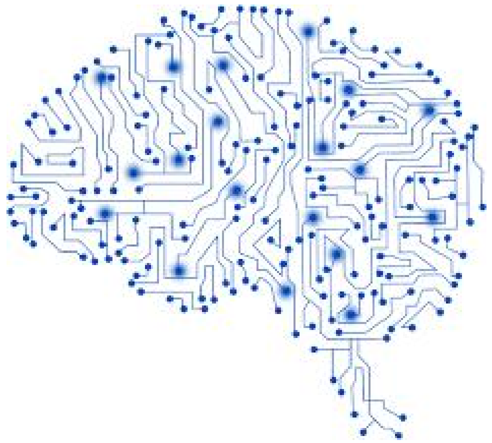
University of Minho
School of Engineering

ISLab



Dados e Aprendizagem Automática

Data Exploration and Preparation

DAA @ MEI-1º/MiEI-4º – 1º Semestre

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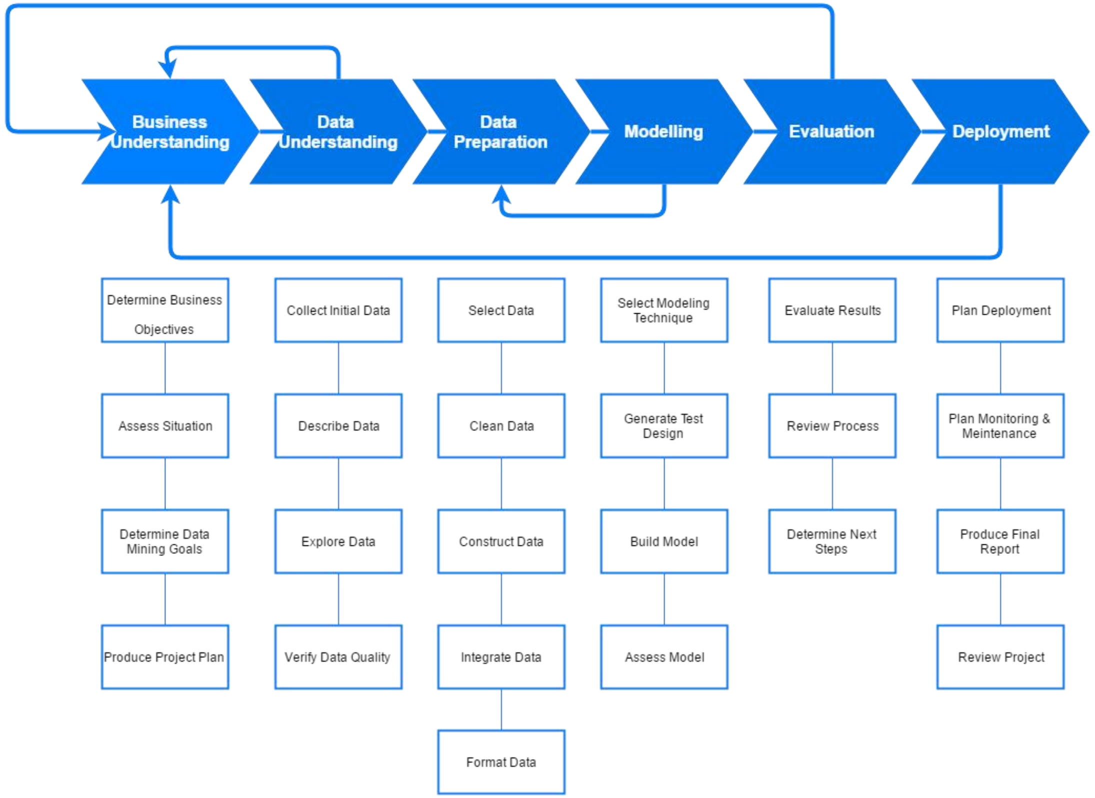
Part II

Contents

Understanding the problem

We must look to our data… We must understand it!

Data understanding is a huge step of the process and, as so, it will take its time! Nonetheless, it will give us a flavor of our dataset, at each variable, their meaning, and their relevance to this problem



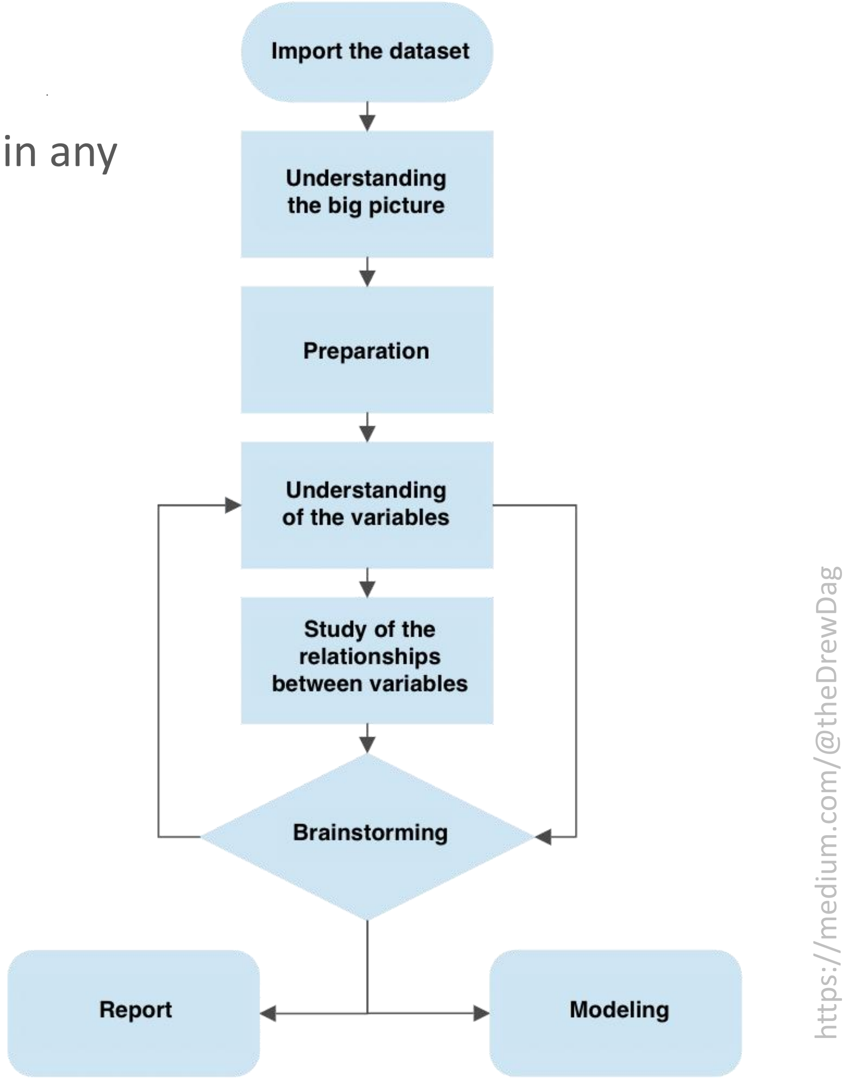
(http://crisp-dm.eu/business-understanding/)

Understanding the problem

We must look to our data… We must understand it!

Let’s understand the features’ type, how important it may be, if it is described in any other feature, … Let’s use the **wine dataset**, available here:

https://tinyurl.com/4cshpfac



Imports

Import libraries

```
import sklearn as skl
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

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

Data Understanding

What about actual data? What can we see/get/understand from these data?

```
'''
Inspect 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 Understanding


```
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 that refer to the type of wine.

Data Understanding


```
#df.dtypes
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
```

There aren’t null values and the attributes are all numeric except the Class.

Data Understanding

We can also get some descriptive stats (for the entire numerical data or just the desired ones)…

```
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 Understanding

What about missing values?

```
'''
Missing data
'''
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 Understanding

With our analysis, we can characterize better the dataset:

- It has **178 entries**
- **14 attributes** - 13 are physical-chemical properties of the wine and 1 is the classification
- All **non-null values**
- There **aren't missing values**

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

If used for **modeling**, the features of the wine can be used to **predict its type**.

Data Preparation

It consists of multiple steps… Many times (in reality, a lot of times), you'll need to check the API of the lib you are using… Hera are some links you may save for future reference:

- Numpy (https://numpy.org/doc/stable/)
- Pandas (https://pandas.pydata.org/docs/)
- Matplotlib (https://matplotlib.org/stable/contents.html)
- Seaborn (https://seaborn.pydata.org/api.html)
- Scikit Learn (https://scikit-learn.org/stable/modules/classes.html)

Data Preparation

And here are some basic Pandas functions you'll need (somewhen) in the future for data prep.:

- 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

And here are some basic sklearn functions/classes you'll need (somewhen) in the future for data prep.:

- sklearn.preprocessing.MinMaxScaler
- sklearn.preprocessing.StandardScaler
- sklearn.preprocessing.KBinsDiscretizer
- sklearn.preprocessing.LabelEncoder
- sklearn.feature_selection
- sklearn.metrics
- …

Data Preparation and Transformation

Remove duplicate values

```python
'''
Drop Duplicates
'''
print(df.duplicated().sum())
print(df.drop_duplicates(inplace=True))
print(df.info())
```

```
0
None
<class 'pandas.core.frame.DataFrame'>
Int64Index: 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: 20.9+ KB
None
```

Rename attributes

```python
'''
Rename complicated columns' names
'''
df.rename(columns={"OD280/OD315 of diluted wines": "Protein Concentration"}, inplace=True)
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 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: 20.9+ KB
```

Data Preparation and Transformation


```
'''
Remove values (Ash smaller than 2, Alcalinity bigger than 15)
'''
df_clean = df.drop(df.loc[(df['Ash']<2) & (df['Alcalinity of ash']>15)].index)
print(df_clean)
#df.drop(df.loc[(df['Ash']<2) & (df['Alcalinity of ash']>15)].index, inplace=True) ##alternative
```

```
     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
...
```

Since all the variables appear to be physical-chemical measures, they could all be useful and help define the segmentation of the type of wine. There is no reason to remove columns.

Univariate Analysis

Iterate through each and every relevant variable and get basic information.

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

```
12.37    6
13.05    6
12.08    5
12.29    4
12.00    3
        ..
13.34    1
13.69    1
13.90    1
13.84    1
13.75    1
Name: Alcohol, Length: 126, dtype: int64
```

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

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

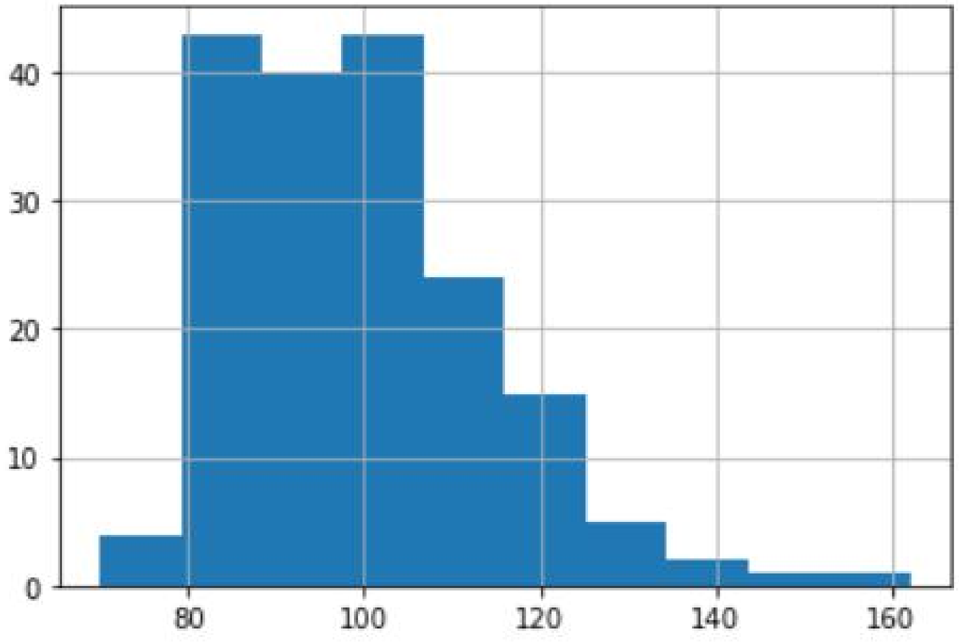
```
'''
Numeric variables
'''
df['Magnesium'].describe()
```

```
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


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

Histogram: AxesSubplot(0.125,0.125;0.775x0.755)



Does not follow a normal curve and has spikes.

```
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.

Univariate Analysis

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

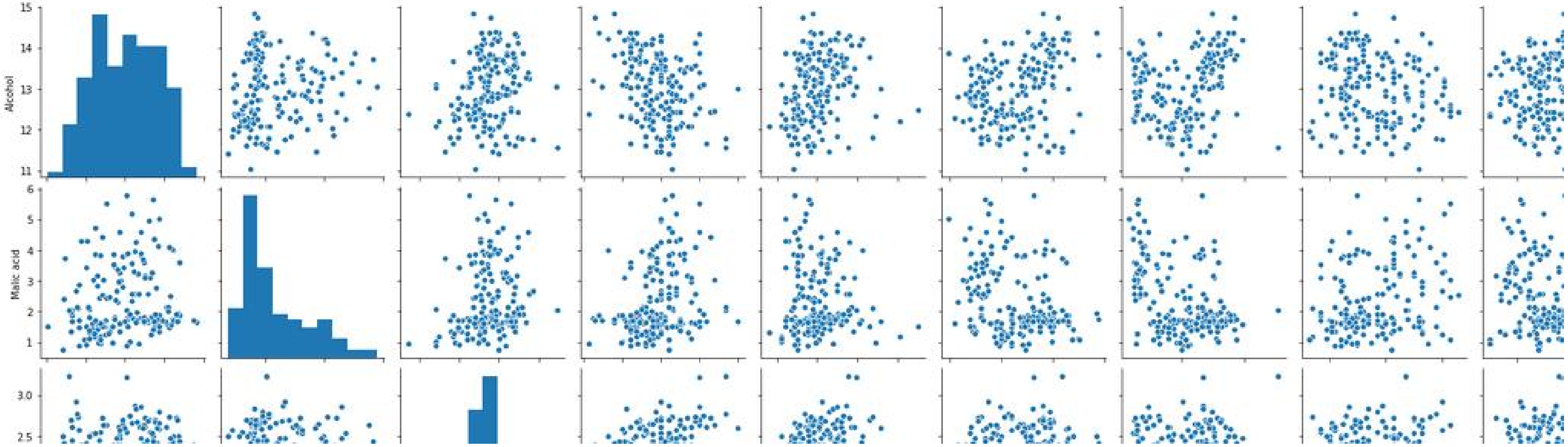
- *Variable*: name of the variable
- *Type*: the type or format of the variable. This can be categorical, numeric, Boolean, and so on
- *Context*: useful information to understand the semantic space of the variable. In the case of our dataset, the context is always the chemical-physical one
- *Expectation*: how relevant is this variable with respect to our task? We can use a scale “High, Medium, Low”.
- *Comments*: whether or not we have any comments to make on the variable

Multivariate Analysis

We can start by seeing the relation between all variables:

```
'''
All variables
'''
sns.pairplot(df)
```

```
<seaborn.axisgrid.PairGrid at 0x7f08ccac79d0>
```



...

Multivariate Analysis

We can group by variables:

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

	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	P ...
Class									
one	13.744746	2.010678	2.455593	17.037288	106.338983	2.840169	2.982373	0.290000	
three	13.153750	3.333750	2.437083	21.416667	99.312500	1.678750	0.781458	0.447500	
two	12.278732	1.932676	2.244789	20.238028	94.549296	2.258873	2.080845	0.363662	

Multivariate Analysis


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

Class	Proline	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	…
one	**680**	13.240	3.980	2.290	17.5	103.0	2.640	2.630	0.32	
	735	13.240	2.590	2.870	21.0	118.0	2.800	2.690	0.39	
	760	14.220	3.990	2.510	13.2	128.0	3.000	3.040	0.20	
	770	12.930	3.800	2.650	18.6	102.0	2.410	2.410	0.25	
	780	14.060	1.630	2.280	16.0	126.0	3.000	3.170	0.24	
...	**...**	...	...	...	...	...	...	...	...	
two	**750**	12.835	0.965	2.155	15.9	123.0	2.215	1.575	0.45	

…

Multivariate Analysis

We can group by variables:

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

```
              Malic acid           Ash Alcalinity of ash Total phenols  \
Alcohol
11.03               1.51           2.2              21.5          2.46
11.41               0.74           2.5                21          2.48
11.45                2.4          2.42                20           2.9
11.46               3.74          1.82              19.5          3.18
11.56               2.05          3.23              28.5          3.18
...                  ...           ...               ...           ...
14.37               1.95           2.5              16.8          3.85
14.38       [1.87, 3.59]  [2.28, 2.38]      [12.0, 16.0]   [3.25, 3.3]
14.39               1.87          2.45              14.6           2.5
14.75               1.73          2.39              11.4           3.1
14.83               1.64          2.17                14           2.8

              Flavanoids Nonflavanoid phenols Proanthocyanins Color intensity  \
Alcohol
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
 ...
```

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

```
                    Malic acid   Ash  Alcalinity of ash  Magnesium  \
Alcohol Flavanoids
11.03   2.17              1.51  2.20               21.5         85
11.41   2.01              0.74  2.50               21.0         88
11.45   2.79              2.40  2.42               20.0         96
11.46   2.58              3.74  1.82               19.5        107
11.56   5.08              2.05  3.23               28.5        119
...                        ...   ...                ...        ...
14.38   3.17              3.59  2.28               16.0        102
        3.64              1.87  2.38               12.0        102
14.39   2.52              1.87  2.45               14.6         96
14.75   3.69              1.73  2.39               11.4         91
14.83   2.98              1.64  2.17               14.0         97

                    Total phenols  Nonflavanoid phenols  Proanthocyanins  \
Alcohol Flavanoids
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
 ...
```

Multivariate Analysis

We can create bins.

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

Binning is a technique for data smoothing. Data smoothing is employed to remove noise from data.

```
'''
Bins
'''
# https://scikit-learn.org/stable/modules/preprocessing.html#discretization
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
```

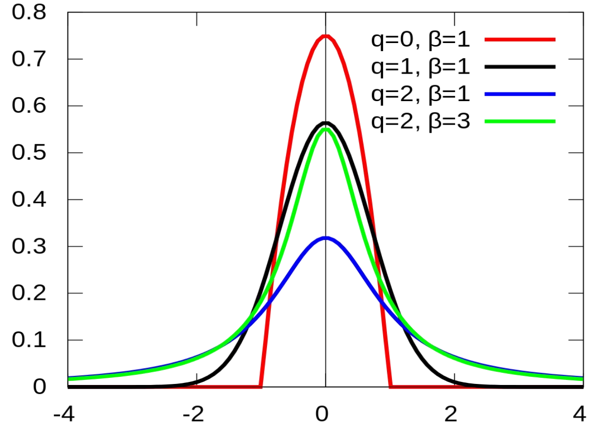
...

Multivariate Analysis

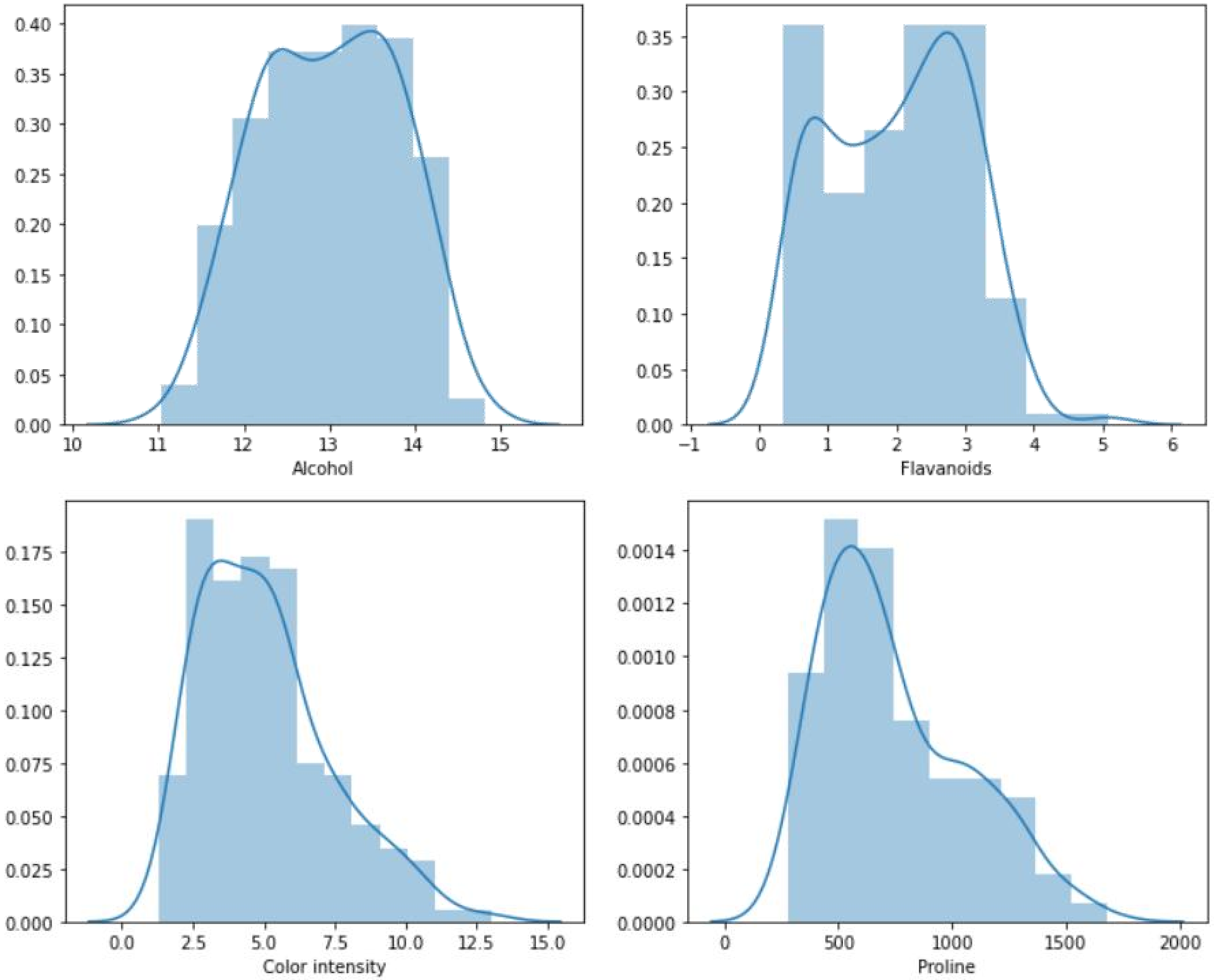
Dispersion: does it follow a Gaussian distribution?

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

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



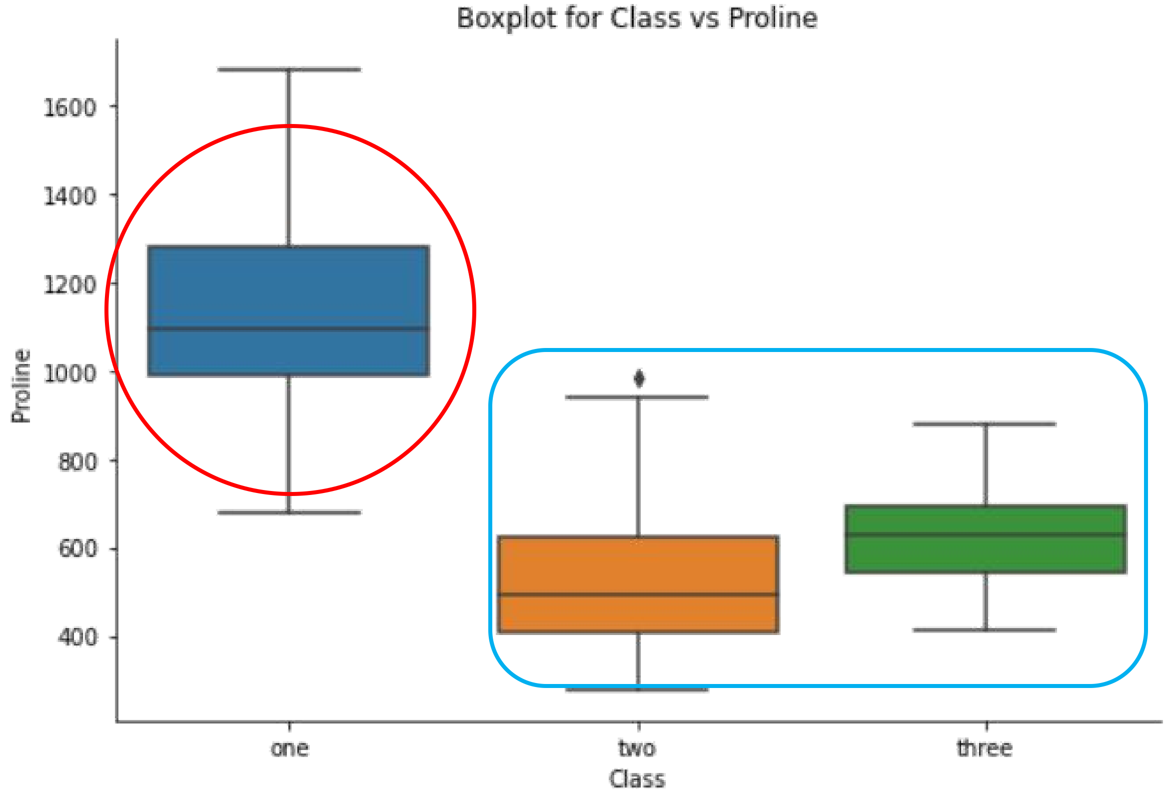
https://en.wikipedia.org/wiki/Q-Gaussian_distribution



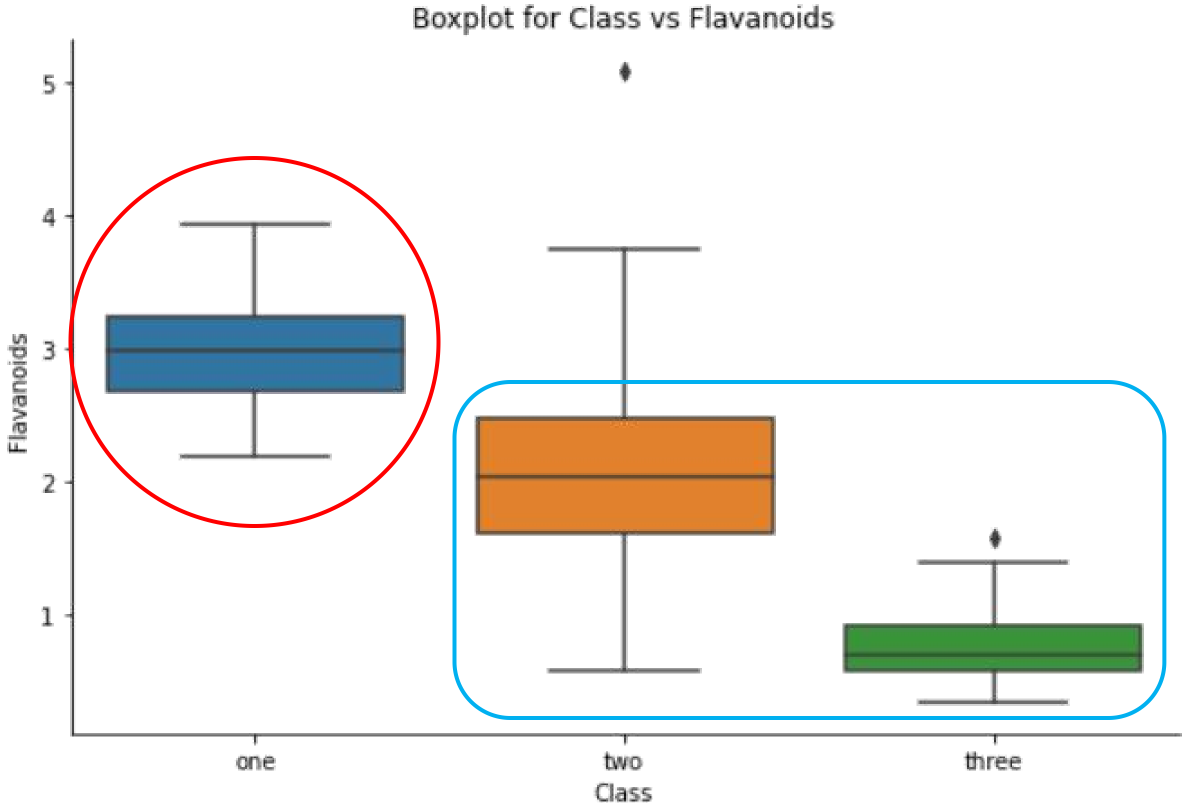
Multivariate Analysis

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

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



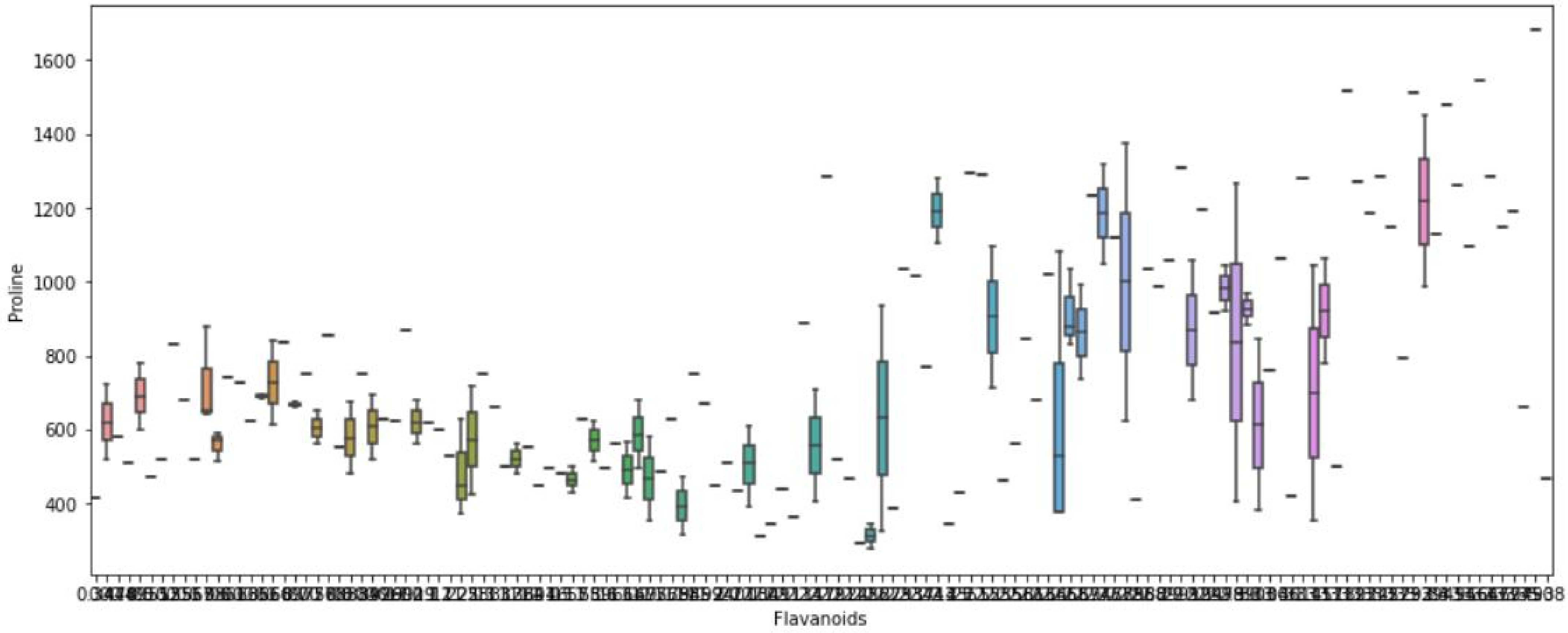

```
sns.catplot(x="Class", y="Flavanoids", data=df, kind="box", aspect=1.5)
plt.title("Boxplot for Class vs Flavanoids")
plt.show()
```



Multivariate Analysis

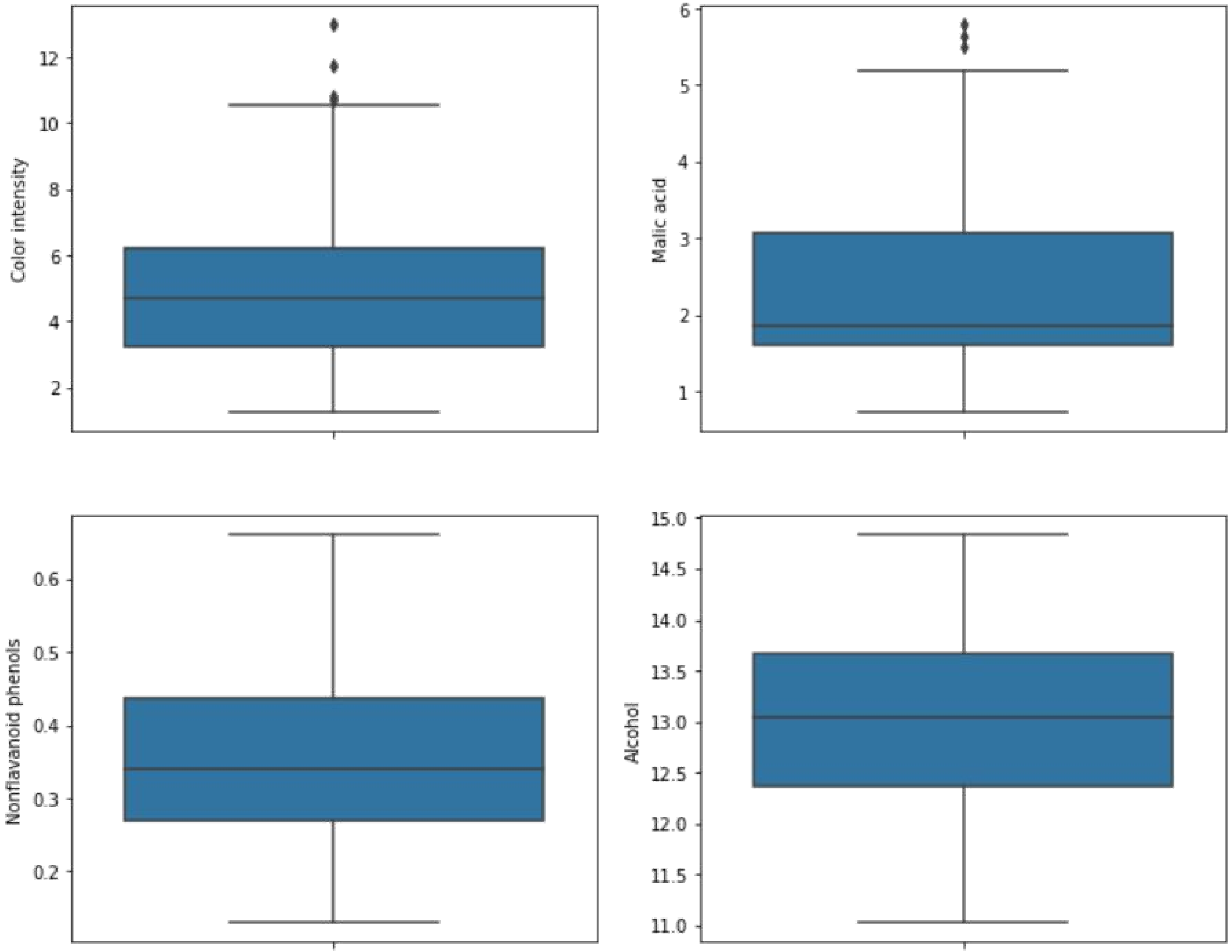

```
_, ax = plt.subplots(figsize=(15, 6))
fig.suptitle('Boxplot for Flavanoids vs Proline')
sns.boxplot(x=df["Flavanoids"], y=df["Proline"])
```

```
<AxesSubplot:xlabel='Flavanoids', ylabel='Proline'>
```



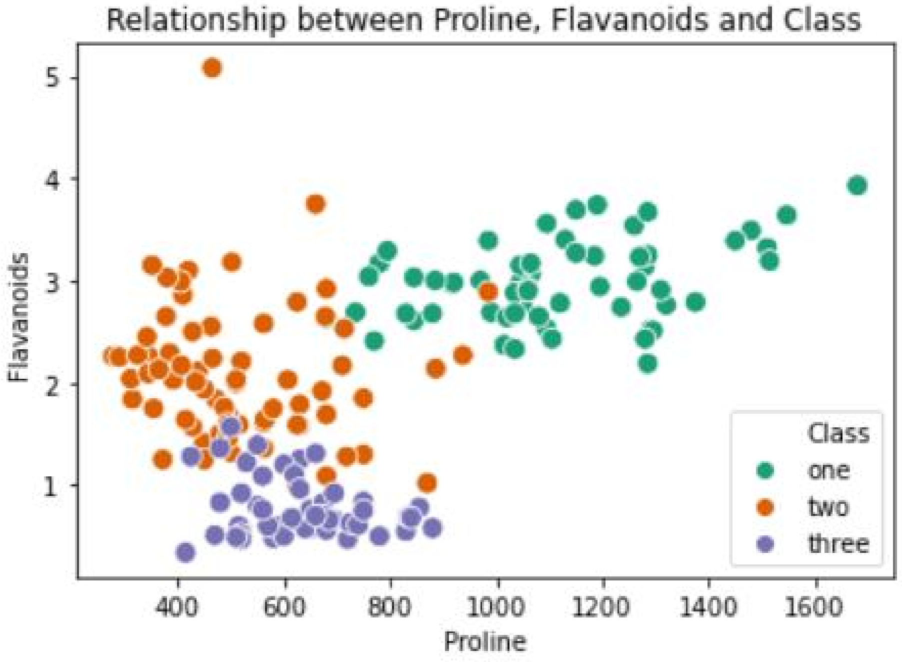
Multivariate Analysis


```python
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

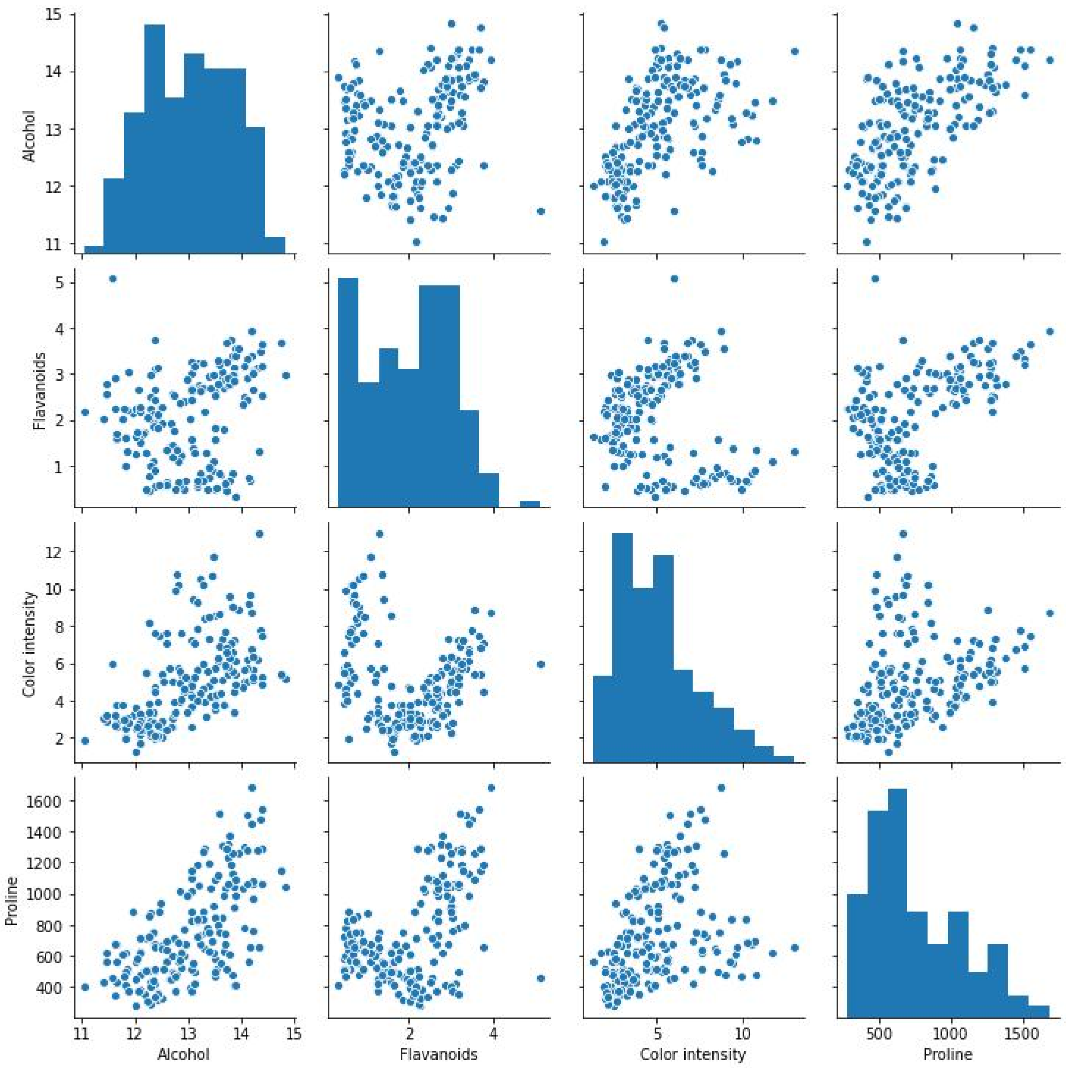

```
'''
Scatter plots
'''
sns.scatterplot(x="Proline", y="Flavanoids", hue="Class", data=df, palette="Dark2", s=80)
plt.title("Relationship between Proline, Flavanoids and Class")
plt.show()
```



For class one the proline levels are much higher while the flavanoid level is stable around the value of 3.

Multivariate Analysis


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

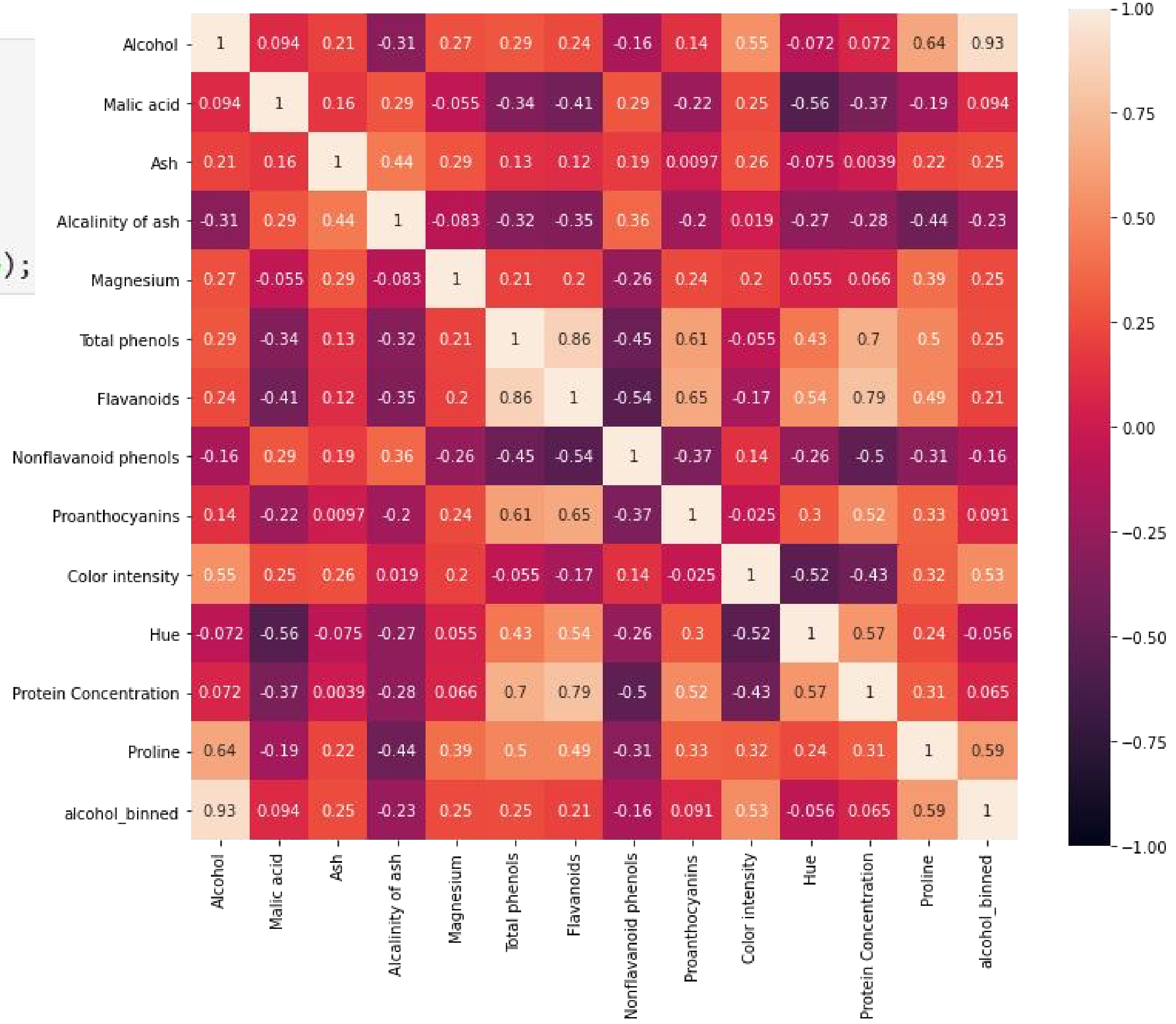


Multivariate Analysis


```
'''
Correlation
'''
corr_matrix = df.corr()
f, ax = plt.subplots(figsize=(12, 10))
sns.heatmap(corr_matrix, vmin=-1, vmax=1, square=True, annot=True);
```

When the Class variable decreases (tendency to go to 0) the flavanoids, total phenols, proline and other proteins tend to increase. And viceversa.

There is a very strong correlation between alcohol and proline. High levels of alcohol correspond to high levels of proline.



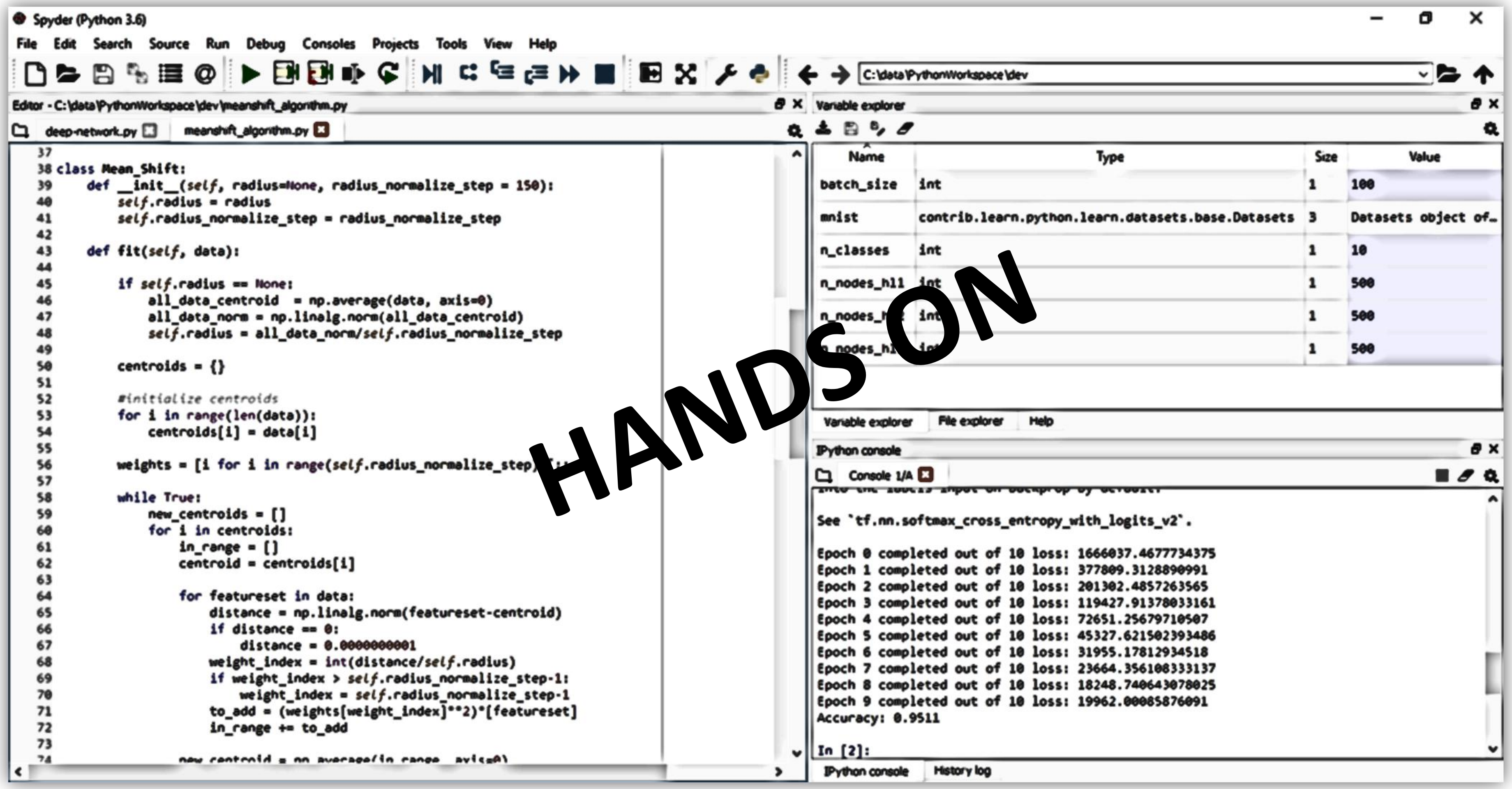
Critical Analysis

Which components characterize the various types of wine?

Which component is the most significant?

…

Hands On


Spyder (Python 3.6)
File Edit Search Source Run Debug Consoles Projects Tools View Help
C:\data\PythonWorkspace\dev
Editor - C:\data\PythonWorkspace\dev\meanshift_algorithm.py
deep-network.py
meanshift_algorithm.py
class Mean_Shift:
def __init__(self, radius=None, radius_normalize_step = 150):
self.radius = radius
self.radius_normalize_step = radius_normalize_step
def fit(self, data):
if self.radius == None:
all_data_centroid = np.average(data, axis=0)
all_data_norm = np.linalg.norm(all_data_centroid)
self.radius = all_data_norm/self.radius_normalize_step
centroids = {}
#initialize centroids
for i in range(len(data)):
centroids[i] = data[i]
while True:
new_centroids = []
for i in centroids:
in_range = []
centroid = centroids[i]
for featureset in data:
distance = np.linalg.norm(featureset-centroid)
if distance == 0:
distance = 0.0000000001
weight_index = int(distance/self.radius)
if weight_index > self.radius_normalize_step-1:
weight_index = self.radius_normalize_step-1
to_add = (weights[weight_index]**2)*[featureset]
in_range += to_add
Variable explorer
Name
Type
Size
Value
batch_size
int
1
100
mnist
contrib.learn.python.learn.datasets.base.Datasets
3
Datasets object of…
n_classes
int
1
10
n_nodes_hl1
int
1
500
1
500
1
500
Variable explorer
File explorer
Help
IPython console
Console 1/A
See `tf.nn.softmax_cross_entropy_with_logits_v2`.
Epoch 0 completed out of 10 loss: 1666037.4677734375
Epoch 1 completed out of 10 loss: 377809.3128890991
Epoch 2 completed out of 10 loss: 201302.4857263565
Epoch 3 completed out of 10 loss: 119427.91378033161
Epoch 4 completed out of 10 loss: 72651.25679710507
Epoch 5 completed out of 10 loss: 45327.621502393486
Epoch 6 completed out of 10 loss: 31955.17812934518
Epoch 7 completed out of 10 loss: 23664.356108333137
Epoch 8 completed out of 10 loss: 18248.740643078025
Epoch 9 completed out of 10 loss: 19962.00085876091
Accuracy: 0.9511
In [2]:
IPython console
History log
HANDS ON