```
pip install ucimlrepo
```

```
Requirement already satisfied: ucimlrepo in /usr/local/lib/python3.10/dist-packages (0.0.6)
```

```
from ucimlrepo import fetch_ucirepo

# fetch dataset
wine = fetch_ucirepo(id=109)

# data (as pandas dataframes)
X = wine.data.features
y = wine.data.targets

# metadata
print(wine.metadata)

# variable information
print(wine.variables)
```

```
{'uci_id': 109, 'name': 'Wine', 'repository_url': 'https://archive.ics.uci.edu/dataset/109/wine', 'data_url': 'https://archive.ics.uci.e
                          name     role         type demographic  \
0                        class   Target  Categorical        None
1                      Alcohol  Feature   Continuous        None
2                    Malicacid  Feature   Continuous        None
3                          Ash  Feature   Continuous        None
4              Alcalinity_of_ash  Feature   Continuous        None
5                    Magnesium  Feature      Integer        None
6                Total_phenols  Feature   Continuous        None
7                   Flavanoids  Feature   Continuous        None
8           Nonflavanoid_phenols  Feature   Continuous        None
9                Proanthocyanins  Feature   Continuous        None
10               Color_intensity  Feature   Continuous        None
11                           Hue  Feature   Continuous        None
12  0D280_0D315_of_diluted_wines  Feature   Continuous        None
13                       Proline  Feature      Integer        None

   description units missing_values
0         None  None             no
1         None  None             no
2         None  None             no
3         None  None             no
4         None  None             no
5         None  None             no
6         None  None             no
7         None  None             no
8         None  None             no
9         None  None             no
10        None  None             no
11        None  None             no
12        None  None             no
13        None  None             no
```

```
X
```

	Alcohol	Malicacid	Ash	Alcalinity_of_ash	Magnesium	Total_phenols	Flavanoids	Nonflavanoid_phenols	Proanthocyanins	Color_inte
0	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	2.29	
1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	1.28	
2	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	2.81	
3	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	2.18	
4	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	1.82	
...	...	...	...	...	...	...	...	...	...	
173	13.71	5.65	2.45	20.5	95	1.68	0.61	0.52	1.06	
174	13.40	3.91	2.48	23.0	102	1.80	0.75	0.43	1.41	
175	13.27	4.28	2.26	20.0	120	1.59	0.69	0.43	1.35	
176	13.17	2.59	2.37	20.0	120	1.65	0.68	0.53	1.46	
177	14.13	4.10	2.74	24.5	96	2.05	0.76	0.56	1.35	

178 rows × 13 columns

Next steps: View recommended plots

```
y
```

	class
0	1
1	1
2	1
3	1
4	1
...	...
173	3
174	3
175	3
176	3
177	3

178 rows × 1 columns

Next steps: View recommended plots

```
!pip install hvplot
```

```
Requirement already satisfied: hvplot in /usr/local/lib/python3.10/dist-packages (0.9.2)
Requirement already satisfied: bokeh>=1.0.0 in /usr/local/lib/python3.10/dist-packages (from hvplot) (3.3.4)
Requirement already satisfied: colorcet>=2 in /usr/local/lib/python3.10/dist-packages (from hvplot) (3.1.0)
Requirement already satisfied: holoviews>=1.11.0 in /usr/local/lib/python3.10/dist-packages (from hvplot) (1.17.1)
Requirement already satisfied: pandas in /usr/local/lib/python3.10/dist-packages (from hvplot) (2.0.3)
Requirement already satisfied: numpy>=1.15 in /usr/local/lib/python3.10/dist-packages (from hvplot) (1.25.2)
Requirement already satisfied: packaging in /usr/local/lib/python3.10/dist-packages (from hvplot) (24.0)
Requirement already satisfied: panel>=0.11.0 in /usr/local/lib/python3.10/dist-packages (from hvplot) (1.3.8)
Requirement already satisfied: param<3.0,>=1.12.0 in /usr/local/lib/python3.10/dist-packages (from hvplot) (2.1.0)
Requirement already satisfied: Jinja2>=2.9 in /usr/local/lib/python3.10/dist-packages (from bokeh>=1.0.0->hvplot) (3.1.3)
Requirement already satisfied: contourpy>=1 in /usr/local/lib/python3.10/dist-packages (from bokeh>=1.0.0->hvplot) (1.2.1)
Requirement already satisfied: pillow>=7.1.0 in /usr/local/lib/python3.10/dist-packages (from bokeh>=1.0.0->hvplot) (9.4.0)
Requirement already satisfied: PyYAML>=3.10 in /usr/local/lib/python3.10/dist-packages (from bokeh>=1.0.0->hvplot) (6.0.1)
Requirement already satisfied: tornado>=5.1 in /usr/local/lib/python3.10/dist-packages (from bokeh>=1.0.0->hvplot) (6.3.3)
Requirement already satisfied: xyzservices>=2021.09.1 in /usr/local/lib/python3.10/dist-packages (from bokeh>=1.0.0->hvplot) (2024.4.0)
Requirement already satisfied: pyviz-comms>=0.7.4 in /usr/local/lib/python3.10/dist-packages (from holoviews>=1.11.0->hvplot) (3.0.2)
Requirement already satisfied: python-dateutil>=2.8.2 in /usr/local/lib/python3.10/dist-packages (from pandas->hvplot) (2.8.2)
Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.10/dist-packages (from pandas->hvplot) (2023.4)
Requirement already satisfied: tzdata>=2022.1 in /usr/local/lib/python3.10/dist-packages (from pandas->hvplot) (2024.1)
Requirement already satisfied: markdown in /usr/local/lib/python3.10/dist-packages (from panel>=0.11.0->hvplot) (3.6)
Requirement already satisfied: markdown-it-py in /usr/local/lib/python3.10/dist-packages (from panel>=0.11.0->hvplot) (3.0.0)
Requirement already satisfied: linkify-it-py in /usr/local/lib/python3.10/dist-packages (from panel>=0.11.0->hvplot) (2.0.3)
Requirement already satisfied: mdit-py-plugins in /usr/local/lib/python3.10/dist-packages (from panel>=0.11.0->hvplot) (0.4.0)
Requirement already satisfied: requests in /usr/local/lib/python3.10/dist-packages (from panel>=0.11.0->hvplot) (2.31.0)
```

```
Requirement already satisfied: tqdm>=4.48.0 in /usr/local/lib/python3.10/dist-packages (from panel>=0.11.0->hvplot) (4.66.2)
Requirement already satisfied: bleach in /usr/local/lib/python3.10/dist-packages (from panel>=0.11.0->hvplot) (6.1.0)
Requirement already satisfied: typing-extensions in /usr/local/lib/python3.10/dist-packages (from panel>=0.11.0->hvplot) (4.11.0)
Requirement already satisfied: MarkupSafe>=2.0 in /usr/local/lib/python3.10/dist-packages (from Jinja2>=2.9->bokeh>=1.0.0->hvplot) (2.1.
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.10/dist-packages (from python-dateutil>=2.8.2->pandas->hvplot) (1.16.0
Requirement already satisfied: webencodings in /usr/local/lib/python3.10/dist-packages (from bleach->panel>=0.11.0->hvplot) (0.5.1)
Requirement already satisfied: uc-micro-py in /usr/local/lib/python3.10/dist-packages (from linkify-it-py->panel>=0.11.0->hvplot) (1.0.3
Requirement already satisfied: mdurl~=0.1 in /usr/local/lib/python3.10/dist-packages (from markdown-it-py->panel>=0.11.0->hvplot) (0.1.2
Requirement already satisfied: charset-normalizer<4,>=2 in /usr/local/lib/python3.10/dist-packages (from requests->panel>=0.11.0->hvplot
Requirement already satisfied: idna<4,>=2.5 in /usr/local/lib/python3.10/dist-packages (from requests->panel>=0.11.0->hvplot) (3.7)
Requirement already satisfied: urllib3<3,>=1.21.1 in /usr/local/lib/python3.10/dist-packages (from requests->panel>=0.11.0->hvplot) (2.0
Requirement already satisfied: certifi>=2017.4.17 in /usr/local/lib/python3.10/dist-packages (from requests->panel>=0.11.0->hvplot) (202
```

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

from sklearn.model_selection import train_test_split
from sklearn import metrics
from sklearn.linear_model import LinearRegression
%matplotlib inline
```

```
data = pd.concat([X, y], axis = 1)
data
```

	Alcohol	Malicacid	Ash	Alcalinity_of_ash	Magnesium	Total_phenols	Flavanoids	Nonflavanoid_phenols	Proanthocyanins	Color_inte
0	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	2.29	
1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	1.28	
2	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	2.81	
3	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	2.18	
4	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	1.82	
...	...	...	...	...	...	...	...	...	...	
173	13.71	5.65	2.45	20.5	95	1.68	0.61	0.52	1.06	
174	13.40	3.91	2.48	23.0	102	1.80	0.75	0.43	1.41	
175	13.27	4.28	2.26	20.0	120	1.59	0.69	0.43	1.35	
176	13.17	2.59	2.37	20.0	120	1.65	0.68	0.53	1.46	
177	14.13	4.10	2.74	24.5	96	2.05	0.76	0.56	1.35	

178 rows × 14 columns

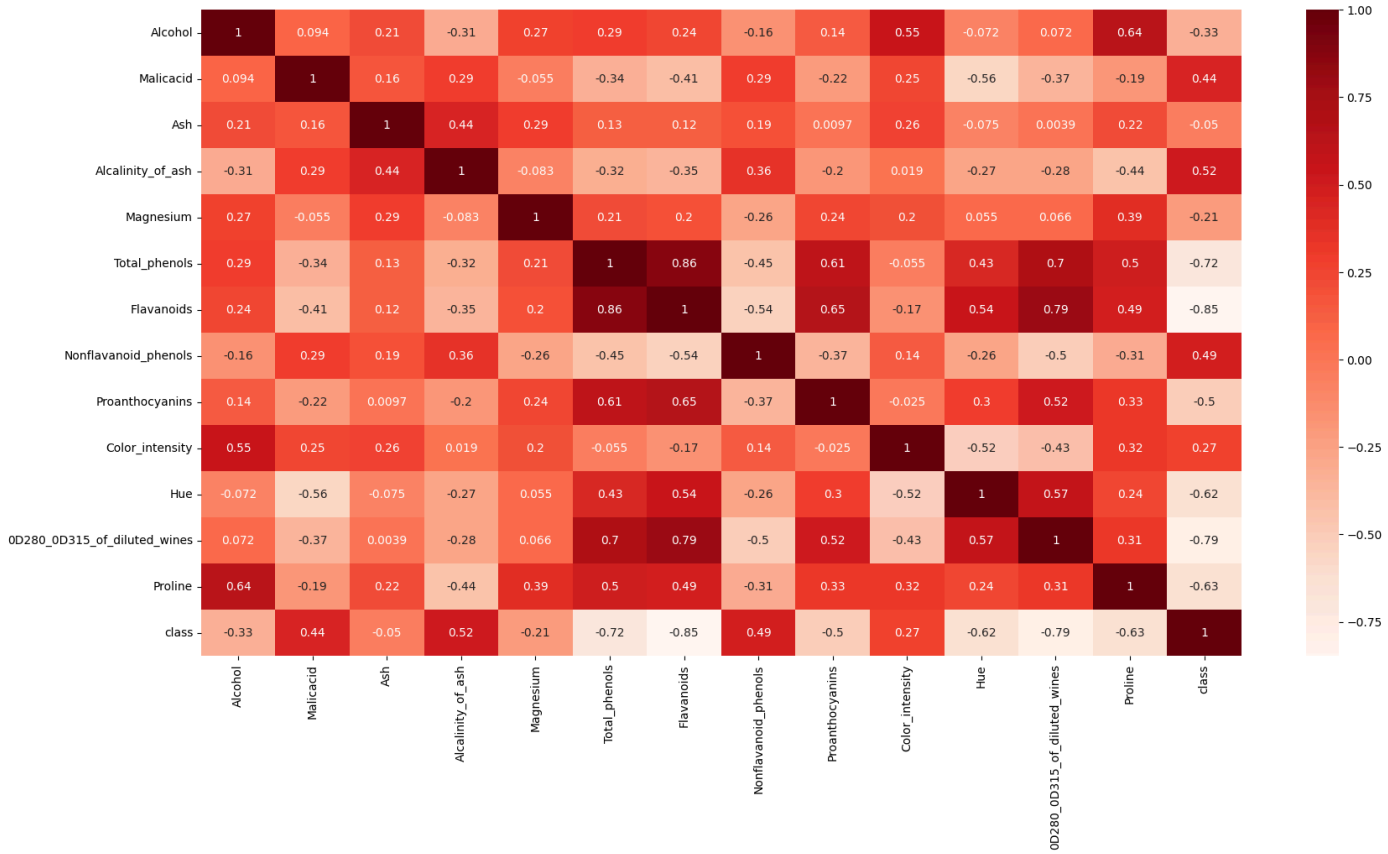
Next steps: View recommended plots

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 178 entries, 0 to 177
Data columns (total 14 columns):
 #   Column                        Non-Null Count  Dtype  
---  ------                        --------------  -----  
 0   Alcohol                       178 non-null    float64
 1   Malicacid                     178 non-null    float64
 2   Ash                           178 non-null    float64
 3   Alcalinity_of_ash             178 non-null    float64
 4   Magnesium                     178 non-null    int64  
 5   Total_phenols                 178 non-null    float64
 6   Flavanoids                    178 non-null    float64
 7   Nonflavanoid_phenols          178 non-null    float64
 8   Proanthocyanins               178 non-null    float64
 9   Color_intensity               178 non-null    float64
 10  Hue                           178 non-null    float64
 11  0D280_0D315_of_diluted_wines  178 non-null    float64
 12  Proline                       178 non-null    int64  
 13  class                         178 non-null    int64  
dtypes: float64(11), int64(3)
memory usage: 19.6 KB
```

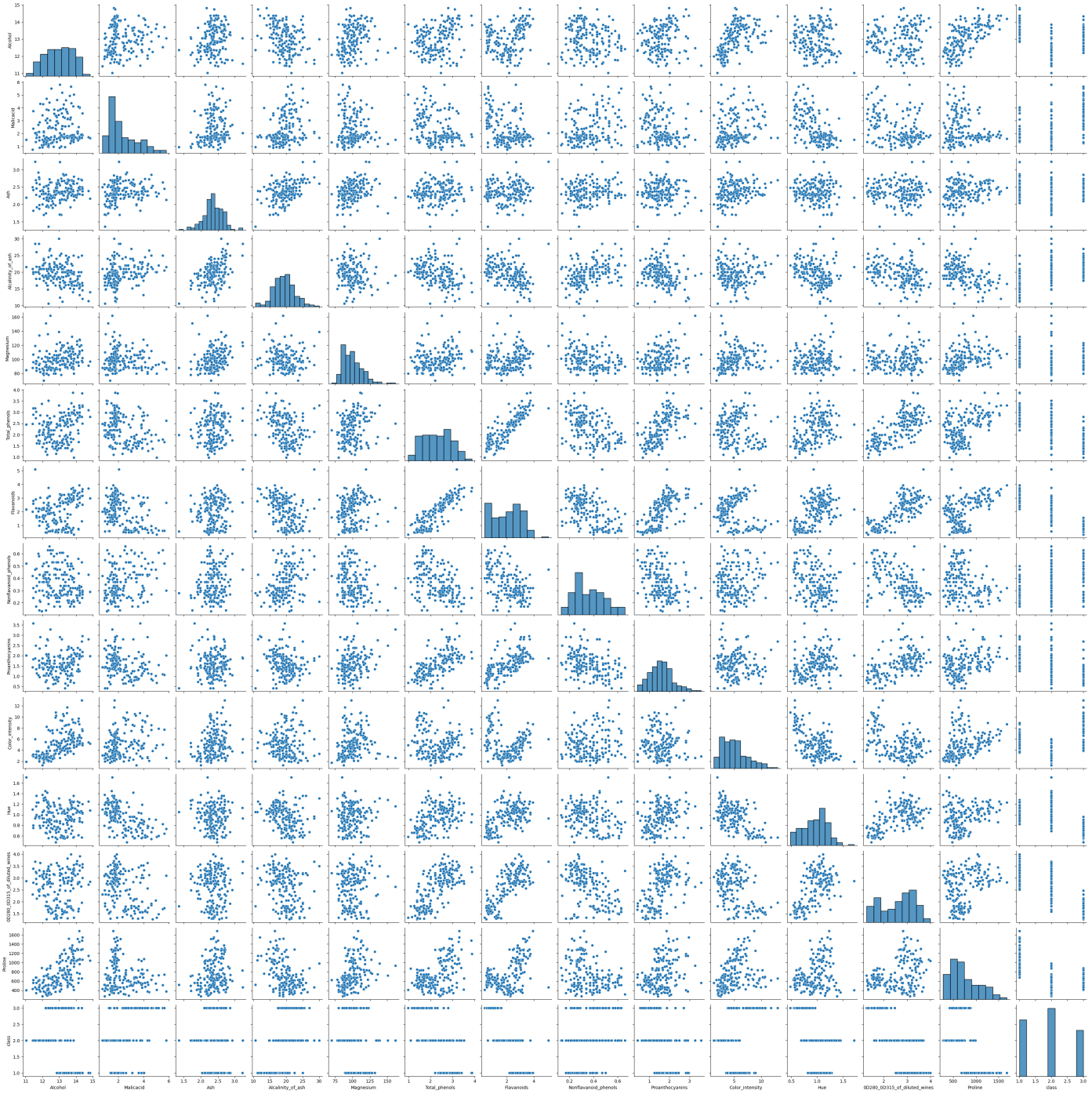
Correlation between columns using heatmap

```
plt.figure(figsize = (20,10))
ax = sns.heatmap(data.corr(), annot = True, cmap = 'Reds')
```




```
sns.pairplot(data)
```

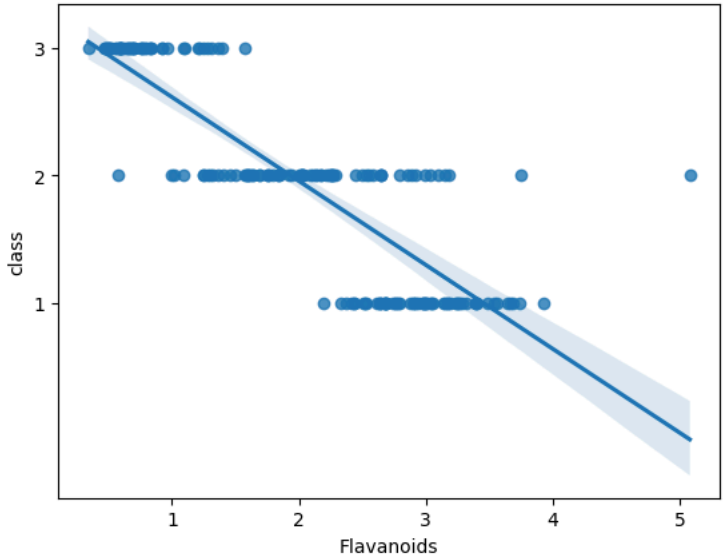
```
<seaborn.axisgrid.PairGrid at 0x7d5c07d47640>
```



Logicstic regression is used to find or examine the association between categorical variables with dependent variables. In this case, we only have 1 categorical varable, which is the 'class' column.

```
sns.regplot(data = data, x = 'Flavanoids', y = 'class')
plt.yticks(data['class'].unique())
```

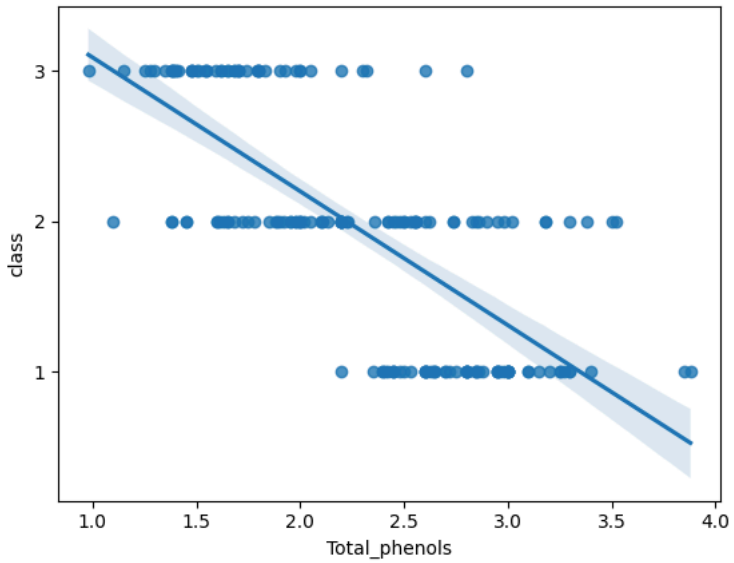
```
([<matplotlib.axis.YTick at 0x7d5c00069db0>,
  <matplotlib.axis.YTick at 0x7d5bfffc6ec0>,
  <matplotlib.axis.YTick at 0x7d5bfffc7d90>],
 [Text(0, 1, '1'), Text(0, 2, '2'), Text(0, 3, '3')])
```



Observing our plot, we can see that the higher the class of our wine, it will most likely contain less flavanoids

```
sns.regplot(data = data, x = 'Total_phenols', y = 'class')
plt.yticks(data['class'].unique())
```

```
([<matplotlib.axis.YTick at 0x7d5bffec8d00>,
  <matplotlib.axis.YTick at 0x7d5bffec86a0>,
  <matplotlib.axis.YTick at 0x7d5c00062470>],
 [Text(0, 1, '1'), Text(0, 2, '2'), Text(0, 3, '3')])
```



The phenols in wine is the taste of its bitterness and acidity. According to our graph, we can see that the higher the class of the wine, the lower its phenols which means less bitter and less acidic