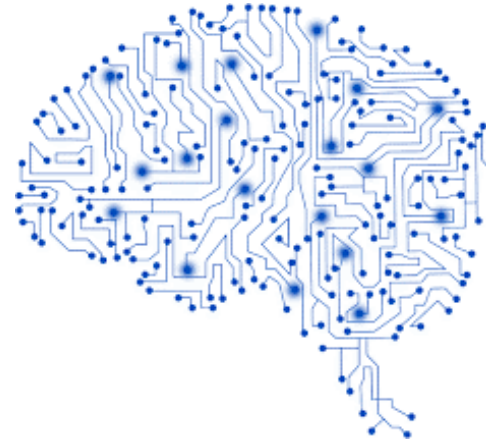




University of Minho
School of Engineering



Dados e Aprendizagem Automática

Data Exploration and Preparation

DAA @ MEI-1º/MiEI-4º – 1º Semestre

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Part III

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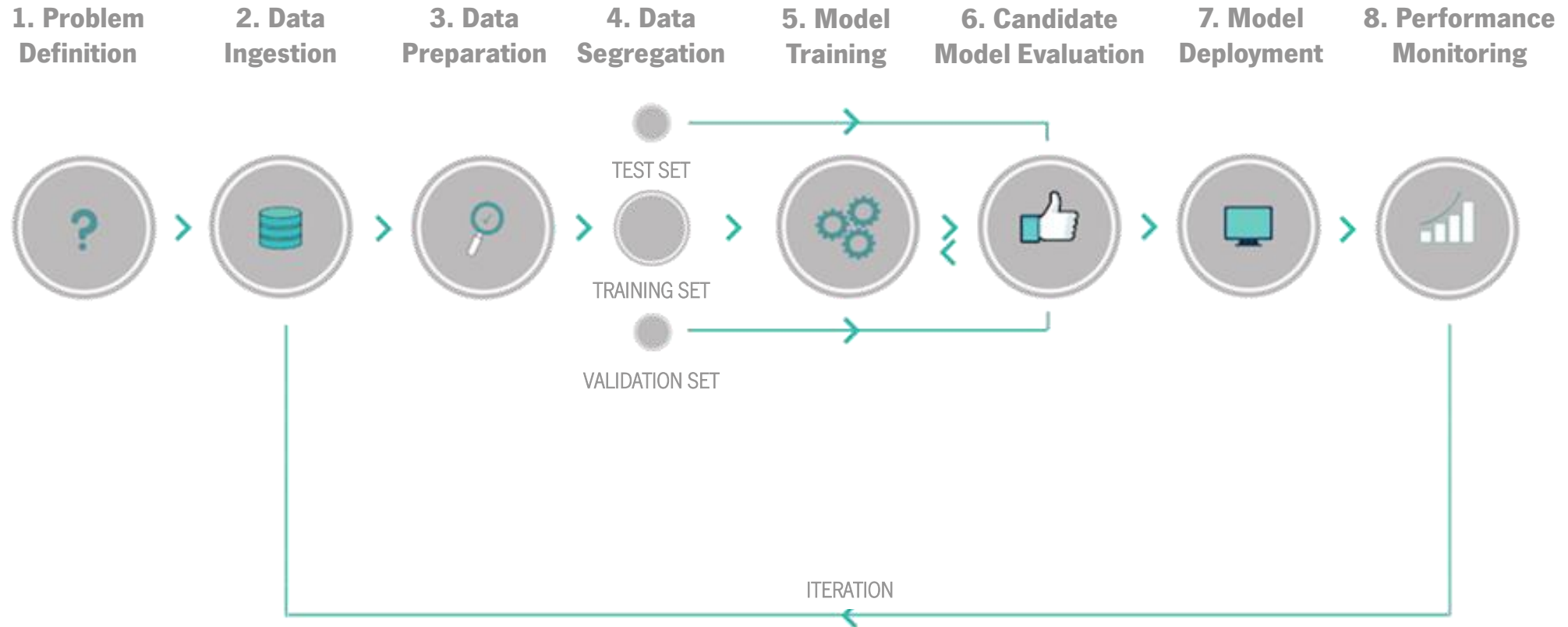
- Understanding The Problem
- Data Exploration
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Understanding The Problem

Understanding The Problem

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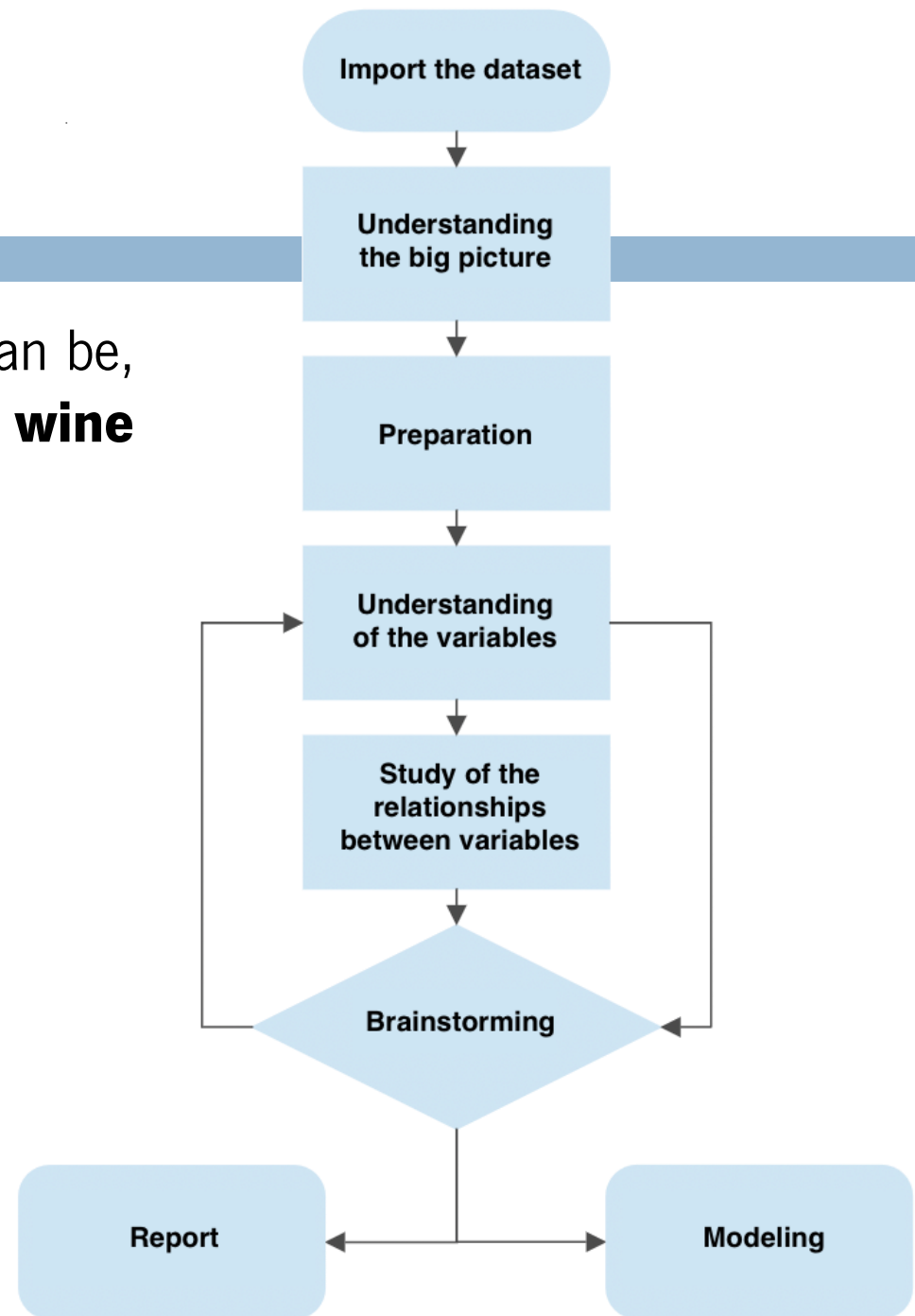


We need to look at our data and understand it.

Understanding the data is a huge step in the process and, as such, will take time. Nevertheless, it will give us a flavour of our dataset, each variable, its meaning and its relevance to this problem.

Understanding The Problem

Let's understand the type of features, how important it can be, if it is described in another feature, etc. Let's use the **wine dataset** available here: <https://tinyurl.com/4cshpfac>



Imports

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Let's import the necessary libraries:

```
import sklearn as skl
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn import preprocessing
```

Load the dataset and inspect some meta-data:

```
df = pd.read_csv('wine.csv')
```



Data Exploration

Data Exploration

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What about actual data? What can we **see/learn/understand** from this data?

```
print(df.columns)
```

```
Index(['Alcohol', 'Malic acid', 'Ash', 'Alcalinity of ash', 'Magnesium',  
      'Total phenols', 'Flavanoids', 'Nonflavanoid phenols',  
      'Proanthocyanins', 'Color intensity', 'Hue',  
      'OD280/OD315 of diluted wines', 'Proline', 'Class'],  
      dtype='object')
```

```
df.head()
```

	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue	OD280/OD315 of diluted wines	Proline	Class
0	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	2.29	5.64	1.04	3.92	1065	one
1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	1.28	4.38	1.05	3.40	1050	one
2	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	2.81	5.68	1.03	3.17	1185	one
3	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	2.18	7.80	0.86	3.45	1480	one
4	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	1.82	4.32	1.04	2.93	735	one

Data Exploration

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```
df.tail()
```

	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue	OD280/OD315 of diluted wines	Proline	Class
173	13.71	5.65	2.45	20.5	95	1.68	0.61	0.52	1.06	7.7	0.64	1.74	740	three
174	13.40	3.91	2.48	23.0	102	1.80	0.75	0.43	1.41	7.3	0.70	1.56	750	three
175	13.27	4.28	2.26	20.0	120	1.59	0.69	0.43	1.35	10.2	0.59	1.56	835	three
176	13.17	2.59	2.37	20.0	120	1.65	0.68	0.53	1.46	9.3	0.60	1.62	840	three
177	14.13	4.10	2.74	24.5	96	2.05	0.76	0.56	1.35	9.2	0.61	1.60	560	three

```
df.shape
```

```
(178, 14)
```

We can see that we have 178 entries with 14 attributes each.

The Class has **3 classifications**: one, two and three, which refer to the type of wine.

Data Exploration

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There are **no null values**, and the attributes are all numeric except for the Class.

```
df.dtypes
```

```
Alcohol          float64
Malic acid       float64
Ash              float64
Alcalinity of ash float64
Magnesium        int64
Total phenols    float64
Flavanoids       float64
Nonflavanoid phenols float64
Proanthocyanins  float64
Color intensity  float64
Hue              float64
OD280/OD315 of diluted wines float64
Proline          int64
Class            object
dtype: object
```

```
df.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   Malic acid                             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  OD280/OD315 of diluted wines           178 non-null    float64
12  Proline                                178 non-null    int64
13  Class                                  178 non-null    object
dtypes: float64(11), int64(2), object(1)
memory usage: 19.6+ KB
```

Data Exploration

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We can also get some descriptive statistics (for all numeric data or only desired):

```
df.describe()
```

	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue	OD280/OD315 of diluted wines	Proline
count	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000
mean	13.000618	2.336348	2.366517	19.494944	99.741573	2.295112	2.029270	0.361854	1.590899	5.058090	0.957449	2.611685	746.893258
std	0.811827	1.117146	0.274344	3.339564	14.282484	0.625851	0.998859	0.124453	0.572359	2.318286	0.228572	0.709990	314.907474
min	11.030000	0.740000	1.360000	10.600000	70.000000	0.980000	0.340000	0.130000	0.410000	1.280000	0.480000	1.270000	278.000000
25%	12.362500	1.602500	2.210000	17.200000	88.000000	1.742500	1.205000	0.270000	1.250000	3.220000	0.782500	1.937500	500.500000
50%	13.050000	1.865000	2.360000	19.500000	98.000000	2.355000	2.135000	0.340000	1.555000	4.690000	0.965000	2.780000	673.500000
75%	13.677500	3.082500	2.557500	21.500000	107.000000	2.800000	2.875000	0.437500	1.950000	6.200000	1.120000	3.170000	985.000000
max	14.830000	5.800000	3.230000	30.000000	162.000000	3.880000	5.080000	0.660000	3.580000	13.000000	1.710000	4.000000	1680.000000

```
df['Color intensity'].describe()
```

```
count    178.000000
mean         5.058090
std         2.318286
min         1.280000
25%         3.220000
50%         4.690000
75%         6.200000
max        13.000000
Name: Color intensity, dtype: float64
```

Data Exploration

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What about missing values?

```
df.isna().any()
```

Alcohol	False
Malic acid	False
Ash	False
Alcalinity of ash	False
Magnesium	False
Total phenols	False
Flavanoids	False
Nonflavanoid phenols	False
Proanthocyanins	False
Color intensity	False
Hue	False
OD280/OD315 of diluted wines	False
Proline	False
Class	False
dtype: bool	

```
print(df.isna().sum())
```

Alcohol	0
Malic acid	0
Ash	0
Alcalinity of ash	0
Magnesium	0
Total phenols	0
Flavanoids	0
Nonflavanoid phenols	0
Proanthocyanins	0
Color intensity	0
Hue	0
OD280/OD315 of diluted wines	0
Proline	0
Class	0
dtype: int64	

Data Exploration

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Our analysis allows us to better characterize the dataset:

- It has **178 entries**
- **14 attributes** - 13 are physicochemical properties of the wine and 1 is the classification
- All **non-null values**
- There **are no missing values**

The **goal** of working with this dataset can be to **identify the type of wine by its properties** - the target is a numeric categorical variable that covers the values of one, two and three.
When used for modelling, the characteristics of the wine can be used to **predict its type**.



Data Preparation

Data Preparation

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It consists of several steps. Often (in fact, a lot of times), you will need to check the API of the library you are using.

Here are some links you can save for future reference:

- **Numpy** (<https://numpy.org/doc/stable/>)
- **Pandas** (<https://pandas.pydata.org/docs/>)
- **Matplotlib** (<https://matplotlib.org/stable/users/index.html>)
- **Seaborn** (<https://seaborn.pydata.org/api.html>)
- **Scikit Learn** (<https://scikit-learn.org/stable/api/index.html>)

Data Preparation

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And here are some basic Pandas functions that you will need (sometime) in the future for data preparation:

```
pandas.DataFrame.drop  
pandas.DataFrame.drop_duplicates  
pandas.DataFrame.fillna  
pandas.DataFrame.isna  
pandas.DataFrame.interpolate  
pandas.DataFrame.dropna  
pandas.DataFrame.groupby  
pandas.DataFrame.loc  
pandas.DataFrame.iloc
```


Data Preparation

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Some basic Sklearn functions/classes you will need as well:

`sklearn.preprocessing.MinMaxScaler`

`sklearn.preprocessing.StandardScaler`

`sklearn.preprocessing.KBinsDiscretizer`

`sklearn.preprocessing.LabelEncoder`

`sklearn.feature_selection`

`sklearn.metrics`

Data Preparation and Transformation

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Remove duplicate values

```
print(df.duplicated().sum())
print(df.drop_duplicates(inplace=True))
print(df.info())
```

```
0
None
<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   Malic acid                            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  OD280/OD315 of diluted wines          178 non-null    float64
12  Proline                               178 non-null    int64
13  Class                                 178 non-null    object
dtypes: float64(11), int64(2), object(1)
memory usage: 19.6+ KB
None
```

Rename attributes

```
df.rename(columns={"OD280/OD315 of diluted wines": "Protein Concentration"}, inplace=True)
df.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   Malic acid                            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  Protein Concentration                  178 non-null    float64
12  Proline                               178 non-null    int64
13  Class                                 178 non-null    object
dtypes: float64(11), int64(2), object(1)
memory usage: 19.6+ KB
```

Data Preparation and Transformation

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```
df_clean = df.drop(df.loc[(df['Ash']<2) & (df['Alcalinity of ash']>15)].index)
print(df_clean)
```

As all the variables appear to be physicochemical measures, they could all be useful and help to define the segmentation of the wine type. There is **no reason to remove columns**.

	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	\
0	14.23	1.71	2.43	15.6	127	2.80	
1	13.20	1.78	2.14	11.2	100	2.65	
2	13.16	2.36	2.67	18.6	101	2.80	
3	14.37	1.95	2.50	16.8	113	3.85	
4	13.24	2.59	2.87	21.0	118	2.80	
..	
173	13.71	5.65	2.45	20.5	95	1.68	
174	13.40	3.91	2.48	23.0	102	1.80	
175	13.27	4.28	2.26	20.0	120	1.59	
176	13.17	2.59	2.37	20.0	120	1.65	
177	14.13	4.10	2.74	24.5	96	2.05	

	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue	\
0	3.06		0.28	2.29	5.64	1.04
1	2.76		0.26	1.28	4.38	1.05
2	3.24		0.30	2.81	5.68	1.03
3	3.49		0.24	2.18	7.80	0.86
4	2.69		0.39	1.82	4.32	1.04
..
173	0.61		0.52	1.06	7.70	0.64
174	0.75		0.43	1.41	7.30	0.70
175	0.69		0.43	1.35	10.20	0.59
176	0.68		0.53	1.46	9.30	0.60
177	0.76		0.56	1.35	9.20	0.61

	Protein Concentration	Proline	Class
0	3.92	1065	one
1	3.40	1050	one
2	3.17	1185	one
3	3.45	1480	one
4	2.93	735	one
..
173	1.74	740	three
174	1.56	750	three
175	1.56	835	three
176	1.62	840	three
177	1.60	560	three

[164 rows x 14 columns]



Univariate Analysis

Univariate Analysis

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Get basic information by iterating through each relevant variable:

```
df['Alcohol'].value_counts()
```

```
Alcohol
13.05    6
12.37    6
12.08    5
12.29    4
12.42    3
..
13.72    1
13.29    1
13.74    1
13.77    1
14.13    1
Name: count, Length: 126, dtype: int64
```

```
df['Class'].value_counts(normalize=True)
```

```
Class
two      0.398876
one      0.331461
three    0.269663
Name: proportion, dtype: float64
```

```
...
Numeric variables
...
df['Magnesium'].describe()
```

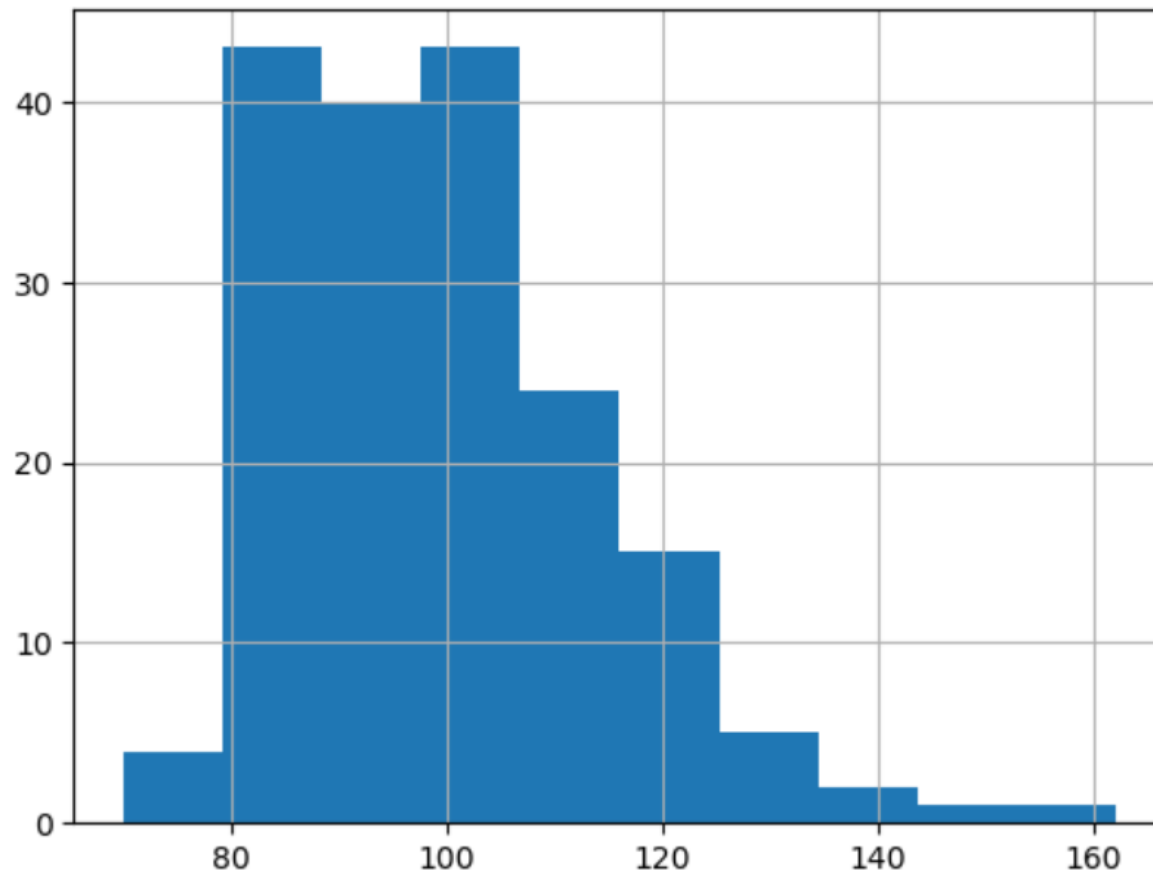
```
count      178.000000
mean       99.741573
std        14.282484
min        70.000000
25%        88.000000
50%        98.000000
75%       107.000000
max       162.000000
Name: Magnesium, dtype: float64
```

Univariate Analysis

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```
print(f"Histogram: {df['Magnesium'].hist()}")
```

Histogram: Axes(0.125,0.11;0.775x0.77)



Does **not follow a normal curve** and **has spikes**.

Univariate Analysis

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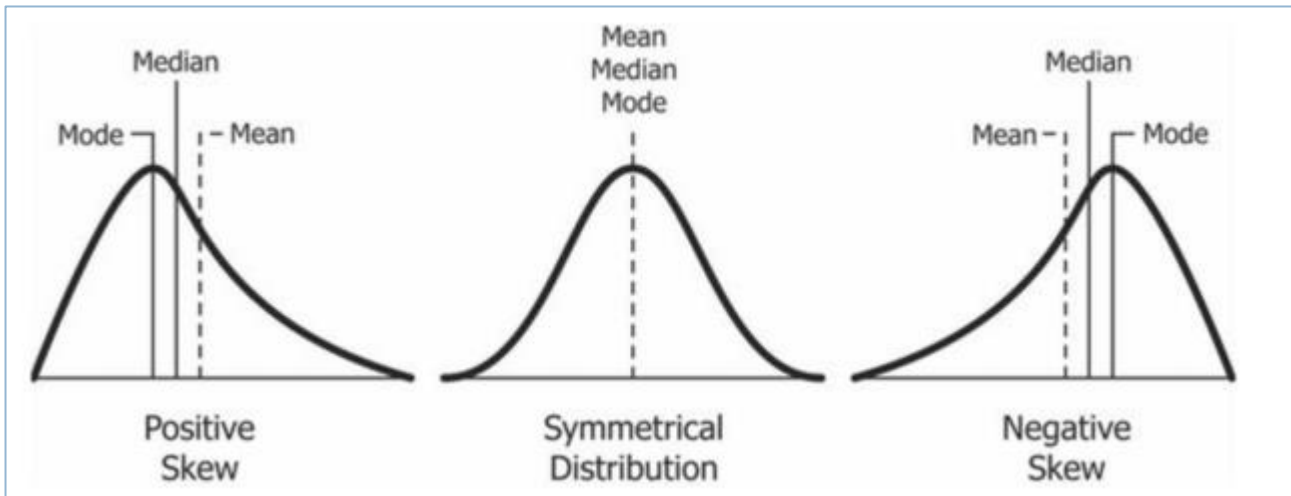
```
print(f"Skewness: {df['Magnesium'].skew()}")
```

Skewness: 1.098191054755161

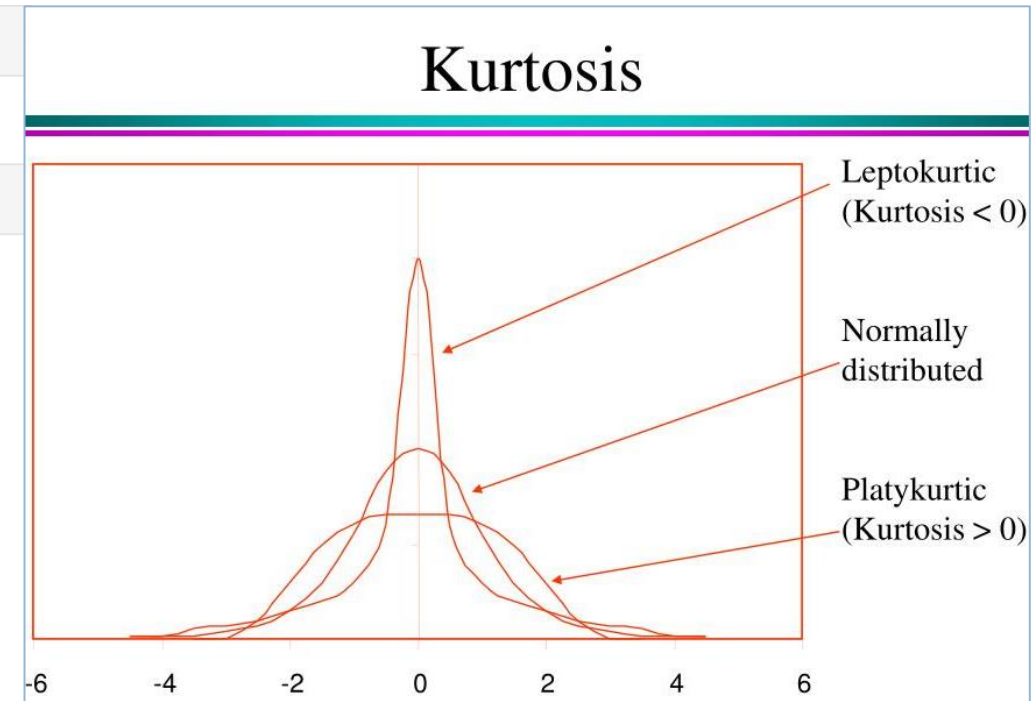
```
print(f"Kurtosis: {df['Magnesium'].kurt()}")
```

Kurtosis: 2.1049913235905557

Kurtosis and asymmetry values are **greater than 1**.



<https://t.ly/rISUJ>



<https://t.ly/us-2l>

Univariate Analysis

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Now we can summarize the dataset by creating a small document with detailed information:

- ***Variable***: the name of the variable
- ***Type***: the type or format of the variable. This can be categorical, numerical, Boolean, etc.
- ***Context***: useful information to understand the semantic space of the variable. In the case of our dataset, the context is always the physicochemical one
- ***Expectation***: how relevant is this variable for our task? We can use a scale “High, Medium, Low”
- ***Comments***: if we have any comments to make about the variable



Multivariate Analysis

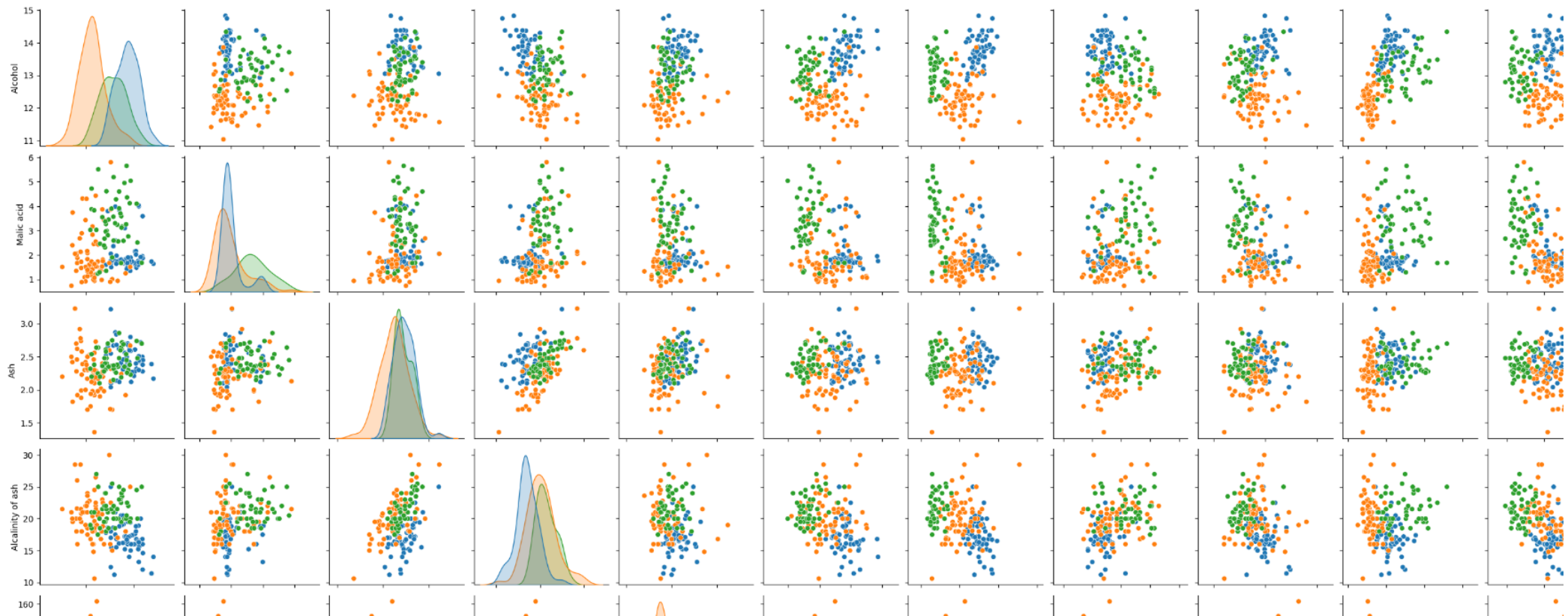
Multivariate Analysis

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We can start by looking at the **relationship** between all the variables:

```
sns.pairplot(df, hue="Class")
```

<seaborn.axisgrid.PairGrid at 0x1e31c6eb620>



Multivariate Analysis

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We can **group** by variables:

```
df.groupby(by=['Class']).mean(numeric_only=True)
```

	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue	Protein Concentration	Proline
Class													
one	13.744746	2.010678	2.455593	17.037288	106.338983	2.840169	2.982373	0.290000	1.899322	5.528305	1.062034	3.157797	1115.711864
three	13.153750	3.333750	2.437083	21.416667	99.312500	1.678750	0.781458	0.447500	1.153542	7.396250	0.682708	1.683542	629.895833
two	12.278732	1.932676	2.244789	20.238028	94.549296	2.258873	2.080845	0.363662	1.630282	3.086620	1.056282	2.785352	519.507042

Multivariate Analysis

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```
df.groupby(by=['Class', 'Proline']).mean(numeric_only=True)
```

		Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue	Protein Concentration
Class	Proline												
one	680	13.240	3.980	2.290	17.5	103.0	2.640	2.630	0.32	1.66	4.360	0.820	3.00
	735	13.240	2.590	2.870	21.0	118.0	2.800	2.690	0.39	1.82	4.320	1.040	2.93
	760	14.220	3.990	2.510	13.2	128.0	3.000	3.040	0.20	2.08	5.100	0.890	3.53
	770	12.930	3.800	2.650	18.6	102.0	2.410	2.410	0.25	1.98	4.500	1.030	3.52
	780	14.060	1.630	2.280	16.0	126.0	3.000	3.170	0.24	2.10	5.650	1.090	3.71
...
two	750	12.835	0.965	2.155	15.9	123.0	2.215	1.575	0.45	1.59	3.285	1.040	2.12
	870	12.290	1.610	2.210	20.4	103.0	1.100	1.020	0.37	1.46	3.050	0.906	1.82
	886	11.960	1.090	2.300	21.0	101.0	3.380	2.140	0.13	1.65	3.210	0.990	3.13
	937	12.470	1.520	2.200	19.0	162.0	2.500	2.270	0.32	3.28	2.600	1.160	2.63
	985	12.990	1.670	2.600	30.0	139.0	3.300	2.890	0.21	1.96	3.350	1.310	3.50

138 rows × 12 columns

Multivariate Analysis

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```
print(df.groupby(by=['Alcohol']).agg([pd.Series.mode]))
```

Alcohol	Malic acid mode	Ash mode	Alcalinity of ash mode	Magnesium mode	Total phenols mode	\
11.03	1.51	2.2	21.5	85	2.46	
11.41	0.74	2.5	21.0	88	2.48	
11.45	2.4	2.42	20.0	96	2.9	
11.46	3.74	1.82	19.5	107	3.18	
11.56	2.05	3.23	28.5	119	3.18	
...	
14.37	1.95	2.5	16.8	113	3.85	
14.38	[1.87, 3.59]	[2.28, 2.38]	[12.0, 16.0]	102	[3.25, 3.3]	
14.39	1.87	2.45	14.6	96	2.5	
14.75	1.73	2.39	11.4	91	3.1	
14.83	1.64	2.17	14.0	97	2.8	

Alcohol	Flavanoids mode	Nonflavanoid phenols mode	Proanthocyanins mode	Color intensity mode	\
11.03	2.17	0.52	2.01	1.9	
11.41	2.01	0.42	1.44	3.08	
11.45	2.79	0.32	1.83	3.25	
11.46	2.58	0.24	3.58	2.9	
11.56	5.08	0.47	1.87	6.0	
...	
14.37	3.49	0.24	2.18	7.8	
14.38	[3.17, 3.64]	[0.27, 0.29]	[2.19, 2.96]	[4.9, 7.5]	
14.39	2.52	0.3	1.98	5.25	
14.75	3.69	0.43	2.81	5.4	
14.83	2.98	0.29	1.98	5.2	

```
print(df.groupby(by=['Alcohol', 'Flavanoids']).mean(numeric_only=True))
```

Alcohol	Flavanoids	Malic acid	Ash	Alcalinity of ash	Magnesium	\
11.03	2.17	1.51	2.20	21.5	85.0	
11.41	2.01	0.74	2.50	21.0	88.0	
11.45	2.79	2.40	2.42	20.0	96.0	
11.46	2.58	3.74	1.82	19.5	107.0	
11.56	5.08	2.05	3.23	28.5	119.0	
...	
14.38	3.17	3.59	2.28	16.0	102.0	
	3.64	1.87	2.38	12.0	102.0	
14.39	2.52	1.87	2.45	14.6	96.0	
14.75	3.69	1.73	2.39	11.4	91.0	
14.83	2.98	1.64	2.17	14.0	97.0	

Alcohol	Flavanoids	Total phenols	Nonflavanoid phenols	Proanthocyanins	\
11.03	2.17	2.46	0.52	2.01	
11.41	2.01	2.48	0.42	1.44	
11.45	2.79	2.90	0.32	1.83	
11.46	2.58	3.18	0.24	3.58	
11.56	5.08	3.18	0.47	1.87	
...	
14.38	3.17	3.25	0.27	2.19	
	3.64	3.30	0.29	2.96	
14.39	2.52	2.50	0.30	1.98	
14.75	3.69	3.10	0.43	2.81	
14.83	2.98	2.80	0.29	1.98	

Multivariate Analysis

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We can create **bins**.

Data binning (or bucketing) groups data into bins (or buckets) in the sense that it replaces values contained in a small interval with a single representative value for that interval. It is a **type of data pre-processing**, a mechanism that also includes missing value handling, formatting, normalization and standardization.

Binning is a **data smoothing technique**. Data smoothing is **used to remove noise from data**.

```
estimator = preprocessing.KBinsDiscretizer(n_bins=3, encode='ordinal', strategy='quantile')
df['alcohol_binned'] = estimator.fit_transform(df[['Alcohol']])
```

```
print('Bin Edges')
print(estimator.bin_edges_[0])
print('Alcohol Groups')
print(df.groupby(by=['alcohol_binned']).count())
```

Bin Edges

[11.03 12.52 13.48 14.83]

Alcohol Groups

	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium \
alcohol_binned					
0.0	59	59	59	59	59
1.0	58	58	58	58	58
2.0	61	61	61	61	61

	Total phenols	Flavanoids	Nonflavanoid phenols \
alcohol_binned			
0.0	59	59	59
1.0	58	58	58
2.0	61	61	61

	Proanthocyanins	Color intensity	Hue	Protein Concentration \
alcohol_binned				
0.0	59	59	59	59
1.0	58	58	58	58
2.0	61	61	61	61

	Proline	Class
alcohol_binned		
0.0	59	59
1.0	58	58
2.0	61	61

Multivariate Analysis

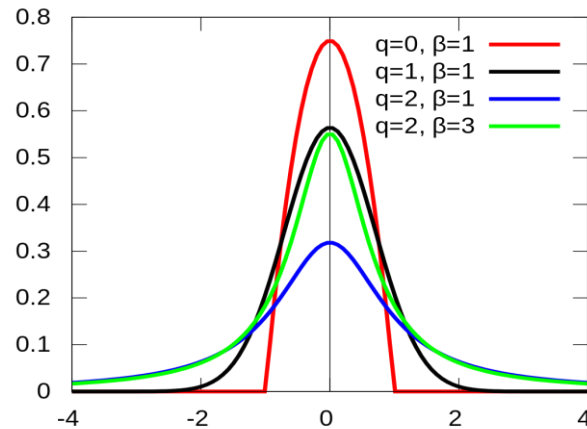
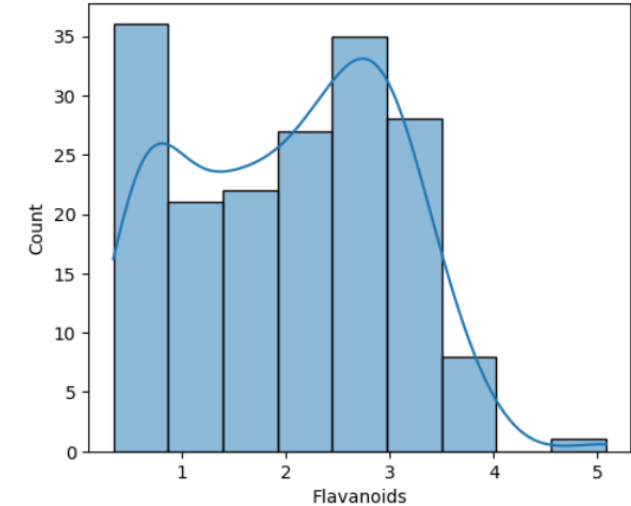
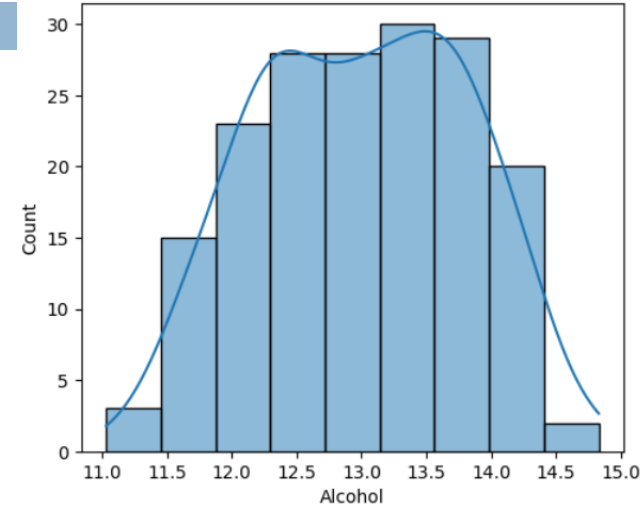
31

Dispersion: does it follow a Gaussian distribution?

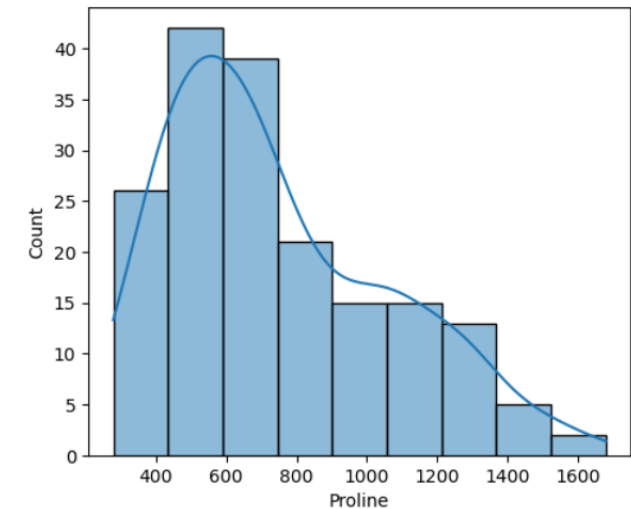
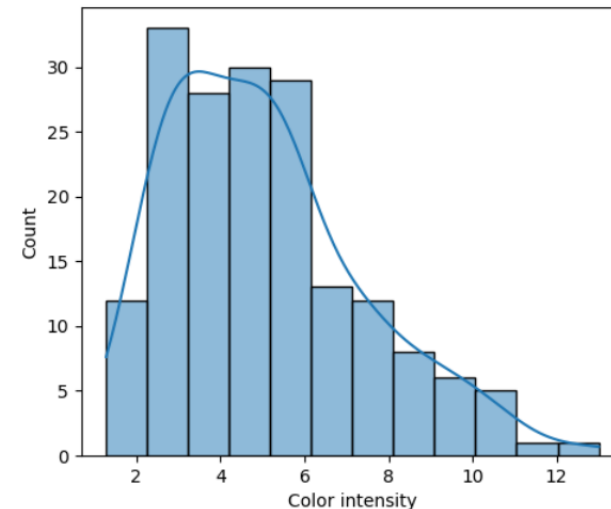
```
fig, axs = plt.subplots(2, 2, figsize=(12, 10))
fig.suptitle('Histograms')

sns.histplot(df['Alcohol'], ax=axs[0, 0], kde=True)
sns.histplot(df['Flavanoids'], ax=axs[0, 1], kde=True)
sns.histplot(df['Color intensity'], ax=axs[1, 0], kde=True)
sns.histplot(df['Proline'], ax=axs[1, 1], kde=True)
```

Histograms



https://en.wikipedia.org/wiki/Q-Gaussian_distribution

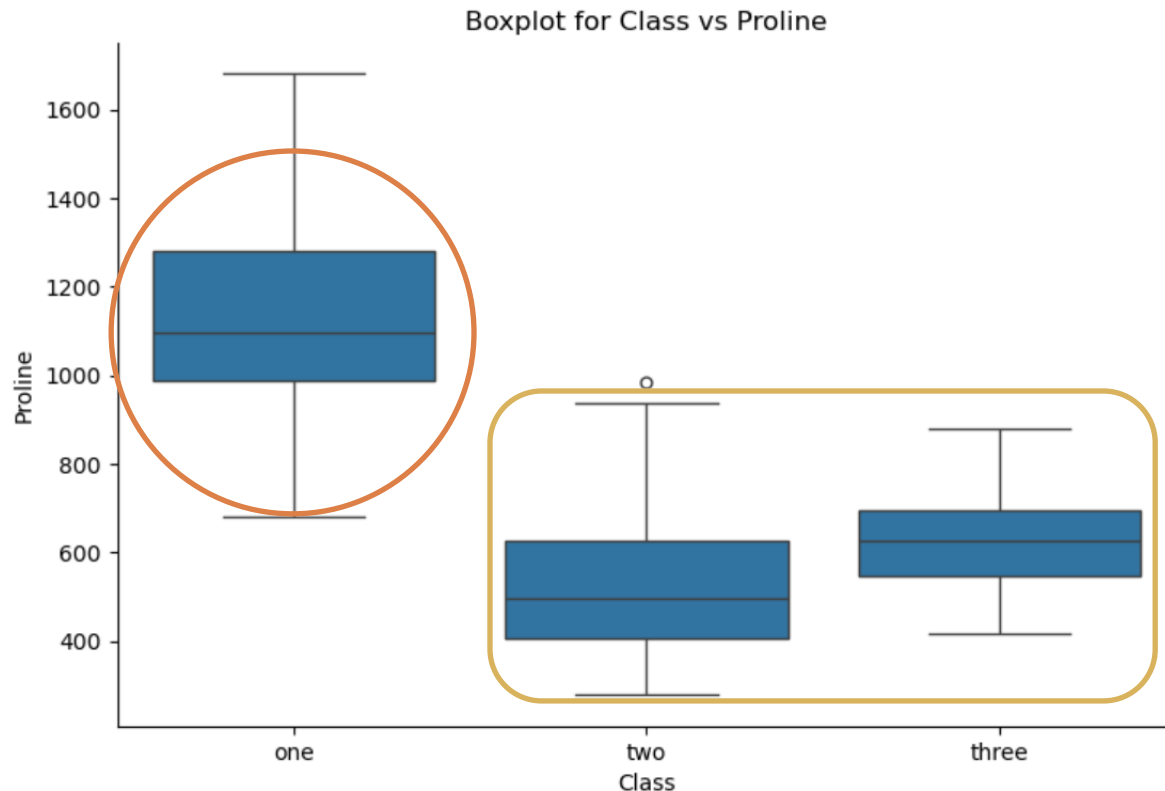


Multivariate Analysis

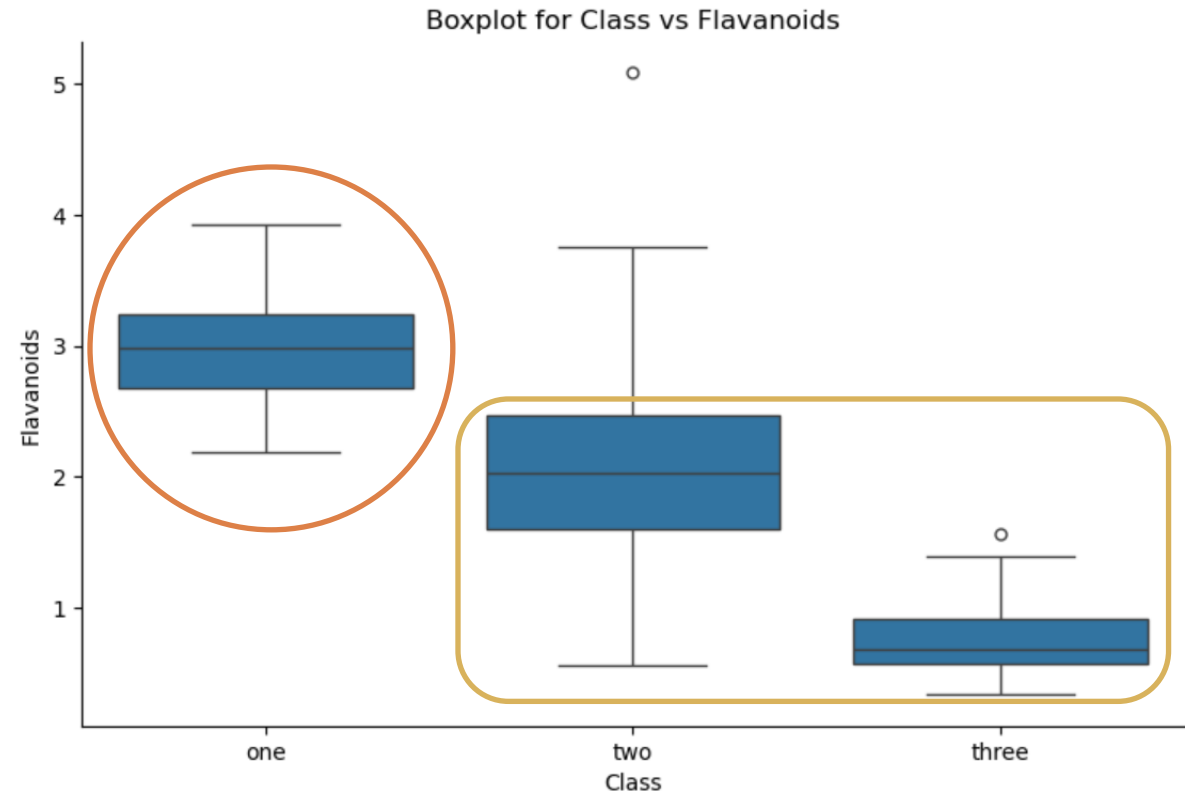
32

The best way to understand the relationship between a numeric variable and a categorical variable is through a boxplot:

```
sns.catplot(x="Class", y="Proline", data=df, kind="box", aspect=1.5)  
plt.title("Boxplot for Class vs Proline")  
plt.show()
```



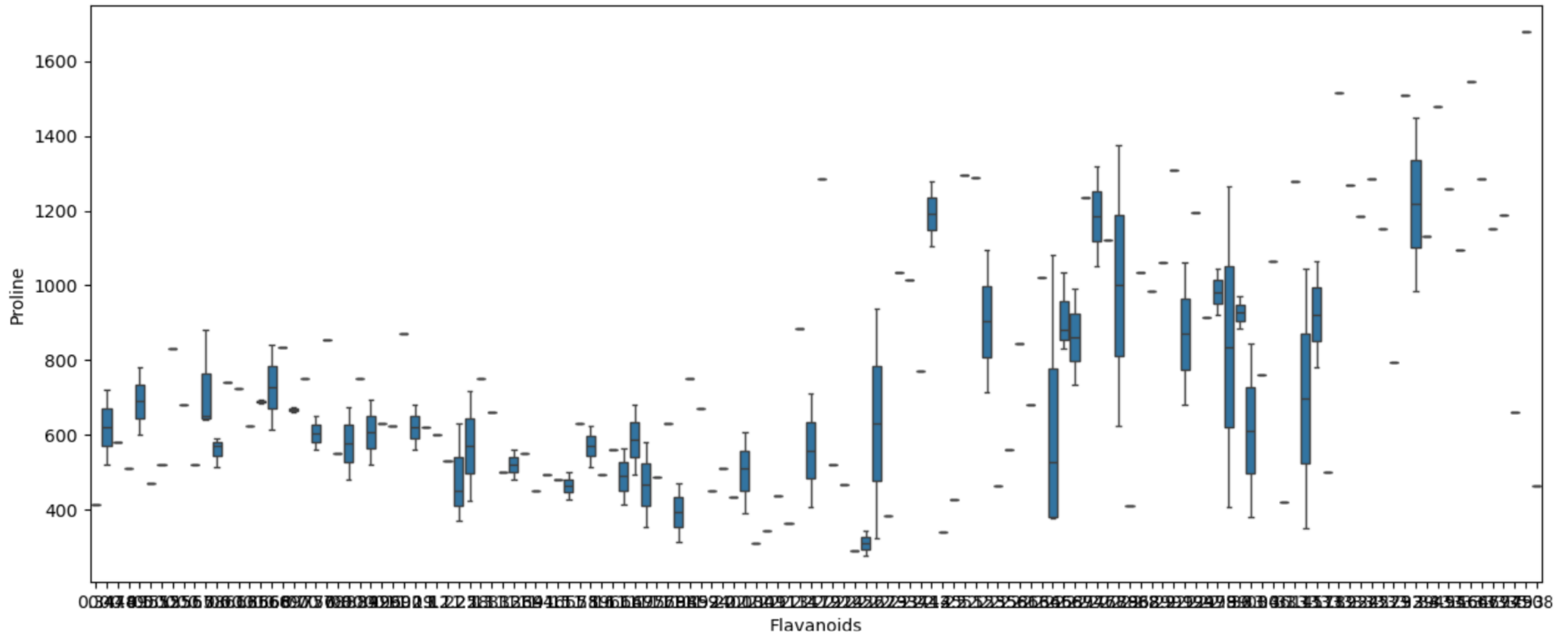
```
sns.catplot(x="Class", y="Flavanoids", data=df, kind="box", aspect=1.5)  
plt.title("Boxplot for Class vs Flavanoids")  
plt.show()
```



Multivariate Analysis

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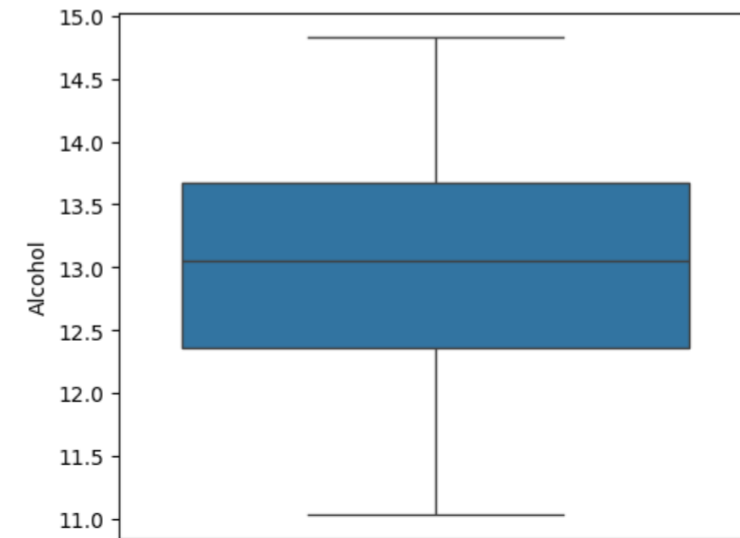
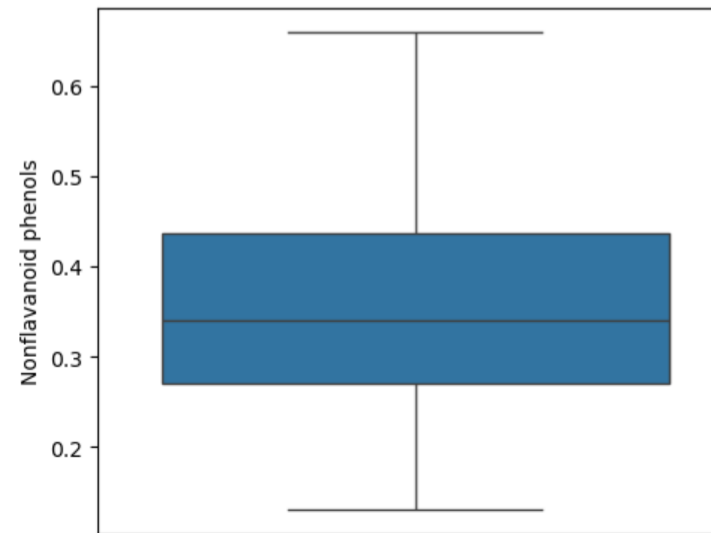
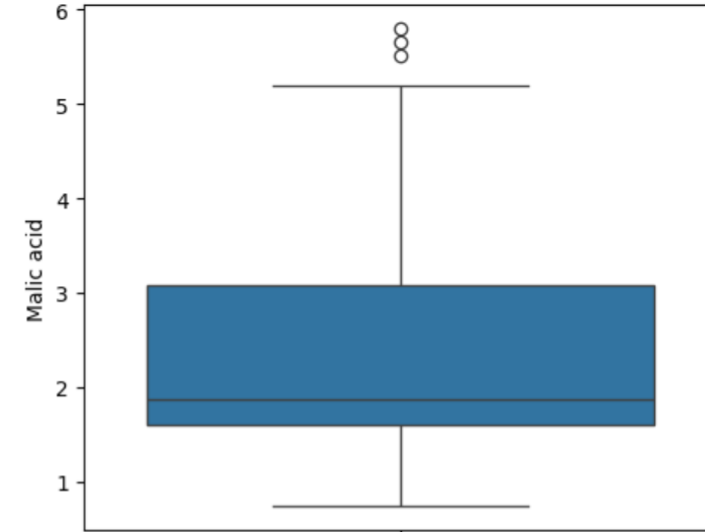
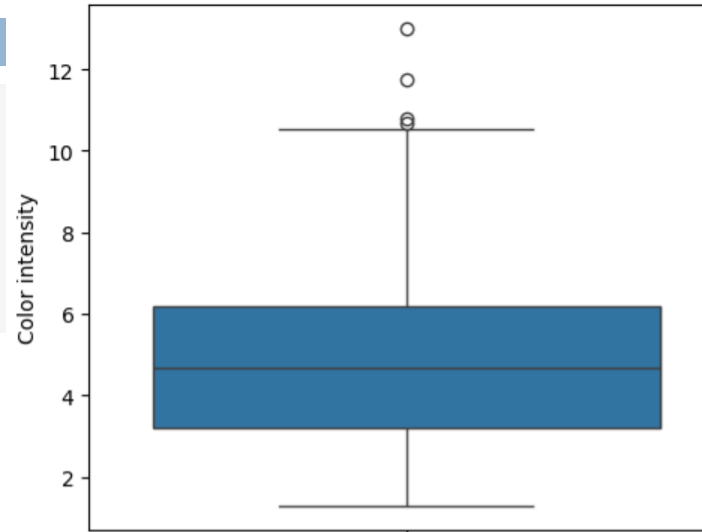
```
_, ax = plt.subplots(figsize=(15, 6))  
fig.suptitle('Boxplot for Flavanoids vs Proline')  
sns.boxplot(x=df["Flavanoids"], y=df["Proline"])
```



Multivariate Analysis

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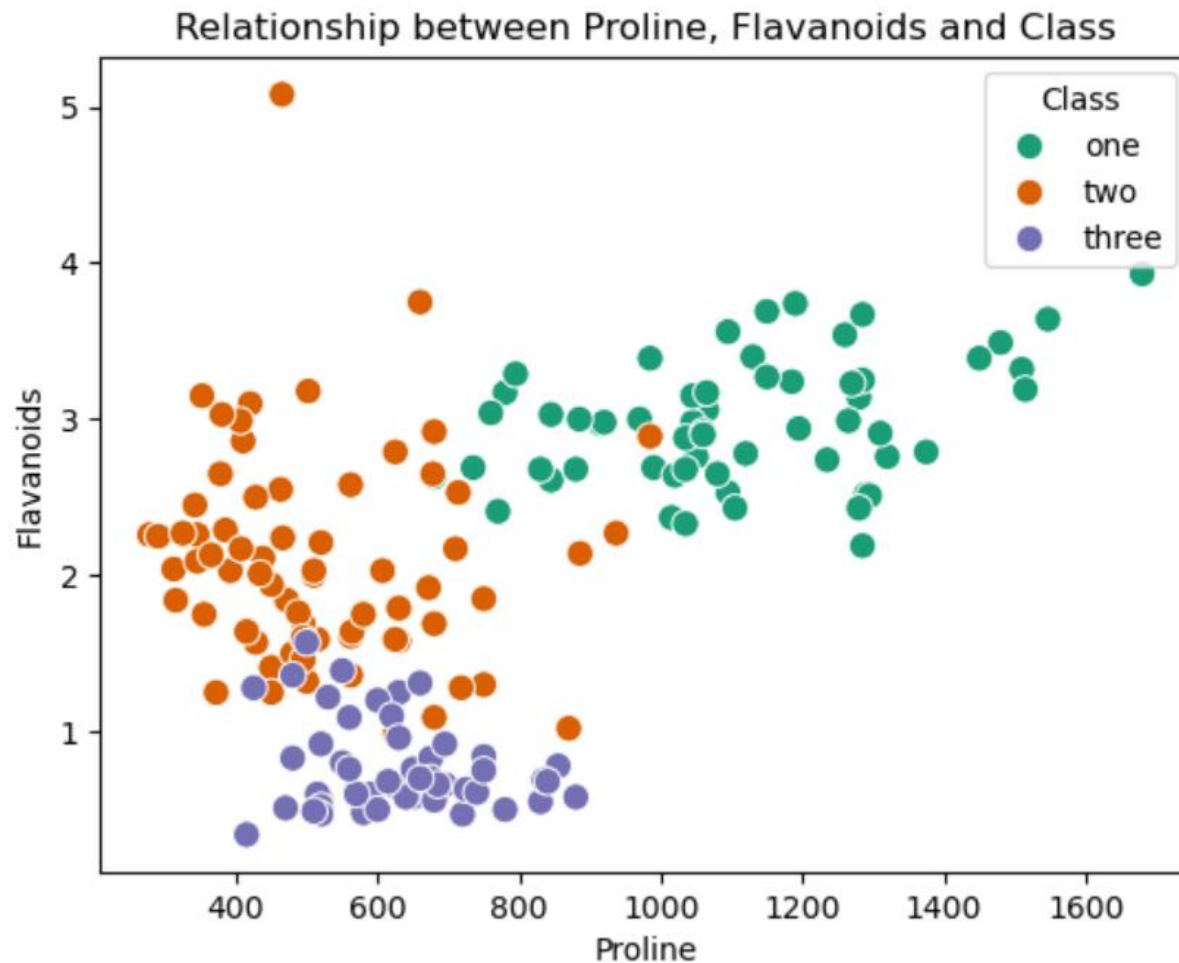
```
fig, axs = plt.subplots(2, 2, figsize=(12, 10))
fig.suptitle('Boxplots for 4 variables')
sns.boxplot(y=df['Color intensity'], ax=axs[0, 0])
sns.boxplot(y=df['Malic acid'], ax=axs[0, 1])
sns.boxplot(y=df['Nonflavanoid phenols'], ax=axs[1, 0])
sns.boxplot(y=df['Alcohol'], ax=axs[1, 1])
```



Multivariate Analysis

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```
sns.scatterplot(x="Proline", y="Flavanoids", hue="Class", data=df, palette="Dark2", s=80)
plt.title("Relationship between Proline, Flavanoids and Class")
plt.show()
```

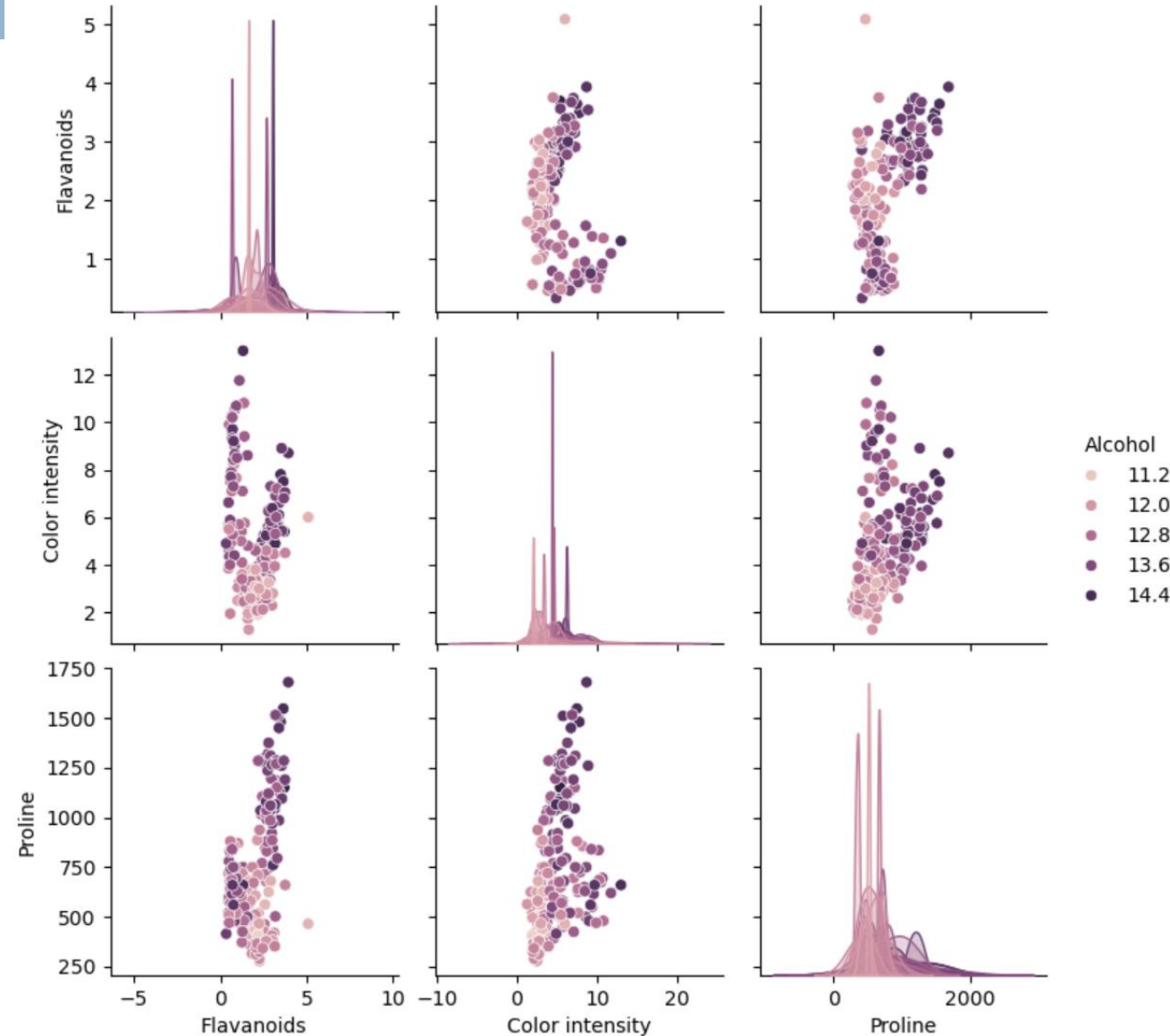


In Class one, Proline levels are much **higher**, while Flavanoids levels are **stable** around the value of 3.

Multivariate Analysis

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```
cols = ['Alcohol', 'Flavanoids', 'Color intensity', 'Proline']  
_ = sns.pairplot(df[cols], hue='Alcohol', height = 2.5)
```



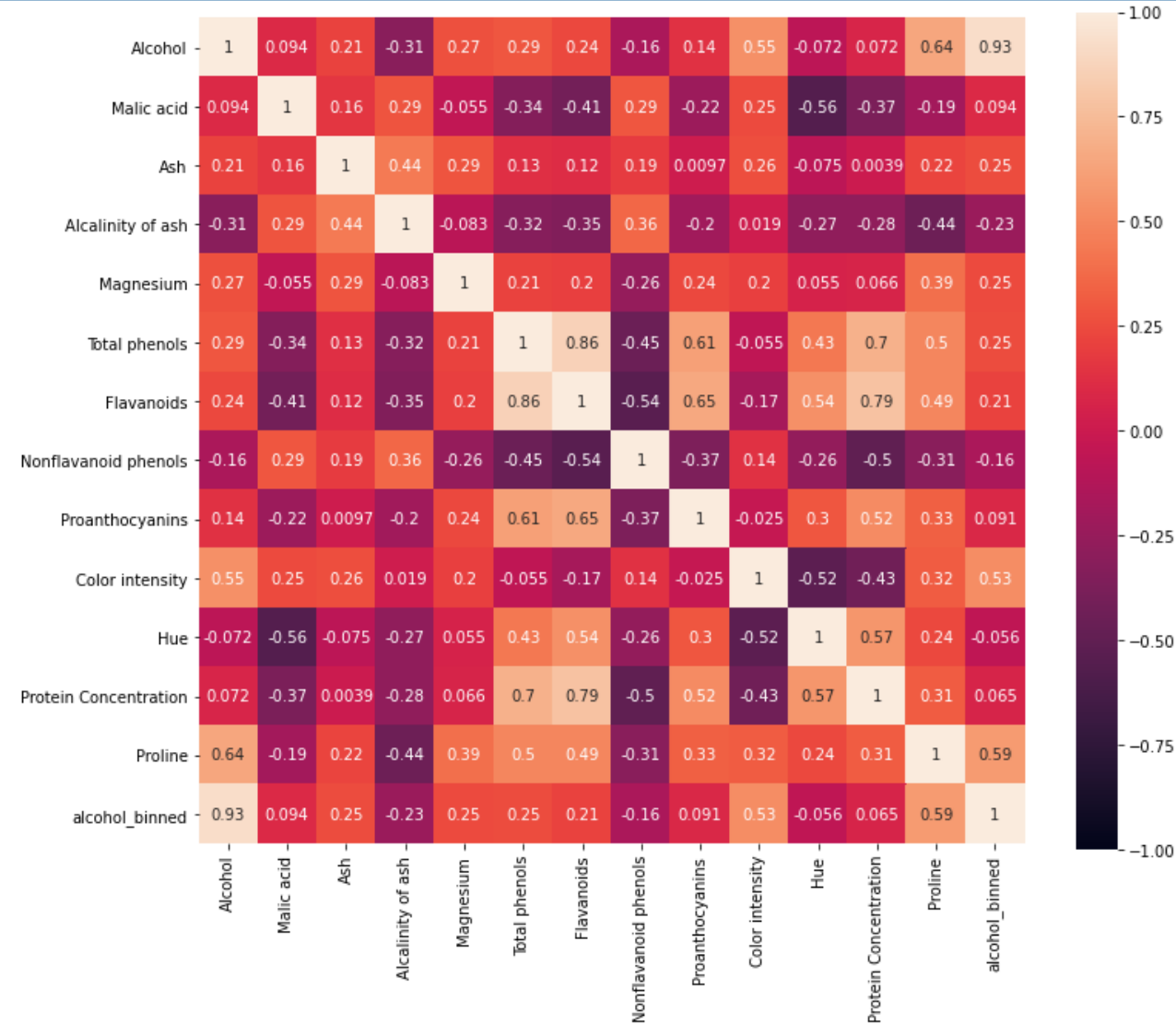
Multivariate Analysis

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```
corr_matrix = df.corr(numeric_only=True)
f, ax = plt.subplots(figsize=(6,4))
sns.heatmap(corr_matrix, vmin=-1, vmax=1, square=True, annot=True)
```

When the Class variable **decreases** (tends to go to 0), Flavanoids, Total phenols, Proline and other proteins tend to **increase**. And vice versa.

There is a **very strong correlation between Alcohol and Proline**. High levels of Alcohol correspond to high levels of Proline.



Critical Analysis

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- Which components characterize the different types of wine?
- Which component is the most important?



Hands On