**MAI Assignment 1 Answers**

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**Question 1(a)**

PCA should be carried out on correlation matrix.

1. The mean for vitA variable is 187 (3s.f). However, the mean for the 5 other variables ranges from 3.70 to 28.3 (3s.f). This indicates that the variables are of different magnitudes.
2. The variables are also measured in different scales since vitA variable is measured in micrograms while the 5 other variables are measured in grams
3. Since the variables have different scales and largely differing magnitudes, PCA on the correlation matrix is preferred to prevent the variable with the largest magnitude from dominating the first PC

Graphical user interface, text

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Chart, histogram

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**Question (b)**

There are 3 criteria that can be used to determine the number of Principal Components to extract:

1. Use Kaiser’s Rule – Kaiser’s Rule states that we should retain PCs whose eigenvalues are greater than 1 as an eigenvalue that is less than 1 explains less variance than a variable would. (Only when correlation matrix is used in the PCA)
2. Look at cumulative explained variance – Retain PCs with cumulative percentage of at least 80% to 90%
3. Retain PCs left to the elbow before the inflection point shows up and the graph starts to flatten

Chart, line chart

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Table

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1. Using Kaiser’s Rule, only the first 2 PCs will be selected as the eigenvalues of PC 1 and 2 are greater than 1.
2. The cumulative explained variance indicates that only the first 2 PCs should be extracted as the first 2 PCs have a cumulative explained variance of 82.6%, which is more than 80% of total variance.
3. The scree plot shows that the elbow is located at PC3, starting from PC3, graph starts to become flat, and the eigenvalues differ a lot from PC 1 and 2, suggesting that only the first 2 PCs on the left of the elbow should be extracted.

Since the 3 criteria all suggest extracting PC 1 and 2, I will only extract the first 2 Principal Components.

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Interpreting PC1

PC1 = -0.288363c1 -0.259392c2 +0.505242c3 +0.475652c4 +0.446642c5 +0.410560c6 (where c1 to c6 are values of each nutrient, in their respective units of measurement)

1. For PC1, the loadings on Protein and Fat are negative while other loadings are positive. PC1 measures a weighted average of nutrients contrasting against Protein and Fat.
2. For PC1 to be positive, the values of Protein and Fat should be below average while the values of Carbohydrate, Sugar, Fiber and Vitamin A should be above average.
3. For PC1 to be negative, the values of Protein and Fat should be above average while the values of Carbohydrate, Sugar, Fiber and Vitamin A should be below average

Interpreting PC2

PC2 = 0.628268c1 +0.654692c2 +0.224962c3 +0.119515c4 +0.115814c5 +0.313612c6 (where c1 to c6 are values of each nutrient, in their respective units of measurement)

1. The loading for every nutrient in PC2 is positive.
2. For PC2 to be positive, all nutrients should be above average (as this is a scaled dataset, values below the mean are negative)
3. For PC2 to be negative, values of all the nutrients should be below average.

**Question 1(c)**

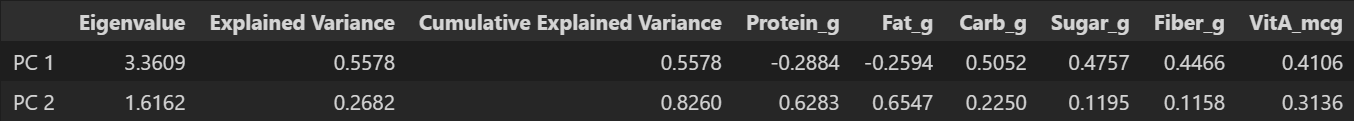
Loading Plot, Score Plot and Linear System of PC1 and PC2 used to answer part (c).

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**Chart, scatter chart

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This is the function used to calculate the direction of line based on nutrient values. I will be using this function to determine the Type of food.

1. The nutrient values passed into this function are standardized using StandardScaler which was fit on the original dataset.
2. PC1 and PC2 for the nutrient values entered is calculated using the linear equations of PC1 and PC2.
3. A line is drawn from the origin to the point of the calculated PC1 and PC2

**Text

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**Question 1(c)(i): Low Protein and Fat, high in all other nutrients**

Chart, scatter chart

Description automatically generated

1. The maximum values of other nutrients are used, while lower quartile values of Protein and Fat is used to mimic the scenario of low Protein and Fat, but high in all other nutrients
2. When Protein and Fat values are low, and values of other nutrients are high, the direction seems to point towards the Breakfast Cereals cluster.
3. The biplot also seems to imply that when all other nutrients except Protein and Fat are high, the possible type of food product would be Breakfast Cereals, since the loadings of all other nutrients are in the direction of Breakfast Cereals cluster.

Thus, the possible type of food product that is low in fat and protein but high in other nutrients is Breakfast Cereals.

**Question 1(c)(ii): High Protein and Fat, low in all other nutrients**

Chart, scatter chart

Description automatically generated

1. The maximum values of Protein and Fat are used, while lower quartile values of all other nutrients are used to mimic the scenario of high Protein and Fat, but low in all other nutrients
2. When protein and fat values are high and other values are low, the direction based on calculated PC1 and PC2 points towards Poultry Products cluster
3. The biplot also seem to suggest that high Protein and Fat food product would be the Poultry Products, since the direction of the loadings of Protein and Fat point towards the Poultry Products Cluster.

Hence, the possible type of food product that has high protein and fat and low in other nutrients is Poultry Products.

**Question 1(d)**

Working:

Values = (0.3, 0.1, 19.6, 16.7, 2.9 ,2)

Scaled Values = (-0.87758779, -0.71856717, -0.27066624, 0.44930193, -0.18267824, -0.70928026)

Score = Scaled Values x Transposed

Score =

(-0.87758779, -0.71856717, -0.27066624, 0.44930193, -0.18267824, -0.70928026) x Transposed

Score = (0.14362031, -1.27258756)

Text

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Chart, scatter chart

Description automatically generated

When the calculated score is plotted in the score plot, the point lies within the Fruits and Fruit Juices cluster, and the nearby datapoints surrounding it are all from the Fruits and Fruit Juices type. Thus, the type of the food product is likely to be Fruits and Fruit Juices.

**Question 2(a)**

PCA should be carried out on correlation matrix.

Chart, histogram

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Graphical user interface, text, application

Description automatically generated

Reasons:

1. The 7 variables have different units of measurement such as grams/milligrams per litre, colour intensity units and alcohol percentage of total volume.
2. From the boxplot and descriptive summary, it is seen that the variables have different magnitudes and standard deviation. Proline has the highest median of 672mg/L and a large standard deviation of 322.56mg/L. Meanwhile, nonflavonoid phenols has the lowest median of 0.37mg/L and a very low standard deviation of 0.118mg/L

Thus, as the variables have different units of measurement and differing magnitudes, PCA should be done on the correlation matrix to avoid an inaccurate analysis (e.g., The variable with the largest magnitude dominating PC1.)

**Question 2(b)**

Since we should only retain the PCs with cumulative explained variance of at least 80% of total variance, the decision is only needed to be based on this factor.

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From the PCA results table above, PC3 has a cumulative explained variance of 81.78%, thus only the first 3 PCs are to be extracted.

Graphical user interface, text, application

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Interpreting PC1

PC1 = 0.411787c1 -0.216623c2 +0.392271c3 +0.431704c4 -0.388771c5 +0.184531c6 +0.508003c7

1. For PC1, the loadings on malic acid and nonflavonoid phenols is negative. This PC seems to measure a weighted average of constituents in wine, contrasting against malic acid and nonflavonoid phenols.
2. For a positive PC1, the values of malic acid and nonflavonoid phenols should be below average and alcohol, magnesium, flavonoids, colour intensity and proline should be above average
3. For a negative PC1, the values of malic acid and nonflavonoid phenols should be above average, while the other constituents should be below average

Interpreting PC2

PC2 = 0.358439c1 +0.507626c2 +0.218459c3 -0.370840c4 +0.326525c5 +0.554404c6 +0.120866c7

The loading on flavonoids is negative. This PC seems to measure a weighted average of constituents in wine contrasting against flavonoids.

For a positive PC2, the values of the other constituents should be above average while value of flavonoids should be below average

For a negative PC2, the value of flavonoids should be above average, and the values other constituents should be below average.

Interpreting PC3

PC3 = -0.320359c1 +0.350294c2 +0.791780c3 +0.045703c4 -0.126181c5 -0.268342c6 -0.240274c7

1. The loadings on alcohol, nonflavonoid phenols, colour intensity and proline are negative. This PC seems to measure a weighted average of constituents in wine contrasting against alcohol, nonflavonoid phenols, colour intensity and proline.
2. For PC3 to be positive, the values of alcohol, nonflavonoid phenols, colour intensity and proline should be below average and other constituents should be above average.
3. For PC3 to be negative, the values of alcohol, nonflavonoid phenols, colour intensity and proline should be above average while the other values should be below average.

**Question 2(c)**

**Text

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This function will be used to calculate PC1, PC2 and PC3 based on the attributes of the wine

Chart, scatter chart

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When the point calculated is plotted in PC1 against PC2 graph, the point lies within the Cultivator 2 cluster. Its immediate neighbours are also of Cultivator 2 type

Chart, scatter chart

Description automatically generated

When the point is plotted in the score plot of PC1 and PC3, the calculated point is located within the mixed cluster of Cultivator 1 and 2, and a decision cannot be made as it is a mixed cluster, where there is no clear indication of Cultivator 1 and Cultivator 2 clusters

Chart, scatter chart

Description automatically generated

When the point is plotted in the score plot of PC2 and PC3, the point lies in between the cluster of Cultivator 0 and 2. However in this plot we can see that some points of Cultivator 2 are mixed within the cluster of Cultivator 0.

Thus, based on the insights the 3 plots gave, since all 3 plots suggest Cultivator 2 as one of the possible Cultivators, this wine is likely to have come from Cultivator 2.

**Question 2(d)**

Chart, scatter chart

Description automatically generated

Using the score plot of PC3 and PC1, plotting the point calculated using the wine’s attributes in part (c). The point calculated lies in the mixed cluster of Cultivator 1 and Cultivator 2. Hence, this score plot of PC3 and PC1 is not useful in helping to identify the cultivator of wine in part (c) as a conclusion cannot be drawn between Cultivator 1 and 2.

Chart, scatter chart

Description automatically generated

When using the score plot of PC3 and PC2, when plotting the calculated point using the same wine attributes from part (c), the point lies in the middle of Cultivator 0 cluster and Cultivator 2 cluster. From this plot, it cannot be decided that whether the point calculated belongs to Cultivator 0 or Cultivator 2. Thus, this plot itself is not useful in helping to identify whether the point belongs to Cultivator 0 or 2.

Both plots which are using PC3 suggested Cultivator 2 as a possible cultivator. Even though PC3 plotted with PC1 and PC2 respectively cannot give as a solid conclusion on identifying the cultivator, it still was not completely useless and provided useful information as it constantly suggested Cultivator 2 as one of the possible cultivators when plotted against PC1 and PC2.

Thus, my conclusion is that PC3 was useful in helping to identify the cultivator of the wine in part (c) since it provided us some useful information.