

# Let's create 2 sets, one for disease, and another for healthy
disease = df_clean[df_clean['cardio'] == 1]
disease.reset_index(inplace = True)

healthy = df_clean[df_clean['cardio'] == 0]
disease.reset_index(inplace = True)
```

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```
var='bmi'

# diff = disease[var] - healthy[var]
# stats.probplot(diff, plot= plt)
# plt.title('BMI P-P Plot')
# stats.ttest_ind(disease[var], healthy[var]))

descriptives, results = rp.ttest(disease[var], healthy[var], equal_variances=False)
results
```

[74]:

```
                Welch's t-test     results
0  Difference (bmi - bmi) =       1.8505
1      Degrees of freedom =   69185.9581
2                       t =      51.2621
3   Two side test p value =       0.0000
4  Difference < 0 p value =       1.0000
5  Difference > 0 p value =       0.0000
6               Cohen's d =       0.3876
7               Hedge's g =       0.3876
8           Glass's delta =       0.3686
9                       r =       0.1913
```

We could also create a BMI category to represent the following four cases. Source

- Underweight: BMI is less than 18.5.
- Normal weight: BMI is 18.5 to 24.9.
- Overweight: BMI is 25 to 29.9.
- Obese: BMI is 30 or more.

As expected, we can see from that a higher BMI group correlates with a higher chance of being diagnosed with cardiovascular disease.

[75]:

```
df_clean['bmiGrp'] = np.where((df_clean.bmi < 18.5), 1, 0)
df_clean['bmiGrp'] = np.where((df_clean.bmi >= 18.5) & (df_clean.bmi < 25), 2, df_
↪clean.bmiGrp)
df_clean['bmiGrp'] = np.where((df_clean.bmi >= 25) & (df_clean.bmi < 30), 3, df_clean.
↪bmiGrp)
df_clean['bmiGrp'] = np.where((df_clean.bmi >= 30), 4, df_clean.bmiGrp)

df_grouped = df_clean.groupby(by=['bmiGrp'])
print ("Percentage of Caridovascular Disease in each BMI group:")
print (df_grouped.cardio.sum() / df_grouped.cardio.count() *100)
```

```
Percentage of Caridovascular Disease in each BMI group:
bmiGrp
1    26.917058
2    40.545001
3    51.286476
4    62.745980
Name: cardio, dtype: float64
```

[76]:

```
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(15,8))

sns.boxplot(x='cardio', y='bmiGrp', data=df_clean, ax=ax1)
#sns.barplot(x='bp', y='cardio', data=df, ax=ax2)
```

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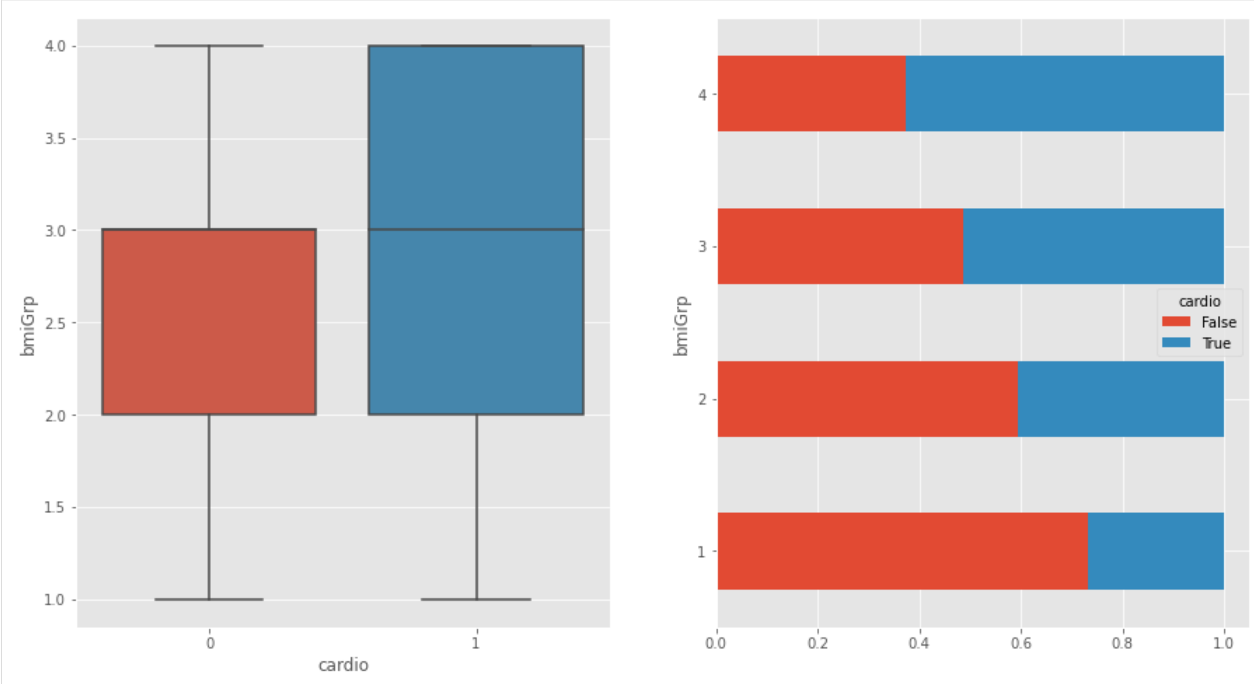
```
cardio = pd.crosstab([df_clean['bmiGrp']],df_clean.cardio.astype(bool))
cardo_rate = cardio.div(cardio.sum(1).astype(float), axis=0) # normalize the value
cardo_rate.plot(kind='barh', stacked=True, ax=ax2)

plt.show()
```



We can also create a new feature to categorize the Blood Pressure values. Source

Blood Pressure Categories

American Heart Association | American Stroke Association

BLOOD PRESSURE CATEGORY	SYSTOLIC mm Hg (upper number)		DIASTOLIC mm Hg (lower number)
NORMAL	LESS THAN 120	and	LESS THAN 80
ELEVATED	120 – 129	and	LESS THAN 80
HIGH BLOOD PRESSURE (HYPERTENSION) STAGE 1	130 – 139	or	80 – 89
HIGH BLOOD PRESSURE (HYPERTENSION) STAGE 2	140 OR HIGHER	or	90 OR HIGHER
HYPERTENSIVE CRISIS (consult your doctor immediately)	HIGHER THAN 180	and/or	HIGHER THAN 120

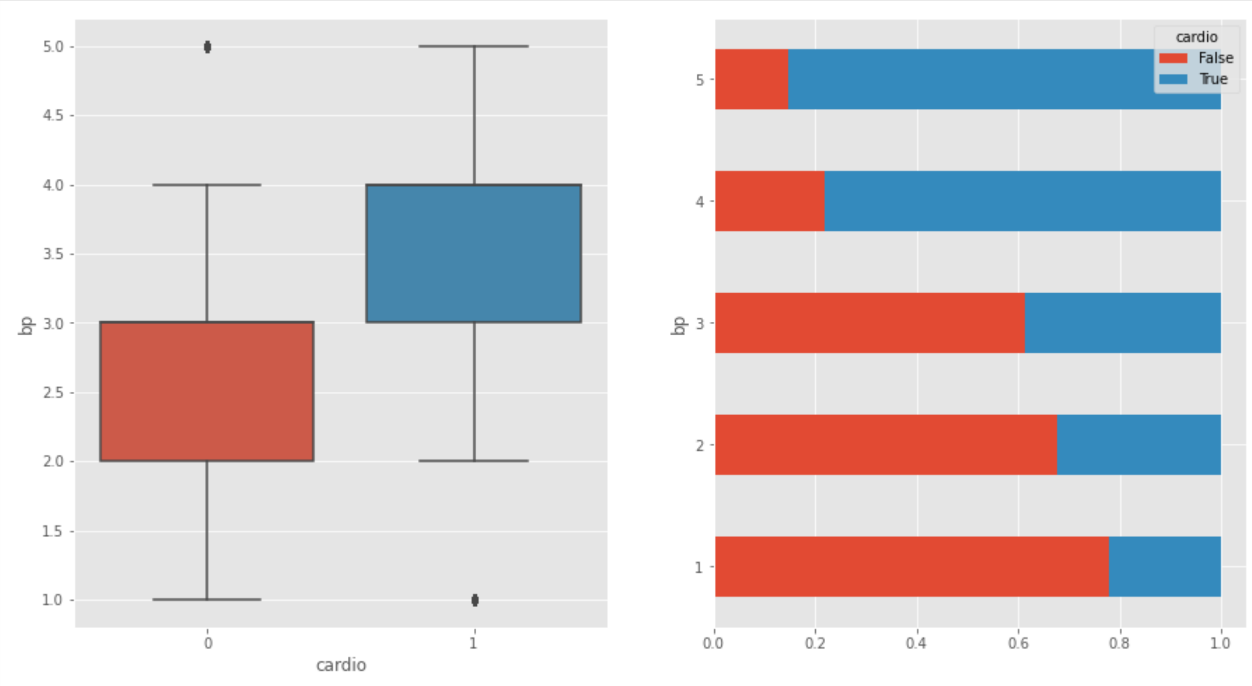
heart.org/bplevels

As with BMI Categories, we can see that a higher BP group corresponds to a higher chance of being diagnosed with cardiovascular disease.

[77]:
```
# Create blood pressure categories

df_clean['bp'] = np.where((df_clean.ap_hi < 120) & (df_clean.ap_lo < 80), 1, 0)
df_clean['bp'] = np.where((df_clean.ap_hi >= 120) & (df_clean.ap_hi < 130) & (df_
↪clean.ap_lo < 80), 2, df_clean.bp)
df_clean['bp'] = np.where((df_clean.ap_hi >= 130) & (df_clean.ap_hi < 140) | ((df_
↪clean.ap_lo >= 80) & (df_clean.ap_lo < 90)), 3, df_clean.bp)
df_clean['bp'] = np.where((df_clean.ap_hi >= 140) | (df_clean.ap_lo >= 90), 4, df_
↪clean.bp)
df_clean['bp'] = np.where((df_clean.ap_hi > 180) | (df_clean.ap_lo > 120), 5, df_
↪clean.bp)

df_grouped = df_clean.groupby(by=['bp'])
print ("Percentage of cardio disease in each Blood Pressure group:")
print (df_grouped.cardio.sum() / df_grouped.cardio.count() *100)
```

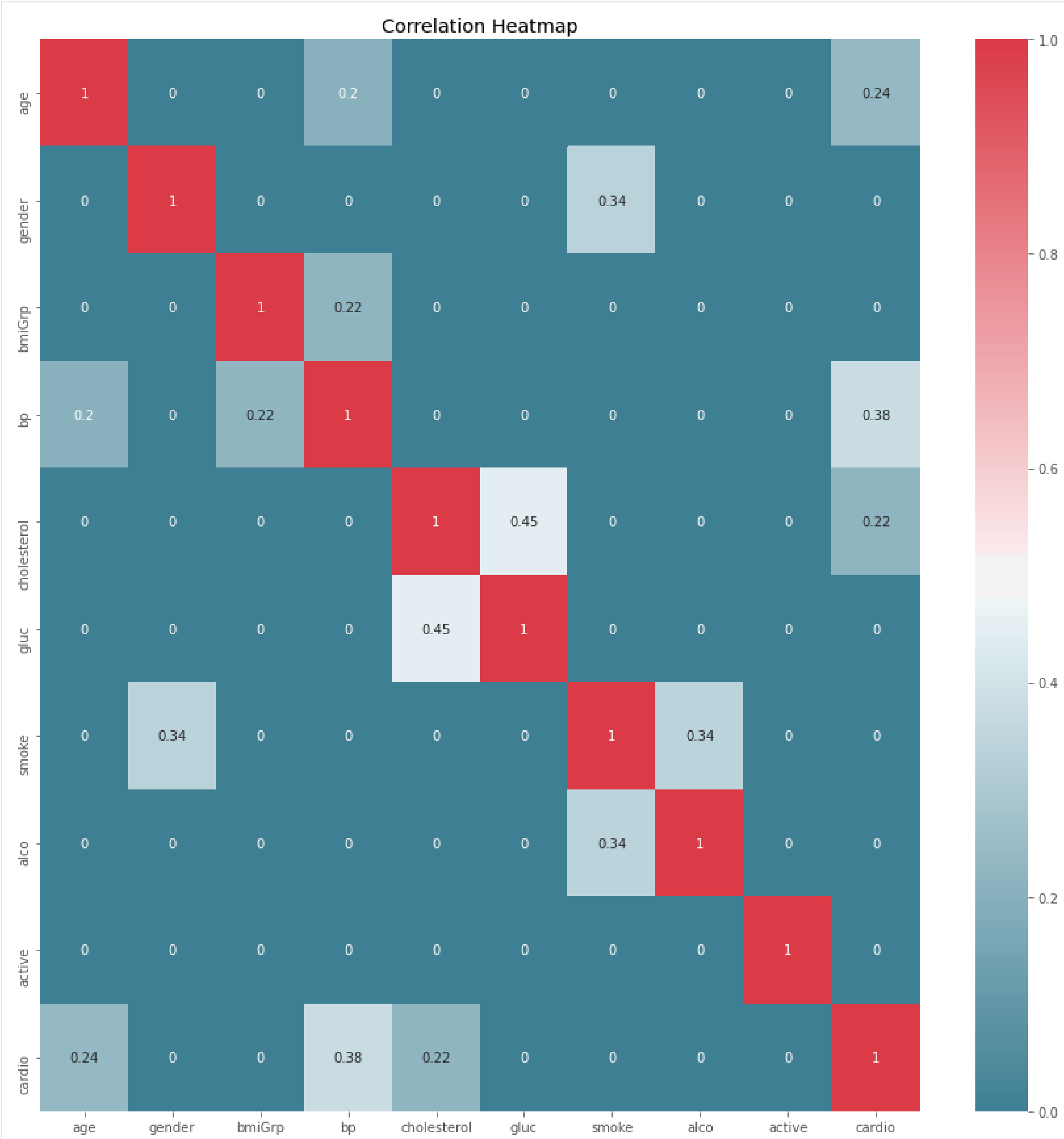
```
Percentage of cardio disease in each Blood Pressure group:
bp
1    22.155939
2    32.253968
3    38.524389
4    78.158972
5    85.250000
Name: cardio, dtype: float64
```

[78]:
```
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(15,8))

sns.boxplot(x='cardio', y='bp', data=df_clean, ax=ax1)
#sns.barplot(x='bp', y='cardio', data=df, ax=ax2)

cardio = pd.crosstab([df_clean['bp']],df_clean.cardio.astype(bool))
cardo_rate = cardio.div(cardio.sum(1).astype(float), axis=0) # normalize the value
cardo_rate.plot(kind='barh', stacked=True, ax=ax2)

plt.show()
```



Let's create a new feature correlation heatmap, but instead use the new features we created. In this case, we can see a better correlation between our groups for BMI and BP with respect to our reponse variable (cardio). Please note, we used a mask below to set correlations less than .2 to 0, for a better visualization.

[79]:
```
features = ['age', 'gender', 'bmiGrp', 'bp', 'cholesterol', 'gluc', 'smoke', 'alco',
↪'active', 'cardio']

plt.figure(figsize=(15,15))

# Use an easier to see colormap
cmap = sns.diverging_palette(220, 10, as_cmap=True)

correlation = df_clean[features].corr()
correlation[np.abs(correlation)<.2] = 0

sns.heatmap(correlation, annot = True, cmap=cmap).set(title = 'Correlation Heatmap')
plt.show()
```


Correlation Heatmap
age
gender
bmiGrp
bp
cholesterol
gluc
smoke
alco
active
cardio
1 0 0 0.2 0 0 0 0 0 0.24
0 1 0 0 0 0 0.34 0 0 0
0 0 1 0.22 0 0 0 0 0 0
0.2 0 0.22 1 0 0 0 0 0 0.38
0 0 0 0 1 0.45 0 0 0 0.22
0 0 0 0 0.45 1 0 0 0 0
0 0.34 0 0 0 0 1 0.34 0 0
0 0 0 0 0 0 0.34 1 0 0
0 0 0 0 0 0 0 0 1 0
0.24 0 0 0.38 0.22 0 0 0 0 1
1.0
0.8
0.6
0.4
0.2
0.0

CHAPTER

NINE

EXCEPTIONAL WORK

9.1 Store feature matrix as an ndarray

```
[80]: # Full Model
X_cols = ['age', 'gender', 'height', 'weight', 'ap_hi', 'ap_lo', 'cholesterol', 'gluc
↪', 'smoke', 'alco', 'active']
# *dcrouthamel - test with new features
# X_cols = ['age', 'gender', 'bmiGrp', 'bp', 'cholesterol', 'gluc', 'smoke', 'alco',
↪'active']
X = df_clean[X_cols].to_numpy()
```

```
[81]: type(X)
```

```
[81]: numpy.ndarray
```

9.2 Store response vector

```
[82]: y = df_clean['cardio'].to_numpy()
```

Full Model consisting of all features with standardized values.

```
[83]: from sklearn import metrics
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import StandardScaler
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_
↪state=0)

sc = StandardScaler()
X_train_std = sc.fit_transform(X_train)
X_test_std = sc.transform(X_test)

# logreg = LogisticRegression()
# logreg.fit(X_train, y_train)
logreg = LogisticRegression()
logreg.fit(X_train_std, y_train)
```

```
[83]: LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
                   intercept_scaling=1, l1_ratio=None, max_iter=100,
                   multi_class='auto', n_jobs=None, penalty='l2',
                   random_state=None, solver='lbfgs', tol=0.0001, verbose=0,
                   warm_start=False)
```

[84]:
```
y_pred = logreg.predict(X_test_std)
print('Accuracy of the log reg model on the test data: {:.2f}'.format(logreg.score(X_
↪test_std, y_test)))
```

```
Accuracy of the log reg model on the test data: 0.73
```

[85]:
```
from sklearn.metrics import confusion_matrix
confusion_matrix = confusion_matrix(y_test, y_pred)
print(confusion_matrix)
```

```
[[8136 2293]
 [3436 7128]]
```

[86]:
```
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred))
```

```
precision    recall  f1-score   support

           0       0.70      0.78      0.74     10429
           1       0.76      0.67      0.71     10564

    accuracy                           0.73     20993
   macro avg       0.73      0.73      0.73     20993
weighted avg       0.73      0.73      0.73     20993
```

[87]:
```
from IPython.display import Markdown as md
```

[88]:
```
### Logistic Regression Metrics

md(f"**True Positives:**  {confusion_matrix[1, 1]} \n\n **True Negatives:**
↪{confusion_matrix[0, 0]} \n\n **False Positives:**  {confusion_matrix[0, 1]} \n\n␣
↪**False Negatives:**  {confusion_matrix[1, 0]}")
```

[88]: **True Positives:** 7128

True Negatives: 8136

False Positives: 2293

False Negatives: 3436

[89]:
```
md(f"**Accuracy:**  { format(( confusion_matrix[1, 1] + confusion_matrix[0, 0] ) /␣
↪confusion_matrix.sum(), '.3f')}\n\n-how often we were correct overall")
```

[89]: **Accuracy:** 0.727

-how often we were correct overall

[90]:
```
md(f"**Error:**  { format(( confusion_matrix[0, 1] + confusion_matrix[1, 0] ) /␣
↪confusion_matrix.sum(), '.3f')}\n\n-how often we were incorrect overall")
```

[90]: **Error:** 0.273

-how often we were incorrect overall

[91]:
```
md(f"**Sensitivity/ Recall:**  { format(( confusion_matrix[1, 1] ) / confusion_
↪matrix[1].sum(axis=0), '.3f')}\n\n-when the patient actually had CVD, how often␣
↪were we correct")
```

[91]: **Sensitivity/ Recall:** 0.675

-when the patient actually had CVD, how often were we correct

[92]:
```
md(f"**Specificity:**  { format(( confusion_matrix[0, 0] ) / confusion_matrix[0].
↪sum(), '.3f')}\n\n-when the patient did not had CVD, how often were we correct")
```

[92]: **Specificity:** 0.780

-when the patient did not had CVD, how often were we correct

[93]:
```
md(f"**False Postive Rate:**  { format(( confusion_matrix[0, 1] ) / ( confusion_
↪matrix[0, 0] + confusion_matrix[0, 1] ), '.3f')}\n\n-when the patient did not had␣
↪CVD, how often were we incorrect")
```

[93]: **False Postive Rate:** 0.220

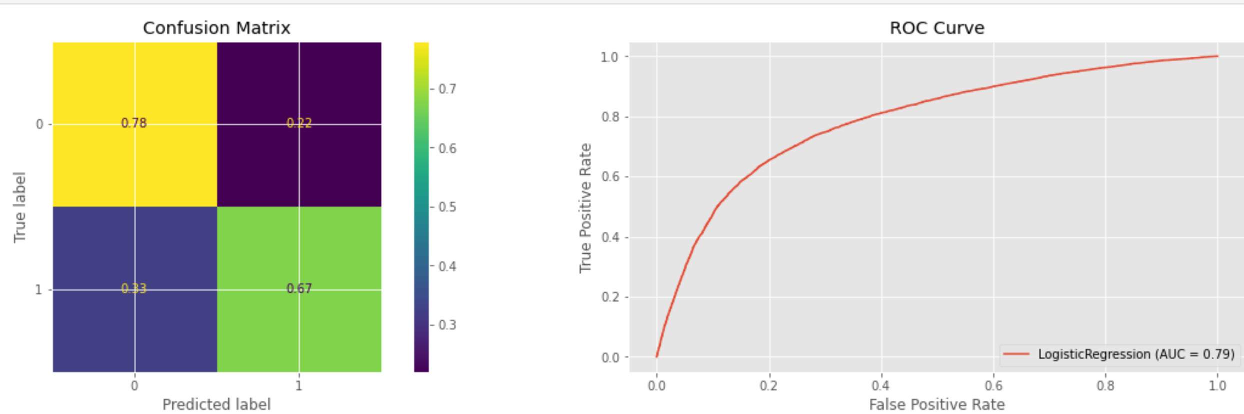
-when the patient did not had CVD, how often were we incorrect

[94]:
```
md(f"**Precision:**  { format(( confusion_matrix[1, 1] ) / ( confusion_matrix[1, 1] +␣
↪confusion_matrix[0, 1] ), '.3f')}\n\n-how precise were we when classifying the␣
↪patient as having CVD")
```

[94]: **Precision:** 0.757

-how precise were we when classifying the patient as having CVD

[95]:
```
from sklearn.metrics import plot_confusion_matrix
from sklearn.metrics import plot_roc_curve

fig = plt.figure(1, figsize=(20, 5))

chart_1 = fig.add_subplot(121)
chart_2 = fig.add_subplot(122)

plot_confusion_matrix(logreg, X_test_std, y_test, normalize='true', ax=chart_1)
chart_1.set_title('Confusion Matrix')

plot_roc_curve(logreg, X_test_std, y_test, ax=chart_2)
chart_2.set_title('ROC Curve')

plt.show()
```



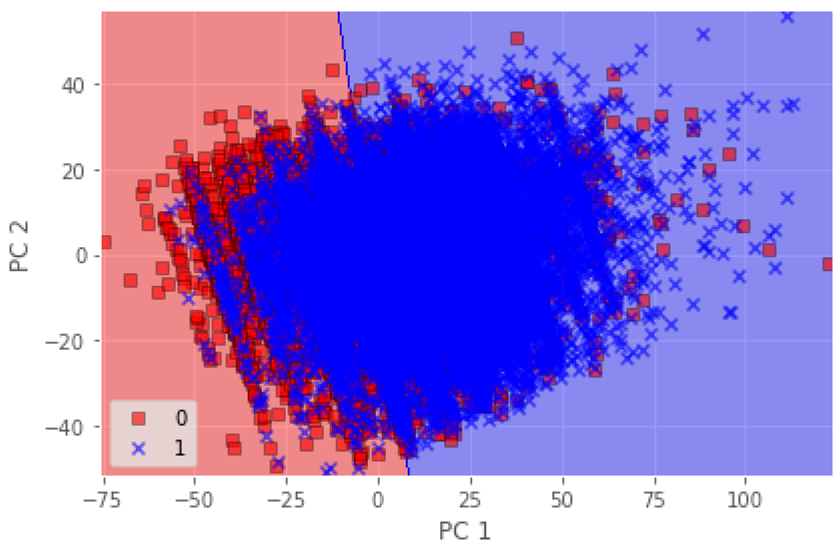
Principal Component Analysis is a data compression technique that can reduce the dimensionality of a data set. It does this by finding the maximum variance in a higher dimensional space and project that onto a new space with fewer dimensions. Although our data set doesn't have a hugh number a features, let's explore what PCA can do for us.

First, we'll define a function that can plot two principal components and a decison boundary. This code was taken from chapter 4 of Python Machine Learning, by Vahid Mirjalili and Sebastian Raschka.

[96]:
```
# Chapter 4 of book
from matplotlib.colors import ListedColormap
def plot_decision_regions(X, y, classifier, resolution=0.02):

    # setup marker generator and color map
    markers = ('s', 'x', 'o', '^', 'v')
    colors = ('red', 'blue', 'lightgreen', 'gray', 'cyan')
    cmap = ListedColormap(colors[:len(np.unique(y))])

    # plot the decision surface
    x1_min, x1_max = X[:, 0].min() - 1, X[:, 0].max() + 1
    x2_min, x2_max = X[:, 1].min() - 1, X[:, 1].max() + 1
    xx1, xx2 = np.meshgrid(np.arange(x1_min, x1_max, resolution),
                           np.arange(x2_min, x2_max, resolution))
    Z = classifier.predict(np.array([xx1.ravel(), xx2.ravel()]).T)
    Z = Z.reshape(xx1.shape)
    plt.contourf(xx1, xx2, Z, alpha=0.4, cmap=cmap)
    plt.xlim(xx1.min(), xx1.max())
    plt.ylim(xx2.min(), xx2.max())

    # plot examples by class
    for idx, cl in enumerate(np.unique(y)):
        plt.scatter(x=X[y == cl, 0],
                    y=X[y == cl, 1],
                    alpha=0.6,
                    color=cmap(idx),
                    edgecolor='black',
                    marker=markers[idx],
                    label=cl)
```

Below, we'll create a pca classifier with two components and fit the reduced data set to a logistic regression model.

[97]:
```
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler

pca = PCA(n_components=2)
# sc = StandardScaler()
# X_train_std = sc.fit_transform(X_train)
# X_test_std = sc.transform(X_test)

# dimensionality reduction:
X_train_pca = pca.fit_transform(X_train)
X_test_pca = pca.transform(X_test)

# fitting the logistic regression model on the reduced dataset:
logreg = LogisticRegression()
logreg.fit(X_train_pca, y_train)
plot_decision_regions(X_train_pca, y_train, classifier=logreg)
plt.xlabel('PC 1')
plt.ylabel('PC 2')
plt.legend(loc='lower left')
plt.tight_layout()
plt.show()
```



[98]:
```
pca.explained_variance_ratio_
```

[98]:
```
array([0.55118299, 0.24041201])
```

Above, we can see that the two components account nearly 80 percent of the variance. The figure though doesn't show a good separation. This could be due to the fact that we need to visualize it in more than 2 dimensions, i.e., run PCA to account for a higher number of components and variance.

Below we output some metrics related to using the reduced dimensionality set in a Logistic Regression model. We see that the accuracy is comparable to the full model created previously. Accuracy is an acceptable metric for a balance data set. However, in the case of medical diagnosis, Recall or Sensitivity is an important metric. It desribes the proportion of patients correctly diagnosed with CVD. If this number is low, patients won't be corretly identified and won't receive the treatment they should.

PCA shows .62 for recall, whereas the previous model is .67. Because of that, I would go with the full model.

[99]:
```
y_pred = logreg.predict(X_test_pca)
print('Accuracy of the log reg model on the test data: {:.2f}'.format(logreg.score(X_
↪test_pca, y_test)))
```

```
Accuracy of the log reg model on the test data: 0.71
```

[100]:
```
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred))
```

```
precision    recall  f1-score   support

           0       0.68      0.80      0.74     10429
           1       0.76      0.62      0.69     10564

    accuracy                           0.71     20993
   macro avg       0.72      0.71      0.71     20993
weighted avg       0.72      0.71      0.71     20993
```

[101]:
```
from sklearn.metrics import plot_confusion_matrix
from sklearn.metrics import plot_roc_curve
```

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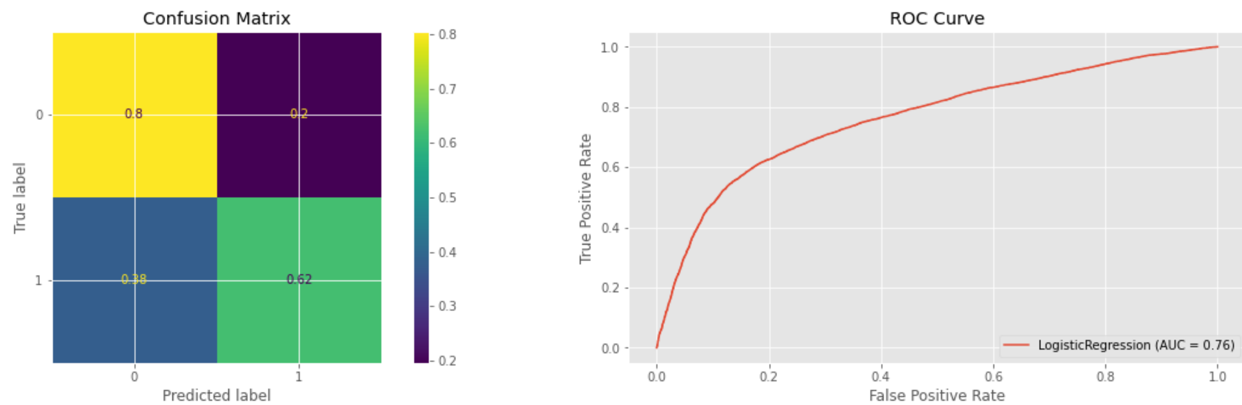
```
fig = plt.figure(1, figsize=(20, 5))

chart_1 = fig.add_subplot(121)
chart_2 = fig.add_subplot(122)

plot_confusion_matrix(logreg, X_test_pca, y_test, normalize='true', ax=chart_1)
chart_1.set_title('Confusion Matrix')

plot_roc_curve(logreg, X_test_pca, y_test, ax=chart_2)
chart_2.set_title('ROC Curve')

plt.show()
```



PCA (unsupervised) does not use the target variable. It attempts to maximize the variance in the feature set. LDA (supervised) can use our target information and maximize the class separability.

Note that LDA will produce N-1 components, where N is the number of classes in our target. So in our case, it would produce 1 components.

We can use the below to generate an LDA feature space and train a logistic regression model against it.

[102]:
```
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.preprocessing import StandardScaler

lda = LinearDiscriminantAnalysis()
# sc = StandardScaler()
# X_train_std = sc.fit_transform(X_train)
# X_test_std = sc.transform(X_test)

X_train_lda = lda.fit_transform(X_train, y_train)
X_test_lda = lda.transform(X_test)

# fitting the logistic regression model on the lda dataset:
logreg = LogisticRegression()
logreg.fit(X_train_lda, y_train)
```

[102]:
```
LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
                   intercept_scaling=1, l1_ratio=None, max_iter=100,
                   multi_class='auto', n_jobs=None, penalty='l2',
                   random_state=None, solver='lbfgs', tol=0.0001, verbose=0,
                   warm_start=False)
```

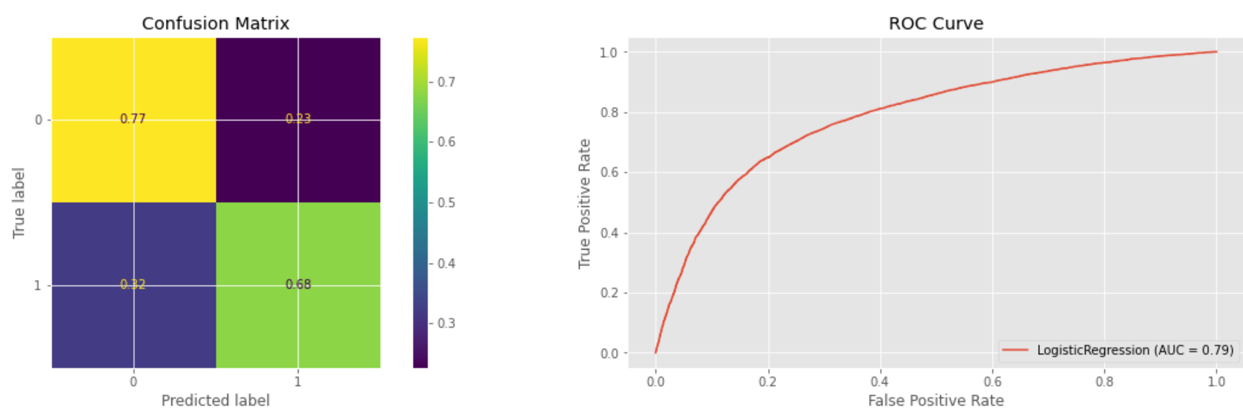
[103]:
```
y_pred = logreg.predict(X_test_lda)
print('Accuracy of the log reg model on the test data: {:.2f}'.format(logreg.score(X_
↪test_lda, y_test)))
```

```
Accuracy of the log reg model on the test data: 0.73
```

[104]:
```
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred))
```

```
precision    recall  f1-score   support

           0       0.70      0.77      0.74     10429
           1       0.75      0.68      0.71     10564

    accuracy                           0.73     20993
   macro avg       0.73      0.73      0.73     20993
weighted avg       0.73      0.73      0.73     20993
```

[105]:
```
from sklearn.metrics import plot_confusion_matrix
from sklearn.metrics import plot_roc_curve

fig = plt.figure(1, figsize=(20, 5))

chart_1 = fig.add_subplot(121)
chart_2 = fig.add_subplot(122)

plot_confusion_matrix(logreg, X_test_lda, y_test, normalize='true', ax=chart_1)
chart_1.set_title('Confusion Matrix')

plot_roc_curve(logreg, X_test_lda, y_test, ax=chart_2)
chart_2.set_title('ROC Curve')

plt.show()
```



Above we can see that our accuracy increased to .73 using LDA, vs .71 with PCA. Additionally, the AUC value is higher and maybe more importantly, the Recall/Sensitivity value increased to .68. I think this helps demonstrate that LDA did a better job since it was able to use our target information.