In [281…
```
%time
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from scipy.stats import zscore
```

```
CPU times: user 4 µs, sys: 0 ns, total: 4 µs
Wall time: 8.11 µs
```

Data Cleaning

In [282…
```
df = pd.read_csv("../data/merged_data_cleaned.csv")
df.head()
```

Out[282…

	Unnamed: 0	Species	Owner	Country.of.Origin	Farm.Name	Lot.Number	Mi
0	0	Arabica	metad plc	Ethiopia	metad plc	NaN	meta p
1	1	Arabica	metad plc	Ethiopia	metad plc	NaN	meta p
2	2	Arabica	grounds for health admin	Guatemala	san marcos barrancas "san cristobal cuch	NaN	Na
3	3	Arabica	yidnekachew dabessa	Ethiopia	yidnekachew dabessa coffee plantation	NaN	wolens
4	4	Arabica	metad plc	Ethiopia	metad plc	NaN	meta p

5 rows × 44 columns

We have a lot of columns with data that are irrelevant for our analysis. We'll drop them to reduce dimensionality of the dataset

In [283…
```
df = df.drop(["Unnamed: 0", "Farm.Name", "Lot.Number", "Mill", "ICO.Numbe
```

In [284…
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1339 entries, 0 to 1338
Data columns (total 21 columns):
 #   Column                Non-Null Count  Dtype
---  ------                --------------  -----
 0   Species               1339 non-null   object
 1   Country.of.Origin     1338 non-null   object
 2   Variety               1113 non-null   object
 3   Processing.Method     1169 non-null   object
 4   Aroma                 1339 non-null   float64
 5   Flavor                1339 non-null   float64
 6   Aftertaste            1339 non-null   float64
 7   Acidity               1339 non-null   float64
 8   Body                  1339 non-null   float64
 9   Balance               1339 non-null   float64
 10  Uniformity            1339 non-null   float64
 11  Clean.Cup             1339 non-null   float64
 12  Sweetness             1339 non-null   float64
 13  Cupper.Points         1339 non-null   float64
 14  Total.Cup.Points      1339 non-null   float64
 15  Moisture              1339 non-null   float64
 16  Category.One.Defects  1339 non-null   int64
 17  Quakers               1338 non-null   float64
 18  Color                 1069 non-null   object
 19  Category.Two.Defects  1339 non-null   int64
 20  altitude_mean_meters  1109 non-null   float64
dtypes: float64(14), int64(2), object(5)
memory usage: 219.8+ KB
```

In [285…
```
df.isna().sum()
```

Out[285…
```
Species                   0
Country.of.Origin         1
Variety                 226
Processing.Method       170
Aroma                     0
Flavor                    0
Aftertaste                0
Acidity                   0
Body                      0
Balance                   0
Uniformity                0
Clean.Cup                 0
Sweetness                 0
Cupper.Points             0
Total.Cup.Points          0
Moisture                  0
Category.One.Defects      0
Quakers                   1
Color                   270
Category.Two.Defects      0
altitude_mean_meters    230
dtype: int64
```

We replace rows with a lot of missing nominal data with the mode of the column, to retain the variance of the rest of the row data

In [286…
```
df = df.fillna({'Variety': df['Variety'].mode()[0]})
df = df.fillna({'Processing.Method': df['Processing.Method'].mode()[0]})
```

```
df = df.fillna({'Color': df['Color'].mode()[0]})
```

We drop the rows with a single row missing nominal data. Especially "Country of Origin", since we can not just put in a mode value, since it might create significant wrong data

In [287…
```
df = df.dropna(how='any')
```

In [288…
```
df.isna().sum()
```

Out[288…
```
Species                 0
Country.of.Origin       0
Variety                 0
Processing.Method       0
Aroma                   0
Flavor                  0
Aftertaste              0
Acidity                 0
Body                    0
Balance                 0
Uniformity              0
Clean.Cup               0
Sweetness               0
Cupper.Points           0
Total.Cup.Points        0
Moisture                0
Category.One.Defects    0
Quakers                 0
Color                   0
Category.Two.Defects    0
altitude_mean_meters    0
dtype: int64
```

No more missing values!

Outliers

In [289…
```
df.describe()
```

Out[289…

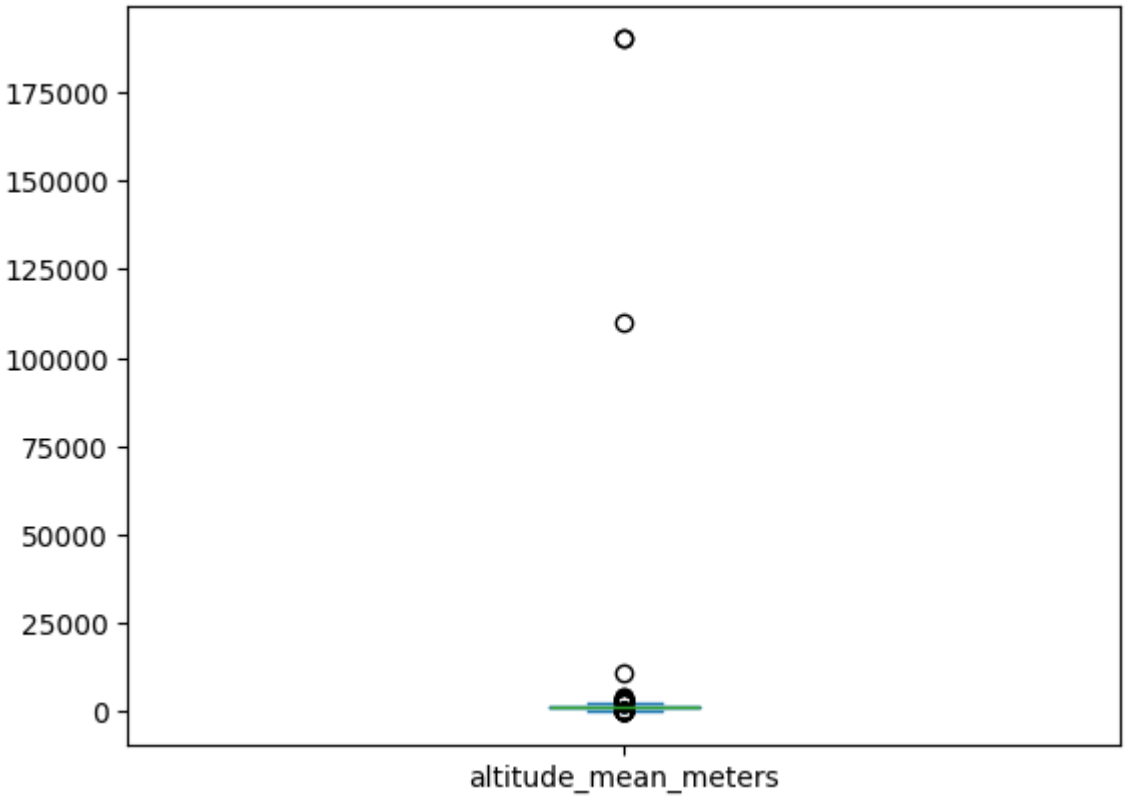
	Aroma	Flavor	Aftertaste	Acidity	Body	Balance
count	1108.000000	1108.00000	1108.000000	1108.000000	1108.000000	1108.000000
mean	7.570569	7.52056	7.394269	7.528953	7.506670	7.505542
std	0.383837	0.40059	0.405867	0.386075	0.366717	0.419311
min	0.000000	0.00000	0.000000	0.000000	0.000000	0.000000
25%	7.420000	7.33000	7.250000	7.330000	7.330000	7.330000
50%	7.580000	7.58000	7.420000	7.500000	7.500000	7.500000
75%	7.750000	7.75000	7.580000	7.750000	7.670000	7.750000
max	8.750000	8.83000	8.670000	8.750000	8.580000	8.750000

We have some columns with very high standard deviations

In [290…
```
fig = plt.figure()
```

```
df.altitude_mean_meters.plot.box()
```

Out[290… <Axes: >



The column contains significant outliers. Since its only a couple of rows, we'll drop them

In [291…
```
# We'll remove the outlying rows based on z-score
df = df[np.abs(zscore(df['altitude_mean_meters'])) < 1]
```

In [292…
```
df
```

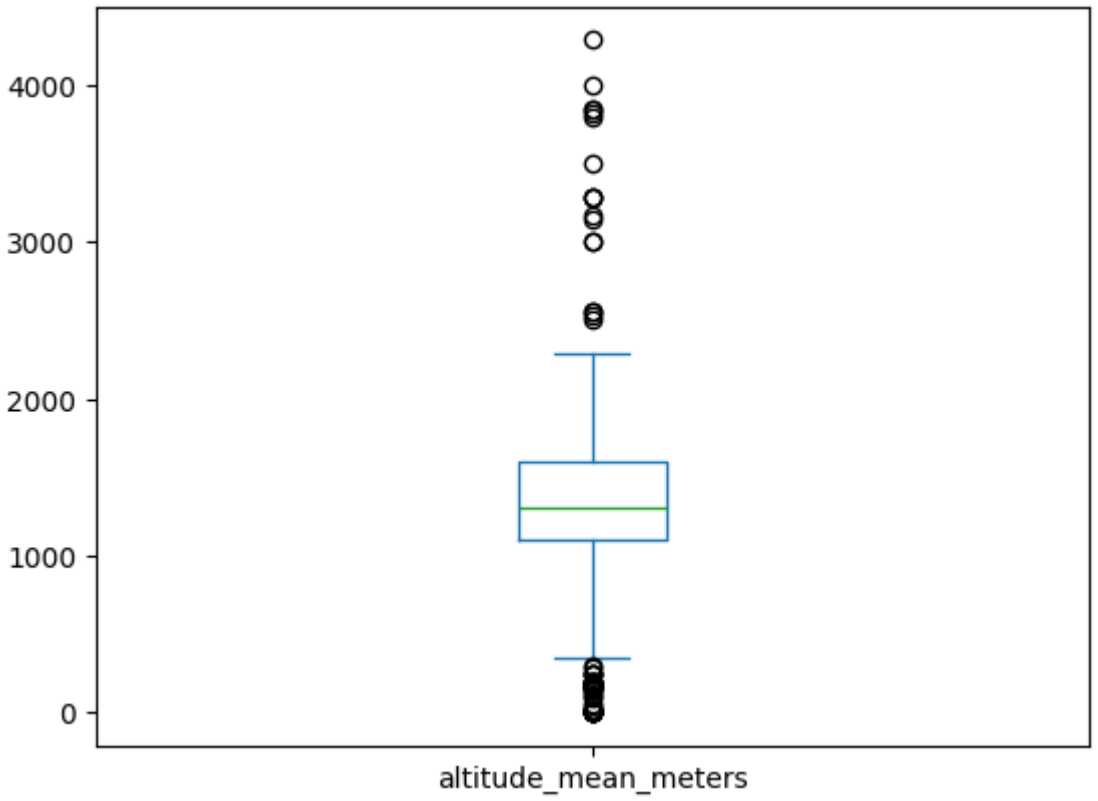
Out[292…

	Species	Country.of.Origin	Variety	Processing.Method	Aroma	Flavor	Aftertast
0	Arabica	Ethiopia	Caturra	Washed / Wet	8.67	8.83	8.6
1	Arabica	Ethiopia	Other	Washed / Wet	8.75	8.67	8.5
2	Arabica	Guatemala	Bourbon	Washed / Wet	8.42	8.50	8.4
3	Arabica	Ethiopia	Caturra	Natural / Dry	8.17	8.58	8.4
4	Arabica	Ethiopia	Other	Washed / Wet	8.25	8.50	8.2
...	...	...	...	...	...	...	...
1331	Robusta	India	Caturra	Washed / Wet	7.67	7.67	7.5
1332	Robusta	India	Caturra	Natural / Dry	7.58	7.42	7.4
1333	Robusta	United States	Arusha	Natural / Dry	7.92	7.50	7.4
1335	Robusta	Ecuador	Caturra	Washed / Wet	7.50	7.67	7.7
1336	Robusta	United States	Caturra	Natural / Dry	7.33	7.33	7.1

1104 rows × 21 columns

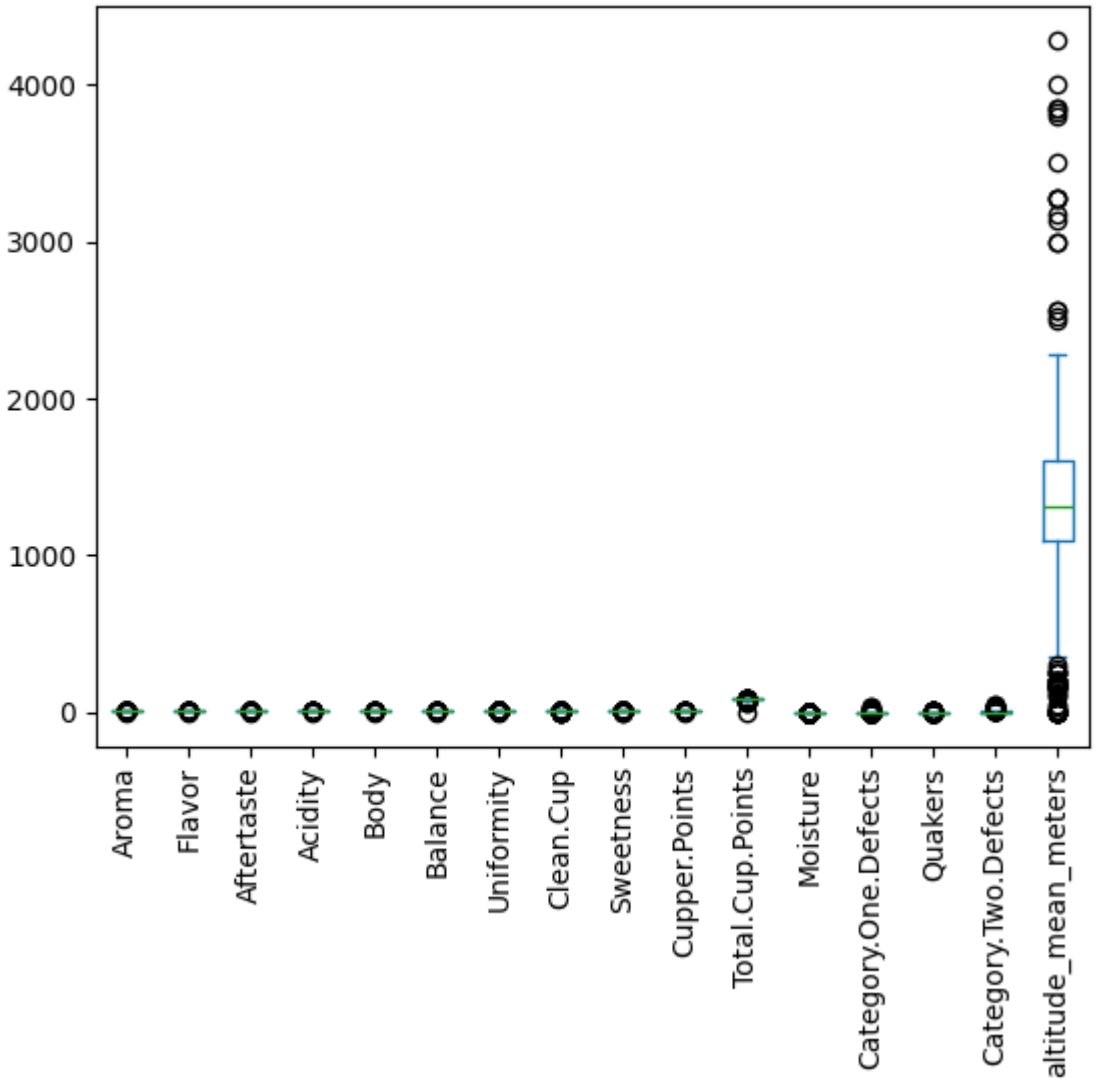
In [293…
```
df.altitude_mean_meters.plot.box()
```

Out[293… <Axes: >



In [294…
```
df.plot.box(rot=90)
```

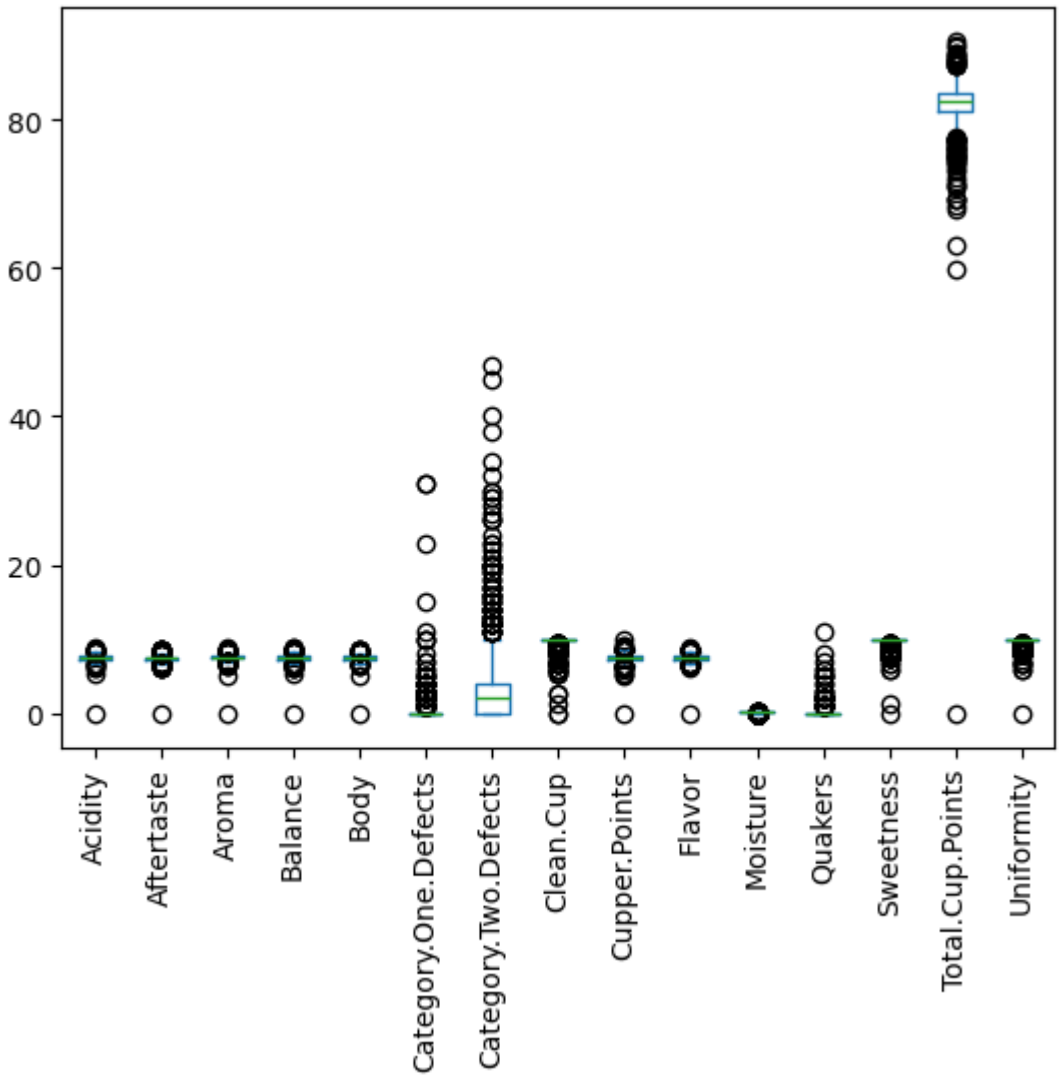
Out[294… <Axes: >



Even after removing the worst outliers, the mean altitude still distributes over large values. We'll exclude it in the plot to dentify other problematic features

In [295…
```
df[df.columns.difference(['altitude_mean_meters'])].plot.box(rot=90)
```

Out[295… <Axes: >



It seems a lot of the features contain unnatural zero-values. We'll replace the zero values, with the median of the feature

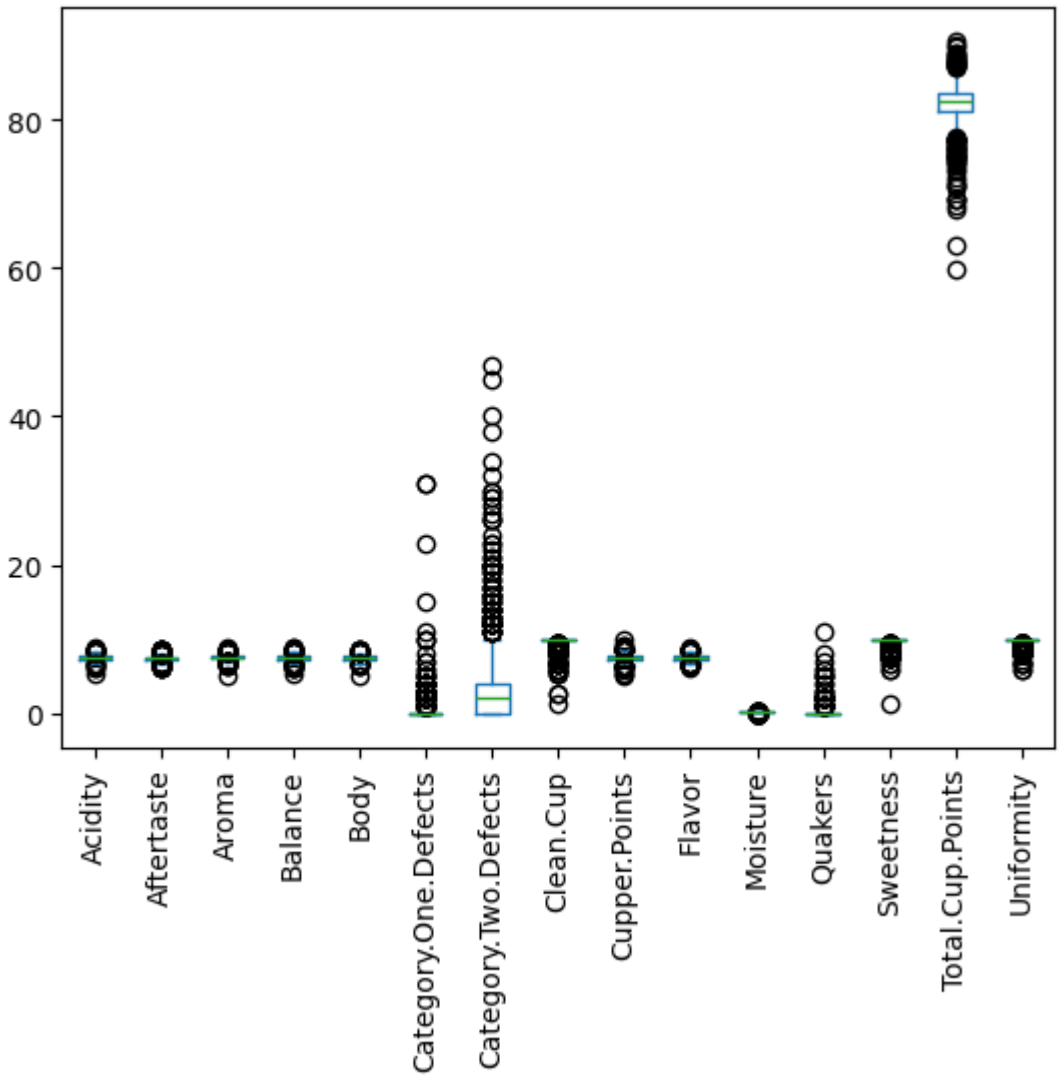
In [296…
```
df['Acidity'] = df['Acidity'].replace(0, df['Acidity'].median())
df['Aftertaste'] = df['Aftertaste'].replace(0, df['Aftertaste'].median())
df['Aroma'] = df['Aroma'].replace(0, df['Aroma'].median())
df['Balance'] = df['Balance'].replace(0, df['Balance'].median())
df['Body'] = df['Body'].replace(0, df['Body'].median())
df['Clean.Cup'] = df['Clean.Cup'].replace(0, df['Clean.Cup'].median())
df['Cupper.Points'] = df['Cupper.Points'].replace(0, df['Cupper.Points'].
df['Flavor'] = df['Flavor'].replace(0, df['Flavor'].median())
df['Moisture'] = df['Moisture'].replace(0, df['Moisture'].median())
df['Sweetness'] = df['Sweetness'].replace(0, df['Sweetness'].median())
df['Uniformity'] = df['Uniformity'].replace(0, df['Uniformity'].median())
```

Except the Total cup points. We'll drop the row since it is our target value, and an unnatural zero might mess with correlations

In [297…
```
df = df[df['Total.Cup.Points'] != 0]
```

In [298…
```
df[df.columns.difference(['altitude_mean_meters'])].plot.box(rot=90)
```

Out[298… <Axes: >



In [299…
```
df.describe()
```

Out[299…

	Aroma	Flavor	Aftertaste	Acidity	Body	Balanc
count	1103.000000	1103.000000	1103.000000	1103.000000	1103.000000	1103.00000
mean	7.578368	7.527824	7.401496	7.535739	7.513654	7.51266
std	0.309181	0.331268	0.340065	0.313192	0.289467	0.35402
min	5.080000	6.170000	6.170000	5.250000	5.170000	5.25000
25%	7.420000	7.330000	7.250000	7.330000	7.330000	7.33000
50%	7.580000	7.580000	7.420000	7.500000	7.500000	7.50000
75%	7.750000	7.750000	7.580000	7.750000	7.670000	7.75000
max	8.750000	8.830000	8.670000	8.750000	8.580000	8.75000

In [300…
```
df.to_csv('cleaned_dataset_no_zeros.csv', index=False)
```

The datset is now ready for analysis!

In [2]:
```
%time
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import sklearn as sk
from sklearn.decomposition import PCA
from sklearn.cluster import KMeans, DBSCAN
from scipy.stats import zscore
import scipy.cluster.hierarchy as ch
from sklearn.cluster import AgglomerativeClustering
from sklearn.preprocessing import LabelEncoder
pd.options.display.max_columns = None
```

```
CPU times: user 4 µs, sys: 0 ns, total: 4 µs
Wall time: 9.06 µs
```

In [3]:
```
df = pd.read_csv("../data_cleaned/cleaned_dataset_no_zeros.csv")
df.head(20)
```

Out[3]:

	Species	Country.of.Origin	Variety	Processing.Method	Aroma	Flavor	Afterta
0	Arabica	Ethiopia	Caturra	Washed / Wet	8.67	8.83	8
1	Arabica	Ethiopia	Other	Washed / Wet	8.75	8.67	8
2	Arabica	Guatemala	Bourbon	Washed / Wet	8.42	8.50	8
3	Arabica	Ethiopia	Caturra	Natural / Dry	8.17	8.58	8
4	Arabica	Ethiopia	Other	Washed / Wet	8.25	8.50	8
5	Arabica	Ethiopia	Caturra	Washed / Wet	8.25	8.33	8
6	Arabica	Ethiopia	Caturra	Washed / Wet	8.67	8.67	8
7	Arabica	Ethiopia	Other	Natural / Dry	8.08	8.58	8
8	Arabica	Ethiopia	Caturra	Natural / Dry	8.17	8.67	8
9	Arabica	United States	Other	Washed / Wet	8.25	8.42	8
10	Arabica	United States	Other	Washed / Wet	8.08	8.67	8
11	Arabica	United States (Hawaii)	Caturra	Washed / Wet	8.33	8.42	8
12	Arabica	Ethiopia	Caturra	Washed / Wet	8.25	8.33	8
13	Arabica	United States	Other	Washed / Wet	8.00	8.50	8
14	Arabica	Indonesia	Caturra	Washed / Wet	8.33	8.25	7
15	Arabica	China	Catimor	Washed / Wet	8.42	8.25	8
16	Arabica	Ethiopia	Ethiopian Yirgacheffe	Natural / Dry	8.17	8.17	8
17	Arabica	United States	Other	Washed / Wet	8.00	8.25	8
18	Arabica	Costa Rica	Caturra	Washed / Wet	8.08	8.25	8
19	Arabica	Mexico	Other	Washed / Wet	8.17	8.25	8

In [4]:
```
df.columns
```

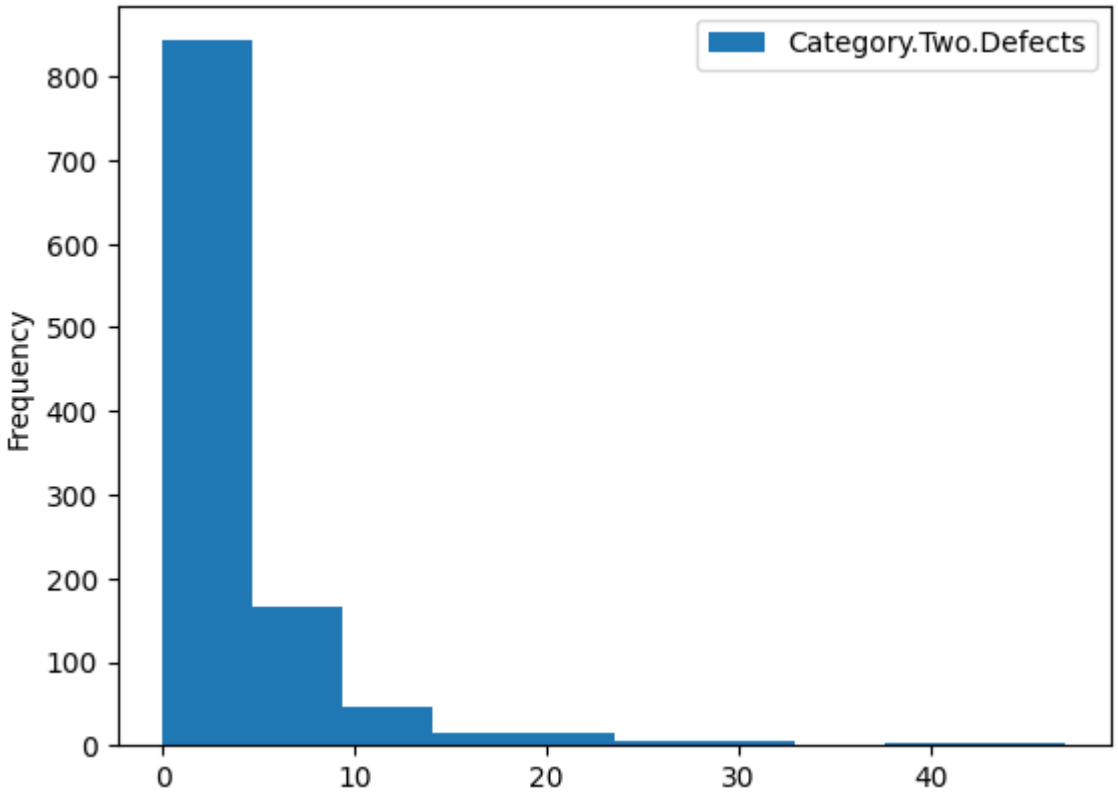
Out[4]:
```
Index(['Species', 'Country.of.Origin', 'Variety', 'Processing.Method', 'Aroma',
       'Flavor', 'Aftertaste', 'Acidity', 'Body', 'Balance', 'Uniformity',
       'Clean.Cup', 'Sweetness', 'Cupper.Points', 'Total.Cup.Points',
       'Moisture', 'Category.One.Defects', 'Quakers', 'Color',
       'Category.Two.Defects', 'altitude_mean_meters'],
      dtype='object')
```

In [5]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1103 entries, 0 to 1102
Data columns (total 21 columns):
 #   Column                Non-Null Count  Dtype  
---  ------                --------------  -----  
 0   Species               1103 non-null   object 
 1   Country.of.Origin     1103 non-null   object 
 2   Variety               1103 non-null   object 
 3   Processing.Method     1103 non-null   object 
 4   Aroma                 1103 non-null   float64
 5   Flavor                1103 non-null   float64
 6   Aftertaste            1103 non-null   float64
 7   Acidity               1103 non-null   float64
 8   Body                  1103 non-null   float64
 9   Balance               1103 non-null   float64
 10  Uniformity            1103 non-null   float64
 11  Clean.Cup             1103 non-null   float64
 12  Sweetness             1103 non-null   float64
 13  Cupper.Points         1103 non-null   float64
 14  Total.Cup.Points      1103 non-null   float64
 15  Moisture              1103 non-null   float64
 16  Category.One.Defects  1103 non-null   int64  
 17  Quakers               1103 non-null   float64
 18  Color                 1103 non-null   object 
 19  Category.Two.Defects  1103 non-null   int64  
 20  altitude_mean_meters  1103 non-null   float64
dtypes: float64(14), int64(2), object(5)
memory usage: 181.1+ KB
```

In [6]:
```
df[['Category.Two.Defects']].plot.hist()
```

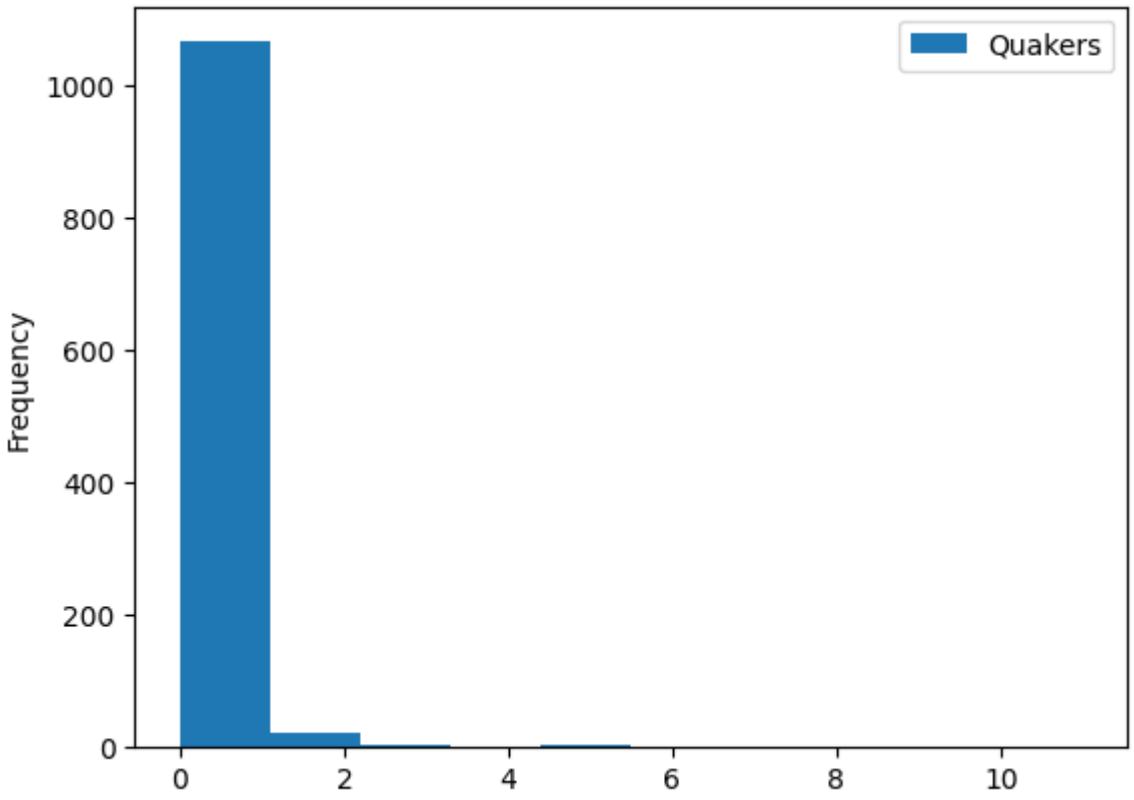
Out[6]:
```
<Axes: ylabel='Frequency'>
```



We're gonna keep these outlying values, as they might have a high impact on the quality score

In [7]:
```
df[['Quakers']].plot.hist()
```

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



Data Exploration

Lets see which countries can boast the highest cup grades

In [8]:
```
df.groupby('Country.of.Origin')['Total.Cup.Points'].mean().reset_index().s
```

Out[8]:

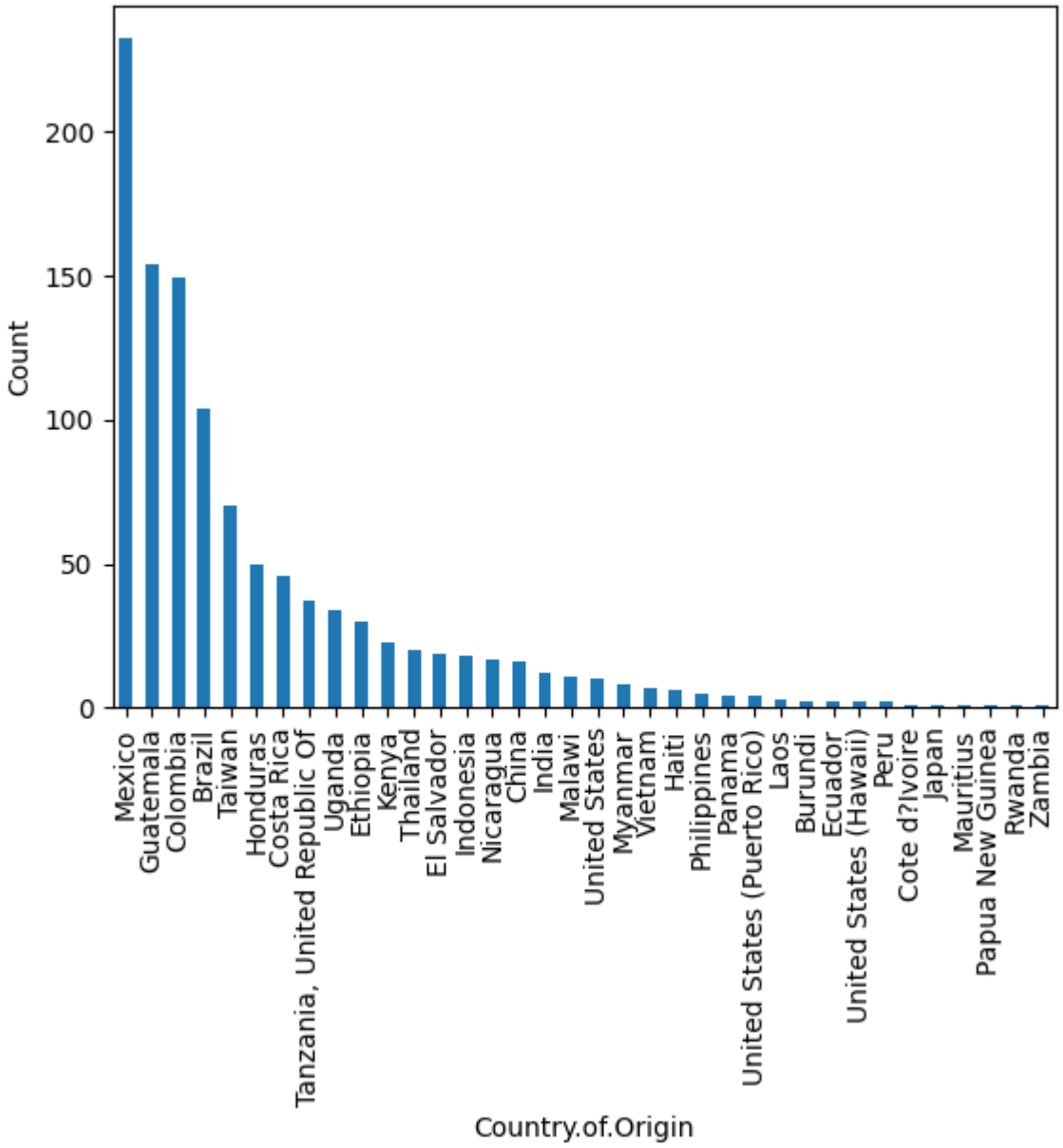
	Country.of.Origin	Total.Cup.Points
32	United States (Hawaii)	86.960000
8	Ethiopia	85.916333
23	Papua New Guinea	85.750000
14	Japan	84.670000
31	United States	84.433000
15	Kenya	84.271304
22	Panama	83.707500
30	Uganda	83.382941
3	Colombia	83.224832
7	El Salvador	83.115263
2	China	82.927500
26	Rwanda	82.830000
4	Costa Rica	82.800435
0	Brazil	82.711442
13	Indonesia	82.528333
29	Thailand	82.430000
28	Tanzania, United Republic Of	82.309459
34	Vietnam	82.274286
9	Guatemala	82.024221
27	Taiwan	81.947714
12	India	81.937500
35	Zambia	81.920000
16	Laos	81.833333
1	Burundi	81.830000
33	United States (Puerto Rico)	81.727500
17	Malawi	81.711818
6	Ecuador	80.955000
19	Mexico	80.863060
25	Philippines	80.834000
11	Honduras	80.832200
20	Myanmar	80.750000
18	Mauritius	80.500000
21	Nicaragua	80.010000
5	Cote d?Ivoire	79.330000
24	Peru	78.000000

	Country.of.Origin	Total.Cup.Points
10	Haiti	77.180000

Seems like a mixed bag from around the world. Quality doens't seem to be linked rigonally, but there is a small majority of african countries in the top half, and Hawaiian coffee seems to be a specialty!

In [9]:
```
df.groupby('Country.of.Origin').size().sort_values(ascending=False).plot.
```

Out[9]:
```
<Axes: xlabel='Country.of.Origin', ylabel='Count'>
```



Though we see that there is a very skewed representation of countries in the dataset. About 1/4 of the coffee in the dataset is from Mexico!

In [10]:
```
df.groupby('Country.of.Origin')['Total.Cup.Points'].median().reset_index()
```

Out[10]:

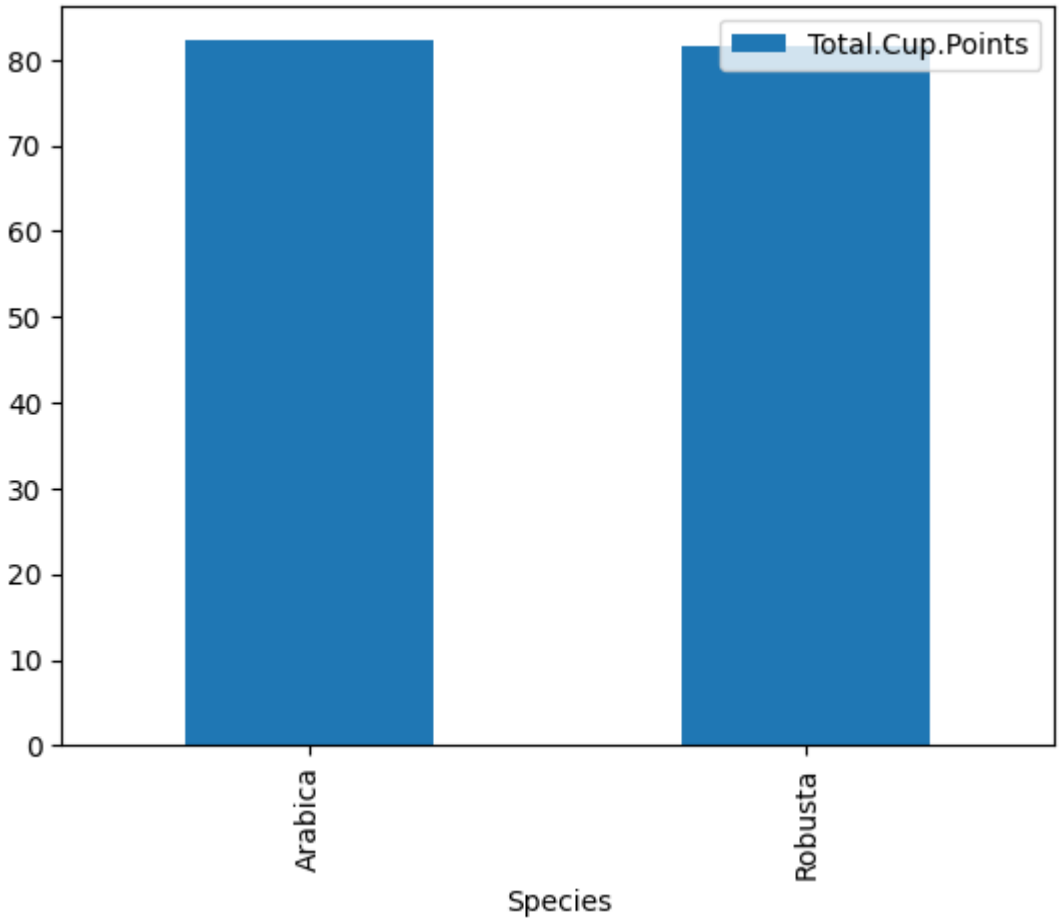
	Country.of.Origin	Total.Cup.Points
32	United States (Hawaii)	86.960
31	United States	86.625
23	Papua New Guinea	85.750
8	Ethiopia	85.250
14	Japan	84.670
15	Kenya	84.580
22	Panama	84.125
3	Colombia	83.250
2	China	83.170
4	Costa Rica	83.165
30	Uganda	83.085
7	El Salvador	82.920
34	Vietnam	82.830
26	Rwanda	82.830
13	Indonesia	82.665
29	Thailand	82.540
9	Guatemala	82.540
0	Brazil	82.500
28	Tanzania, United Republic Of	82.170
12	India	82.040
33	United States (Puerto Rico)	82.040
16	Laos	82.000
35	Zambia	81.920
27	Taiwan	81.875
1	Burundi	81.830
11	Honduras	81.625
17	Malawi	81.580
19	Mexico	81.580
25	Philippines	81.330
6	Ecuador	80.955
21	Nicaragua	80.920
20	Myanmar	80.625
18	Mauritius	80.500
5	Cote d?Ivoire	79.330
10	Haiti	79.000

	Country.of.Origin	Total.Cup.Points
24	Peru	78.000

Taking the median values, it seems about the same

In [11]:
```
df.groupby('Species')['Total.Cup.Points'].mean().reset_index().sort_values
```

Out[11]: <Axes: xlabel='Species'>



Surprinsingly, The Robusta species does not seem to have a much lower average score than Arabica, which we thought were far superior in taste

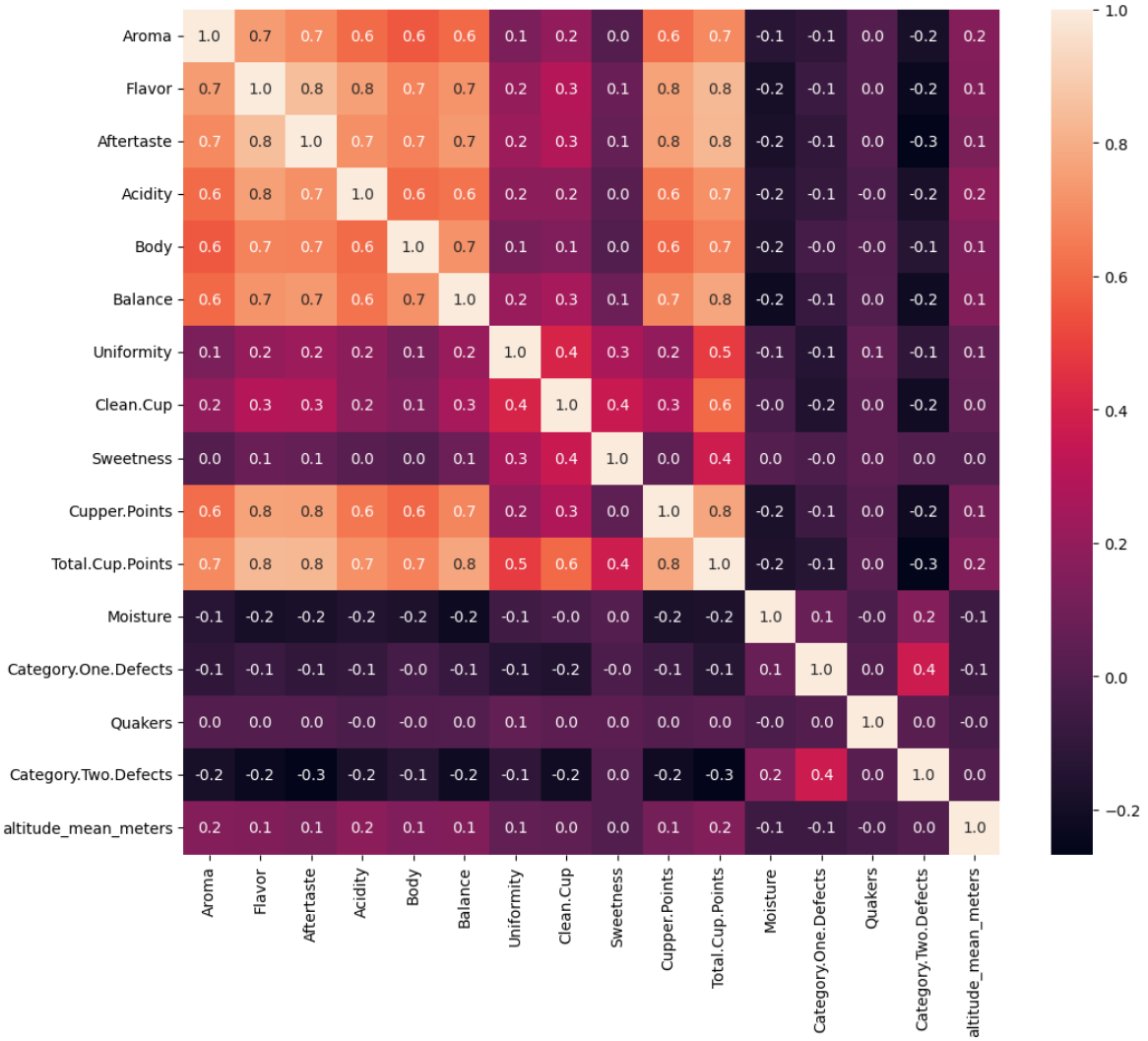
In [12]:
```
corr_mat = df.corr(numeric_only=True)
corr_mat
```

Out[12]:

	Aroma	Flavor	Aftertaste	Acidity	Body	Balance
Aroma	1.000000	0.743109	0.688130	0.606707	0.558217	0.602133
Flavor	0.743109	1.000000	0.849983	0.757027	0.668397	0.722149
Aftertaste	0.688130	0.849983	1.000000	0.705410	0.666111	0.737439
Acidity	0.606707	0.757027	0.705410	1.000000	0.604118	0.624788
Body	0.558217	0.668397	0.666111	0.604118	1.000000	0.715045
Balance	0.602133	0.722149	0.737439	0.624788	0.715045	1.000000
Uniformity	0.126962	0.207079	0.226183	0.178229	0.116480	0.215432
Clean.Cup	0.196811	0.297936	0.288698	0.176823	0.140021	0.254276
Sweetness	0.008310	0.077417	0.063372	0.022285	0.002498	0.083593
Cupper.Points	0.611088	0.764423	0.761057	0.642121	0.590999	0.679213
Total.Cup.Points	0.688725	0.836167	0.827814	0.708001	0.665436	0.775314
Moisture	-0.131316	-0.189600	-0.178685	-0.151101	-0.171327	-0.227089
Category.One.Defects	-0.104645	-0.069596	-0.103180	-0.090468	-0.035044	-0.079425
Quakers	0.007763	0.009010	0.007843	-0.017353	-0.002792	0.001002
Category.Two.Defects	-0.184304	-0.233813	-0.263210	-0.181162	-0.138092	-0.218804
altitude_mean_meters	0.155328	0.148021	0.133273	0.181499	0.142243	0.144477

In [13]:
```
plt.figure(figsize=(12, 10))
sns.heatmap(corr_mat, annot = True, fmt = ".1f")
```

Out[13]: <Axes: >



Unsurprisingly the different flavor parameters seems to correlate a lot with the Total Cup Points, and with each other. It seems that the main parameters that drags down the score is the amount of Category One and Two Defects, which we also suspected. Quakers doesn't seem to have a big impact on the overall Cup Point score. This might, of course, be biased by the low amount of values above zero

In [14]:
```
df.dtypes
```

Out[14]:
```
Species                  object
Country.of.Origin        object
Variety                  object
Processing.Method        object
Aroma                   float64
Flavor                  float64
Aftertaste              float64
Acidity                 float64
Body                    float64
Balance                 float64
Uniformity              float64
Clean.Cup               float64
Sweetness               float64
Cupper.Points           float64
Total.Cup.Points        float64
Moisture                float64
Category.One.Defects      int64
Quakers                 float64
Color                    object
Category.Two.Defects      int64
altitude_mean_meters    float64
dtype: object
```

Lets label encode the categorical data into discrete values, so we can see how the nominal data affects the correlation score as well.

In [15]:
```
le = LabelEncoder()
cols_to_enc = df.select_dtypes(include='object').columns
enc_df = df.copy()

for col in cols_to_enc:
    enc_df[col] = le.fit_transform(df[col]).astype(int)

enc_df
```

Out[15]:

	Species	Country.of.Origin	Variety	Processing.Method	Aroma	Flavor	Aftertast
0	0	8	5	4	8.67	8.83	8.6
1	0	8	13	4	8.75	8.67	8.5
2	0	9	2	4	8.42	8.50	8.4
3	0	8	5	0	8.17	8.58	8.4
4	0	8	13	4	8.25	8.50	8.2
...	...	...	...	...	...	...	.
1098	1	12	5	4	7.67	7.67	7.5
1099	1	12	5	0	7.58	7.42	7.4
1100	1	31	0	0	7.92	7.50	7.4
1101	1	6	5	4	7.50	7.67	7.7
1102	1	31	5	0	7.33	7.33	7.1

1103 rows × 21 columns

In [16]:
```
enc_df.to_csv("../data_cleaned/encoded_df.csv", index=False)
```

Lets see how much variance it give us

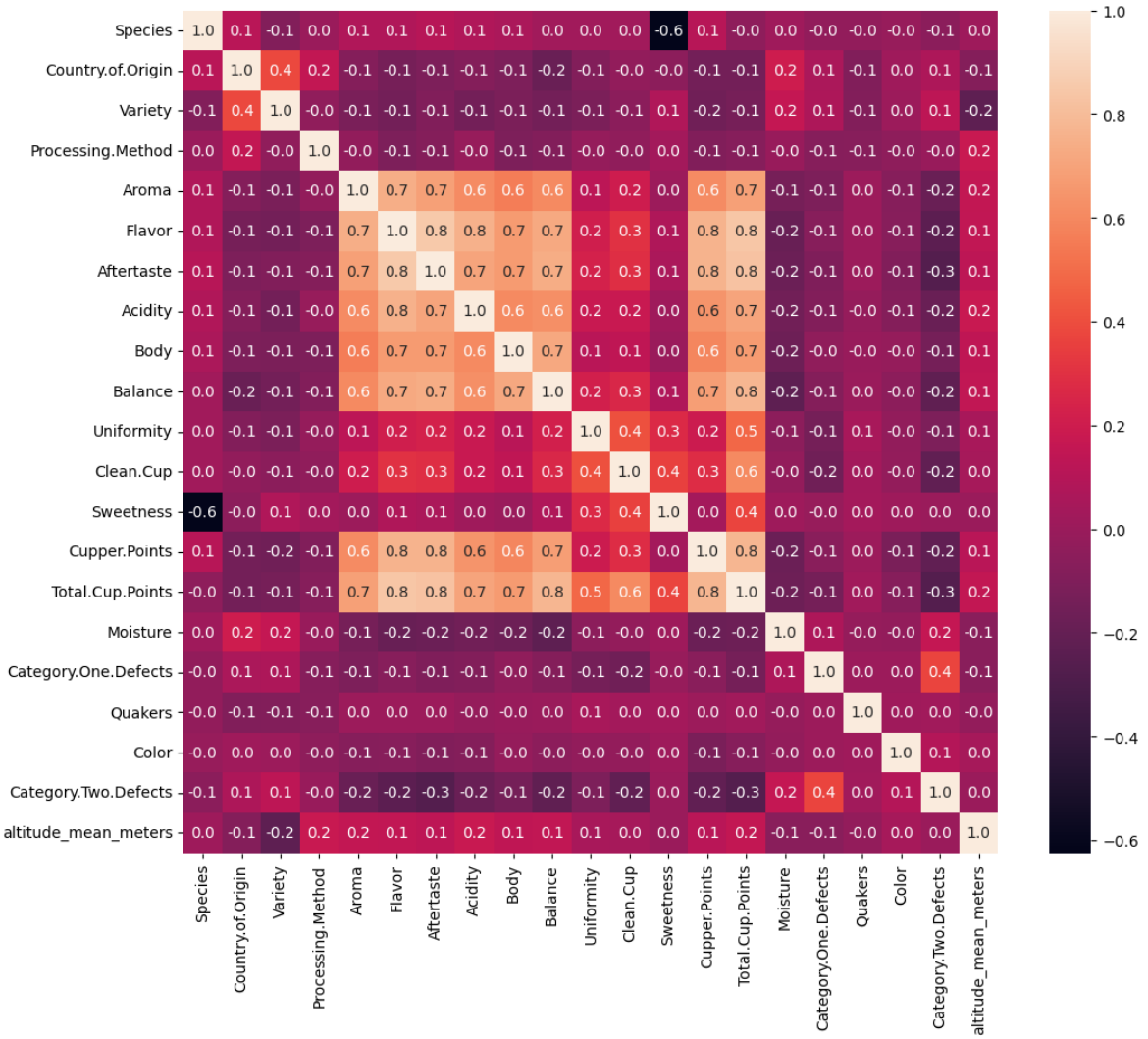
In [17]:
```
df.describe()
```

Out[17]:

	Aroma	Flavor	Aftertaste	Acidity	Body	Balance
count	1103.000000	1103.000000	1103.000000	1103.000000	1103.000000	1103.000000
mean	7.578368	7.527824	7.401496	7.535739	7.513654	7.512665
std	0.309181	0.331268	0.340065	0.313192	0.289467	0.354021
min	5.080000	6.170000	6.170000	5.250000	5.170000	5.250000
25%	7.420000	7.330000	7.250000	7.330000	7.330000	7.330000
50%	7.580000	7.580000	7.420000	7.500000	7.500000	7.500000
75%	7.750000	7.750000	7.580000	7.750000	7.670000	7.750000
max	8.750000	8.830000	8.670000	8.750000	8.580000	8.750000

In [18]:
```
enc_corr_mat = enc_df.corr()
plt.figure(figsize=(12, 10))
sns.heatmap(enc_corr_mat, annot = True, fmt = ".1f")
```

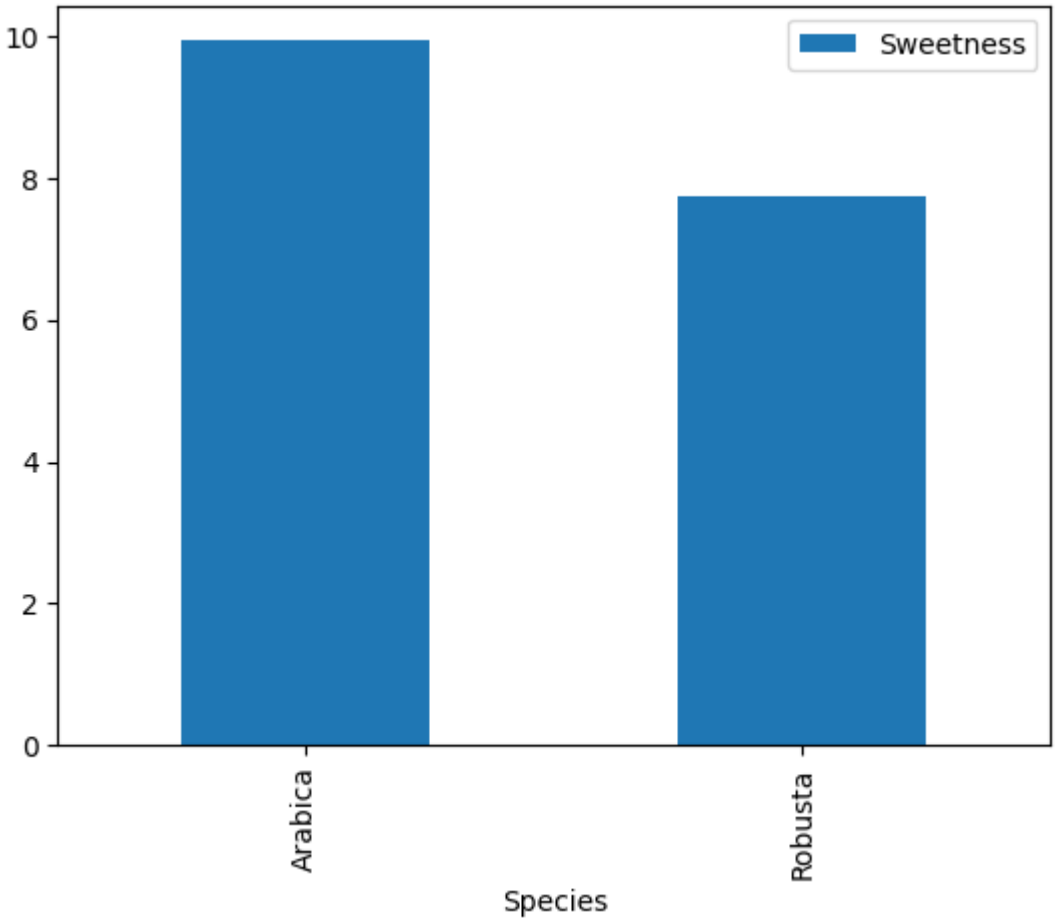
Out[18]: <Axes: >



The species of the coffee seems to have a significant impact on the sweetness

In [19]:
```
# Sweetnes grouped by species
df.groupby('Species')['Sweetness'].mean().reset_index().plot.bar(x='Specie
```

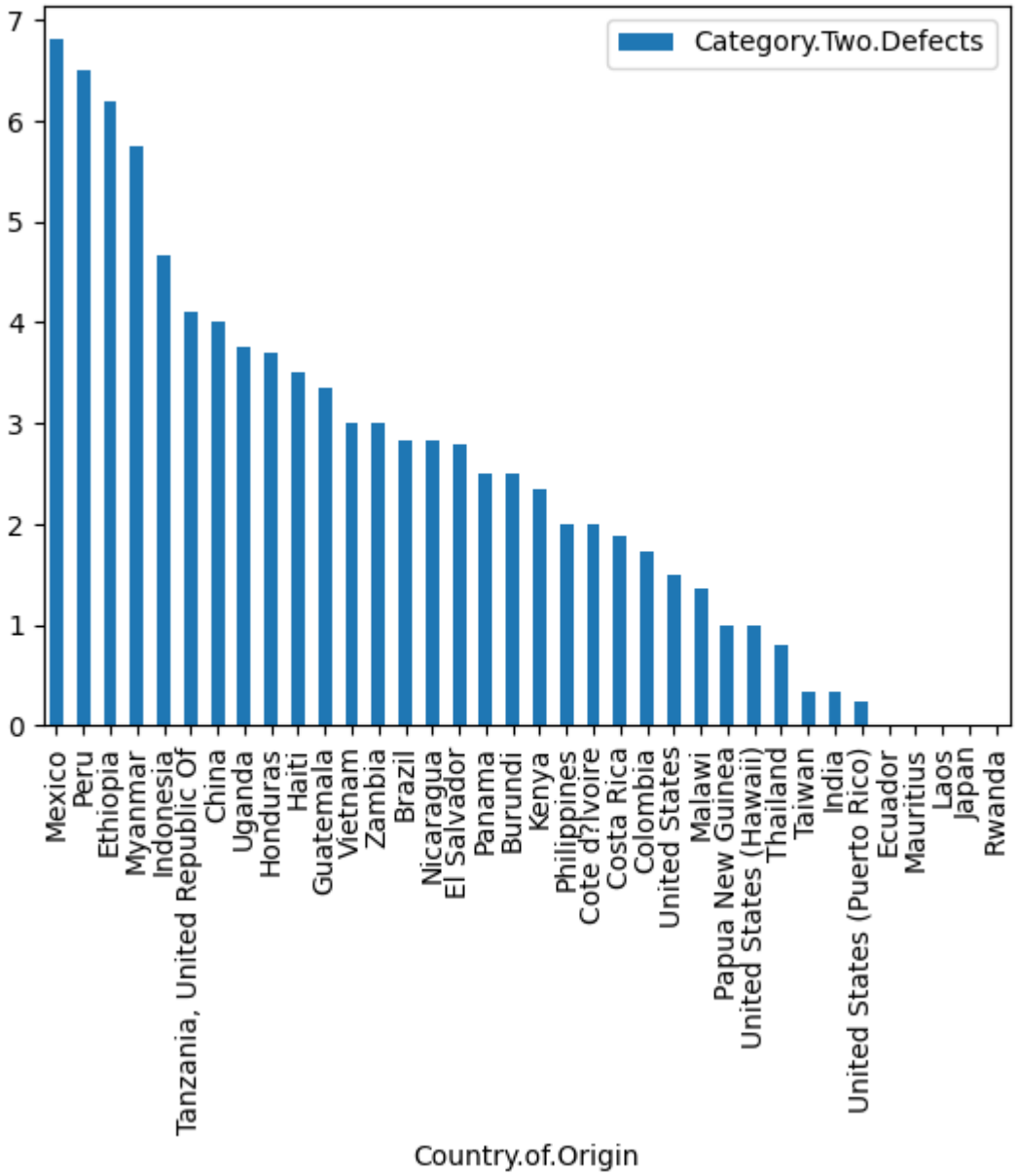
Out[19]: <Axes: xlabel='Species'>



So this is where the Arabica beans stand out! It's on average around 20% sweeter than Robousta beans

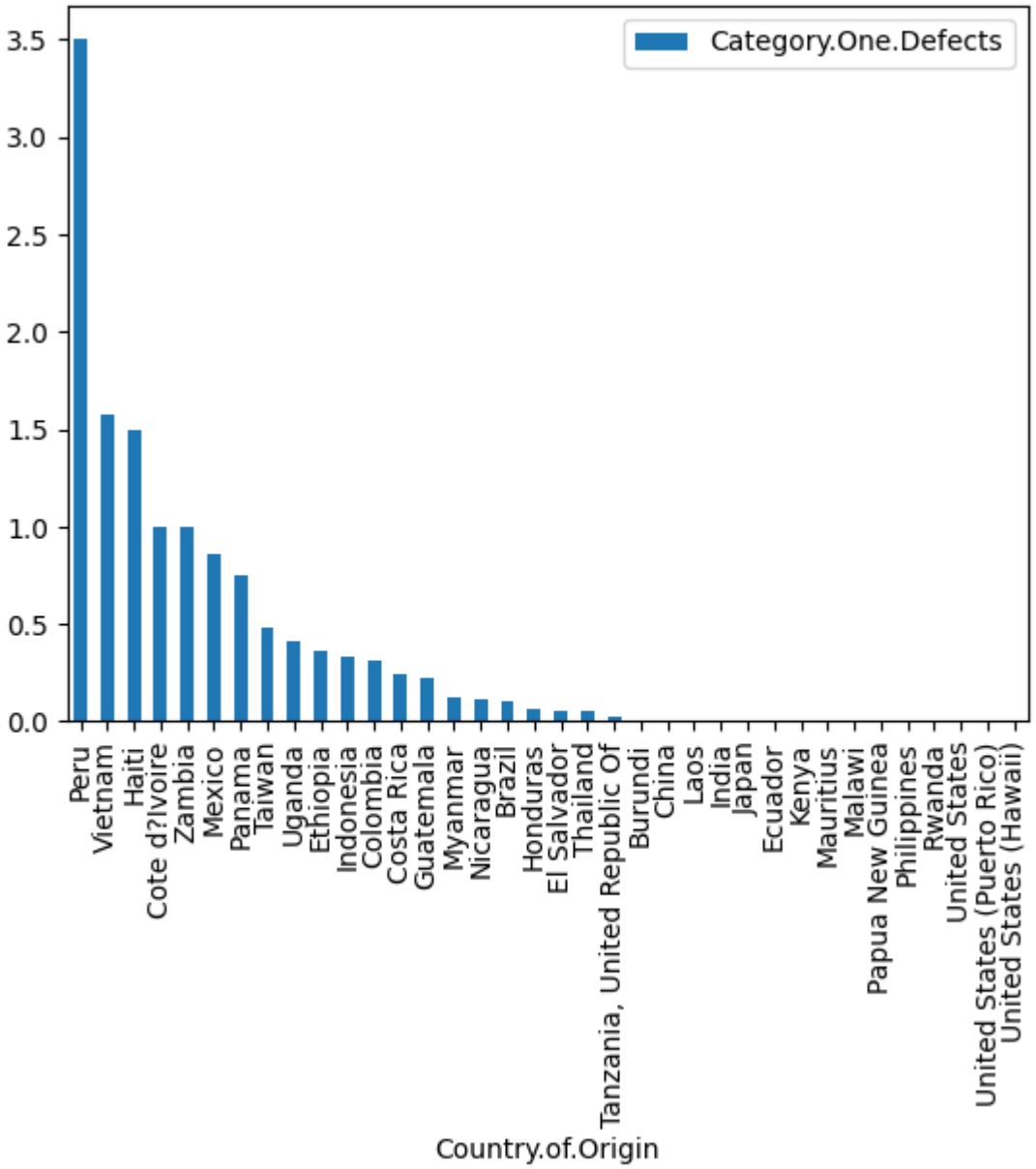
In [20]:
```
df.groupby('Country.of.Origin')['Category.Two.Defects'].mean().reset_index
```

Out[20]:
```
<Axes: xlabel='Country.of.Origin'>
```



In [21]:
```
df.groupby('Country.of.Origin')['Category.One.Defects'].mean().reset_index
```

Out[21]: <Axes: xlabel='Country.of.Origin'>



Interestingly though, we also find Ethiopia among the countries with the highest mean in Category 2 defect parameters, even though it is the country with the 4th averagely highest scoring coffee. This indicates that it takes rather large amounts of defects in the coffee to really make an impact on the overall score.

Clustering model training

We'll try to extract more information with clustering models. For this purpose we drop our previous target feature "Total Cup Points" and scale the feature values in the dataset, so we can do a principal component analysis

In [23]:
```
df_cls = enc_df.drop('Total.Cup.Points', axis=1)
# df_cls = enc_df.copy()
```

In [24]:
```
df_cls[df_cls.columns] = sk.preprocessing.StandardScaler().fit_transform(d
```

In [25]:
```
df_cls.sample(5)
```

Out[25]:

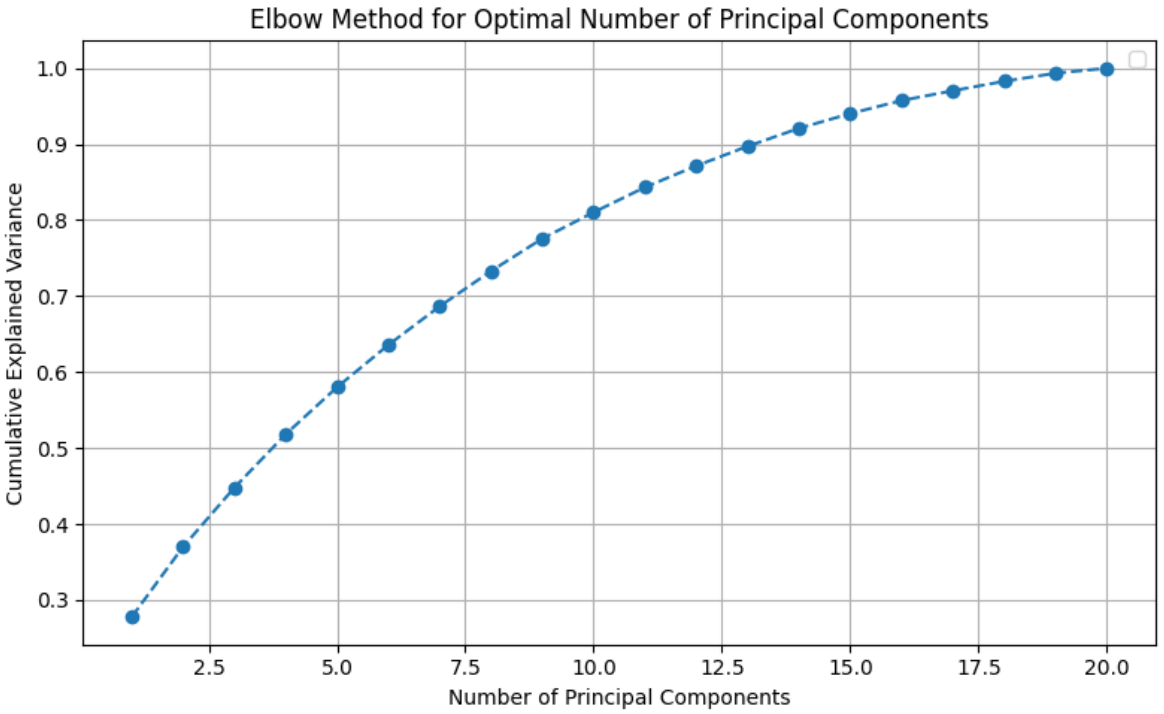
	Species	Country.of.Origin	Variety	Processing.Method	Aroma	Flavor
113	-0.152286	-1.070443	0.282078	0.526081	0.814236	0.429382
150	-0.152286	1.652957	-0.845622	-2.102535	0.814236	0.670988
49	-0.152286	-0.651458	-0.958392	-0.131073	0.814236	1.426007
828	-0.152286	2.071941	0.282078	0.526081	0.296504	0.670988
958	-0.152286	0.605495	1.635319	0.526081	-1.062540	-2.107482

In [26]:
```
pca = PCA()
pca.fit(df_cls)
explained_variance = pca.explained_variance_ratio_
cumulative_variance = np.cumsum(explained_variance)
# 3 principal components
cumulative_variance[2]
```

Out[26]:
```
np.float64(0.4478511071920876)
```

In [27]:
```
plt.figure(figsize=(8, 5))
plt.plot(range(1, len(cumulative_variance) + 1), cumulative_variance, marl
plt.xlabel('Number of Principal Components')
plt.ylabel('Cumulative Explained Variance')
plt.title('Elbow Method for Optimal Number of Principal Components')
plt.grid(True)
plt.legend()
plt.tight_layout()
plt.show()
```

```
/tmp/ipykernel_11022/3103998374.py:7: UserWarning: No artists with labels
found to put in legend.  Note that artists whose label start with an under
score are ignored when legend() is called with no argument.
  plt.legend()
```



Not as much as we hoped for. For 3 principal components, we get just above 50% explained variance, which is not a lot. Lets try and extract high correlating features and

do the PCA again

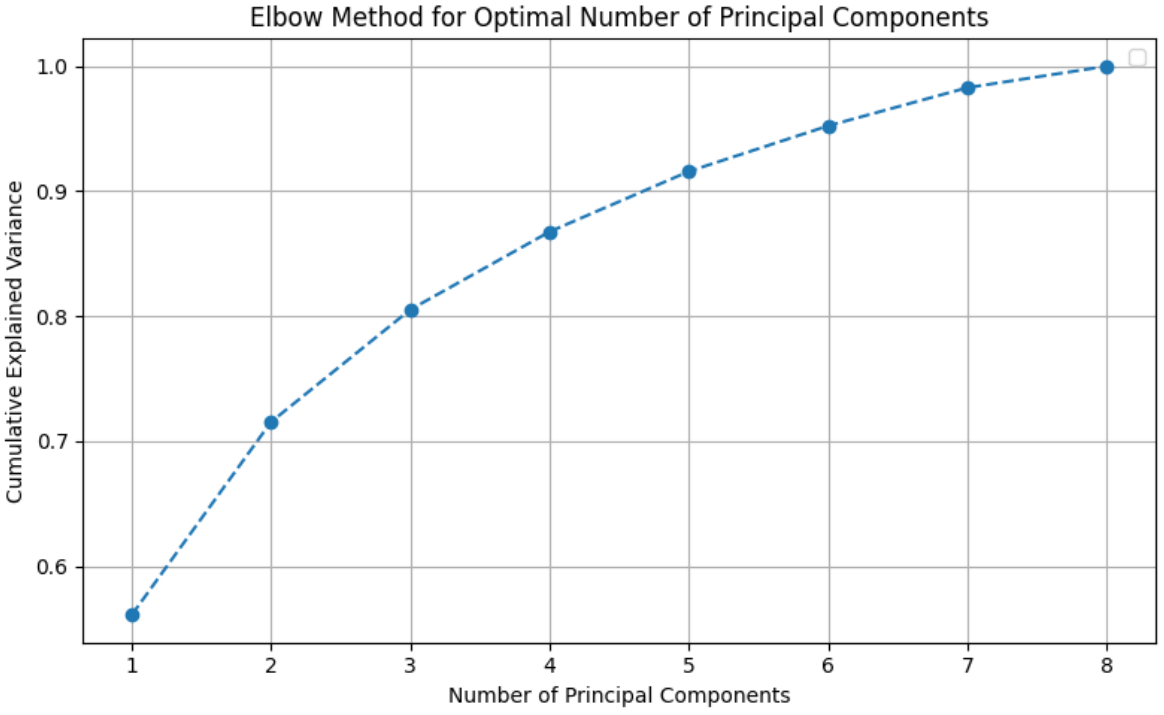
In [28]:
```
df_cls_ext = enc_df[["Aroma","Flavor","Acidity","Body","Balance","Aftertas
df_cls_ext[df_cls_ext.columns] = sk.preprocessing.StandardScaler().fit_trar
```

In [29]:
```
pca = PCA()
pca.fit(df_cls_ext)
explained_variance = pca.explained_variance_ratio_
cumulative_variance = np.cumsum(explained_variance)
# 3 principal components
cumulative_variance[2]
```

Out[29]:
```
np.float64(0.8053004618615184)
```

In [30]:
```
plt.figure(figsize=(8, 5))
plt.plot(range(1, len(cumulative_variance) + 1), cumulative_variance, marl
plt.xlabel('Number of Principal Components')
plt.ylabel('Cumulative Explained Variance')
plt.title('Elbow Method for Optimal Number of Principal Components')
plt.grid(True)
plt.legend()
plt.tight_layout()
plt.show()
```

```
/tmp/ipykernel_11022/3103998374.py:7: UserWarning: No artists with labels
found to put in legend.  Note that artists whose label start with an under
score are ignored when legend() is called with no argument.
  plt.legend()
```



Now we have an explained variance of above 70% with 2 principal components. Much better!

In [31]:
```
pca_2 = PCA(n_components=2)
pca_2_result = pca_2.fit_transform(df_cls_ext)
dataset_pca = pd.DataFrame(abs(pca_2.components_), columns=df_cls_ext.colu
dataset_pca
```

Out[31]:

	Aroma	Flavor	Acidity	Body	Balance	Aftertaste	Uniformity	Sweet
PC_1	0.381225	0.436044	0.392771	0.381476	0.404040	0.428197	0.128396	0.04
PC_2	0.103547	0.019839	0.057700	0.113975	0.009413	0.009358	0.659328	0.73

Here is our principal components. We see that PC1 is weighted across all the features, with a dive in Uniformity and Sweetness, while PC2 is mostly weighted be these.

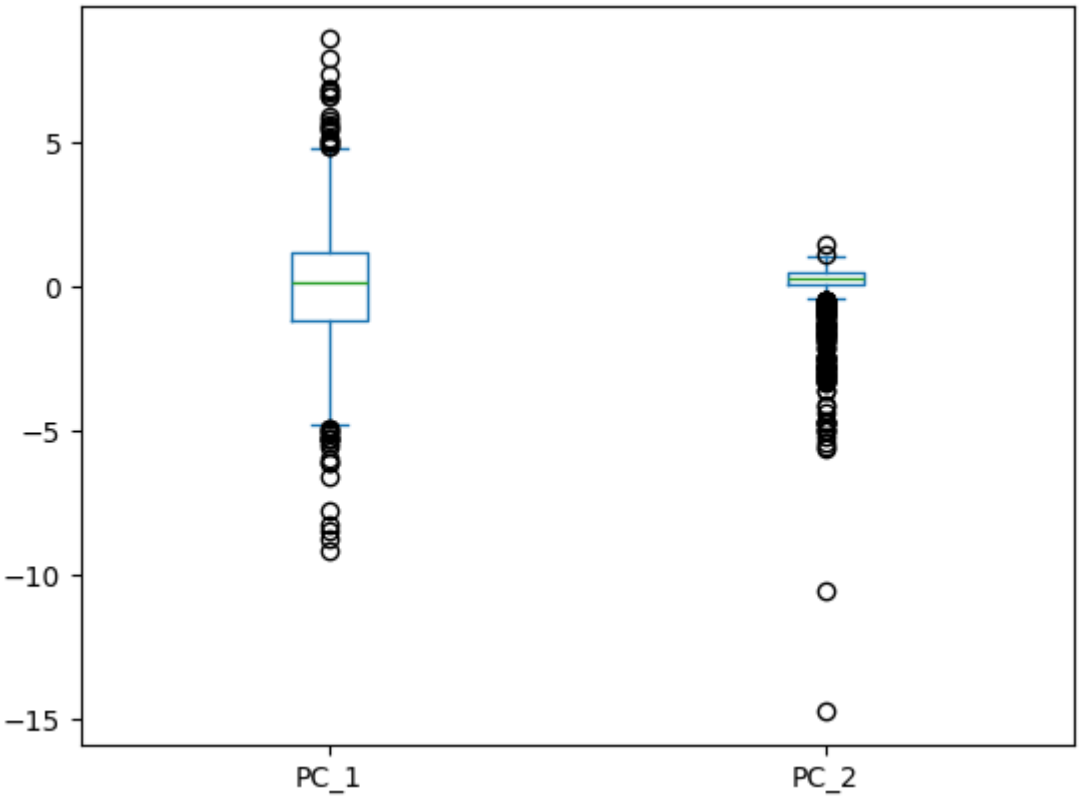
In [32]:
```
df_pca = pd.DataFrame(pca_2_result, columns=['PC_1', 'PC_2'])
df_pca.head()
```

Out[32]:

	PC_1	PC_2
0	8.565309	-0.713374
1	7.920370	-0.663066
2	6.869235	-0.475166
3	6.696222	-0.467683
4	6.561643	-0.466118

In [33]:
```
df_pca.plot.box()
```

Out[33]: <Axes: >

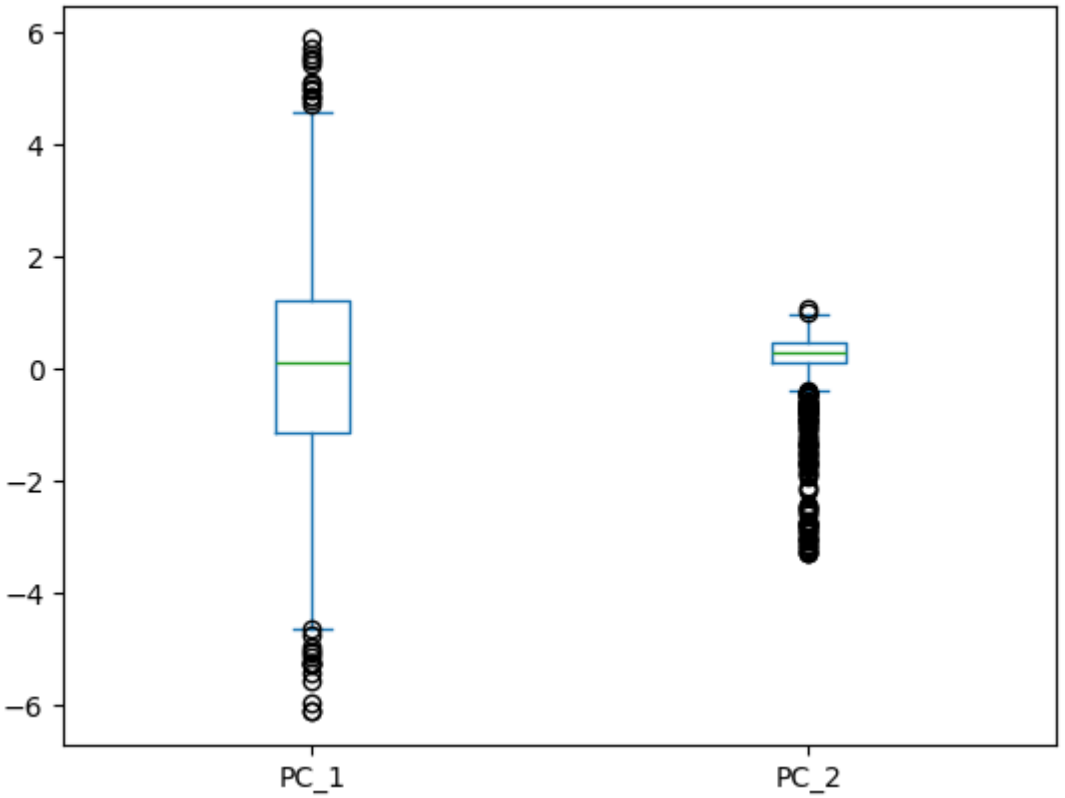


We have also introduced some serious outliers. Lets remove them

In [34]:
```
z_scores = np.abs(zscore(df_pca))
df_pca = df_pca[(z_scores < 3).all(axis=1)]
```

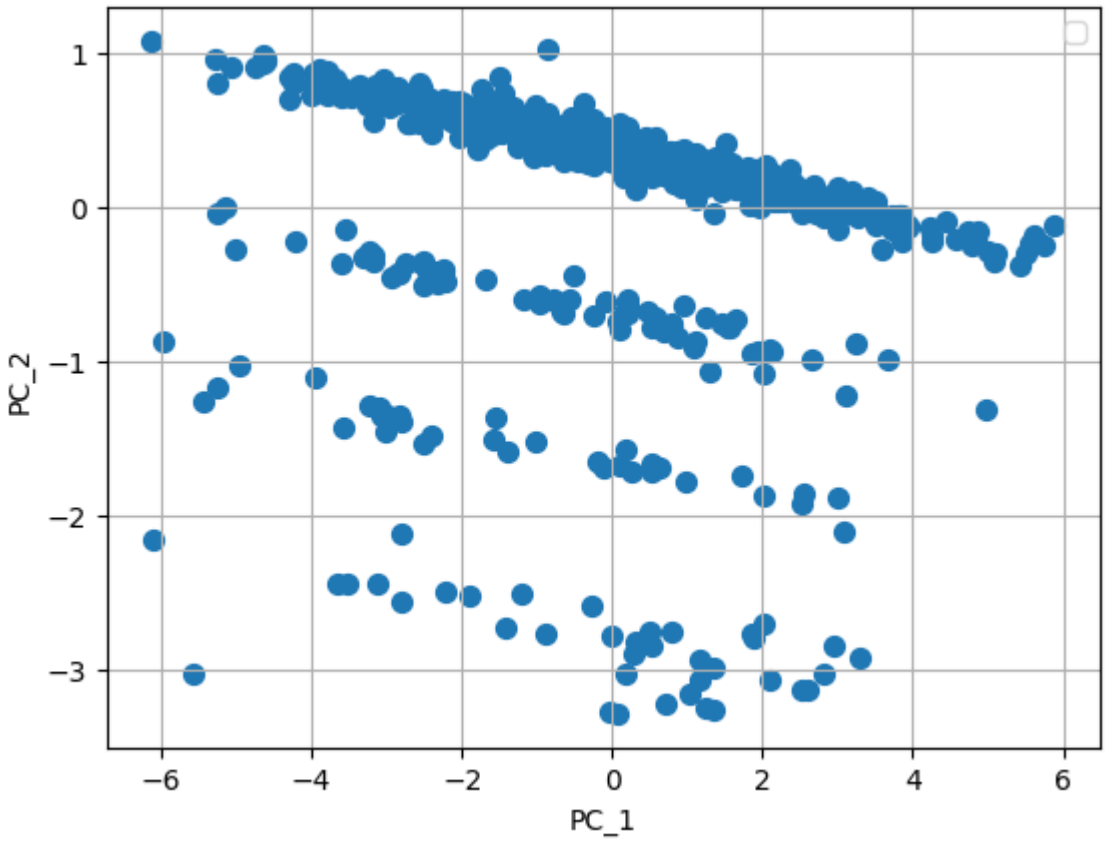
In [35]:
```
df_pca.plot.box()
```

Out[35]: <Axes: >



In [36]:
```
fig = plt.figure()
plt.scatter(df_pca['PC_1'], df_pca['PC_2'], s=50)
plt.xlabel('PC_1')
plt.ylabel('PC_2')
plt.grid(True)
plt.legend()
plt.show()
```

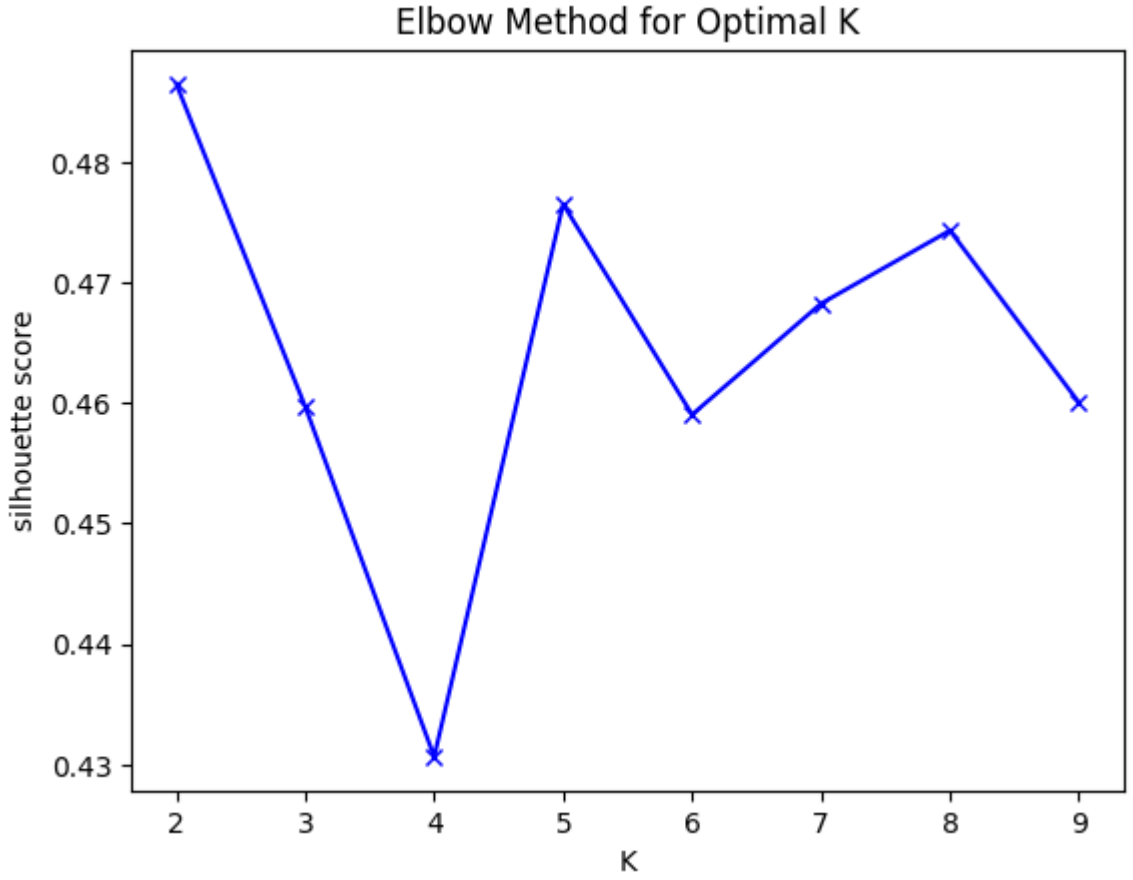
```
/tmp/ipykernel_11022/573061907.py:6: UserWarning: No artists with labels f
ound to put in legend.  Note that artists whose label start with an unders
core are ignored when legend() is called with no argument.
  plt.legend()
```


1
0
−1
−2
−3
PC_2
−6
−4
−2
0
2
4
6
PC_1

In [37]:
```
# Calculating optimal number of clusters in a K-means algorithm using sili
scores = []
K = range(2,10)
for k in K:
    model = KMeans(n_clusters=k, n_init=10)
    model.fit(df_pca)
    score = sk.metrics.silhouette_score(df_pca, model.labels_, metric='euc
    print("\nNumber of clusters =", k)
    print("Silhouette score =", score)
    scores.append([k, score])
```

```
Number of clusters = 2
Silhouette score = 0.4864683885974626

Number of clusters = 3
Silhouette score = 0.4596864222774429

Number of clusters = 4
Silhouette score = 0.4306487916313575

Number of clusters = 5
Silhouette score = 0.4764977680674508

Number of clusters = 6
Silhouette score = 0.4590307090562025

Number of clusters = 7
Silhouette score = 0.468243031713899

Number of clusters = 8
Silhouette score = 0.4743114637983735

Number of clusters = 9
Silhouette score = 0.4600339588086069
```

In [38]:
```
score_df = pd.DataFrame(scores, columns=['k', 'scores'])
fig = plt.figure()
plt.title('Elbow Method for Optimal K')
plt.plot(score_df.k, score_df.scores, 'bx-')
plt.xlabel('K')
plt.ylabel('silhouette score')
plt.show()
```

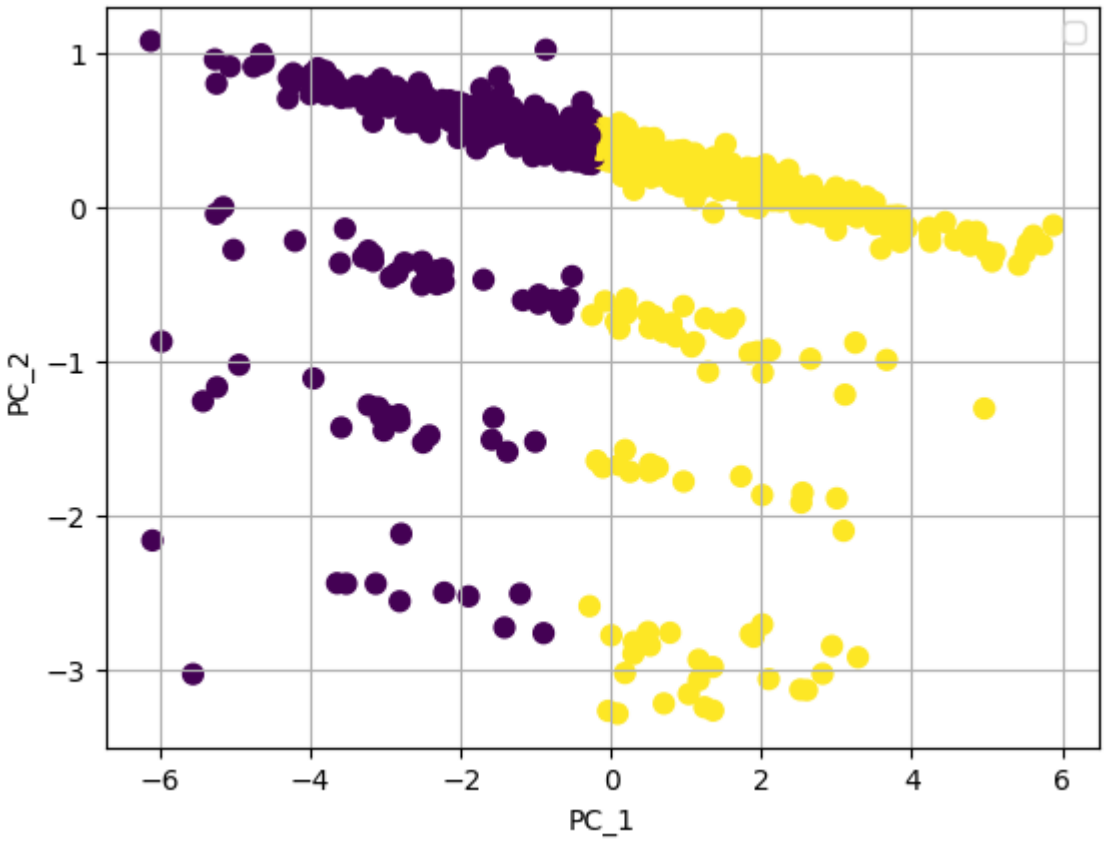


Using silhouette score for each amount of clusters, we se that we achieve a maximum score of 0,473 on 2 clusters. Let's try and visualize them

In [39]:
```
kmeans = KMeans(init='k-means++', n_clusters=2, n_init=10)
prediction = kmeans.fit_predict(df_pca)
```

In [40]:
```
fig = plt.figure()
plt.scatter(df_pca['PC_1'], df_pca['PC_2'], c=prediction, s=50, cmap='vir
plt.xlabel('PC_1')
plt.ylabel('PC_2')
plt.grid(True)
plt.legend()
plt.show()
```

```
/tmp/ipykernel_11022/3703295130.py:6: UserWarning: No artists with labels
found to put in legend.  Note that artists whose label start with an under
score are ignored when legend() is called with no argument.
  plt.legend()
```



Well, its doesn't seem like the K-means algorithm finds any clusters that makes visual sense. Lets try to the PCA again with an additional PC. The extra dimension and 10% added explained variance, might give additional insights

In [41]:
```
pca_3 = PCA(n_components=3)
pca_3_result = pca_3.fit_transform(df_cls_ext)
dataset_pca = pd.DataFrame(abs(pca_3.components_), columns=df_cls_ext.colu
dataset_pca
```

Out[41]:

	Aroma	Flavor	Acidity	Body	Balance	Aftertaste	Uniformity	Sweet
PC_1	0.381225	0.436044	0.392771	0.381476	0.404040	0.428197	0.128396	0.04
PC_2	0.103547	0.019839	0.057700	0.113975	0.009413	0.009358	0.659328	0.73
PC_3	0.049970	0.040739	0.022757	0.067166	0.034935	0.002558	0.731547	0.67

Here are our components. With PC1 weighted across most parameters, PC2 mostly weighted by Sweetness and Uniformity and PC3 weighted mainly by Uniformity

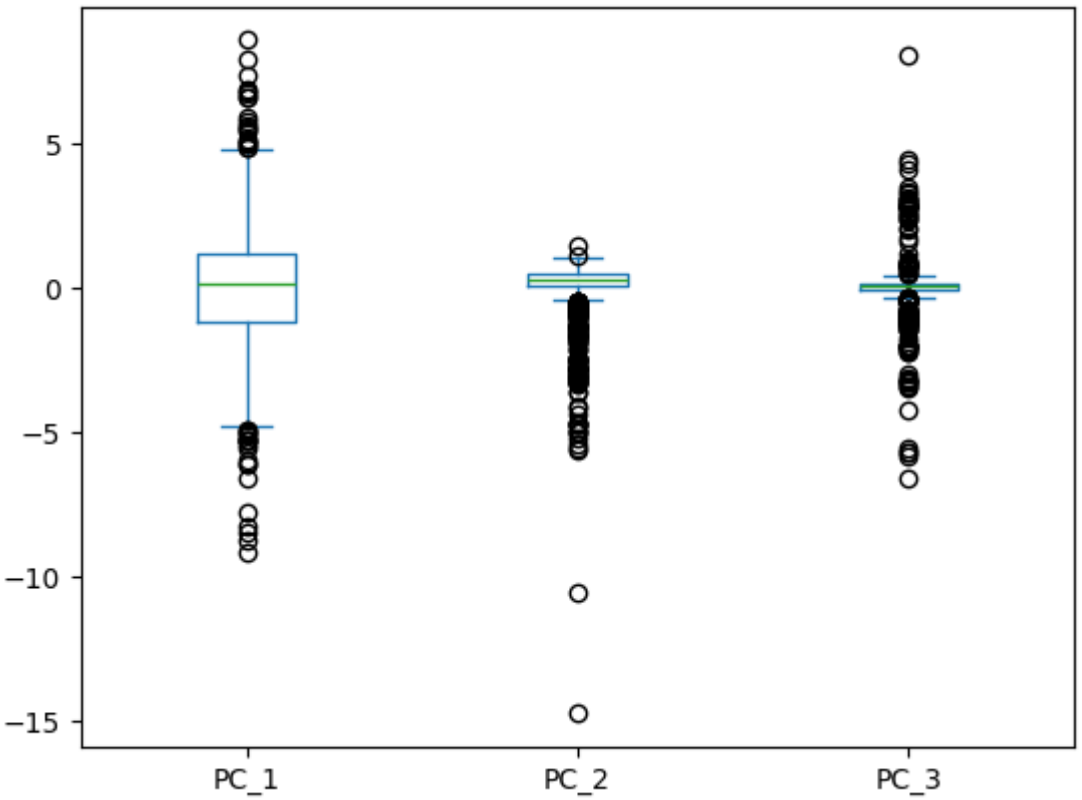
In [42]:
```
df_pca = pd.DataFrame(pca_3_result, columns=['PC_1', 'PC_2', 'PC_3'])
df_pca.head()
```

Out[42]:

	PC_1	PC_2	PC_3
0	8.565309	-0.713374	-0.498447
1	7.920370	-0.663066	-0.486764
2	6.869235	-0.475166	-0.403830
3	6.696222	-0.467683	-0.395929
4	6.561643	-0.466118	-0.383813

In [43]:
```
df_pca.plot.box()
```

Out[43]: <Axes: >

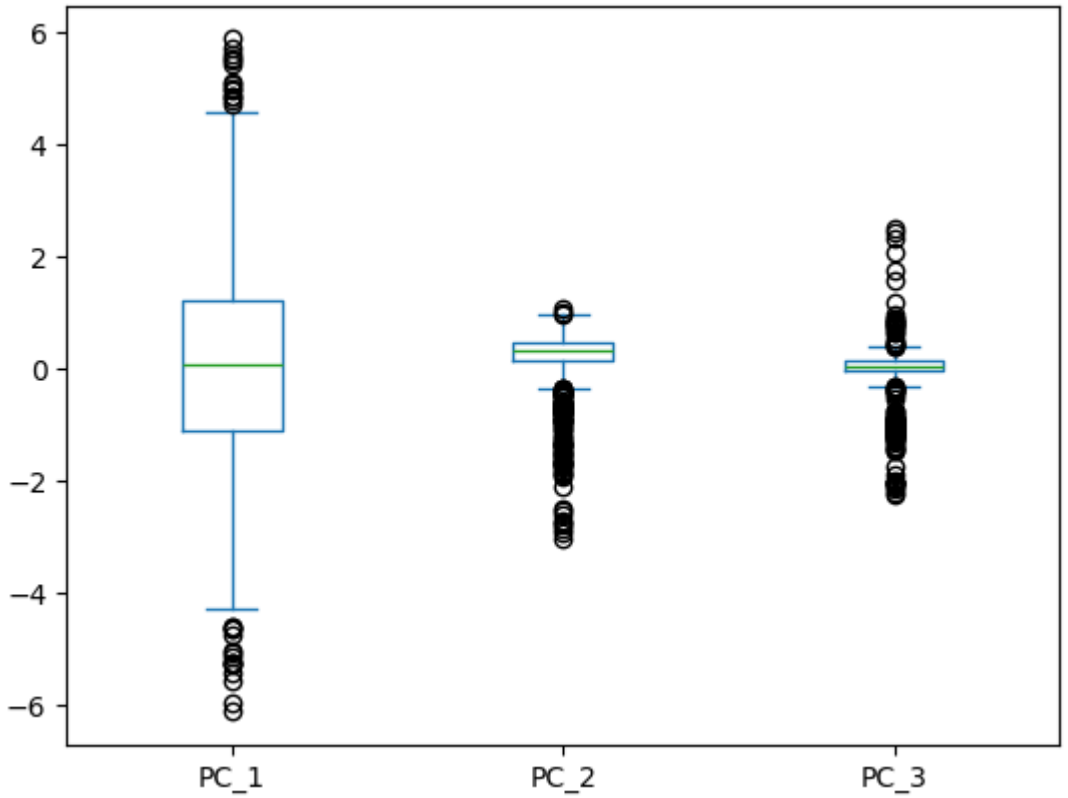


We'll remove the outliers again

In [44]:
```
z_scores = np.abs(zscore(df_pca))
df_pca = df_pca[(z_scores < 3).all(axis=1)]
```

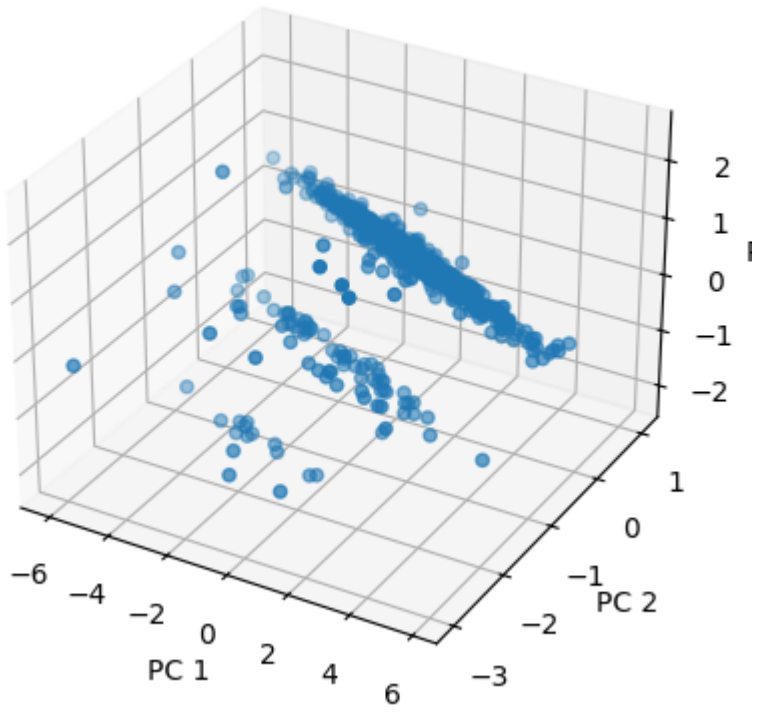
In [45]:
```
df_pca.plot.box()
```

Out[45]: <Axes: >



In [46]:
```
fig = plt.figure()
ax = fig.add_subplot(projection='3d')
ax.scatter(df_pca['PC_1'], df_pca['PC_2'], df_pca['PC_3'])

ax.set_xlabel('PC 1')
ax.set_ylabel('PC 2')
ax.set_zlabel('PC 3')
```

Out[46]:
```
Text(0.5, 0, 'PC 3')
```

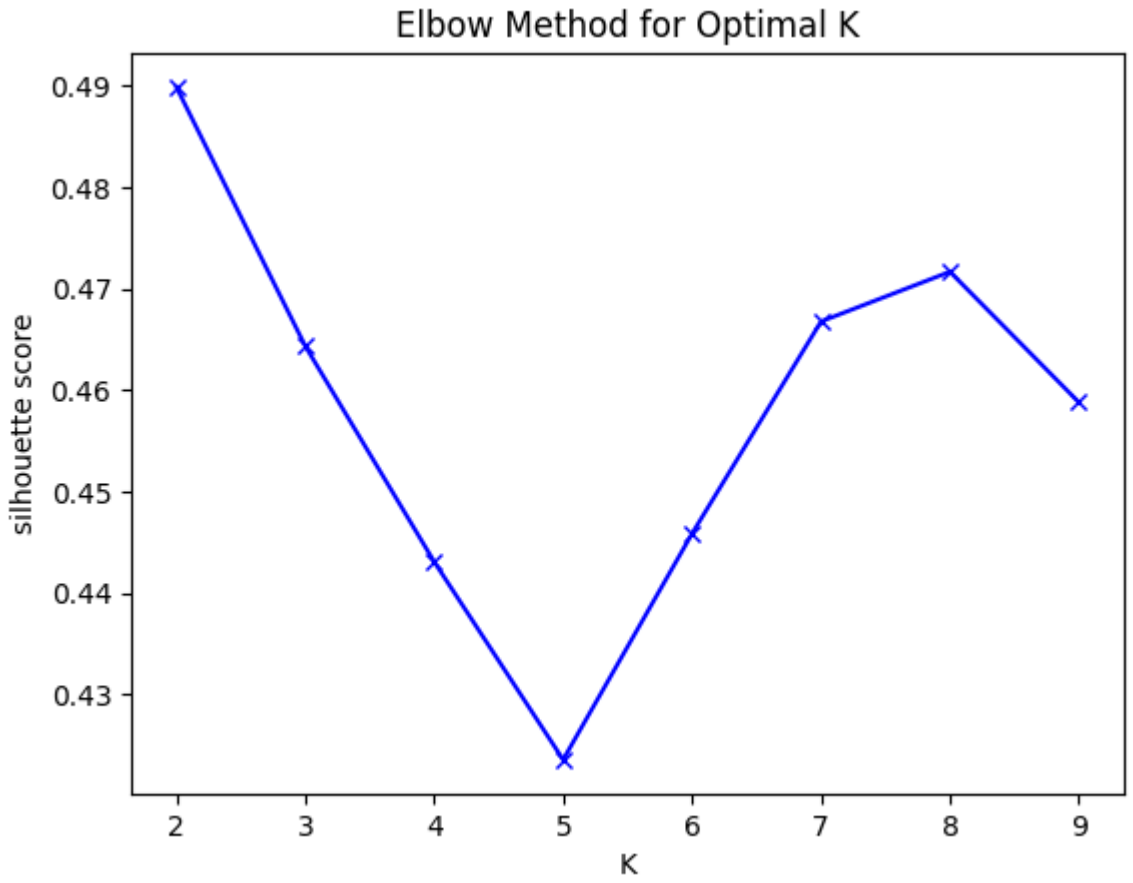


Here is our 3D points. Let's start with doing doing a K-means clustering algorithm. First we need to find the optimal K (Number of clusters)

In [47]:
```
# Calculating optimal number of clusters in a K-means algorithm using sili
scores = []
K = range(2,10)
for k in K:
    model = KMeans(n_clusters=k, n_init=10)
    model.fit(df_pca)
    score = sk.metrics.silhouette_score(df_pca, model.labels_, metric='euc
    print("\nNumber of clusters =", k)
    print("Silhouette score =", score)
    scores.append([k, score])
```

```
Number of clusters = 2
Silhouette score = 0.4898576695192007

Number of clusters = 3
Silhouette score = 0.4643237006986533

Number of clusters = 4
Silhouette score = 0.4430582641319094

Number of clusters = 5
Silhouette score = 0.4235502939312917

Number of clusters = 6
Silhouette score = 0.44583337191385314

Number of clusters = 7
Silhouette score = 0.46673994176770084

Number of clusters = 8
Silhouette score = 0.4716433426294572

Number of clusters = 9
Silhouette score = 0.45877396158210904
```

In [48]:
```
score_df = pd.DataFrame(scores, columns=['k', 'scores'])
fig = plt.figure()
plt.title('Elbow Method for Optimal K')
plt.plot(score_df.k, score_df.scores, 'bx-')
plt.xlabel('K')
plt.ylabel('silhouette score')
plt.show()
```



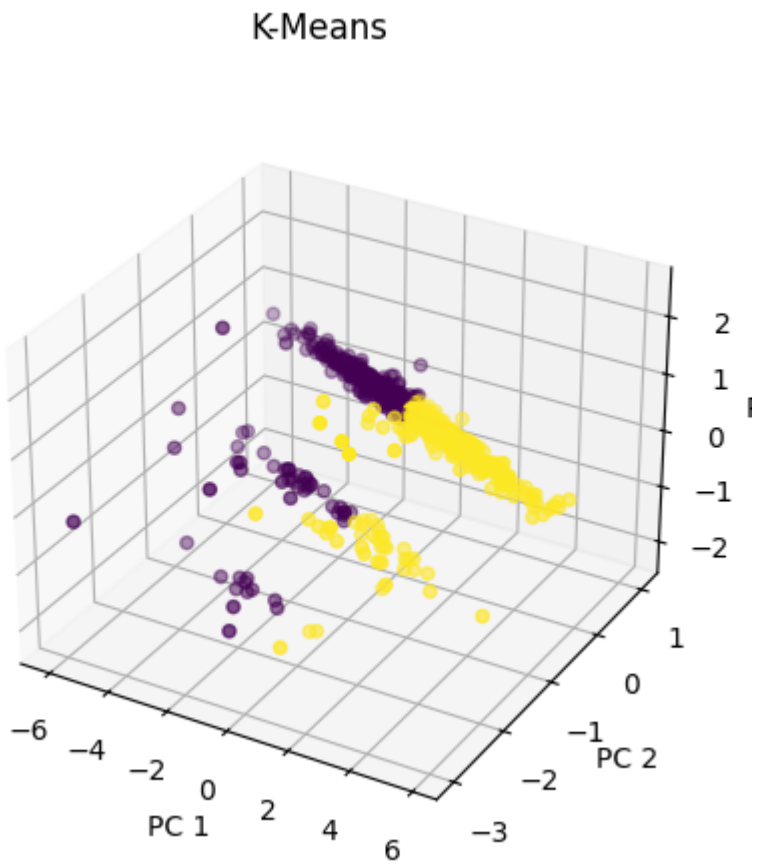
In [49]:
```
kmeans = KMeans(init='k-means++', n_clusters=2, n_init=10)
prediction = kmeans.fit_predict(df_pca)
```

In [50]:
```
prediction
```

Out[50]:
```
array([1, 1, 1, ..., 1, 1, 1], shape=(1042,), dtype=int32)
```

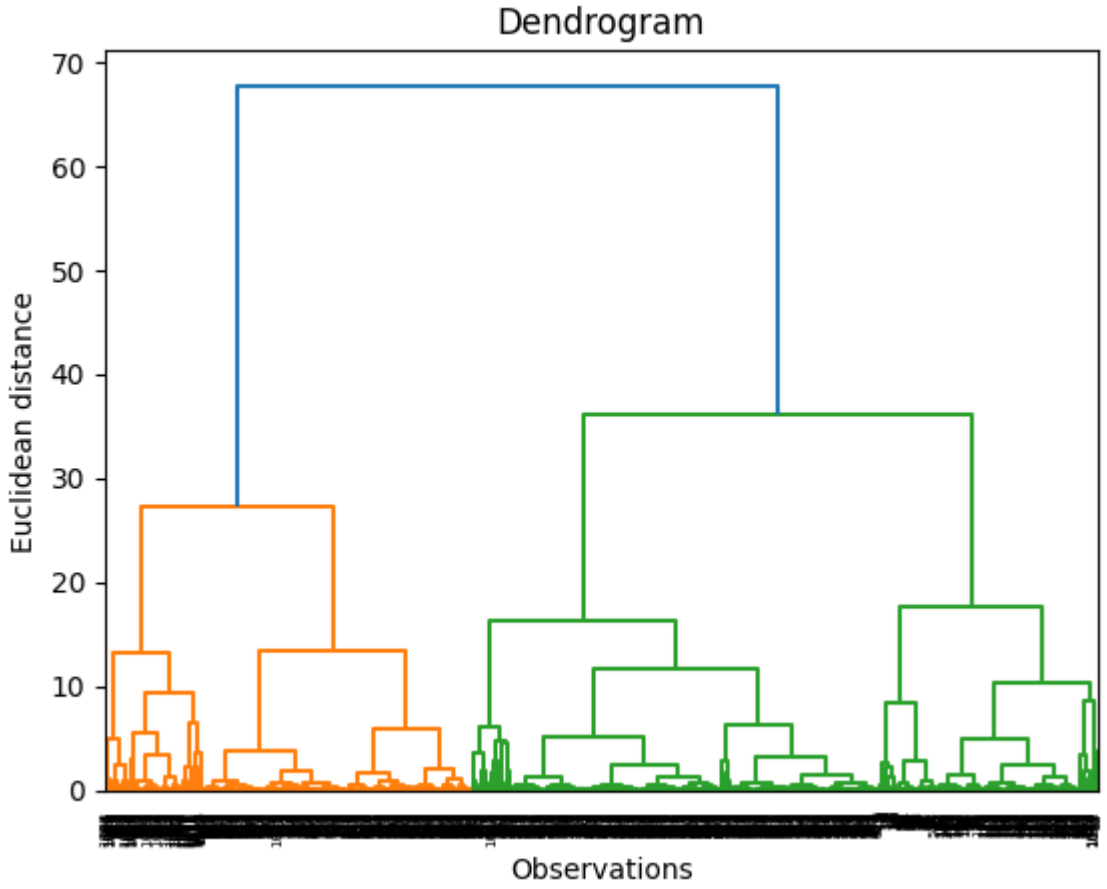
In [51]:
```
fig = plt.figure()
fig.suptitle("K-Means")
ax = fig.add_subplot(projection='3d')
ax.scatter(df_pca['PC_1'], df_pca['PC_2'], df_pca['PC_3'], c=prediction)

ax.set_xlabel('PC 1')
ax.set_ylabel('PC 2')
ax.set_zlabel('PC 3')
```

Out[51]:
```
Text(0.5, 0, 'PC 3')
```



Well, the K-means method doesn't seem to agree with us. Lets try doing agglomerative clustering instead

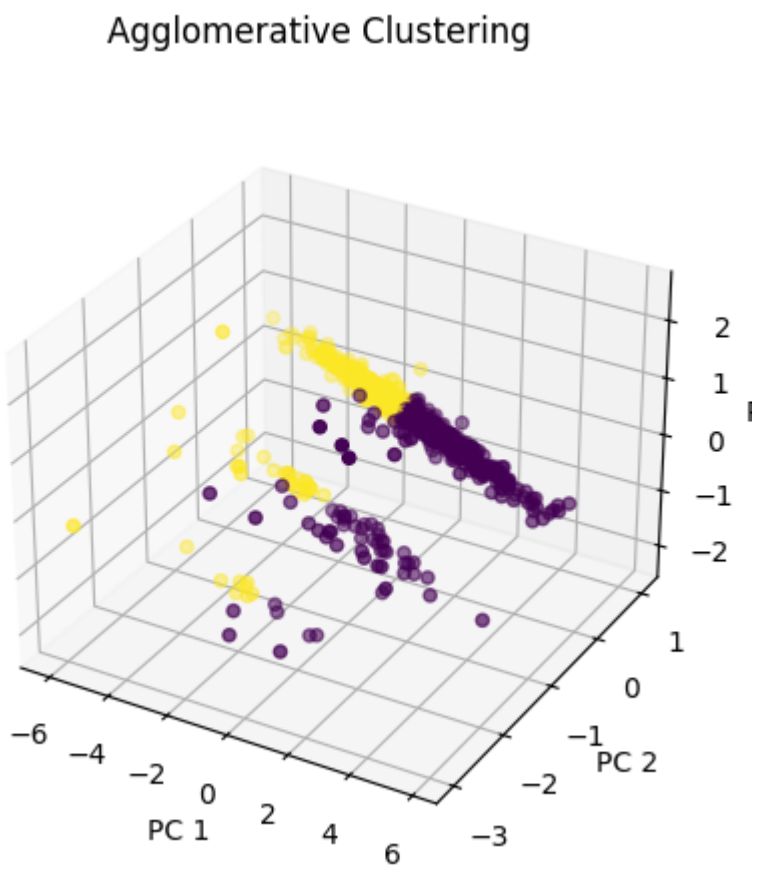
In [52]:
```
# Dendogram for agglomerative clustering
plt.figure()
dendogram = ch.dendrogram(ch.linkage(df_pca, method = 'ward'))
plt.title('Dendrogram')
plt.xlabel('Observations')
plt.ylabel('Euclidean distance')
plt.show()
```



In [53]:
```
model = AgglomerativeClustering(2, linkage = 'ward')
aggmodel_pred = model.fit_predict(df_pca)
```

In [54]:
```
fig = plt.figure()
fig.suptitle("Agglomerative Clustering")
ax = fig.add_subplot(projection='3d')
ax.scatter(df_pca['PC_1'], df_pca['PC_2'], df_pca['PC_3'], c=aggmodel_pred

ax.set_xlabel('PC 1')
ax.set_ylabel('PC 2')
ax.set_zlabel('PC 3')
```

Out[54]:
```
Text(0.5, 0, 'PC 3')
```



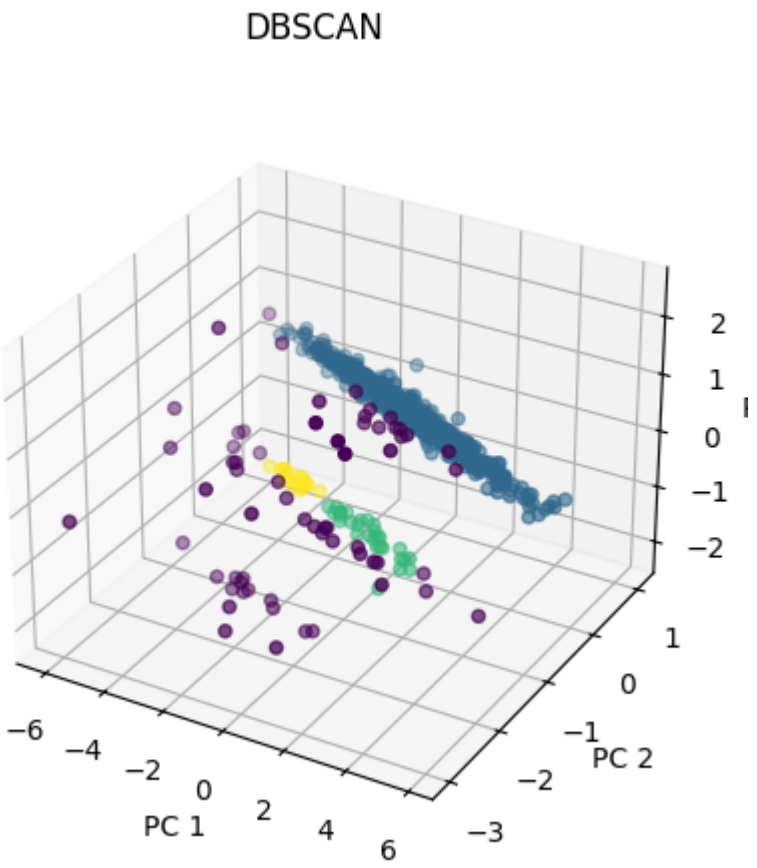
Well that doesn't seem to agree either. Lets try running a DBSCAN

In [57]:
```
#DBSCAN for automatically determining amount of clusters
# Tried to play a little around with eps here
# for finding the optimal separation
dbscan = DBSCAN(eps=0.7, min_samples=10)
dbscan_pred = dbscan.fit_predict(df_pca)
dbscan_pred
```

Out[57]:
```
array([ 0,  0,  0, ..., -1, -1, -1], shape=(1042,))
```

In [56]:
```
fig = plt.figure()
fig.suptitle("DBSCAN")
ax = fig.add_subplot(projection='3d')
ax.scatter(df_pca['PC_1'], df_pca['PC_2'], df_pca['PC_3'], c=dbscan_pred)

ax.set_xlabel('PC 1')
ax.set_ylabel('PC 2')
ax.set_zlabel('PC 3')
```

Out[56]:
```
Text(0.5, 0, 'PC 3')
```



The DBSCAN clustering seems to yield the best results so far. There's a clear large cluster, showing the correlation between PC1 and PC2. Two smaller clusters showing a concentration of data points in the same correlation between PC1 and PC2, but is offset on PC2 and PC3. Showing 2 potential subcategories of data along both axises of PC2 and PC3.

In this case we suspect the clusters mostly represent the bean species, since both PC2 and PC3 are mainly weighted by Unifomity and Sweetness. We found in earlier analysis, that the main difference between Arabica and Robusta beans seem to be in sweetness. This fits with a cluster split along PC2 and PC3 axises, along with the much smaller cluster size in terms of data points, since Robusta beans are less represented in the dataset.

In summary, what we can tell about the dataset is the following:

- The Main quality measures in the coffee seems to be the flavor parameters
- It takes a large amount of defects and quakers to actually worsen the overall quality
- Arabica beans tend to be sweeter than Robusta beans
- There is a very slight indication that higher quality coffee tends to come fom Africa