Question 1

A customer informed their consultant that they have developed several formulations of petrol that gives different characteristics of burning pattern. The formulations are obtaining by adding varying levels of additives that, for example, prevent engine knocking, gum prevention, stability in storage, and etc. However, a third party certification organisation would like to verify if the formulations are significantly different, and request for both physical and statistical proof. Since the formulations are confidential information, they are not named in the dataset.

Please assist the consultant in the area of statistical analysis by doing this;

- A descriptive analysis of the additives (columns named as “a” to “i”), which must include summaries of findings (parametric/non-parametric).
- Correlation and ANOVA, if applicable, is a must.
- A graphical analysis of the additives, including a distribution study.
- A clustering test of your choice (unsupervised learning), to determine the distinctive number of formulations present in the dataset.

```
#import libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings("ignore")
```

```
data = pd.read_csv('ingredient.csv')
```

```
data.head()
```

	a	b	c	d	e	f	g	h	i
0	1.51735	13.02	3.54	1.69	72.73	0.54	8.44	0.00	0.07

```
#analyze descriptive statistics
data.describe()
```

	a	b	c	d	e	f	
count	214.000000	214.000000	214.000000	214.000000	214.000000	214.000000	214.00
mean	1.518365	13.407850	2.684533	1.444907	72.650935	0.497056	8.95
std	0.003037	0.816604	1.442408	0.499270	0.774546	0.652192	1.42
min	1.511150	10.730000	0.000000	0.290000	69.810000	0.000000	5.43
25%	1.516523	12.907500	2.115000	1.190000	72.280000	0.122500	8.24
50%	1.517680	13.300000	3.480000	1.360000	72.790000	0.555000	8.60
75%	1.519157	13.825000	3.600000	1.630000	73.087500	0.610000	9.17
max	1.533930	17.380000	4.490000	3.500000	75.410000	6.210000	16.19

```
#check data types
data.dtypes
```

```
a    float64
b    float64
c    float64
d    float64
e    float64
f    float64
g    float64
h    float64
i    float64
dtype: object
```

```
#check data shape(rows and columns)
data.shape
```

```
(214, 9)
```

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 214 entries, 0 to 213
Data columns (total 9 columns):
 #   Column  Non-Null Count  Dtype  
---  ------  --------------  -----  
 0   a       214 non-null    float64
 1   b       214 non-null    float64
 2   c       214 non-null    float64
 3   d       214 non-null    float64
 4   e       214 non-null    float64
 5   f       214 non-null    float64
 6   g       214 non-null    float64
 7   h       214 non-null    float64
 8   i       214 non-null    float64
dtypes: float64(9)
memory usage: 15.2 KB
```

```
#check if there are any missing or null values. Luckily there is none!
data.isnull().any()
```

```
a    False
b    False
c    False
d    False
e    False
f    False
g    False
h    False
i    False
dtype: bool
```

Summary:

- All the features are numerical in nature.
- There are no missing values.

Lets analyze the numerical(continous and discrete) variables

```
# list of numerical variables
num_vars = [var for var in data.columns if data[var].dtypes != 'O']
```

```
print('Number of numerical variables: ', len(num_vars))

# visualise the numerical variables
data[num_vars].head()
```

```
Number of numerical variables:  9
```

	a	b	c	d	e	f	g	h	i
0	1.51735	13.02	3.54	1.69	72.73	0.54	8.44	0.00	0.07
1	1.53125	10.73	0.00	2.10	69.81	0.58	13.30	3.15	0.28
2	1.52300	13.31	3.58	0.82	71.99	0.12	10.17	0.00	0.03
3	1.51768	12.56	3.52	1.43	73.15	0.57	8.54	0.00	0.00
4	1.51813	13.43	3.98	1.18	72.49	0.58	8.15	0.00	0.00

```
#method to calculate mean and median for every NUMERICAL column
def ingrediants_mean_median(column):
    print(f"{round(column.mean(),2)}\t\t{round(column.median(),2)}")

for var in num_vars:
    if var == num_vars[0]:
        print(f"Mean\t\tMedian")

    ingrediants_mean_median(data[var])
```

```
Mean            Median
1.52            1.52
13.41           13.3
2.68            3.48
1.44            1.36
72.65           72.79
0.5             0.56
8.96            8.6
0.18            0.0
0.06            0.0
```

```
#method to calculate variance and standard deviation for every NUMERICAL column
def ingrediants_var_std(column):
    print(f"{round(column.var(),2)}\t\t{round(column.std(),2)}")

for var in num_vars:
    if var == num_vars[0]:
        print(f"Variance\tStandard Deviation")

    ingrediants_var_std(data[var])
```

```
Variance        Standard Deviation
0.0             0.0
0.67            0.82
2.08            1.44
0.25            0.5
0.6             0.77
0.43            0.65
2.03            1.42
0.25            0.5
0.01            0.1
```

Summary:

- Mean and median are quite close to eache other.
- Not much variance except for two columns c and g.

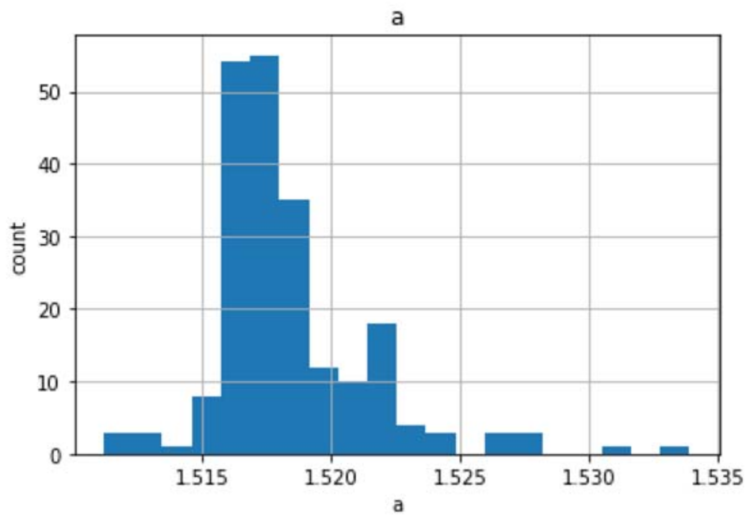
Lets analyze the distributions

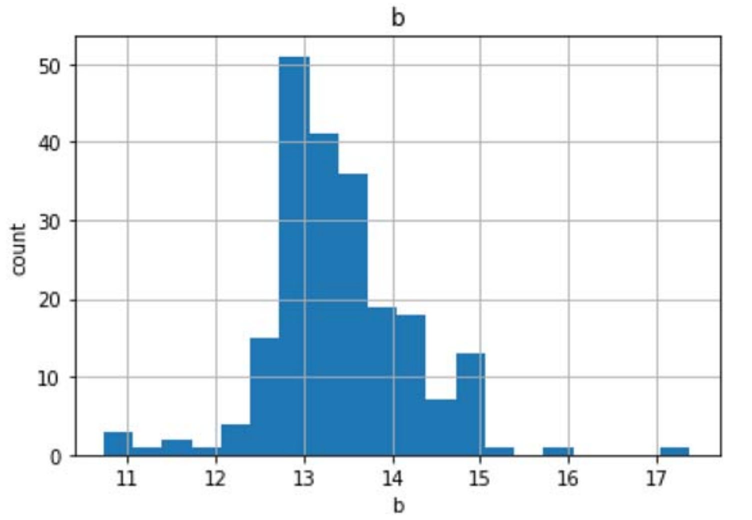
```
#  list of discrete variables - my assumption is that a discrete column has less than 20 unique values
discrete_vars = [var for var in num_vars if len(data[var].unique())<20]

print('Number of discrete variables: ', len(discrete_vars))
```

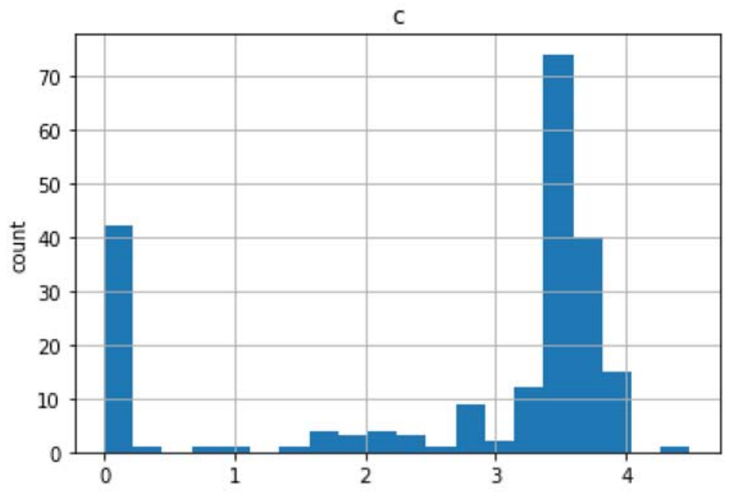
```
Number of discrete variables:  0
```

```
# Let's go ahead and analyse the distributions of these variables
def analyse_continous(df, var):
    df = df.copy()
    df[var].hist(bins=20)
    plt.ylabel('count')
    plt.xlabel(var)
    plt.title(var)
    plt.show()

for var in num_vars:
```

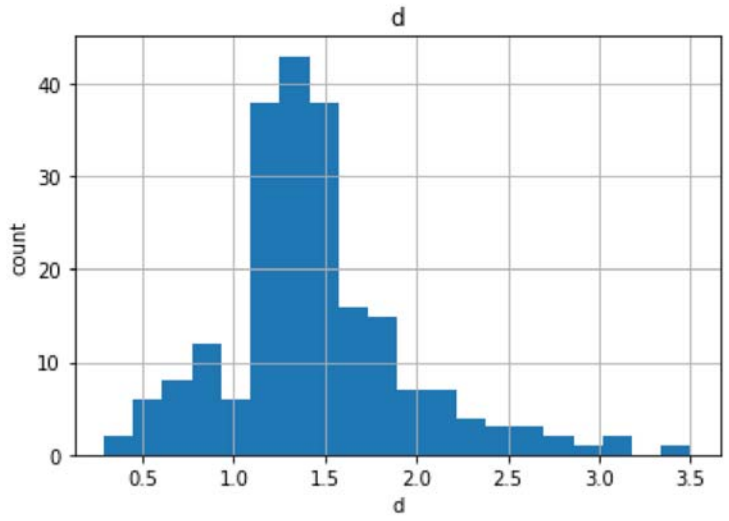
```
for var in num_vars:
    analyse_continous(data, var)
```

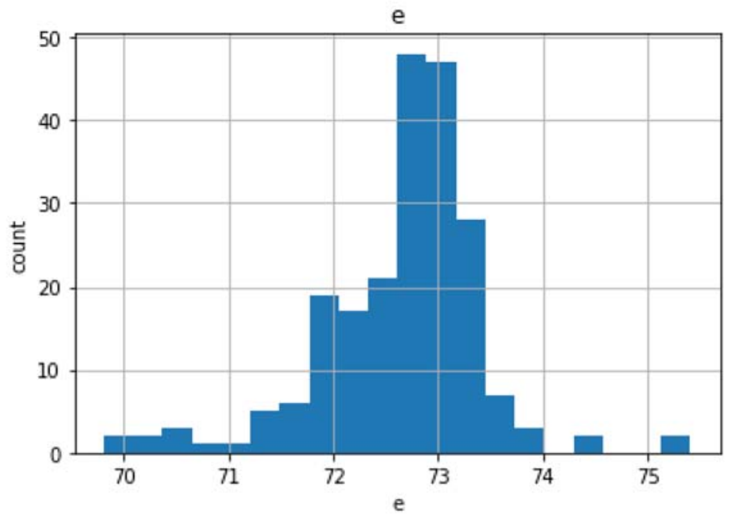

a
count
0
10
20
30
40
50
1.515
1.520
1.525
1.530
1.535
a

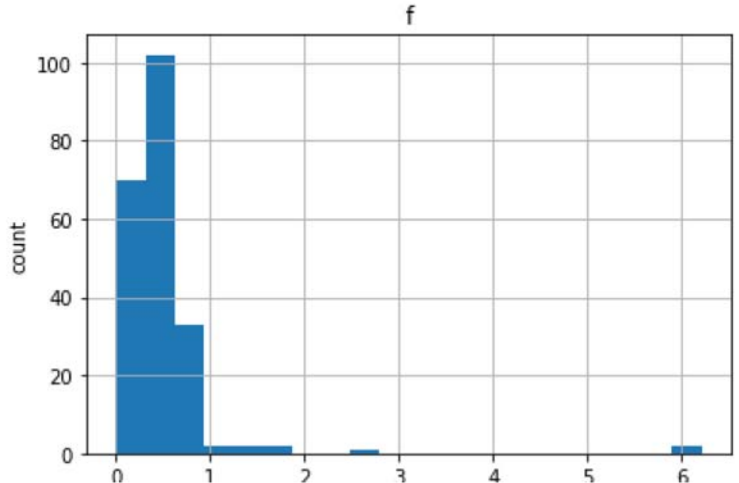

b
count
0
10
20
30
40
50
11
12
13
14
15
16
17
b

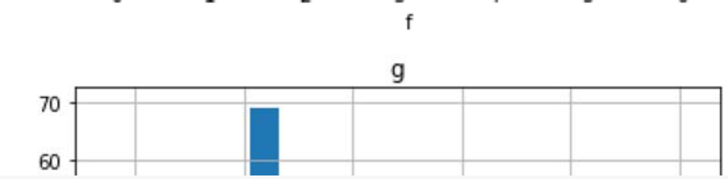

c
count
0
10
20
30
40
50
60
70
0
1
2
3
4

c

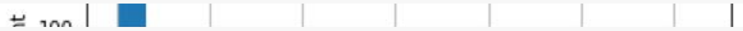

d
count
0
10
20
30
40
0.5
1.0
1.5
2.0
2.5
3.0
3.5
d


e
count
0
10
20
30
40
50
70
71
72
73
74
75
e


f
count
0
20
40
60
80
100
0
1
2
3
4
5
6



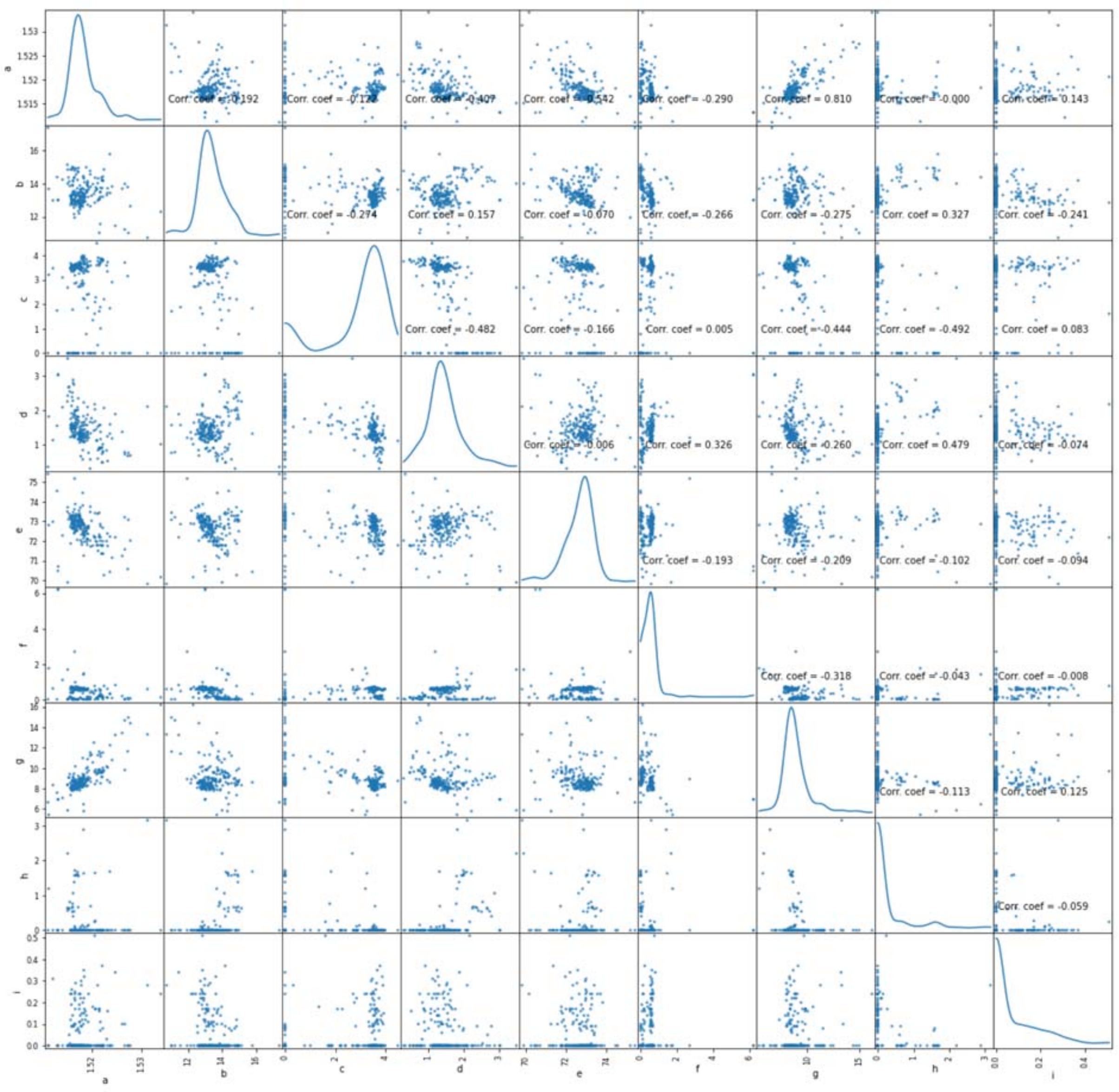
```
# Scatter and density plots
def plotScatterMatrix(df, plotSize, textSize):
    df = df.select_dtypes(include =[np.number]) # keep only numerical columns
    # Remove rows and columns that would lead to df being singular
    df = df.dropna('columns')
    df = df[[col for col in df if df[col].nunique() > 1]] # keep columns where there are more than 1 unique values
    columnNames = list(df)
    if len(columnNames) > 10: # reduce the number of columns for matrix inversion of kernel density plots
        columnNames = columnNames[:10]
    df = df[columnNames]
    ax = pd.plotting.scatter_matrix(df, alpha=0.75, figsize=[plotSize, plotSize], diagonal='kde')
    corrs = df.corr().values
    for i, j in zip(*plt.np.triu_indices_from(ax, k = 1)):
        ax[i, j].annotate('Corr. coef = %.3f' % corrs[i, j], (0.8, 0.2), xycoords='axes fraction', ha='right', va='baseline', size=textSize)
    plt.suptitle('Scatter and Density Plot')
    plt.show()
```



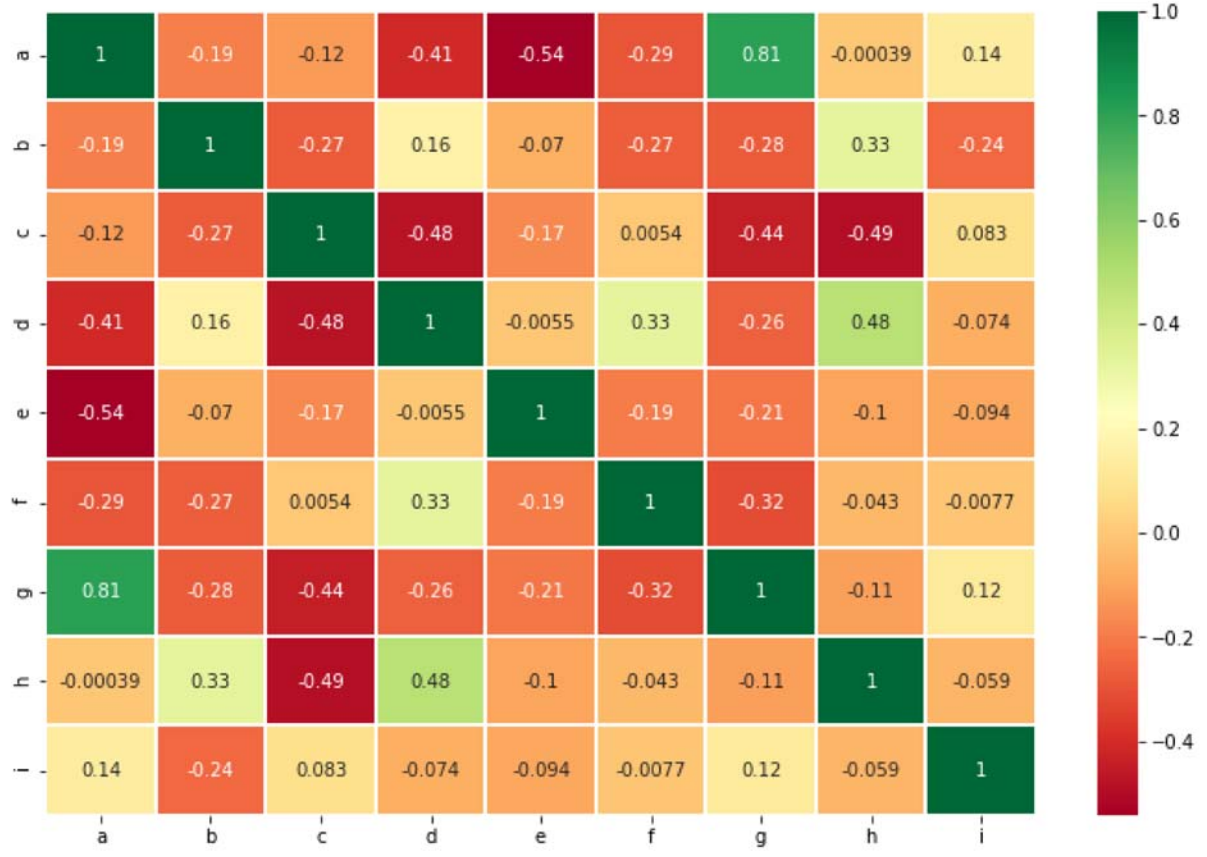
```
# sns.set()
# cols = data.columns
# sns.pairplot(data[cols], size = 8.5)
# plt.show()
```

```
plotScatterMatrix(data, 20, 10)
```

Scatter and Density Plot



```
sns.heatmap(data.corr(),annot=True,cmap='RdYlGn',linewidths=1) #data.corr()-->correlation matrix
fig=plt.gcf()
fig.set_size_inches(12,8)
plt.show()
```



Interpreting The Heatmap The first thing to note is that only the numeric features are compared as it is obvious that we cannot correlate between alphabets or strings. Before understanding the plot, let us see what exactly correlation is.

POSITIVE CORRELATION: If an increase in feature A leads to increase in feature B, then they are positively correlated. A value 1 means perfect positive correlation.

NEGATIVE CORRELATION: If an increase in feature A leads to decrease in feature B, then they are negatively correlated. A value -1 means perfect negative correlation.

Now lets say that two features are highly or perfectly correlated, so the increase in one leads to increase in the other. This means that both the features are containing highly similar information and there is very little or no variance in information. This is known as MultiColinearity as both of them contains almost the same information.

So do you think we should use both of them as one of them is redundant. While making or training models, we should try to eliminate redundant features as it reduces training time and many such advantages.

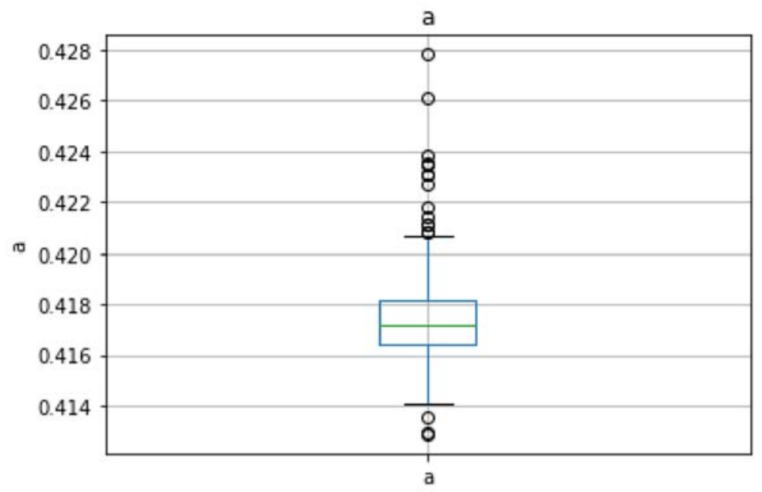
Now from the above heatmap,we can see that the features a & g are highly correlated. So we may delete one of them if we were to perfrom any machine learning.

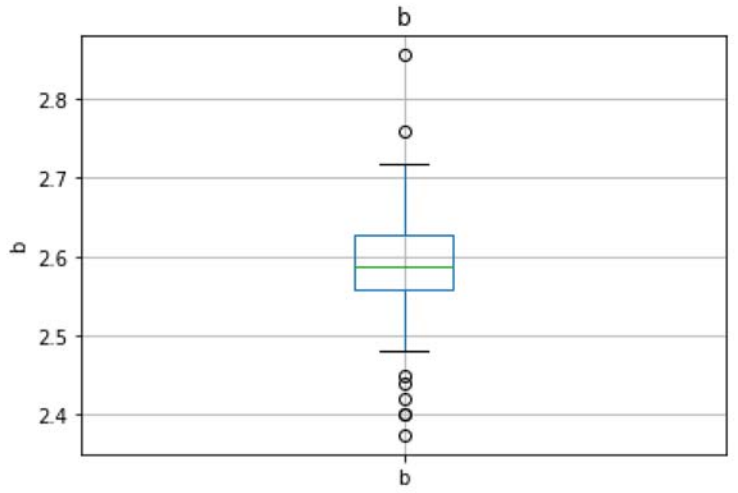
Summary:

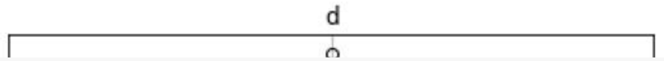
- All the features are normally distributed except for f, h, i.
- a & g are highly positively corelated and e & a are highly negatively corelated.

```
# let's make boxplots to visualise outliers in the continuous variables

def find_outliers(df, var):
    df = df.copy()

    # log does not take negative values, so let's be careful and skip those variables
    if 0 in data[var].unique():
        pass
    else:
        df[var] = np.log(df[var])
        df.boxplot(column=var)
        plt.title(var)
        plt.ylabel(var)
        plt.show()
```

```
for var in num_vars:
    find_outliers(data, var)
```







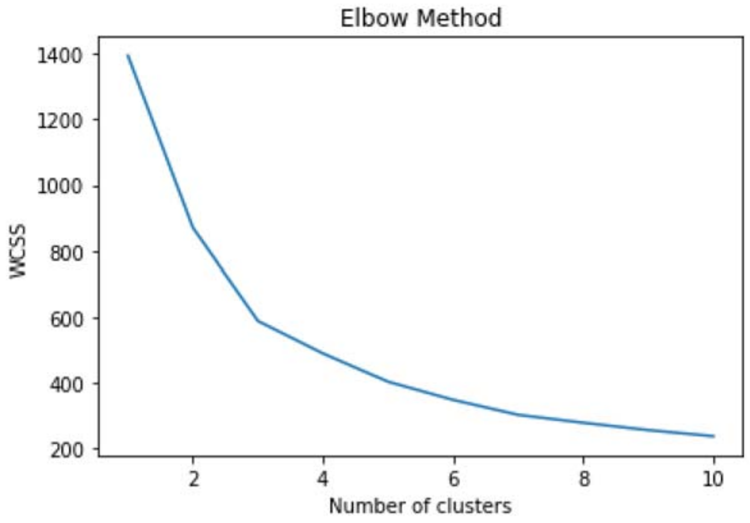
Lets perform some clustering with Kmeans clustering and hierarchical (dendogram) clustering

```
from sklearn.cluster import KMeans
from sklearn.preprocessing import MinMaxScaler
```

```
X = data.copy()
```

e

```
wcss = []
for i in range(1, 11):
    kmeans = KMeans(n_clusters=i, init='k-means++', max_iter=300, n_init=10, random_state=0)
    kmeans.fit(X)
    wcss.append(kmeans.inertia_)
plt.plot(range(1, 11), wcss)
plt.title('Elbow Method')
plt.xlabel('Number of clusters')
plt.ylabel('WCSS')
plt.show()
```



Summary:

- Elbow method suggests we should have 3 clusters

```
kmeans = KMeans(n_clusters=3, init='k-means++', max_iter=300, n_init=10, random_state=0)
pred_y = kmeans.fit_predict(X)
```

```
pred_y
```

```
array([1, 0, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       2, 1, 1, 1, 1, 1, 0, 1, 0, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1,
       0, 1, 1, 1, 2, 2, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1,
       2, 1, 1, 2, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 2,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 0, 1, 2, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 2, 2, 1, 1, 1, 0, 1, 0, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1,
       1, 2, 1, 2, 1, 1, 1, 1, 1, 2, 1, 1, 0, 1, 0, 2, 1, 1, 0, 1, 1, 1,
       1, 1, 0, 1, 1, 2, 1, 1, 1, 1, 2, 2, 1, 1, 1, 0, 1, 2, 1, 1, 1, 1,
       2, 1, 0, 0, 1, 2, 0, 1, 1, 2, 0, 1, 1, 1, 1, 1, 2, 1, 2, 1, 0, 1,
       1, 1, 2, 0, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 2], dtype=int32)
```

```
len(pred_y)
```

```
214
```

```
data['predictions1'] = pd.DataFrame(pred_y)
```

```
data.head()
```

	a	b	c	d	e	f	g	h	i	predictions1
0	1.51735	13.02	3.54	1.69	72.73	0.54	8.44	0.00	0.07	1
1	1.53125	10.73	0.00	2.10	69.81	0.58	13.30	3.15	0.28	0
2	1.52300	13.31	3.58	0.82	71.99	0.12	10.17	0.00	0.03	1
3	1.51768	12.56	3.52	1.43	73.15	0.57	8.54	0.00	0.00	1
4	1.51813	13.43	3.98	1.18	72.49	0.58	8.15	0.00	0.00	1

```
data.predictions1.value_counts()
```

```
1    162
2     31
0     21
Name: predictions1, dtype: int64
```

```
# data.drop(['predictions2'],axis=1, inplace=True)
X.head()
```

	a	b	c	d	e	f	g	h	i	predictions1
0	1.51735	13.02	3.54	1.69	72.73	0.54	8.44	0.00	0.07	1

Lets scale the features using minmaxscaler and see if we can slighlty better results

```
scaler = MinMaxScaler()
X_scaled = scaler.fit_transform(X)
```

```
X_scaled[:5]
```

```
array([[0.27216857, 0.3443609 , 0.78841871, 0.43613707, 0.52142857,
        0.08695652, 0.27973978, 0.        , 0.1372549 ],
       [0.88235294, 0.        , 0.        , 0.56386293, 0.        ,
        0.09339775, 0.73141264, 1.        , 0.54901961],
       [0.52019315, 0.38796992, 0.79732739, 0.16510903, 0.38928571,
        0.01932367, 0.44052045, 0.        , 0.05882353],
       [0.28665496, 0.27518797, 0.78396437, 0.35514019, 0.59642857,
        0.09178744, 0.28903346, 0.        , 0.        ],
       [0.30640913, 0.40601504, 0.88641425, 0.27725857, 0.47857143,
        0.09339775, 0.2527881 , 0.        , 0.        ]])
```

```
pred_y = kmeans.fit_predict(X_scaled)
```

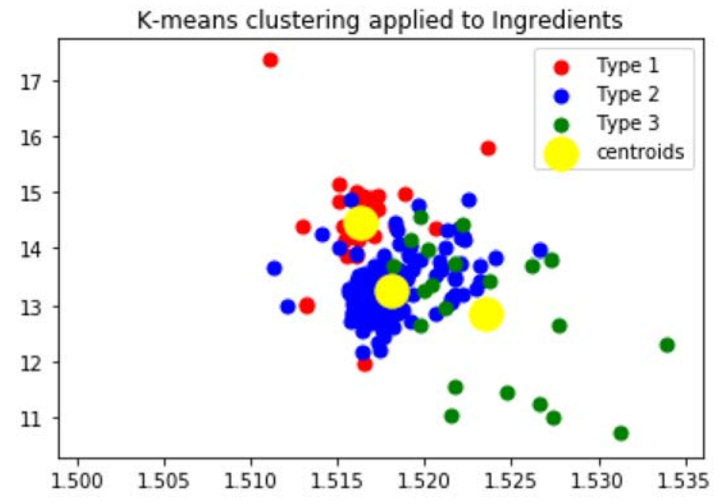
```
pred_y
```

```
array([0, 2, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 2, 0, 0, 0, 0, 0, 0,
       1, 0, 1, 0, 0, 0, 2, 0, 2, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 2, 0,
       2, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0,
       1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 2, 0, 1, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 1, 1, 0, 0, 0, 2, 0, 2, 0, 0, 0, 0, 2, 0, 0, 0, 0, 0,
       0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 2, 0, 2, 1, 0, 0, 0, 0, 0, 0,
       0, 0, 2, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 2, 0, 1, 0, 0, 0, 0,
       1, 0, 2, 2, 0, 1, 2, 0, 0, 1, 2, 0, 0, 0, 0, 0, 1, 0, 1, 0, 2, 0,
       0, 0, 1, 2, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1], dtype=int32)
```

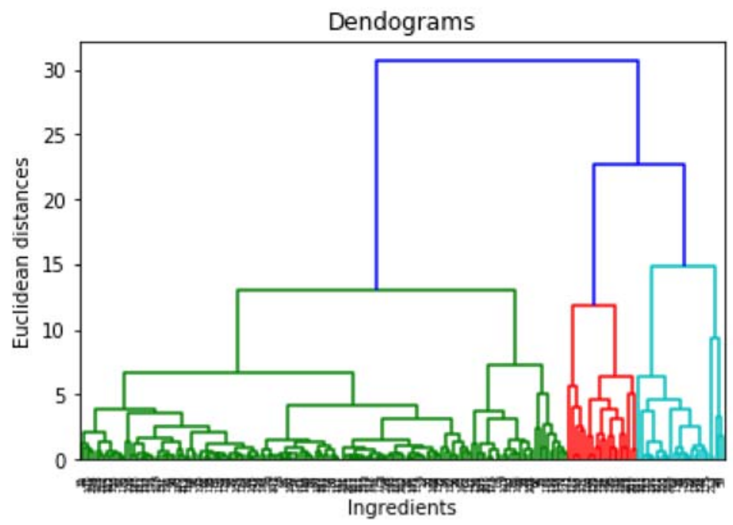
```
data['predictions2'] = pd.DataFrame(pred_y)
```

```
data.predictions3 = data.predictions3.astype(int)
```

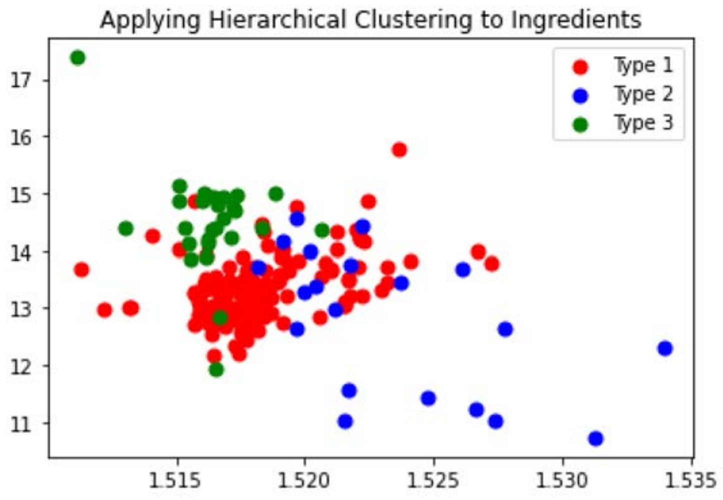
```
#Lets visualize the clusters and their centroids together

plt.figure(2)
plt.scatter(X.iloc[pred_y == 0, 0], X.iloc[pred_y == 0, 1], s = 50, c = 'red', label = 'Type 1')
plt.scatter(X.iloc[pred_y == 1, 0], X.iloc[pred_y == 1, 1], s = 50, c = 'blue', label = 'Type 2')
plt.scatter(X.iloc[pred_y == 2, 0], X.iloc[pred_y == 2, 1], s = 50, c = 'green', label = 'Type 3')

plt.scatter(kmeans.cluster_centers_[:, 0], kmeans.cluster_centers_[:, 1], s = 300, c = 'yellow', label = 'centroids' )
# _centers_ --> also an attribute that can be accessed.
# s --> size of each point
plt.title("K-means clustering applied to Ingredients")

plt.legend()
plt.show()
```



```
#Use dendrogram to find the optimal number of clusters



import scipy.cluster.hierarchy as sch
dendrogram_1 = sch.dendrogram(sch.linkage(X, method = 'ward'))
fig.set_size_inches(12,8)
plt.title('Dendograms')
plt.xlabel('Ingredients')
plt.ylabel('Euclidean distances')
plt.show()
```



```
from sklearn.cluster import AgglomerativeClustering

hc = AgglomerativeClustering(n_clusters = 3, affinity = 'euclidean', linkage = 'ward')
y_hc = hc.fit_predict(X)
plt.scatter(X.iloc[y_hc == 0, 0], X.iloc[y_hc == 0, 1], s = 50, c = 'red', label = 'Type 1')
plt.scatter(X.iloc[y_hc == 1, 0], X.iloc[y_hc == 1, 1], s = 50, c = 'blue', label = 'Type 2')
plt.scatter(X.iloc[y_hc == 2, 0], X.iloc[y_hc == 2, 1], s = 50, c = 'green', label = 'Type 3')
plt.title('Applying Hierarchical Clustering to Ingredients')

plt.legend()
plt.show()
```



```
data['predictions4'] = pd.DataFrame(y_hc)
```

```
data.drop(['predictions2','predictions1'], axis=1, inplace=True)
```

```
data.head()
```

	a	b	c	d	e	f	g	h	i	predictions3	predictic
0	1.51735	13.02	3.54	1.69	72.73	0.54	8.44	0.00	0.07	1	
1	1.53125	10.73	0.00	2.10	69.81	0.58	13.30	3.15	0.28	2	
2	1.52300	13.31	3.58	0.82	71.99	0.12	10.17	0.00	0.03	1	
3	1.51768	12.56	3.52	1.43	73.15	0.57	8.54	0.00	0.00	1	
4	1.51813	13.43	3.98	1.18	72.49	0.58	8.15	0.00	0.00	1	

Summary:

- Lets look at the summary of each clustering techniques and measure the class counts against each other using cross tab
- The predictions from both algorithms looks quite similiar with a few exceptions.

```
pd.crosstab(data.predictions3, data.predictions4,margins=True, margins_name="Total")
```

predictions4	0	1	2	Total
predictions3				
0	27	2	4	33
1	2	159	0	161
2	0	1	19	20
Total	29	162	23	214

✓ 0s completed at 22:27