BIOM5405/SYSC5405

Mock Assignment

Table of Contents

BIOM5405/SYSC5405

Mock Assignment

Question 1: Data Wrangling

Consider two possible features for a new fruit classification system: weight and diameter. Sample data for each feature is provided in assigData2.tsv

100 weight and diameter measurements are given for three types of fruit: apple, orange, and grape. (File can be easily viewed in Excel or MATLAB. Columns are: W_apl W_orng W_grp D_apl D_orng D_grp)

a) To develop a Bayesian classifier, we need to estimate the parameters of the class-conditional distribution for each feature and for each class. Assuming the class-conditional distributions follow normal distributions with unknown mean and variance for each class, estimate the six means and the six estimates of variance.

b) Plot the histograms for each feature showing the distribution of each feature over each class. For each feature, you should have a single plot (single axis) with three potentially overlapping histograms representing the three fruit types.

   i) Use transparency and a different color and/or line style for each class and make sure you can see all the data (i.e., that bars are not completely occluding each other in your figure).

   ii) Which feature would you prefer and why? (150 words)

   iii) Illustrate results using at least two bin widths when generating your histograms.

c) Provide a plot visualizing apple weight vs. diameter. Add a line of best fit and report the Pearson Correlation Coefficient.

BIOM5405/SYSC5405

Mock Assignment

Solutions:

Question 1a)

Table 1 contains the mean, variance, and standard deviation (STD) *(additional info)* of the 6 features in the dataset.

Column	Mean (μ)	Variance (σ^2)	STD (σ)
W_apl	0011.003084	0001.401103	01.183682
W_orng	0011.944999	0006.806620	02.608950
W_grp	0008.733358	0024.787095	04.978664
D_apl	1006.707200	1621.374432	40.266294
D_orng	1114.833850	0383.405810	19.580751
D_grp	0832.546227	8356.381727	91.413247

Table 1: Mean, Variance, and STD for each column in the dataset

Please note, that the question assumes there is a normal distribution in the data, but from the solution in Q1b) it is known that the data is not normally distributed for all the columns.

The formula for each is provided below:

$$\mu = mean = \frac{\sum_{i=1}^{N} x_i}{N}$$

$$\sigma^2 = variance = \frac{\sum_{i=1}^{N} (x_i - \mu)^2}{N}$$

$$\sigma = STD = \sqrt{\frac{\sum_{i=1}^{N} (x_i - \mu)^2}{N}}$$

BIOM5405/SYSC5405

Mock Assignment

Question 1b)

Figure 1 shows the histogram of weight distribution for the three classes with 30 bins for each class. Figure 2 shows the histogram of diameter distribution for the three classes with 20 bins for each class.

Figures 3-6 have a constant bin width for each class. Figures 3 and 4 are histograms for the weight distributions with the bin width being 1 and 2 units of width respectively. (The units are not provided for the data)

Figures 5 and 6 are histograms for the diameter distribution with the bin width being 30 and 60 respectively.

In all of the figures "**line, transparency, and different colours**" have been maintained.

The legend for each figure is provided in the top-right hand corner for all the figures in this section.

For all the figures the class for apples is shown in "Red", the class for oranges is shown in "orange", and the class for grapes is shown in "purple".

> *Please note for Figures 1 and 2 the "bin count" is constant for each class in their respective figures. In the case of Figures 3-6 the "bin width" is constant for each class in their respective figures.*

The feature "Diameter" is the ideal candidate classification. The reason is that there is minimal overlap between the classes in the case of Diameter. When considering the "Weight" we see that there is a very significant **overlap** between "apples" and "oranges", hence models will have a hard time distinguishing between the two in a **generalized** setting.

Note: Classifiers may still manage to give good accuracy on **train data** when using only "Weight" but they will perform poorly on **test or validation data.** This is because of overfitting.

BIOM5405/SYSC5405

Mock Assignment

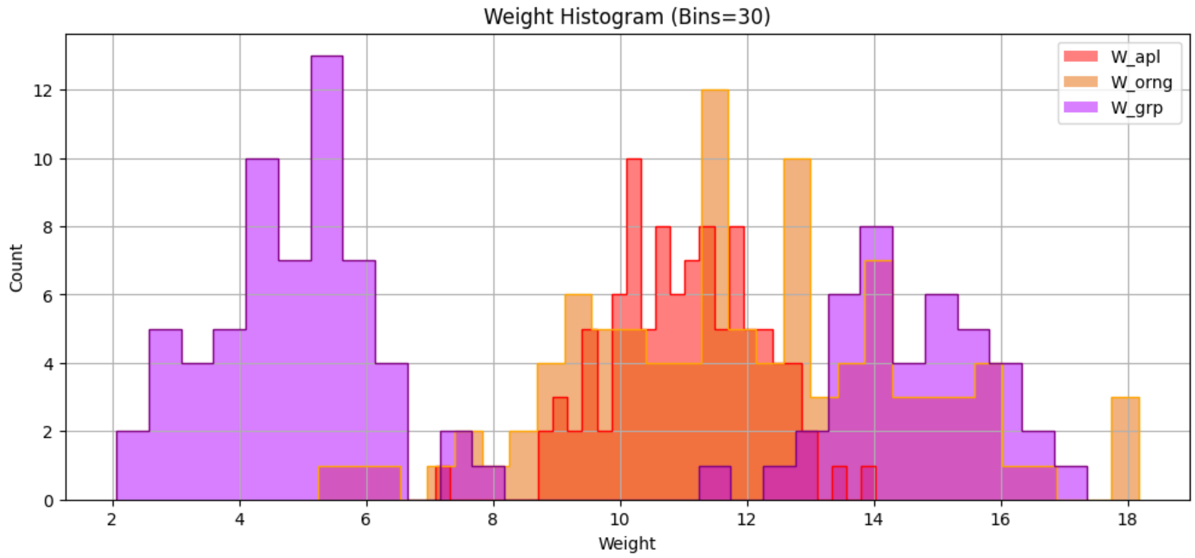


Figure 1: Histogram for "Weight" distribution for apples, oranges, and grapes. The bin count for each class is 30.

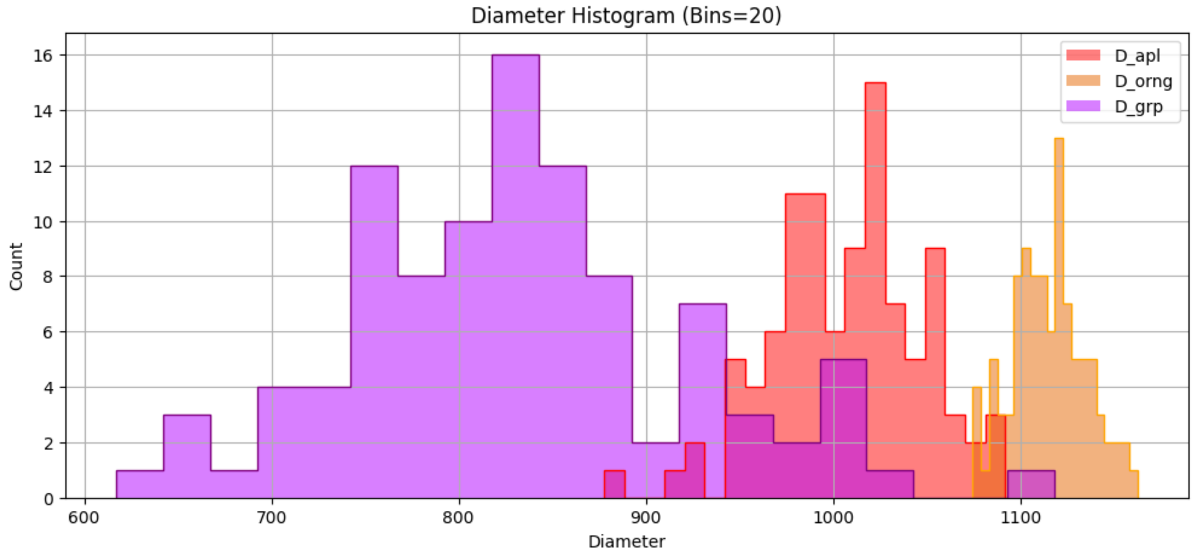


Figure 2: Histogram for "Diameter" distribution for apples, oranges, and grapes. The bin count for each class is 20.

BIOM5405/SYSC5405

Mock Assignment

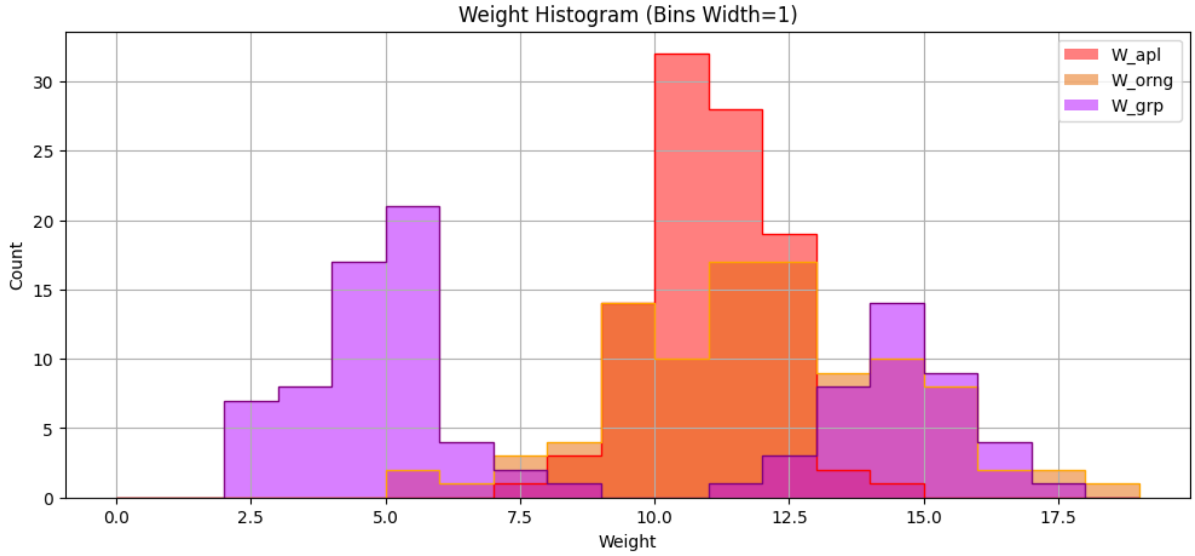


Figure 3: Histogram for "Weight" distribution for apples, oranges, and grapes. The bin width for each class is equal to 1 unit.

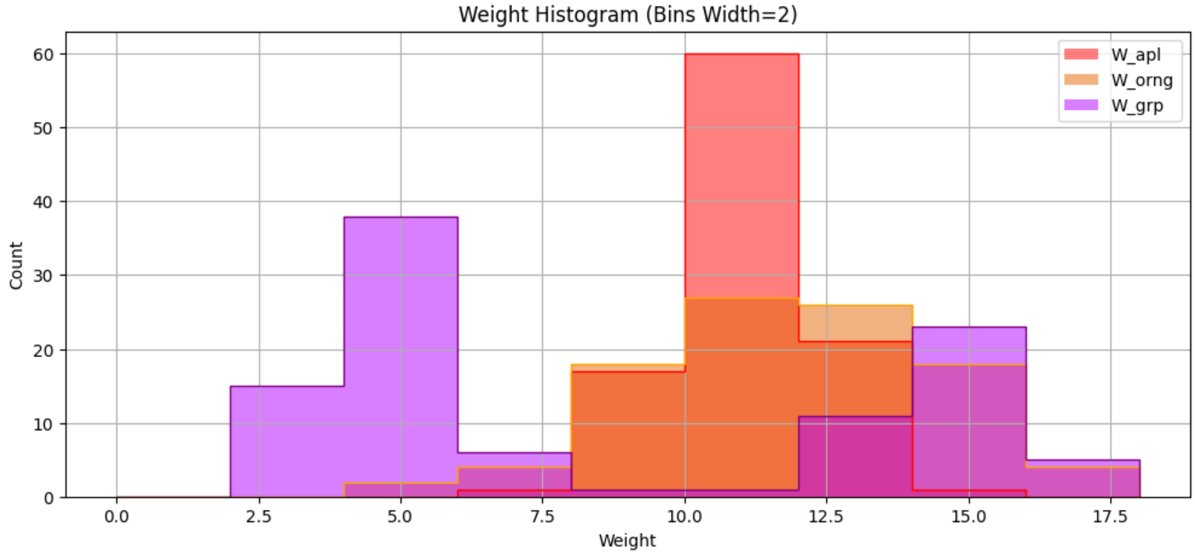


Figure 4: Histogram for "Weight" distribution for apples, oranges, and grapes. The bin width for each class is equal to 2 units.

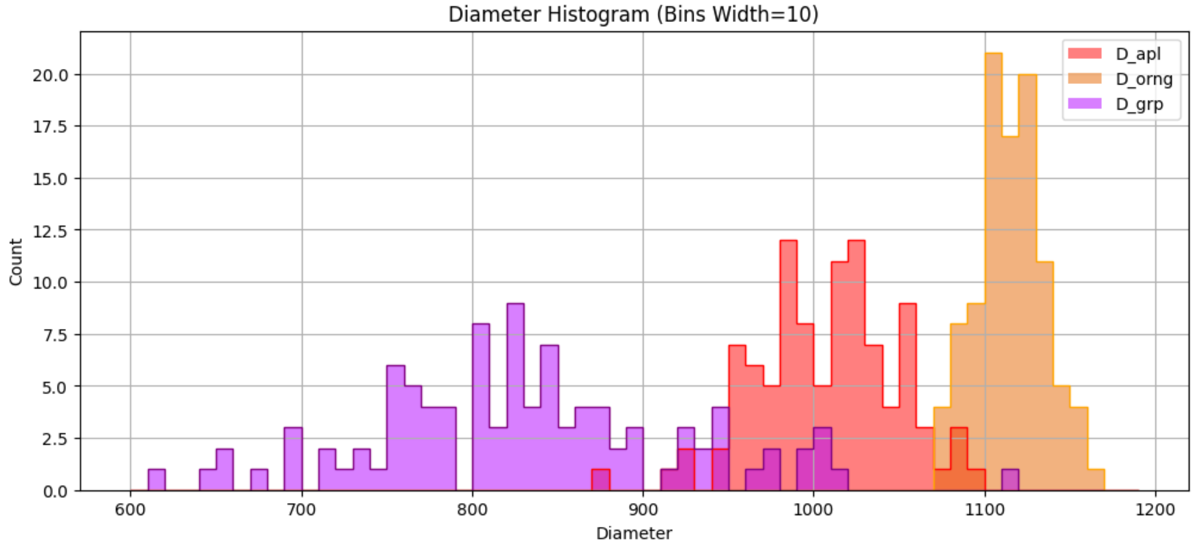


Figure 5: Histogram for "Diameter" distribution for apples, oranges, and grapes. The bin with for each class is equal to 10.

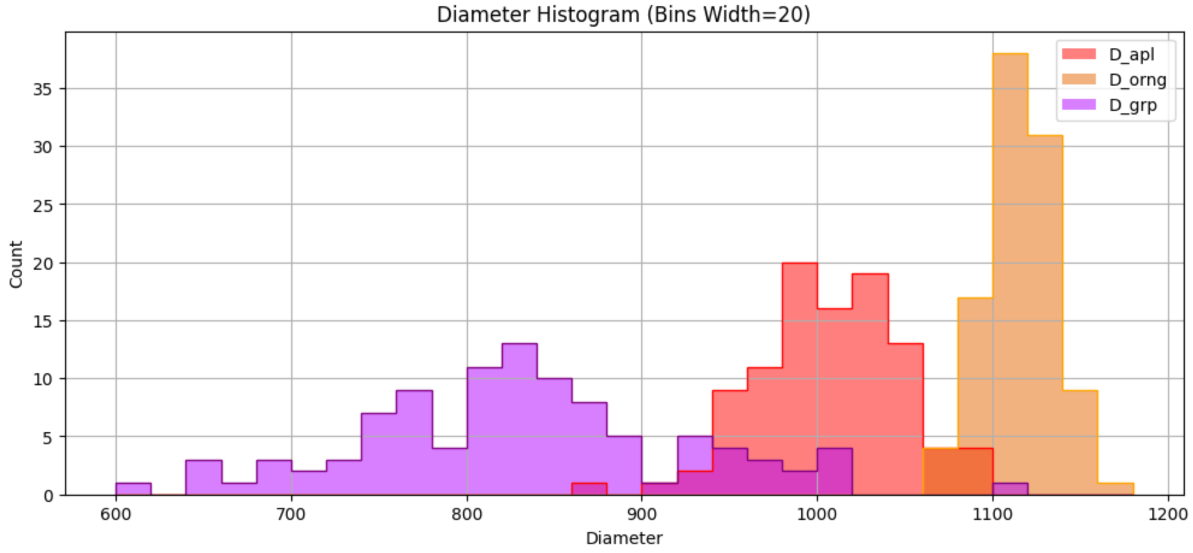


Figure 6: Histogram for "Diameter" distribution for apples, oranges, and grapes. The bin with for each class is equal to 20.

BIOM5405/SYSC5405

Mock Assignment

Question 1C)

Figure 7 represents the scatter plot for weight of apple vs the diameter of apple. The points are marked with “a” in the figure. The line of best fit is shown in the figure in blue. The equation for the best-fit line is shown in the plot’s legend. The x-axis in the figure shows the weight of the apple while the y-axis shows the diameter of the apple.

The Pearson correlation for the weight and diameter of apples is “**0.085**”. The correlation between the remaining features is provided in Table 2. The cell intersection of column and rows provides the correlation among the features.

The line of best fit equation is $\boldsymbol{Y = 2.9X + 974.78}$

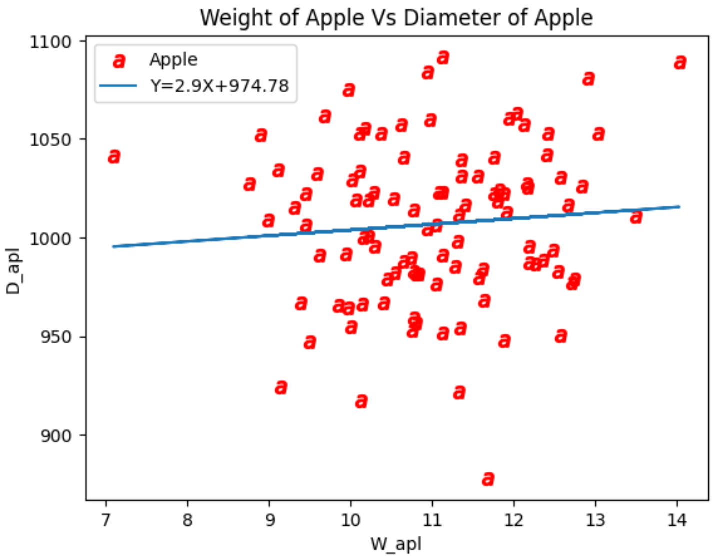
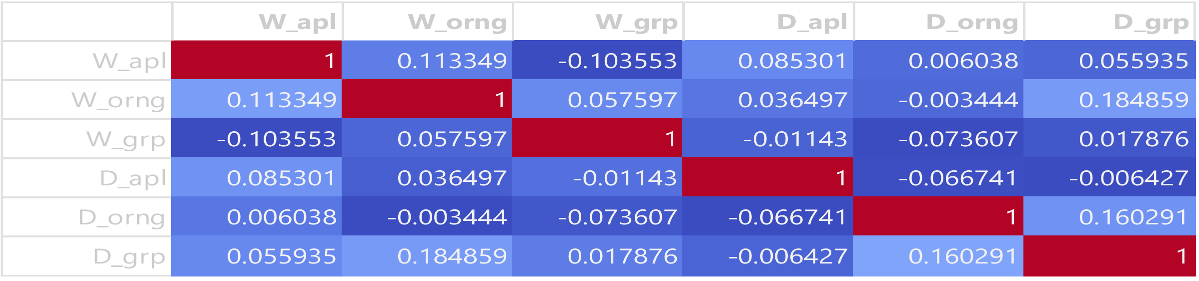


Figure 7: Weight VS Diameter for Apple along with Line of Best Fit using Linear Regression



	W_apl	W_orng	W_grp	D_apl	D_orng	D_grp
W_apl	1	0.113349	-0.103553	0.085301	0.006038	0.055935
W_orng	0.113349	1	0.057597	0.036497	-0.003444	0.184859
W_grp	-0.103553	0.057597	1	-0.01143	-0.073607	0.017876
D_apl	0.085301	0.036497	-0.01143	1	-0.066741	-0.006427
D_orng	0.006038	-0.003444	-0.073607	-0.066741	1	0.160291
D_grp	0.055935	0.184859	0.017876	-0.006427	0.160291	1

Table 2: Pearson Correlation among each column in the dataset.

BIOM5405/SYSC5405

Mock Assignment

Question 2: Generating data & the normal distribution

a) Generate 1000 samples drawn from a trivariate normal distribution with $\mu = \begin{bmatrix} 5 \\ -0.5 \\ 17 \end{bmatrix}, \Sigma = \begin{bmatrix} 4 & 0.5 & 0 \\ 0.5 & 5 & -0.2 \\ 0 & -0.2 & 2 \end{bmatrix}$.
You do not need to provide the actual samples in your assignment submission. Instead, report estimates of the mean and variance of the first dimension based on your 1000 samples. Do your estimates agree with the actual values? (estimates + brief discussion)

b) Create two scatter plots of the data, ensuring that the scale of both axes are equal so that the true shape of the distribution is visible. The first scatter plot should visualize the first two dimensions of your data. The second scatter plot should visualize dimension 1 vs. dimension 3. Why do their shapes differ? (25 words)

c) What is its trace of Σ? Is Σ positive definite? Explain.

d) Calculate and report the eigenvectors and eigenvalues of Σ.

e) Lastly, plot the PDF and CDF for the third dimension of your distribution.

BIOM5405/SYSC5405

Mock Assignment

Solutions:

Question 2a)

The estimated mean and variance for the first dimension are as follows:

- Mean: 4.938153
- Variance: 3.67591658

Yes, the estimates mean agree with the generated data. They are off by a tiny fraction, but this is expected based on the random generation of data.

The remaining generated data's dimension also follow the same mean, and covariance.

Following is a list of means for generated data:

- Dimension 1: 4.938
- Dimension 2: -0.409
- Dimension 3: 16.986

The Covariance matrix is as follows for the generated data

$$\Sigma = \begin{bmatrix} 3.675 & 0.404 & 0.019 \\ 0.404 & 5.221 & -0.143 \\ 0.019 & -0.413 & 1.931 \end{bmatrix}$$

BIOM5405/SYSC5405

Mock Assignment

Question 2b)

Figures 8 and 9 are the scatter plots required in the question. Figure 8 plots dimension 1 vs 2. Figure 9 plots dimension 1 vs 3. The scale of x and y axis are constant in both figures. The colour of markers in each figure has been made unique to distinguish between the two. The colour blue is used for markers in Figure 8 and green has been used in Figure 9.

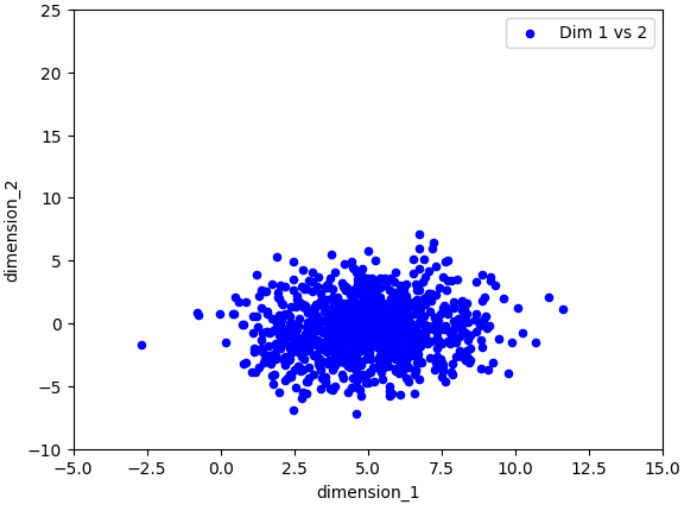


Figure 8: Scatter plot for dimension 1 vs 2

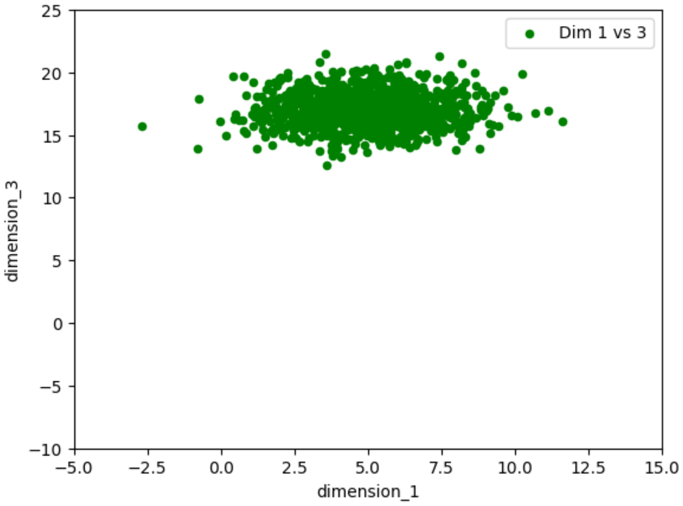


Figure 9: Scatter plot for dimension 1 vs 3d

Differ:

The centre of the cluster in each figure is determined by the mean of the data. The inclination of the cluster is dependent on correlation.

Note: Further explanation could be provided but the limit is 25 words.

BIOM5405/SYSC5405

Mock Assignment

Question 2c)

$Trace(\Sigma) = Sum(4,5,2)$
$\mathrm{Trace}(\Sigma) = \mathbf{11}$

Positive defined:

A matrix is positive definite when:

1. It is symmetric
2. Its eigen values are positive.

Σ is symmetric since $\Sigma = \Sigma^T$ and the eigen values are positive (from solution 2d). **Therefore, it is positive definite.**

Question 2d)

Given a matrix "A" the eigenvalue "λ" and eigenvector "v" follow the formula: Av = λv.

The calculated eigenvalues are: [5.21773098 3.79611128 1.98615774]

The calculated eigenvectors are:

- [0.37920187 -0.9251552 -0.01714037]
- [0.92353174 0.37725742 0.06903598]
- [-0.05740267 -0.04200825 0.99746691]

BIOM5405/SYSC5405

Mock Assignment

Question 2e)

Figures 10 and 11 provide the PDF and CDF respectively for the 3rd dimension of randomly generated data.

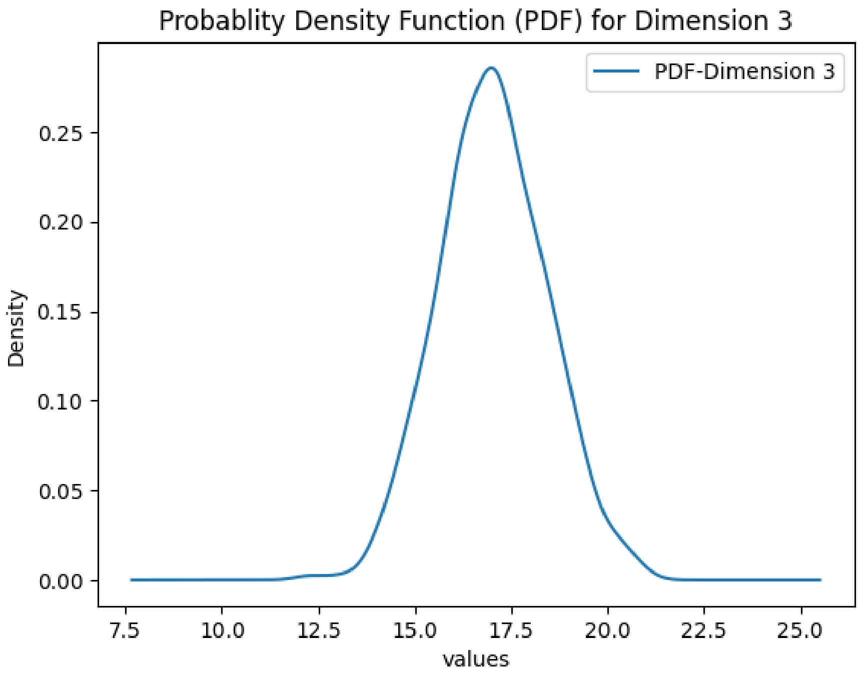


Figure 10: PDF for dimension 3

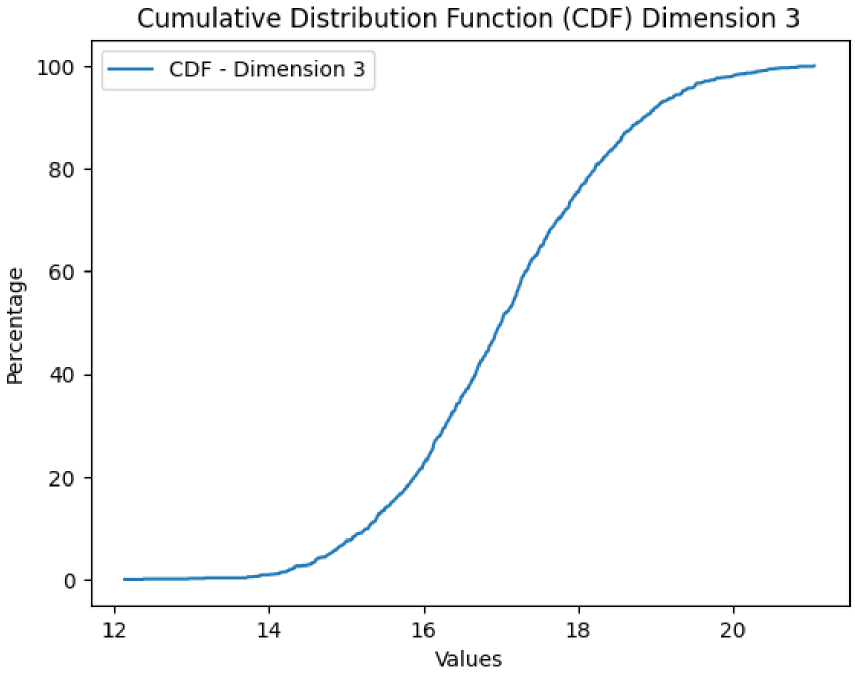


Figure 11 CDF for dimension 3

BIOM5405/SYSC5405

Mock Assignment

Appendix:

Please note, all code is written in Python. Content written in "<>" will change based on the individual.

Question 1:

```
import matplotlib.pyplot as plt
import pandas as pd
import numpy as np
from sklearn.linear_model import LinearRegression


data_loc = “<Your dataset location>"
dataset = pd.read_csv(data_loc, sep="    ")
```

# Get the mean and variance

```
dataset.describe()
```

# Code for plotting histogram

# Repeat this code to plot multiple figures

```
dataset[“<column_name>"].hist(
    bins=<list or range for constant width | integer for constant number of 
bins>,
    color="<provide colour name>",
    histtype=u'step',
    figsize=(12,5)
    )
```

# Build a line of best fit using “Linear regression

```
x = dataset[["W_apl"]]
y = dataset[["D_apl"]]

model = LinearRegression()
model.fit(x,y)

r2_score = model.score(x, y)

print(f"""
      Linear Regression:
      \t R2: {r2_score}
      \t m(slope): {model.coef_}
      \t c(intercept: {model.intercept_})
      """)
```

# visualize apple's weight vd diameter

```
ax = dataset[["W_apl","D_apl"]].plot(
    x="W_apl",
    y="D_apl",
    kind="scatter",
    marker="$a$",
    color="red",
    label="Apple",
    s=50,
)

ax.plot(
    x,
    m*x+c,
    label=f"Y={m:0.2}X+{c:0.2f}",
    )

plt.legend(loc='upper left')
ax.set_title("Weight of Apple Vs Diameter of Apple")
```

# calculate Pearson correlation

```
dataset[["W_apl","D_apl"]].corr(method='pearson')
```

Question 2:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

mean = [5, -0.5, 17]
cov = [[4,0.5,0],[0.5,5,-0.2],[0,-0.2,2]]
sample_size = 1000
```

# generate dataset

```
 pd.DataFrame(
    np.random.multivariate_normal(
        mean=mean,
        cov=cov,
        size=sample_size
    ),
    columns=["dimension_1","dimension_2","dimension_3"]
)
```

# get the mean and variance for generate data

```
dataset.describe()
```

```
dataset.corr()
```

# plot scatter plot

```
dataset.plot.scatter(
    x="dimension_1",
    y="dimension_2",
    label="Dim 1 vs 2",
    color="blue",
    xlim = [-5,15],
    ylim=[-10,25]
)
dataset.plot.scatter(
    x="dimension_1",
    y="dimension_3",
    label="Dim 1 vs 3",
    color="green",
    xlim = [-5,15],
    ylim=[-10,25]
)
```

# Calculate Trace

```
trace = np.trace(cov)

print(f"trace of Sigma: {trace}")
```

# Calculate eigenvalues and eigenvectors

```
eigenvalues, eigenvectors = np.linalg.eig(cov)
print(f"eigen values = {eigenvalues}")
print(f"eigen vectors:\n{eigenvectors}")
```

# plot PDF

```
ax = dataset['dimension_3'].plot.kde(
    title="Probablity Density Function (PDF) for Dimension 3",
    label="PDF-Dimension 3",
    legend=True
)
ax.set_xlabel("values")
```

# plot CDF

```
for i in range(3,4):
    count, bins_count = np.histogram(dataset[f'dimension_{i}'], bins=1000)
    pdf = count / sum(count)
    cdf = np.cumsum(pdf)
    plt.plot(
        bins_count[1:],
        cdf*100,
        label=f"CDF - Dimension {i}"
        )

plt.legend(loc="upper left")
plt.ylabel("Percentage")
plt.xlabel("Values")
plt.title("Cumulative Distribution Function (CDF) Dimension 3")
```