Data Mining Assignment 1

Alex Chau

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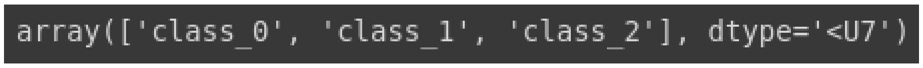
1 Question 1

a) The categorical feature is "Target", this can be shown via the following:

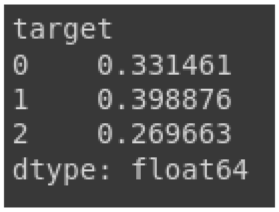
```python
import pandas as pd
from sklearn.datasets import load_wine

data = load_wine()
df = pd.DataFrame(data.data, columns=data.feature_names)
df['target'] = pd.Series(data.target)
```



```
array(['class_0', 'class_1', 'class_2'], dtype='<U7')
```

Getting the frequency of each categorical feature is simple.

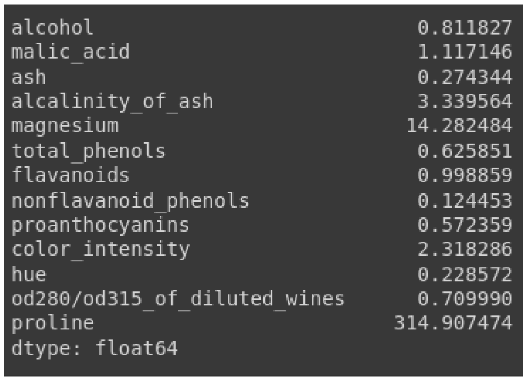
```python
df.groupby('target').size()/len(df)
```



```
target
0    0.331461
1    0.398876
2    0.269663
dtype: float64
```

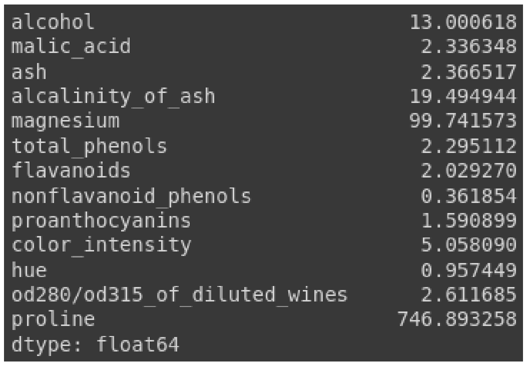
b) For univariate summaries I chose to calculate the standard deviation and the mean of each numerical feature. For multivariate summaries I created a scatter matrix and a covariance matrix of the numerical features.

```
display(df.drop('target', axis = 1).std())
```



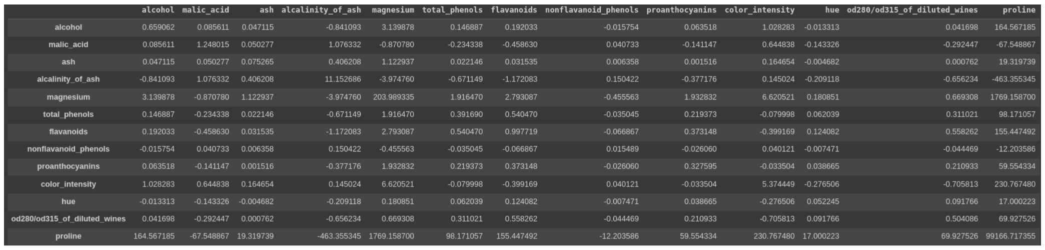
```
alcohol                          0.811827
malic_acid                       1.117146
ash                              0.274344
alcalinity_of_ash                3.339564
magnesium                       14.282484
total_phenols                    0.625851
flavanoids                       0.998859
nonflavanoid_phenols             0.124453
proanthocyanins                  0.572359
color_intensity                  2.318286
hue                              0.228572
od280/od315_of_diluted_wines     0.709990
proline                        314.907474
dtype: float64
```

```
display(df.drop('target', axis = 1).mean())
```



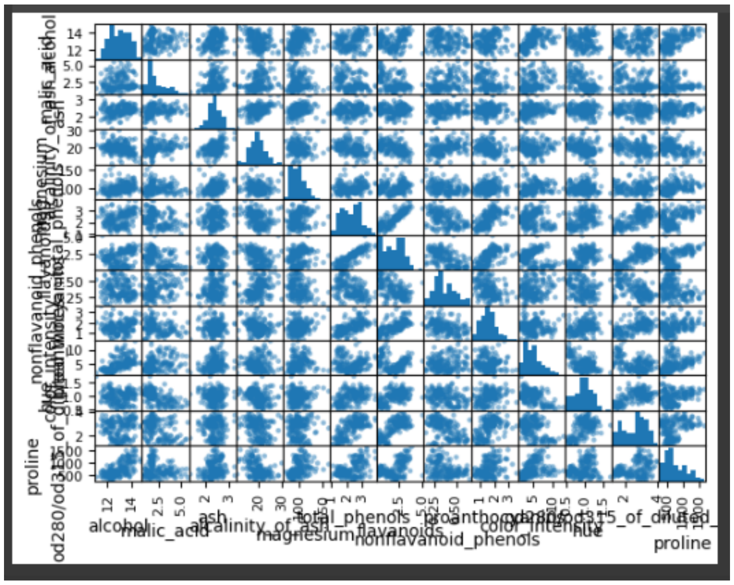
```
alcohol                          13.000618
malic_acid                        2.336348
ash                               2.366517
alcalinity_of_ash                19.494944
magnesium                        99.741573
total_phenols                     2.295112
flavanoids                        2.029270
nonflavanoid_phenols              0.361854
proanthocyanins                   1.590899
color_intensity                   5.058090
hue                               0.957449
od280/od315_of_diluted_wines      2.611685
proline                         746.893258
dtype: float64
```

```
pd.plotting.scatter_matrix(df.drop('target', axis = 1))
```



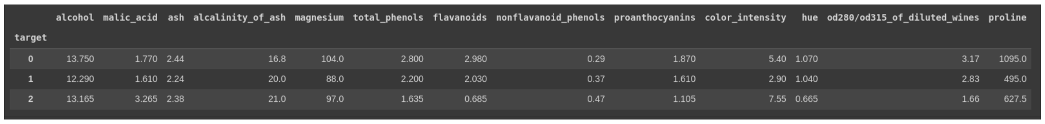
	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phenols	flavanoids	nonflavanoid_phenols	proanthocyanins	color_intensity	hue	od280/od315_of_diluted_wines	proline
alcohol	0.659062	0.085611	0.047115	-0.841093	3.139878	0.146887	0.192033	-0.015754	0.063518	1.028283	-0.013313	0.041698	164.567185
malic_acid	0.085611	1.248015	0.050277	1.076332	-0.870780	-0.234338	-0.458630	0.040733	-0.141147	0.644838	-0.143326	-0.292447	-67.548867
ash	0.047115	0.050277	0.075265	0.406208	1.122937	0.022146	0.031535	0.006358	0.001516	0.164654	-0.004682	0.000762	19.319739
alcalinity_of_ash	-0.841093	1.076332	0.406208	11.152686	-3.974760	-0.671149	-1.172083	0.150422	-0.377176	0.145024	-0.209118	-0.656234	-463.355345
magnesium	3.139878	-0.870780	1.122937	-3.974760	203.989335	1.916470	2.793087	-0.455563	1.932832	6.620521	0.180851	0.669308	1769.158700
total_phenols	0.146887	-0.234338	0.022146	-0.671149	1.916470	0.391690	0.540470	-0.035045	0.219373	-0.079998	0.062039	0.311021	98.171057
flavanoids	0.192033	-0.458630	0.031535	-1.172083	2.793087	0.540470	0.997719	-0.066867	0.373148	-0.399169	0.124082	0.558262	155.447492
nonflavanoid_phenols	-0.015754	0.040733	0.006358	0.150422	-0.455563	-0.035045	-0.066867	0.015489	-0.026060	0.040121	-0.007471	-0.044469	-12.203586
proanthocyanins	0.063518	-0.141147	0.001516	-0.377176	1.932832	0.219373	0.373148	-0.026060	0.327595	-0.033504	0.038665	0.210933	59.554334
color_intensity	1.028283	0.644838	0.164654	0.145024	6.620521	-0.079998	-0.399169	0.040121	-0.033504	5.374449	-0.276506	-0.705813	230.767480
hue	-0.013313	-0.143326	-0.004682	-0.209118	0.180851	0.062039	0.124082	-0.007471	0.038665	-0.276506	0.052245	0.091766	17.000223
od280/od315_of_diluted_wines	0.041698	-0.292447	0.000762	-0.656234	0.669308	0.311021	0.558262	-0.044469	0.210933	-0.705813	0.091766	0.504086	69.927526
proline	164.567185	-67.548867	19.319739	-463.355345	1769.158700	98.171057	155.447492	-12.203586	59.554334	230.767480	17.000223	69.927526	99166.717355

```
df.drop('target', axis = 1).cov()
```



c)

```
df.groupby('target').median()
```

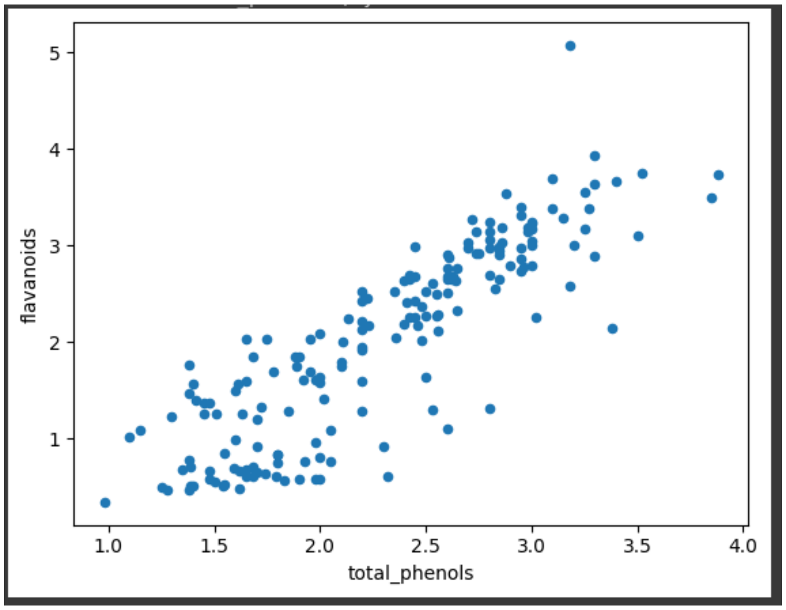


	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phenols	flavanoids	nonflavanoid_phenols	proanthocyanins	color_intensity	hue	od280/od315_of_diluted_wines	proline
target													
0	13.750	1.770	2.44	16.8	104.0	2.800	2.980	0.29	1.870	5.40	1.070	3.17	1095.0
1	12.290	1.610	2.24	20.0	88.0	2.200	2.030	0.37	1.610	2.90	1.040	2.83	495.0
2	13.165	3.265	2.38	21.0	97.0	1.635	0.685	0.47	1.105	7.55	0.665	1.66	627.5

d) First I find, the pair with the highest correlation, flavanoids and total_phenols

```
matrix = df.drop('target', axis = 1).corr()
max_corr = matrix.mask(matrix==1).stack().sort_values(ascending=False).idxmax()
```

I then use this max_corr variable to create a scatter plot



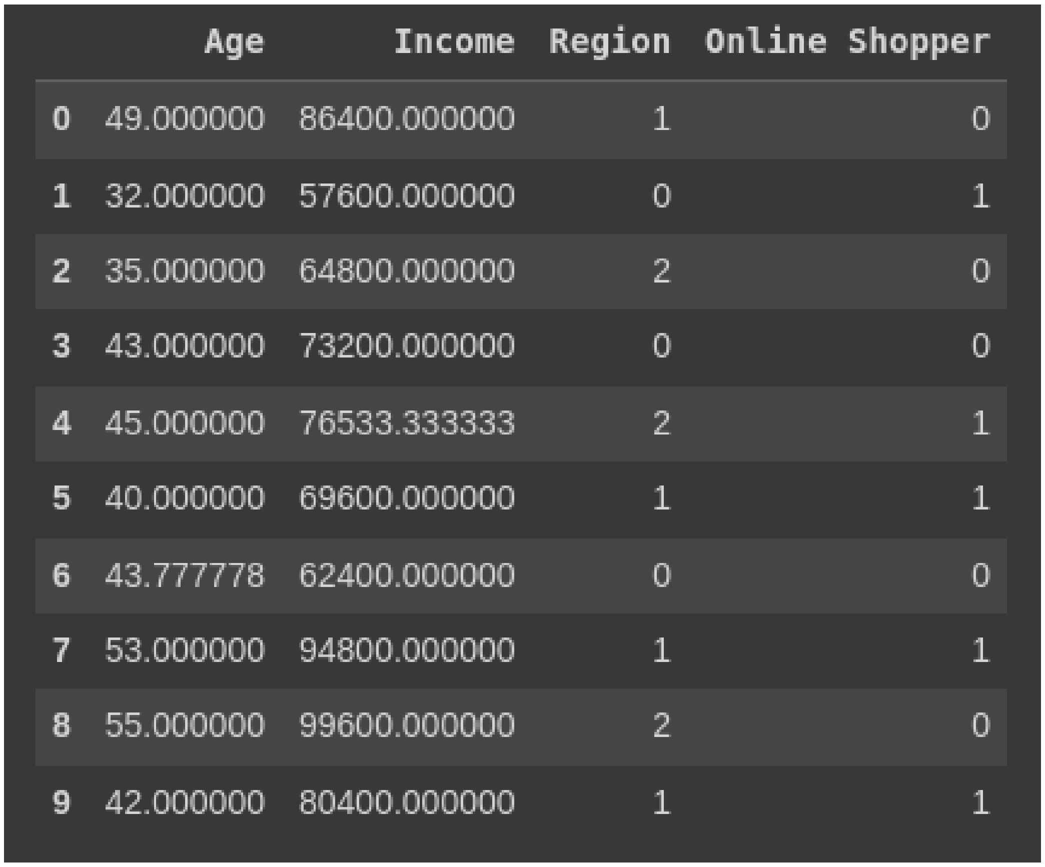
2 Question 2

First I read the csv file into a dataframe, I then created a SimpleImputer which replaces NaN values with the mean. I then created a separate dataframe "numerical_data" which selected only the numerical values of the data. I then applied the imputer to the numerical data which cleaned the NaN values.

Next was to handle the categorical data, like before I split the original dataframe into its categorical features and then created a LabelEncoder and applied it to the categorical data. This normalises the labels into numerical values.

With both numerical and categorical features cleaned I concatenated them back together into a single dataframe "cleaned_data".

```python
import pandas as pd
import numpy as np
from sklearn.impute import SimpleImputer
from sklearn.preprocessing import LabelEncoder

ci = pd.read_csv("country-income.csv")
imp = SimpleImputer(missing_values=np.nan, strategy='mean')
numerical_data = ci.select_dtypes(include = ["number"])
numerical_data = pd.DataFrame(imp.fit_transform(numerical_data),
                              columns = numerical_data.columns)
categorical_data = ci.select_dtypes(include = ["object"])
le = LabelEncoder()
categorical_data = categorical_data.apply(le.fit_transform)
cleaned_data = pd.concat([numerical_data, categorical_data], axis=1)
cleaned_data
```



	Age	Income	Region	Online Shopper
0	49.000000	86400.000000	1	0
1	32.000000	57600.000000	0	1
2	35.000000	64800.000000	2	0
3	43.000000	73200.000000	0	0
4	45.000000	76533.333333	2	1
5	40.000000	69600.000000	1	1
6	43.777778	62400.000000	0	0
7	53.000000	94800.000000	1	1
8	55.000000	99600.000000	2	0
9	42.000000	80400.000000	1	1

3 Question 3

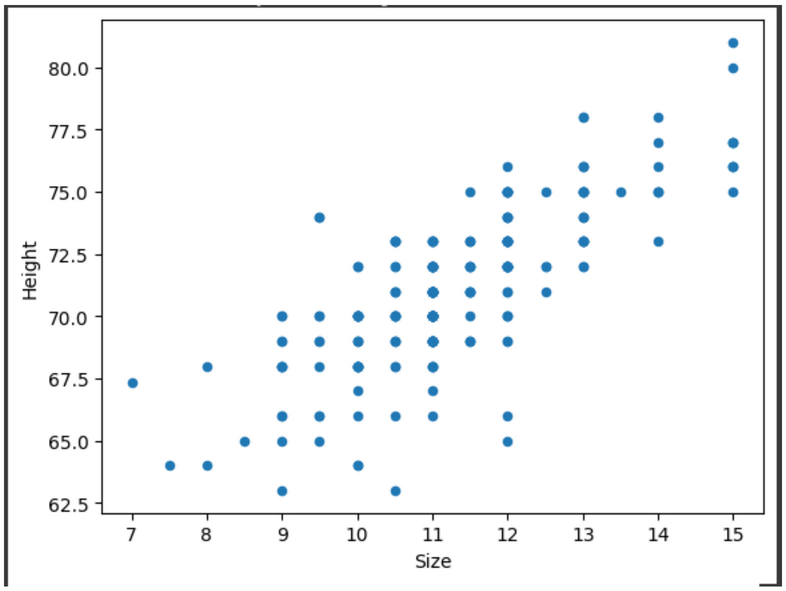
First, load the shoesize csv into a dataframe, I drop the index column since it isn't of any use in this question.

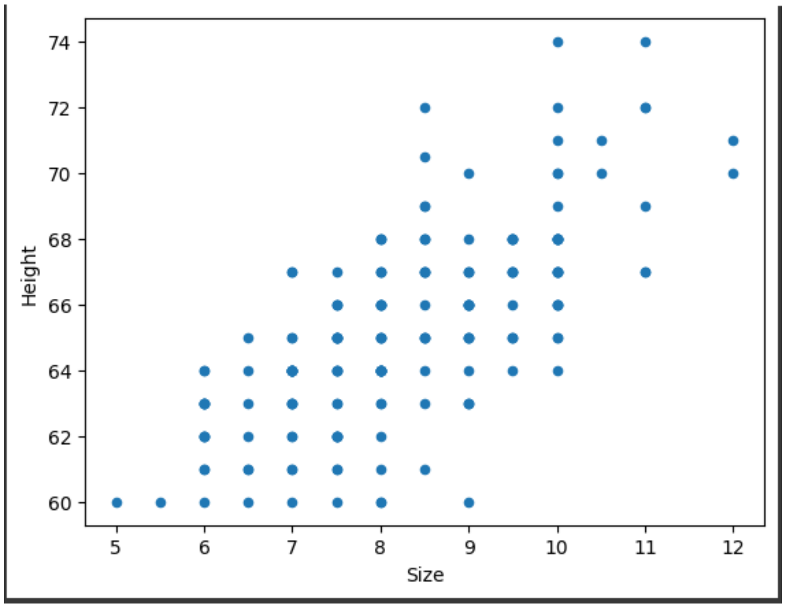
I then separated the dataframe into two dataframes based on the Gender

```
import pandas as pd
ss = pd.read_csv("shoesize.csv")
ss.drop(labels='Index',inplace=True, axis='columns')
female_data = ss[ss['Gender'] == 'F']
male_data = ss[ss['Gender'] == 'M']
```

Then plot the scatter plot of the female and male data using DataFrame.plot()

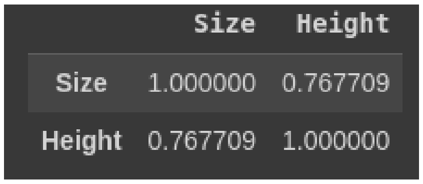
```
male_data.plot(x = 'Size', y = 'Height', kind = 'scatter')
female_data.plot(x = 'Size', y = 'Height', kind = 'scatter')
```





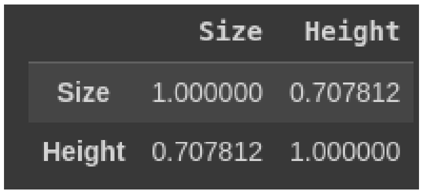
By default, DataFrame.corr() uses the pearson method, the data suggests that both male and female height to shoe size, have a strong linear correlation. In the case of males the male data having higher correlation than the female data.
male pearson correlation coefficient: 0.767709 female pearson correlation coefficient: 0.707812

```
male_data.corr()
female_data.corr()
```



	Size	Height
Size	1.000000	0.767709
Height	0.767709	1.000000

(a) male pearson correlation



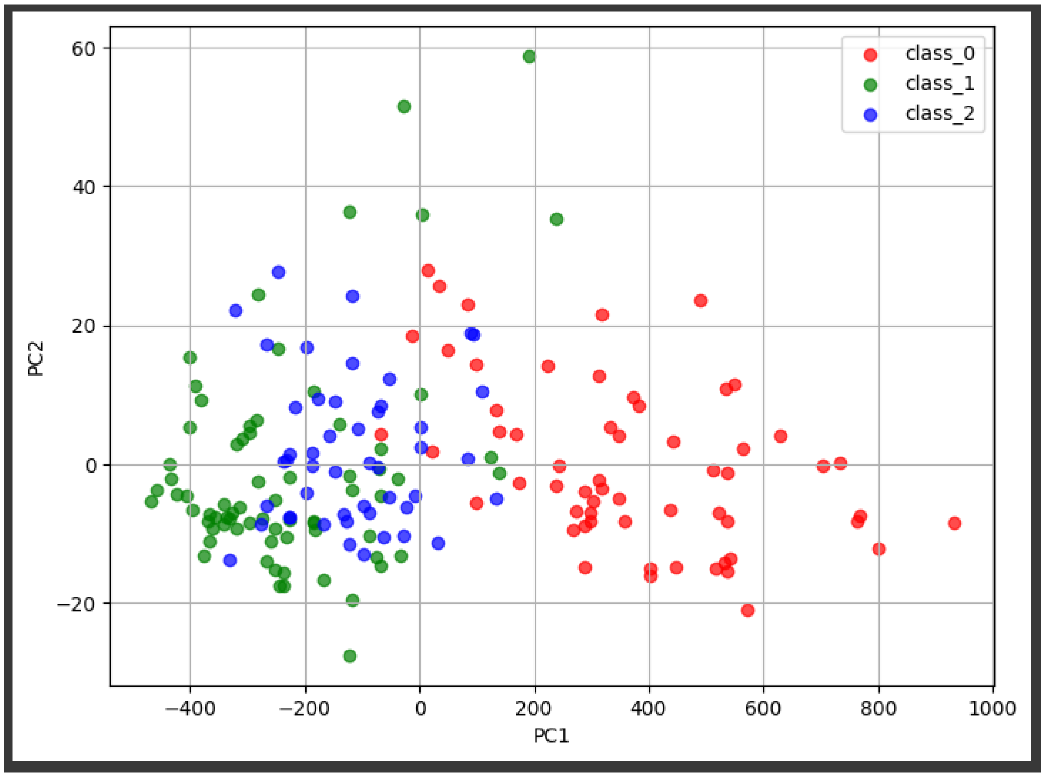
	Size	Height
Size	1.000000	0.707812
Height	0.707812	1.000000

(b) female pearson correlation

4 Question 4

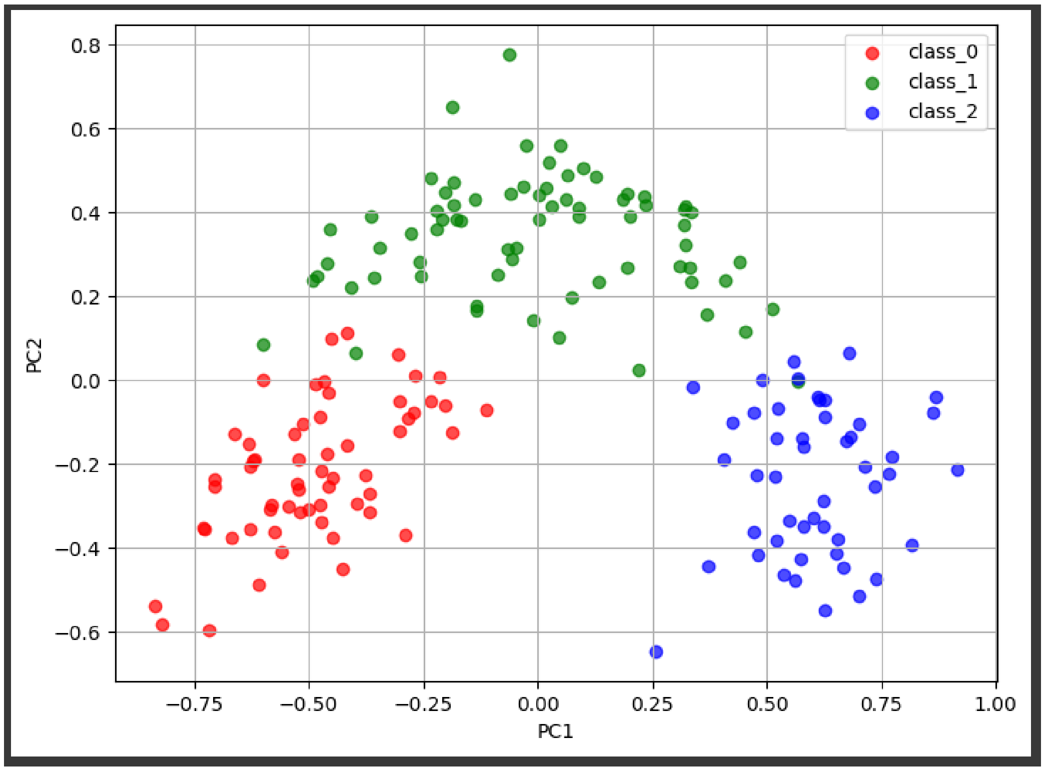
Looking at the below scatterplot of the principal components, you can see that target 0 (red) is somewhat distinguishable from target 2 and 1. There is some overlap. Whereas targets 1 and 2 have significant overlap and are not very distinguishable from each other when PCA is performed. This shows that when Targets 2 and 1 rows are projected into a lower dimension representation via PCA they are hard to distinguish due to having similar features.

```python
from sklearn.decomposition import PCA
import matplotlib.pyplot as plt
import pandas as pd
from sklearn.datasets import load_wine

wine = load_wine()
wdf = pd.DataFrame(wine.data, columns=wine.feature_names)

numComponents = 2
pca = PCA(n_components=numComponents)
pca.fit(wdf)
principal_components = pca.fit_transform(wdf)
principal_df = pd.DataFrame(data=principal_components, columns=['PC1', 'PC2'])
principal_df['target'] = wine.target

colors = ['r', 'g', 'b']
plt.figure(figsize=(8, 6))
for target, color in zip(wine.target_names, colors):
    targetIndex = wine.target_names.tolist().index(target)
    subset = principal_df[principal_df['target'] == targetIndex]
    plt.scatter(subset['PC1'], subset['PC2'], c=color, label=target, alpha=0.7)

plt.xlabel('PC1')
plt.ylabel('PC2')
plt.legend()
plt.grid(True)
```


class_0
class_1
class_2
PC1
PC2
−400
−200
0
200
400
600
800
1000
60
40
20
0
−20

To address the overlap I will normalise the dataframe, using min max normalisation. The resulting scatterplot shows that the target classes are now very distinctive from each other, with very clear separation and extremely minimal overlap.

```
normalized_wdf=(wdf-wdf.min())/(wdf.max()-wdf.min())

numComponents = 2
pca = PCA(n_components=numComponents)
pca.fit(normalized_wdf)
principal_components = pca.fit_transform(normalized_wdf)
principal_df = pd.DataFrame(data=principal_components, columns=['PC1', 'PC2'])
principal_df['target'] = wine.target

colors = ['r', 'g', 'b']
plt.figure(figsize=(8, 6))
for target, color in zip(wine.target_names, colors):
    targetIndex = wine.target_names.tolist().index(target)
    subset = principal_df[principal_df['target'] == targetIndex]
    plt.scatter(subset['PC1'], subset['PC2'], c=color, label=target, alpha=0.7)

plt.xlabel('PC1')
plt.ylabel('PC2')
plt.legend()
plt.grid(True)
```



class_0
class_1
class_2
PC1
PC2
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.75
−0.50
−0.25
0.00
0.25
0.50
0.75
1.00

5 Question 5

$d(x, y)$ is the Euclidean distance between two points x and y. For $x_3 = (3, 2)$:

$$d(x_1, x_3) = \sqrt{(1-3)^2 + (2-2)^2} = 2$$

$$d(x_2, x_3) = \sqrt{(-1-3)^2 + (0-2)^2} = 2\sqrt{5}$$

Since $d(x_1, x_3) < d(x_2, x_3)$, x_3 will be classified with the same class as x_1, which is $y_1 = 1$.

For $x_4 = (0, 1)$:

$$d(x_1, x_4) = \sqrt{(1-0)^2 + (2-1)^2} = \sqrt{2}$$

$$d(x_2, x_4) = \sqrt{(-1-0)^2 + (0-1)^2} = \sqrt{2}$$

The two distances are the same, you can choose either. Or if you want to implement a tie breaking rule a suitable one could be basing it on lowest class index. Being $y_2 = 0$