به نام خدا

تمرین شماره ۱

درس هوش مصنوعی و سیستم های خبره

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زمستان ۱۴۰۲

Assignment 1

Problem 1

Import necessary libraries

First, we need to import basic libraries such as Pandas, NumPy, Seaborn, Matplotlib, Plotly, and cufflinks. these libraries are used accross different sections of the process

In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

%matplotlib inline
from plotly import __version__
from plotly.offline import download_plotlyjs, init_notebook_mode, plot, iplot

print(__version__) # requires version >= 1.9.0
import cufflinks as cf
# For Notebooks
init_notebook_mode(connected=True)

# For offline use
cf.go_offline()
```

```
5.18.0
```

In [2]:
```
import warnings

warnings.filterwarnings("ignore")
```

load Dataset 1

in this section, dataset will be loaded using pandas read_csv method. next, the columns will be renamed, so that we can tell apart 'Vertical', 'Diagonal' and 'Cross' lengths.

In [3]:
```
df = pd.read_csv('Dataset_I.csv')
df.columns = ['Species', 'Weight', 'Vertical', 'Diagonal', 'Cross', 'Height', 'Width']
df
```

Out[3]:

	Species	Weight	Vertical	Diagonal	Cross	Height	Width
0	Bream	242.0	23.2	25.4	30.0	11.5200	4.0200
1	Bream	290.0	24.0	26.3	31.2	12.4800	4.3056
2	Bream	340.0	23.9	26.5	31.1	12.3778	4.6961
3	Bream	363.0	26.3	29.0	33.5	12.7300	4.4555
4	Bream	430.0	26.5	29.0	34.0	12.4440	5.1340
...	...	...	...	...	...	...	...
154	Smelt	12.2	11.5	12.2	13.4	2.0904	1.3936
155	Smelt	13.4	11.7	12.4	13.5	2.4300	1.2690
156	Smelt	12.2	12.1	13.0	13.8	2.2770	1.2558
157	Smelt	19.7	13.2	14.3	15.2	2.8728	2.0672
158	Smelt	19.9	13.8	15.0	16.2	2.9322	1.8792

159 rows × 7 columns

Part a:

Determine the number of fish species present in the dataset and analyze their distribution across each class. (Plot a bar chart too!).

to show the number of fish species, GroupBy method is used. since our dataset does not include any NaN values, the count of elements for each feature is the same. so here we only selected the count of one feature such as Weight to preview the number of each species

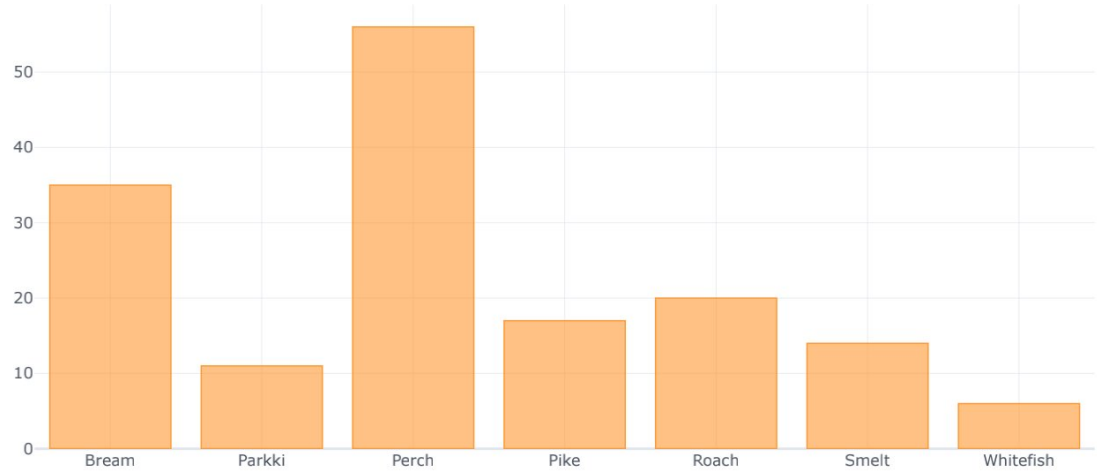
In [4]:
```
1 pd.DataFrame(df.groupby('Species')['Weight'].count())
```

Out[4]:

Species	Weight
Bream	35
Parkki	11
Perch	56
Pike	17
Roach	20
Smelt	14
Whitefish	6

Next, a bar chart is plotted using plotly We can see that Perch and Bream have the highest count among our dataset and WhiteFish and Parkiki have the lowest

In [5]:
```
1 df.groupby('Species')['Weight'].count().iplot(kind = 'bar')
```



Export to plot.ly »

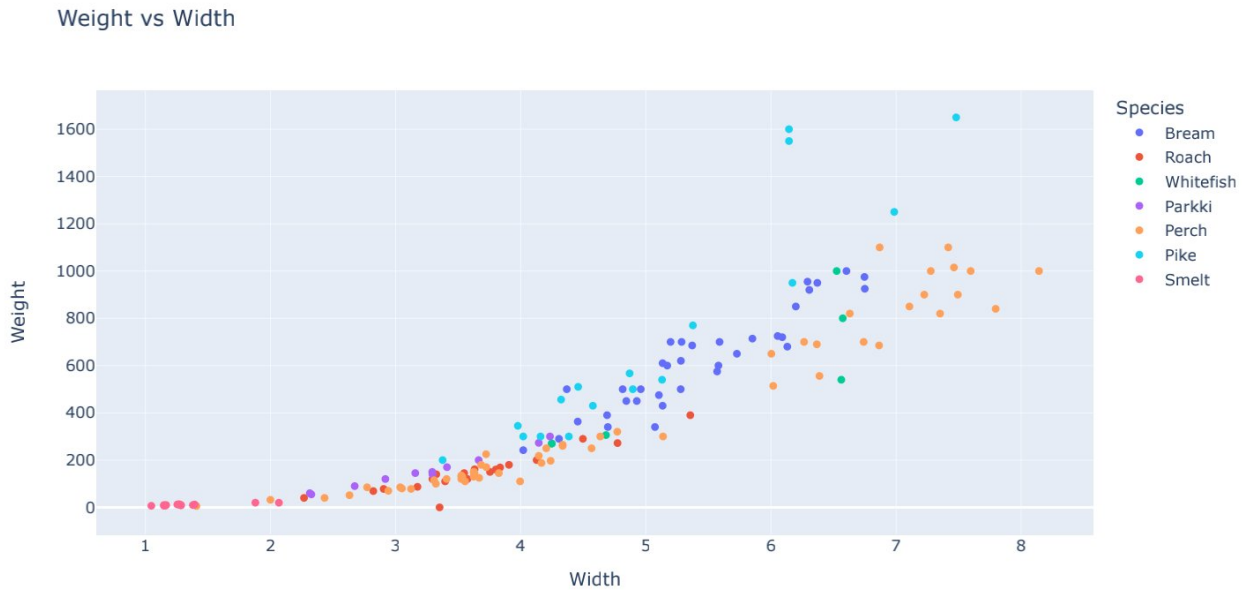
Part b:

Find the relationship between the following features: (weight vs. width) ,(weight vs. diagonal length), (cross length vs. vertical length). Use scatter diagrams to visualize the data and provide a detailed explanation of your findings.

in the following charts, the relationship between desired features are plotted using plotly. the express tool from plotly makes the chart interactive and easy for further exploration besides plotting desired features versus each other, they were also seperated by based on their Species. so that we can analyze the characteristics of each Species. The result of this analyze will be presented below the charts

In [6]:

```
import plotly.express as px

fig = px.scatter(df, y='Weight', x='Width', color='Species' , title='Weight vs Width')
fig.show()
```



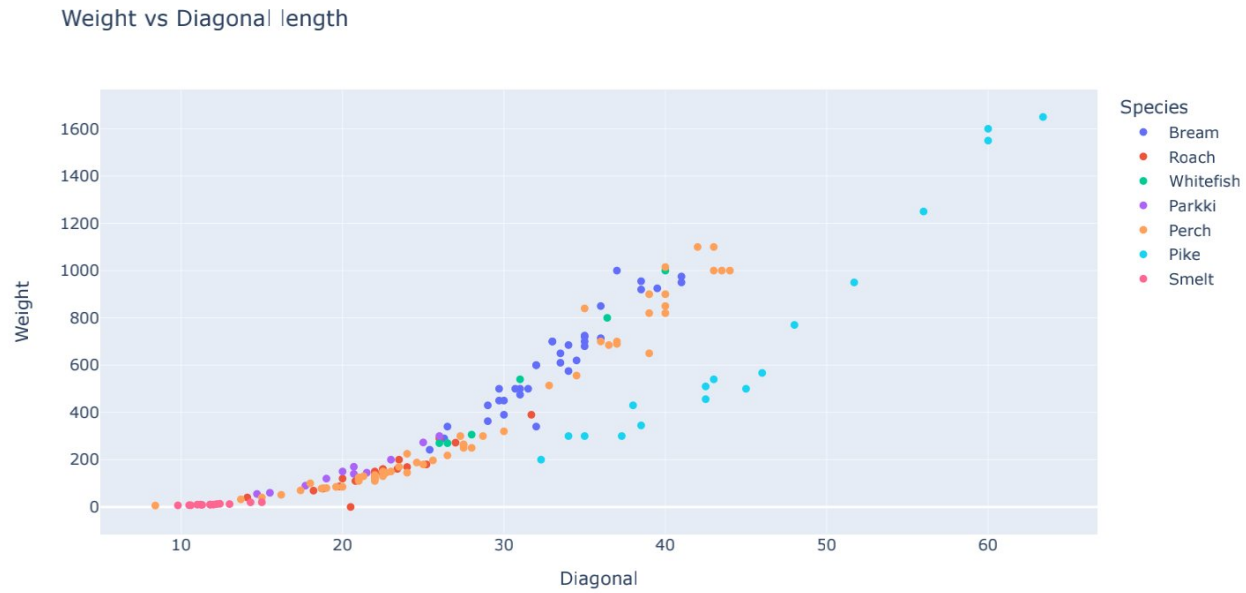
Result:

In the first glance, we can see that Weight has a non linear relation with Width length. We may consider it as a 2nd or 3rd order relation

Next, By looking at the Species, We can conclude the following results:

- 'Smelt' fish are smaller than the others, so they have less weigth and smaller Width length. Their Width range from 1 to 2.5 *
- 'Perch' fish have a wide range of sizes. their Width range from 1 to 8 , while their Weight range from 6 to 1100
- 'Pike' fish is a medium to large sized fish. its Width range from 3 to 7.5, while their weight range from 200 to 1500
- 'Parkiki' is a small sized fish, with the Width of 2 to 4.5, and Weight of 50 to 300
- 'WhiteFish', which have very few samples among dataset have aWidth between 4 to 7, and a Weigth in range of 300 to 1000
- 'Rouch' is considered to be a small sized fish, with the width of 2 to 5, and weigth of 50 to 400
- 'Bream' is a medium sized fish, with the width of 4 to 7 and Weight of 200 to 1000

In [7]:
```
fig = px.scatter(df, y='Weight', x='Diagonal', color='Species' , title='Weight vs Diagonal length')
fig.show()
```



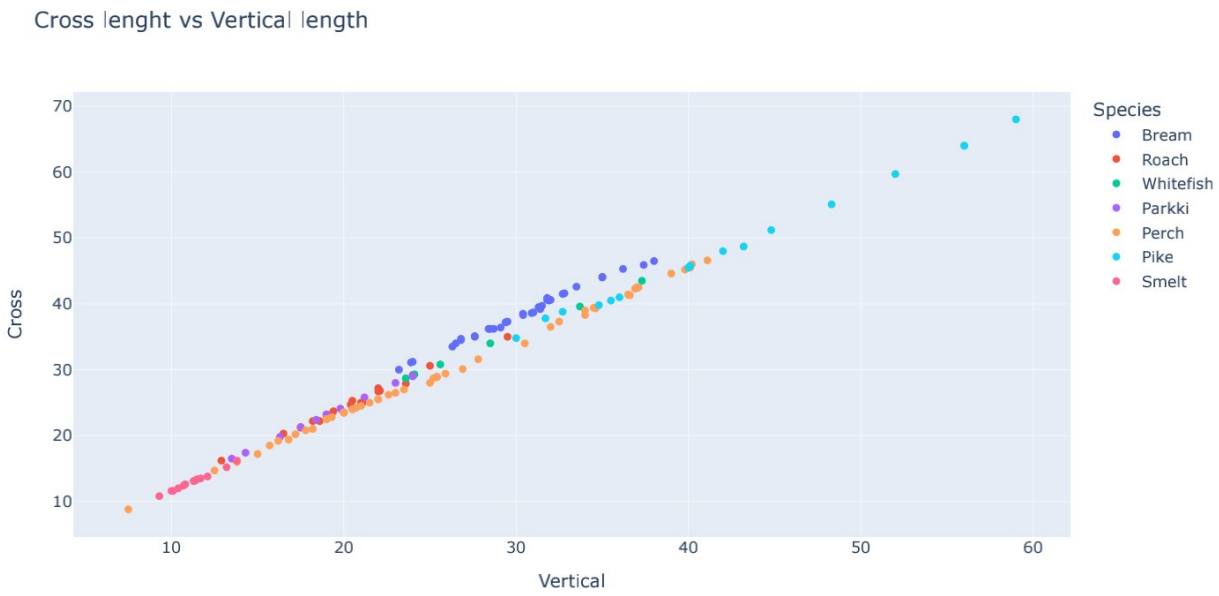
Result:

Just as shown in the distribution of Weigth vs Width, it is observed that Weigth has also a non linear relation with Diagonal Length.

Next, By exploring each Species we conclude that:

- 'Pike' fish has a greater Diagonal length to Weight ratio, which means this type of fish is long and narrower than the others

In [8]:
```
fig = px.scatter(df, y='Cross', x='Vertical', color='Species', title='Cross lenght vs Vertical length')
fig.show()
```



Result:

Unlike the two previous diagrams, we may conclude that Cross Length has a linear relation with Vertical Length.

Part c:

Develop a simple linear regression model for (cross length vs. vertical length). Fit the model and assess its performance using the mean squared error (MSE) and mean absolute error (MAE) metrics. Compare and plot the results.

First, the input and output data is defined. The input, which is 'Vertical' is stored as X1 and the output which is 'Cross' is stored as Y1

Next, this data is seperated to train and test data using sklearn library. finally, a Linear Regression model is fit to train data.

- Important note: Since in this part we had only one feature, the input data had to be reshaped to match the input format of Linear Regression method.

After fitting the model, its constants which are Weight of features and the bias value are stored as 'coef_' and 'intercept_'.

In [9]:
```
X1 = df['Vertical']
Y1 = df['Cross']
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X1, Y1, test_size=0.3 , random_state=101)
from sklearn.linear_model import LinearRegression

model = LinearRegression()
model.fit(np.array(X_train).reshape(-1,1),y_train)

# The coefficients
print('Coefficients: \n', model.coef_)
print('intercept: \n', model.intercept_)
```

```
Coefficients:
 [1.15362994]
intercept:
 1.0212673228352038
```

In the following section, Metrics are imported from sklearn package and three measurements MAE, MSE and RMSE are calculated

In [10]:

```
from sklearn import metrics

predictions = model.predict( np.array(X_test).reshape(-1,1))
print('MAE:', metrics.mean_absolute_error(y_test, predictions))
print('MSE:', metrics.mean_squared_error(y_test, predictions))
print('RMSE:', np.sqrt(metrics.mean_squared_error(y_test, predictions)))
```

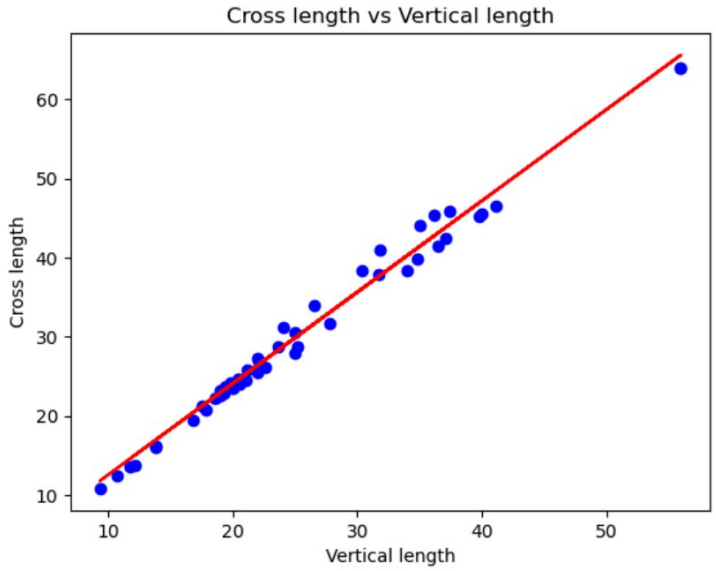
```
MAE: 1.1205663200084255
MSE: 1.8460614768618697
RMSE: 1.358698449569245
```

In the final section of this part, the plot of Actual vs Predicted values is presented. The red line indicate correct answers and the blue dots indicate predicted values. We may conclude that the line is fit satisfyngly to the data and the model is capable of predicting Cross value by a given Vertical value

In [11]:

```
plt.scatter(X_test, y_test,  color='blue')
plt.plot(X_test, model.coef_*X_test + model.intercept_, '-r')
plt.xlabel("Vertical length")
plt.ylabel("Cross length")
plt.title('Cross length vs Vertical length')
```

Out[11]: Text(0.5, 1.0, 'Cross length vs Vertical length')



Part d:

Identify the features that have the most significant impact on fish weight and choose three of these features for further evaluation. Develop a multiple linear regression model to assess the influence of these features on fish weight and evaluate the model using

To show the influence of each feature in predicting the Weigth of a given fish, first we need to find the correlation between features of dataset and Weigth. By examining these values, we will be able to choose only the features with higher correelation value as our inout features for regression models.

In [12]:
```
df.columns
```

Out[12]:
```
Index(['Species', 'Weight', 'Vertical', 'Diagonal', 'Cross', 'Height',
       'Width'],
      dtype='object')
```

Important Note: Since the Species column in our dataset is a categorical column and it contains valuable information about fish, we may not drop this column. so One Hot Encoding is utilized to transform this column into numerical features that consequently we can include them in our analysis. at the end of the proceess, the correlation value of each of these new features are summed up and their mean is calculated, indicating a single number to show the correlation of species with Weigth

In [13]:
```
from sklearn import linear_model
from sklearn.model_selection import train_test_split

df_encoded = pd.get_dummies(df, columns=['Species'])
# Display the resulting DataFrame
df_encoded
```

Out[13]:

	Weight	Vertical	Diagonal	Cross	Height	Width	Species_Bream	Species_Parkki	Species_Perch	Species_Pike	Species_Roach	Species_Smelt	Species_Wt
0	242.0	23.2	25.4	30.0	11.5200	4.0200	True	False	False	False	False	False	
1	290.0	24.0	26.3	31.2	12.4800	4.3056	True	False	False	False	False	False	
2	340.0	23.9	26.5	31.1	12.3778	4.6961	True	False	False	False	False	False	
3	363.0	26.3	29.0	33.5	12.7300	4.4555	True	False	False	False	False	False	
4	430.0	26.5	29.0	34.0	12.4440	5.1340	True	False	False	False	False	False	
...	...	...	...	...	...	...	...	...	...	...	...	...	
154	12.2	11.5	12.2	13.4	2.0904	1.3936	False	False	False	False	False	True	
155	13.4	11.7	12.4	13.5	2.4300	1.2690	False	False	False	False	False	True	
156	12.2	12.1	13.0	13.8	2.2770	1.2558	False	False	False	False	False	True	
157	19.7	13.2	14.3	15.2	2.8728	2.0672	False	False	False	False	False	True	
158	19.9	13.8	15.0	16.2	2.9322	1.8792	False	False	False	False	False	True	

159 rows × 13 columns

In [14]:

```
correlations = df_encoded.corr()['Weight']
species_correlation = correlations.filter(like='Species').abs().mean()
correlations.drop(['Species_Bream', 'Species_Parkki', 'Species_Perch', 'Species_Pike', 'Species_Roach', 'Species_Smelt', 'Speci

# Create a new Series with the species correlation
species_corr_series = pd.Series(species_correlation, index=['species_correlation'])

# Concatenate the two Series
all_correlations = pd.concat([correlations, species_corr_series])

# Display the correlation coefficients
print(all_correlations)

```

```
Weight                1.000000
Vertical              0.915712
Diagonal              0.918618
Cross                 0.923044
Height                0.724345
Width                 0.886507
species_correlation   0.218461
dtype: float64
```

As we can see, the features 'Vertical' ,'Diagonal' and 'Cross' have the highest correlation with our desired parameter Weight. So we just include them as our input features to multiple linear regression model

Having the most important features identified, the input and output dataframes are stored as below:

In [15]:

```
X2 = df[['Vertical', 'Diagonal', 'Cross']]
Y2 = df['Weight']
```

In the following section, input data is seperated to train and test data, and later, a linear regression model is fit to train data. we can access the Coefficients and Intercept of the model using corresponding methods of the model

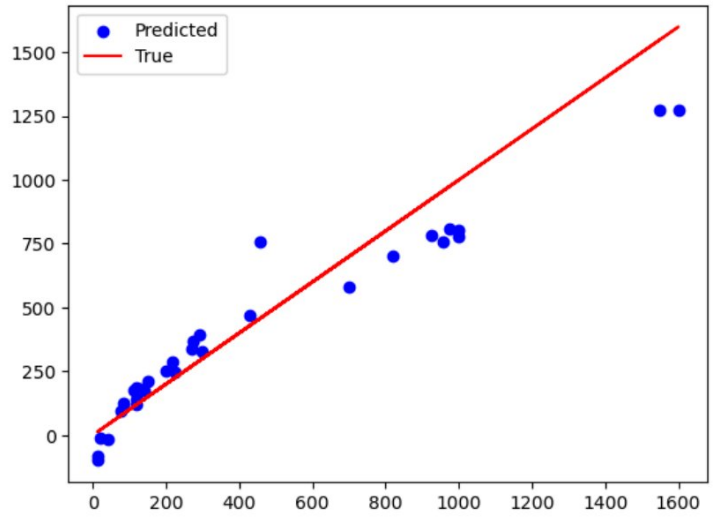
In [16]:
```
model = linear_model.LinearRegression()
X_train, X_test, y_train, y_test = train_test_split(X2, Y2, test_size=0.2 , random_state=101)

model.fit(X_train,y_train)
print ('Coefficients: ', model.coef_)
print ('Intercept: ',model.intercept_)
```

```
Coefficients:  [-39.61009838  40.85056022  23.40081276]
Intercept:  -459.15482470325503
```

Next, test data is given to the trained model and predicts the corresponding Weigth of each input data. In the presented plot, the Actual versus Predicted values are shown.

In [17]:
```
plt.scatter(y_test , model.predict(X_test) , color = 'blue' , label = 'Predicted')
plt.plot(y_test , y_test , color = 'red' , label = 'True')
plt.legend()
```

Out[17]:
```
<matplotlib.legend.Legend at 0x123fcd412a0>
```



In [18]:
```
predictions2 = model.predict(X_test)
from sklearn import metrics

print('MAE:', metrics.mean_absolute_error(y_test, predictions2))
print('MSE:', metrics.mean_squared_error(y_test, predictions2))
print('RMSE:', np.sqrt(metrics.mean_squared_error(y_test, predictions2)))
```

```
MAE: 102.10352455596949
MSE: 17646.012270349038
RMSE: 132.8382936895421
```

Result:

- By considering the Metric values and the diagram, we can see that the model had poor performance in predicting large values of fish weigths, just as very small weigths. This is a logical result, since as presented in part b, we observed that there are non linear relations between Vertical, Croos and Diagonal lengths. In this multiple linear regression model, this nonlinear behaviour was not considered

Part e:

Develop a polynomial regression model for (weight vs. width), as well as (weight vs. height).

(weight vs. width)

Input and Output data are stored in new dataframes named X3 and Y3.

In [19]:
```
X3 = df['Width']
Y3 = df['Weight']
```

In the following section, we first define a 2nd degree polynomial as our model, then the input data is divided into train and test data.

- Important note: Since in this part we had only one feature, the input data had to be reshaped to match the input format of Linear Regression method. The polynimial function is applied to the input features with predefined constants. this makes new features for each of the degrees of input data.

In [20]:
```
from sklearn.preprocessing import PolynomialFeatures

poly = PolynomialFeatures(degree = 2)

train_x, test_x , train_y , test_y = train_test_split(X3,Y3,test_size=0.2,random_state=4)
train_x_poly = poly.fit_transform(np.array(train_x).reshape(-1,1))
test_x_poly = poly.fit_transform(np.array(test_x).reshape(-1,1))
```

In the following section, a linear regression model is defined and fit to the data.

In [21]:
```
model = linear_model.LinearRegression()

model.fit(train_x_poly, train_y)

# The coefficients
print ('Coefficients: ', model.coef_)
print ('Intercept: ', model.intercept_)
```

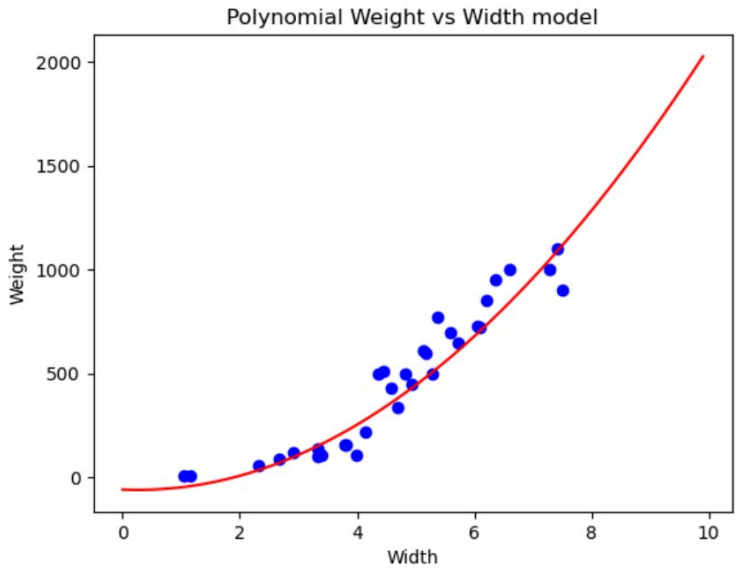
```
Coefficients:  [  0.         -11.88933321  22.45259053]
Intercept:  -57.79725688019863
```

Finally, the Actual vs Predicted diagram is plotted. the red line, is the predicted polynomial function and blue dots indicate true values

In [22]:

```
plt.scatter(test_x , test_y, color = 'blue')

XX = np.arange(0.0, 10.0, 0.1)
yy = model.intercept_+ model.coef_[1]*XX + model.coef_[2]*np.power(XX, 2)

plt.plot(XX, yy, '-r' )
plt.xlabel('Width')
plt.ylabel('Weight')
plt.title('Polynomial Weight vs Width model')
```

Out[22]: Text(0.5, 1.0, 'Polynomial Weight vs Width model')



In [23]:
```
predictions3 = model.predict(test_x_poly)

print('MAE:', metrics.mean_absolute_error(test_y, predictions3))
print('MSE:', metrics.mean_squared_error(test_y, predictions3))
print('RMSE:', np.sqrt(metrics.mean_squared_error(test_y, predictions3)))
```

```
MAE: 81.8972986743567
MSE: 10922.507827726185
RMSE: 104.51080244513571
```

Result:

Based on the diagram above and values of metrics, we can conclude that the model is capable of predicting the value of Weight. Meanwhile, the values of metrics looks higher than metrics calculated in predicting Cross vs Vertical model. This is due to the fact that the scale of output data is different

(weight vs. height)

In [24]:
```
X4 = df['Height']
Y4 = df['Weight']
```

In [25]:
```
from sklearn.preprocessing import PolynomialFeatures
poly = PolynomialFeatures(degree = 2)
train_x, test_x , train_y , test_y = train_test_split(X4,Y4,test_size=0.2,random_state=4)
train_x_poly = poly.fit_transform(np.array(train_x).reshape(-1,1))
test_x_poly = poly.fit_transform(np.array(test_x).reshape(-1,1))
```

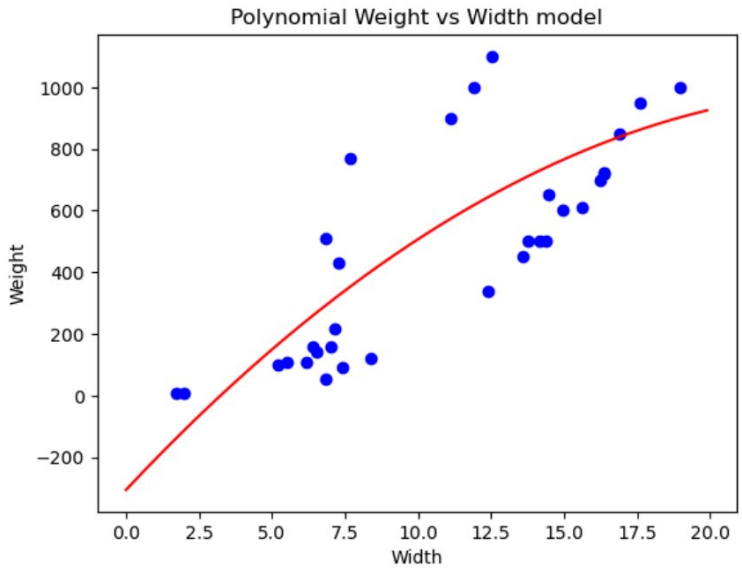
In [26]:
```
model = linear_model.LinearRegression()

model.fit(train_x_poly, train_y)

# The coefficients
print ('Coefficients: ', model.coef_)
print ('Intercept: ', model.intercept_)
```

```
Coefficients:  [  0.         100.92417358  -1.96346368]
Intercept:  -305.9932338395084
```

In [27]:

```
plt.scatter(test_x , test_y, color = 'blue')

XX = np.arange(0.0, 20.0, 0.1)
yy = model.intercept_+ model.coef_[1]*XX + model.coef_[2]*np.power(XX, 2)

plt.plot(XX, yy, '-r' )
plt.xlabel('Width')
plt.ylabel('Weight')
plt.title('Polynomial Weight vs Width model')
```

Out[27]: Text(0.5, 1.0, 'Polynomial Weight vs Width model')



In [28]:

```
predictions4 = model.predict(test_x_poly)

print('MAE:', metrics.mean_absolute_error(test_y, predictions4))
print('MSE:', metrics.mean_squared_error(test_y, predictions4))
print('RMSE:', np.sqrt(metrics.mean_squared_error(test_y, predictions4)))
```

```
MAE: 183.29734463555752
MSE: 44800.22797956126
RMSE: 211.66064343557417
```

Assignment 1

Problem 2

Import necessary libraries

In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

%matplotlib inline
from plotly import __version__
from plotly.offline import download_plotlyjs, init_notebook_mode, plot, iplot

print(__version__) # requires version >= 1.9.0
import cufflinks as cf
# For Notebooks
init_notebook_mode(connected=True)

# For offline use
cf.go_offline()

import warnings

warnings.filterwarnings("ignore")
```

```
5.18.0
```

Read data and plot it

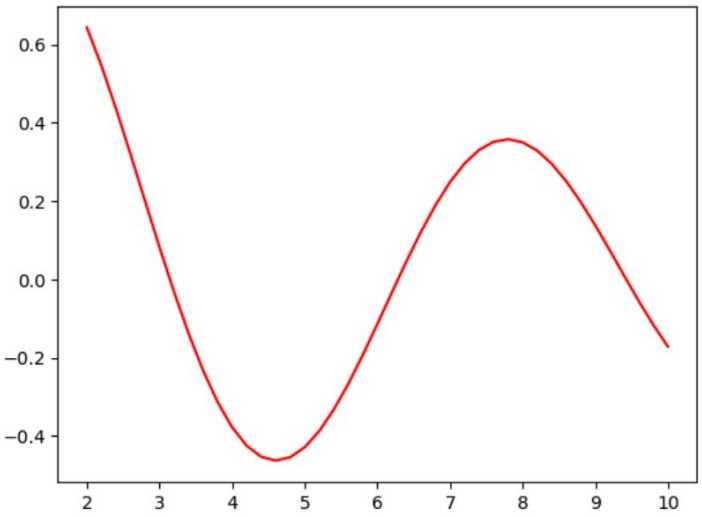
In this part, the dataset is imported using pandas. then, since there was a mismatch in values and indexes, they are manually stored in two new dataframes named x and y.

Next, the signal is plotted

In [2]:
```
df = pd.read_csv('Dataset_II.csv')
x = np.array(df.values[0])
```

```
y = np.array(df.columns, dtype=float)
plt.plot(x,y , color = 'red')
```

Out[2]: [<matplotlib.lines.Line2D at 0x22b2e09c730>]



Here, data is divided into train and test

In [3]:
```
from sklearn.model_selection import train_test_split
train_x, test_x , train_y , test_y = train_test_split(x,y,test_size=0.3,random_state=101)
```

(a) Fit a regression model using the following mathematical formulas:

f1(x) = w1 + w2x + w3x2

f2(x) = w1 + w2x + ... + w10x9

f3(x) = w1 + w2x + sin(x) + cos(x)

Desired mathematical functions are defined in the following code, and using curve_fit method from scipy, a curve is fit to the given train data. This is worth noting that the parameters are already optimized.

In [4]:
```
import numpy as np
from scipy.optimize import curve_fit

# Define the models
def f1(x, w1, w2, w3):
    return w1 + w2*x + w3*x**2

def f2(x, w1, w2, w3, w4, w5, w6, w7, w8, w9, w10):
    return w1 + w2*x + w3*x**2 + w4*x**3 + w5*x**4 + w6*x**5 + w7*x**6 + w8*x**7 + w9*x**8 + w10*x**9

def f3(x, w1, w2):
    return w1 + w2*x + np.sin(x) + np.cos(x)

# Fit the models to the data
popt1, pcov1 = curve_fit(f1, train_x, train_y)
popt2, pcov2 = curve_fit(f2, train_x, train_y)
popt3, pcov3 = curve_fit(f3, train_x, train_y)

# popt1, popt2, and popt3 contain the optimized parameters for each model
```

(b) Evaluate the models using MSE and MAE. Tabulate the results. Look at which models performed better on this dataset and give your conclusion on the results.

Calculate RMSE, MSE and MAE for each model

In [5]:
```
# Calculate the residuals for each model
residuals1 = train_y - f1(train_x, *popt1)
residuals2 = train_y - f2(train_x, *popt2)
residuals3 = train_y - f3(train_x, *popt3)

# Calculate the RMSE for each model
rmse1 = np.sqrt(np.mean(residuals1**2))
rmse2 = np.sqrt(np.mean(residuals2**2))
rmse3 = np.sqrt(np.mean(residuals3**2))

# Calculate the MSE for each model
mse1 = np.mean(residuals1**2)
mse2 = np.mean(residuals2**2)
```

```
mse3 = np.mean(residuals3**2)

# Calculate the MAE for each model
mae1 = np.mean(np.abs(residuals1))
mae2 = np.mean(np.abs(residuals2))
mae3 = np.mean(np.abs(residuals3))

print("MSE for f1: ", mse1)
print("MSE for f2: ", mse2)
print("MSE for f3: ", mse3)
print('.....................................')
print("MAE for f1: ", mae1)
print("MAE for f2: ", mae2)
print("MAE for f3: ", mae3)
print('.....................................')
print("RMSE for f1: ", rmse1)
print("RMSE for f2: ", rmse2)
print("RMSE for f3: ", rmse3)
```

```
MSE for f1:  0.08380058343296011
MSE for f2:  5.026595990308679e-10
MSE for f3:  0.5716359145611148
.....................................
MAE for f1:  0.26054239436901205
MAE for f2:  1.8403865009242728e-05
MAE for f3:  0.6457601651696866
.....................................
RMSE for f1:  0.28948330423870755
RMSE for f2:  2.2420071343126186e-05
RMSE for f3:  0.7560660781711575
```

In [6]:

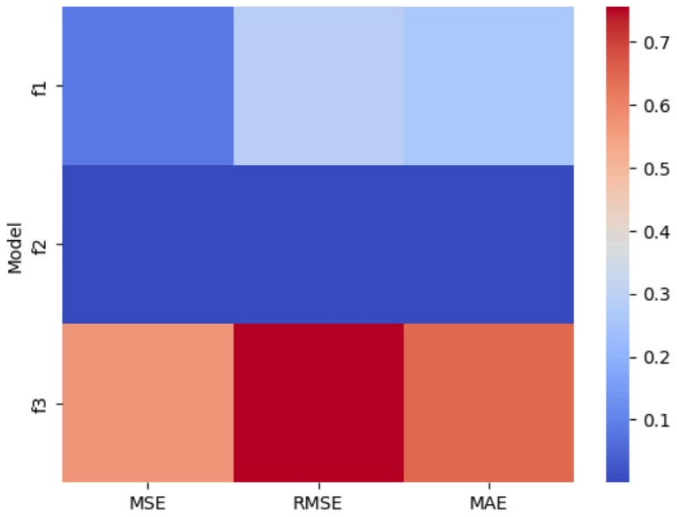
```
import pandas as pd

# Create a dictionary with the calculated values
Measures = {
    'Model': ['f1', 'f2', 'f3'],
    'MSE': [mse1, mse2, mse3],
    'RMSE': [rmse1, rmse2, rmse3],
    'MAE': [mae1, mae2, mae3]
}

# Create a DataFrame from the dictionary
Measures = pd.DataFrame(Measures)
Measures
```

Out[6]:

	Model	MSE	RMSE	MAE
0	f1	8.380058e-02	0.289483	0.260542
1	f2	5.026596e-10	0.000022	0.000018
2	f3	5.716359e-01	0.756066	0.645760

In [7]:
```
# Print the DataFrame
sns.heatmap(Measures.set_index('Model') , cmap = 'coolwarm')
```

Out[7]:
```
<Axes: ylabel='Model'>
```



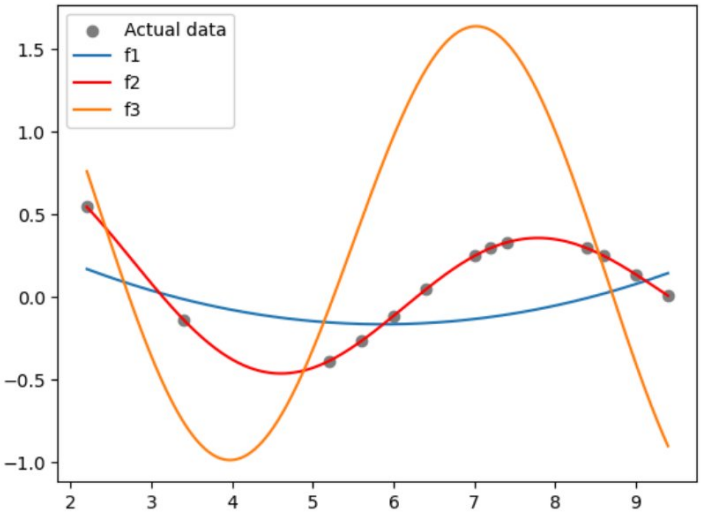
We can observe that function 2, which is 9th degree polynomial has a great performance in comparison to the other models. this might be due to the complexity of this model.

- Important Note:

Since this values are calculated based on training data, it is possible that overfitting had happened and the model has poor performance on test data. in the following sections, performance of these models are examined on test data to verify this issue

Plot Actual vs Predicted values of each model on test data

In [8]:
```
# Generate a sequence of x values from the minimum to the maximum x value in your data
x_seq = np.linspace(min(test_x), max(test_x), 1000)

# Calculate the corresponding y values for each model
y_seq1 = f1(x_seq, *popt1)
y_seq2 = f2(x_seq, *popt2)
y_seq3 = f3(x_seq, *popt3)

# Plot the actual data
plt.scatter(test_x, test_y, label='Actual data' , color = 'gray')

# Plot each model
plt.plot(x_seq, y_seq1, label='f1')
plt.plot(x_seq, y_seq2, label='f2' , color  = 'red')
plt.plot(x_seq, y_seq3, label='f3')

# Add a legend
plt.legend()

# Show the plot
plt.show()
```



Result:

As shown in figure above, we can see that model f2 have a significant advantage to other models in predicting the output value. Also, this calrifies that overfitting did not happen and the performance of this model is still acceptable on unseen data

Assignment 1

Problem 3

Import necessary libraries

In [1]:

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

%matplotlib inline
from plotly import __version__
from plotly.offline import download_plotlyjs, init_notebook_mode, plot, iplot

print(__version__) # requires version >= 1.9.0
import cufflinks as cf
# For Notebooks
init_notebook_mode(connected=True)

# For offline use
cf.go_offline()

import warnings

warnings.filterwarnings("ignore")
```

```
5.18.0
```

(a) Read the text file, how many classes exist in the dataset? Which class has the most amount of data?

Read data and plot it based on type of the drink

In [2]:
```
1 df = pd.read_csv('Dataset_III.csv')
```

In [3]:
```
1 df['type'].unique()
```

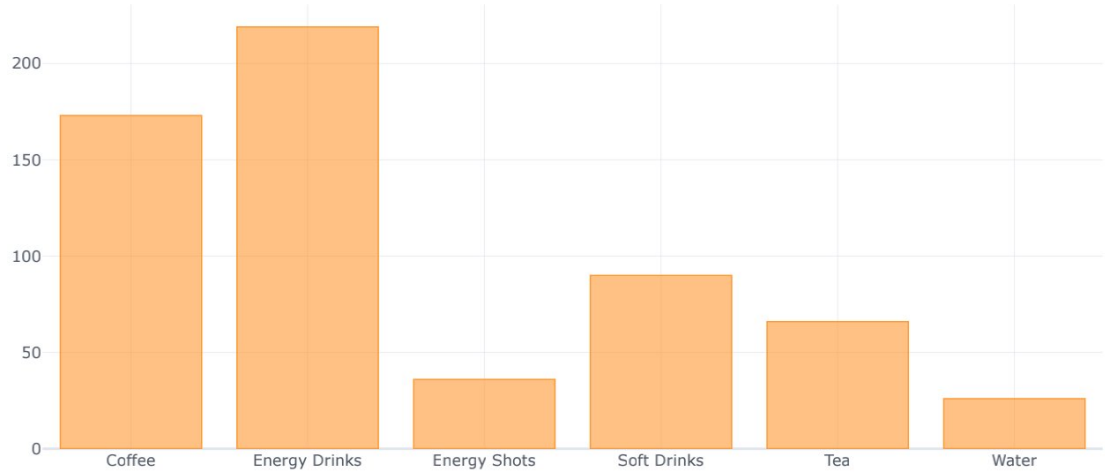
Out[3]:
```
array(['Coffee', 'Energy Drinks', 'Energy Shots', 'Soft Drinks', 'Tea',
       'Water'], dtype=object)
```

In [4]:
```
1 df.groupby('type')['drink'].count()
```

Out[4]:
```
type
Coffee           173
Energy Drinks    219
Energy Shots      36
Soft Drinks       90
Tea               66
Water             26
Name: drink, dtype: int64
```

The distribution of Drinks based on their type is presented in the following plot

In [5]:
```
1 df.groupby('type')['drink'].count().iplot(kind = 'bar')
```



Export to plot.ly »

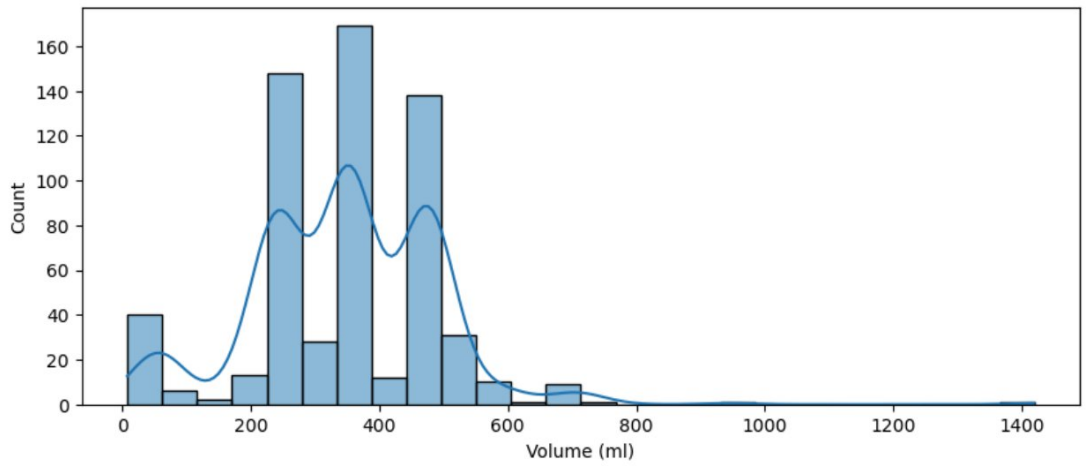
We can see that there are 6 types of drinks among our dataset. Also, this Coffee and Energy Drinks have the most amount of data

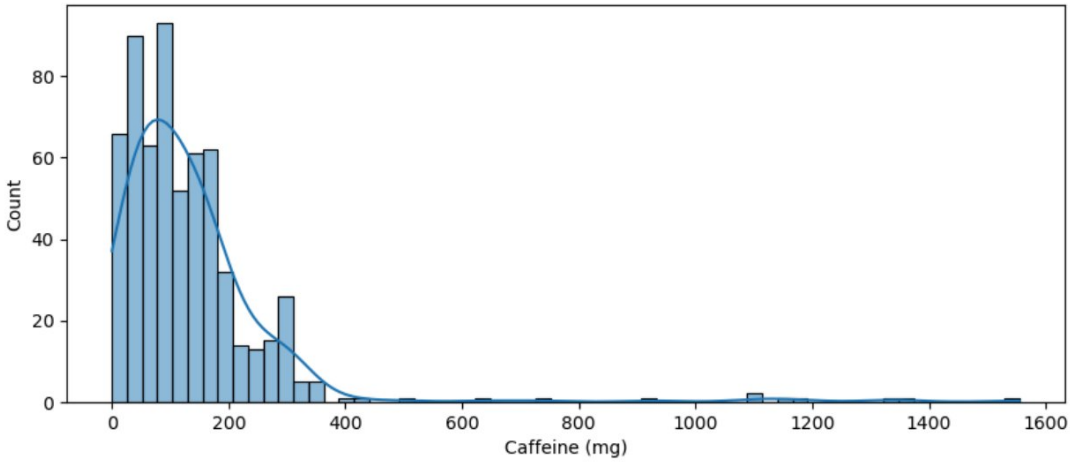
(b) Plot the histogram of the numerical features. Explain what you understand.

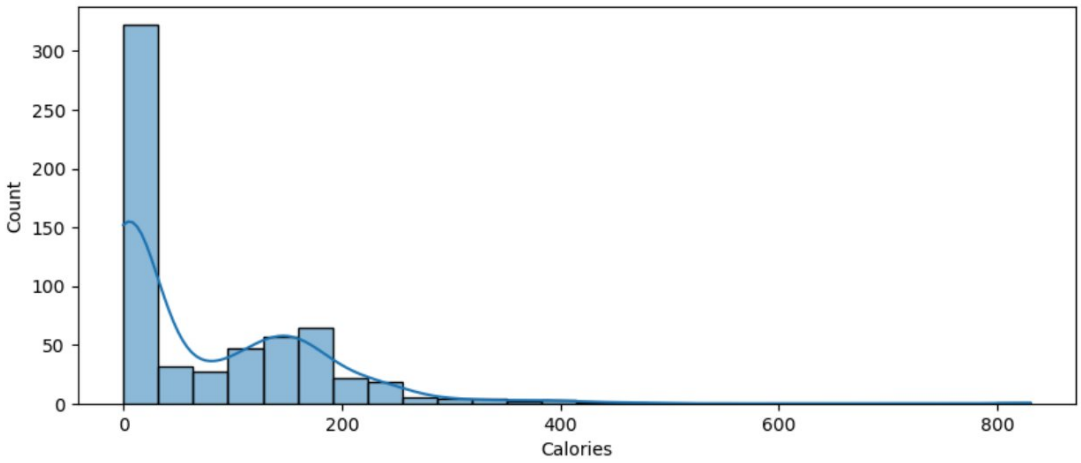
Using Seaborn package, we plot histograms of desired features. also, a kde line in plotted above the bar charts to make it more convenient for analysis

In [6]:

```
# Plot for 'Volume (ml)'
plt.figure(figsize=(10, 4))
sns.histplot(df['Volume (ml)'], kde=True)
plt.show()

# Plot for 'Caffeine (mg)'
plt.figure(figsize=(10, 4))
sns.histplot(df['Caffeine (mg)'], kde=True)
plt.show()

# Plot for 'Calories'
plt.figure(figsize=(10, 4))
sns.histplot(df['Calories'], kde=True)
plt.show()


```




Count
Caffeine (mg)
0
20
40
60
80
0
200
400
600
800
1000
1200
1400
1600

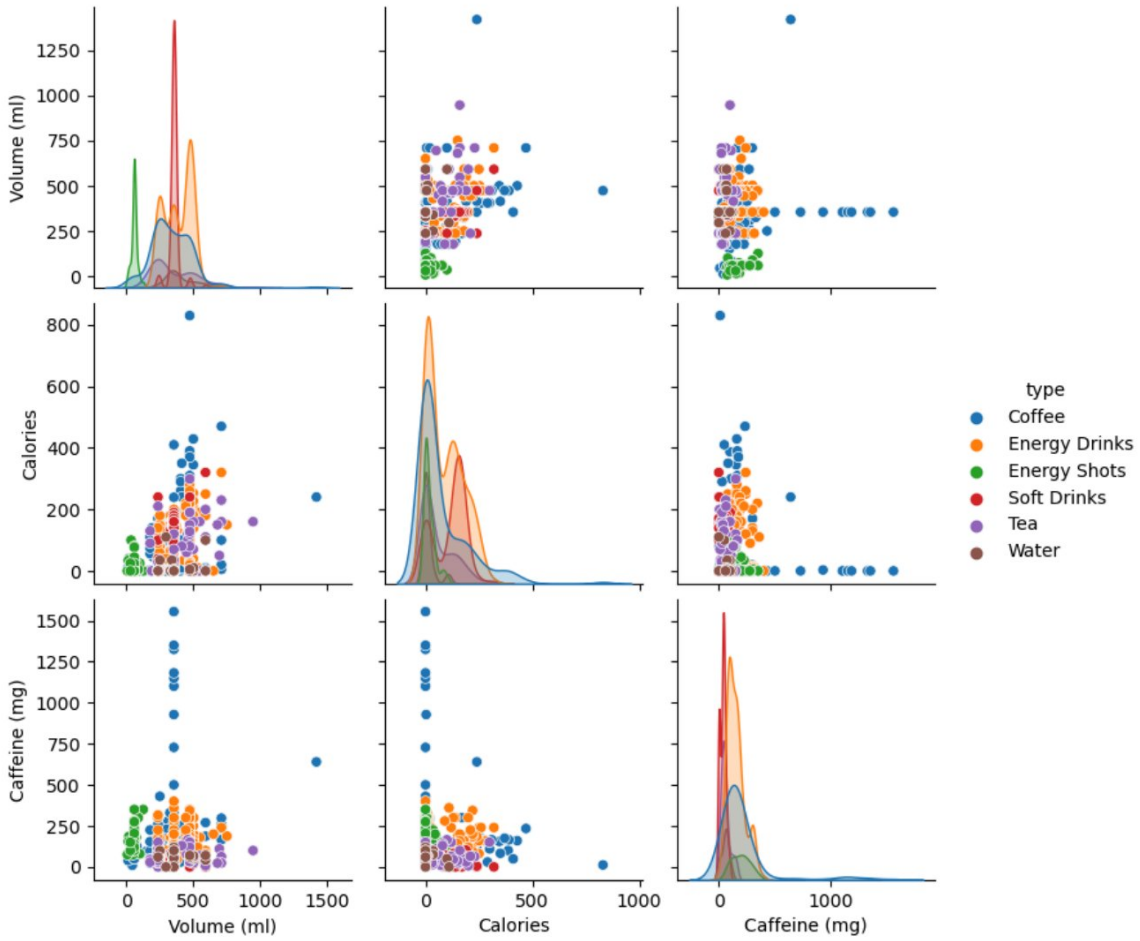

Count
Calories
0
50
100
150
200
250
300
0
200
400
600
800

By analyzing above diagrams,the following results can be concluded:

- Most of drinks in data set, have a volume in range of 200-450 ml. this indicates that there are fewer samples related to small sized drinks, like shots and similar cups.
- Also, the distribution of drinls based on Caffeine shows that there are very few drinks with high amount of Caffeine, and most of the drinks have a normal amount of 0-200 mg. Meanwhile, a significant number of drinks have very little amount of Cafeine
- Most of the drinks present in dataset have very little amount of calories. this can be due to the fact in the description of dataset which indicates that the value of calories are not defined, because of the variable amount of suger which is used besides the drinks

In [7]:
```
1 sns.pairplot(df , hue = 'type')
```

Out[7]:
```
<seaborn.axisgrid.PairGrid at 0x17410a0fe20>
```


Volume (ml)
Calories
Caffeine (mg)
type
Coffee
Energy Drinks
Energy Shots
Soft Drinks
Tea
Water

Scaling feature values to a normalized range

In [8]:
```
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
scaler.fit(df.drop(['type' , 'drink'],axis=1))
```

Out[8]:
```
StandardScaler
StandardScaler()
```

In [9]:
```
scaled_features = scaler.transform(df.drop(['type' , 'drink'],axis=1))
df_feat = pd.DataFrame(scaled_features,columns=df.columns[:-2])
df_feat.head()
```

Out[9]:

	drink	Volume (ml)	Calories
0	-0.623477	-0.797362	0.916714
1	-0.670834	-0.797362	0.066393
2	-0.670834	0.786216	-0.223489
3	-0.670834	-0.797362	1.902314
4	-0.670834	-0.797362	-0.442511

(c) Use KNN to fit the appropriate model. For validation, use the F1 score metric.

Using sklearn, first data is divided into test and train and then a KNN model is trained with initial number of neighbors equalls to 1. This value will be modified later

In [10]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(scaled_features,df['type'], test_size=0.2)
```

In [11]:
```
from sklearn.neighbors import KNeighborsClassifier
knn = KNeighborsClassifier(n_neighbors=1)
knn.fit(X_train,y_train)
```

Out[11]:
```
KNeighborsClassifier(n_neighbors=1)
```

Using the trained model, output values of test data is predicted. Next, we can see the confusion matrix which shows True and False predictions based on each type finally, some metrics are calculated

In [12]:
```
pred = knn.predict(X_test)
```

In [13]:
```
from sklearn.metrics import classification_report,confusion_matrix
print(confusion_matrix(y_test,pred))
```

```
[[19  6  0  0  5  0]
 [ 7 30  0  0  3  2]
 [ 0  0  5  0  0  0]
 [ 1  3  0 18  2  0]
 [ 4  3  0  0  8  0]
 [ 1  0  0  1  3  1]]
```

In [14]:
```
print(classification_report(y_test,pred))
```

```
              precision    recall  f1-score   support

      Coffee       0.59      0.63      0.61        30
Energy Drinks       0.71      0.71      0.71        42
 Energy Shots       1.00      1.00      1.00         5
  Soft Drinks       0.95      0.75      0.84        24
          Tea       0.38      0.53      0.44        15
        Water       0.33      0.17      0.22         6

     accuracy                           0.66       122
    macro avg       0.66      0.63      0.64       122
 weighted avg       0.68      0.66      0.67       122
```

(d) Find the best K.

To optimize the model, we must define the number of neighbors. a convonient method for this is utilizing Elbow Methos. in this method, an error rate is calculated for different number of neighbors. later using this plot, we can choose the best value of K

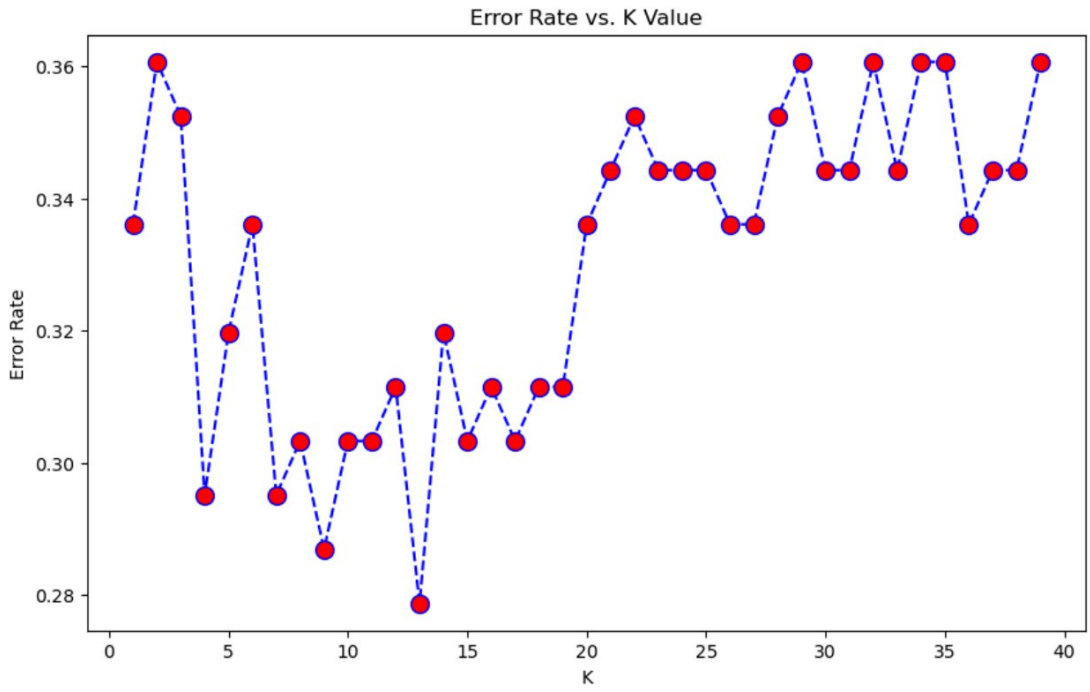
In [15]:

```
error_rate = []

# Will take some time
for i in range(1,40):

    knn = KNeighborsClassifier(n_neighbors=i)
    knn.fit(X_train,y_train)
    pred_i = knn.predict(X_test)
    error_rate.append(np.mean(pred_i != y_test))
```

In [16]:

```
plt.figure(figsize=(10,6))
plt.plot(range(1,40),error_rate,color='blue', linestyle='dashed', marker='o', markerfacecolor='red', markersize=10)
plt.title('Error Rate vs. K Value')
plt.xlabel('K')
plt.ylabel('Error Rate')
```

Out[16]: Text(0, 0.5, 'Error Rate')



As shown on the diagram, the minimum Error Rate is 15. so we set number 15 as our number of neighbors

In [17]:

```
# NOW WITH K=15
knn = KNeighborsClassifier(n_neighbors=15)

knn.fit(X_train,y_train)
pred = knn.predict(X_test)

print('WITH K=15')
print('\n')
confusion_matrix(y_test,pred)
print('\n')
print(classification_report(y_test,pred))
```

```
WITH K=15


              precision    recall  f1-score   support

      Coffee       0.71      0.57      0.63        30
Energy Drinks       0.63      0.86      0.73        42
 Energy Shots       1.00      0.80      0.89         5
  Soft Drinks       0.87      0.83      0.85        24
         Tea        0.62      0.53      0.57        15
       Water        0.00      0.00      0.00         6

    accuracy                           0.70       122
   macro avg       0.64      0.60      0.61       122
weighted avg       0.68      0.70      0.68       122
```

Thank you