Untitled

April 20, 2021

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3.0.1

https://scikit-learn.org/stable/modules/generated/sklearn.datasets.load_wine.html#sklearn.datasets.load_wine

[1]:
```
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
import seaborn as sns
%matplotlib inline
sns.set(style="ticks")

from sklearn.datasets import load_wine
```

[2]:
```
wine = load_wine()
data = pd.DataFrame(wine.data, columns=wine.feature_names)
data['TARGET'] = wine.target
```

[3]:
```
data.head()
```

[3]:

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phenols	\
0	14.23	1.71	2.43	15.6	127.0	2.80	
1	13.20	1.78	2.14	11.2	100.0	2.65	
2	13.16	2.36	2.67	18.6	101.0	2.80	
3	14.37	1.95	2.50	16.8	113.0	3.85	
4	13.24	2.59	2.87	21.0	118.0	2.80	

	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	

	od280/od315_of_diluted_wines	proline	TARGET
0	3.92	1065.0	0
1	3.40	1050.0	0
2	3.17	1185.0	0
3	3.45	1480.0	0
4	2.93	735.0	0

[4]:
```
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   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    float64
 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    float64
```

```
 13  TARGET                          178 non-null    int64
dtypes: float64(13), int64(1)
memory usage: 19.6 KB
```

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[5]:
```
data.describe()
```

[5]:

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium
count	178.000000	178.000000	178.000000	178.000000	178.000000
mean	13.000618	2.336348	2.366517	19.494944	99.741573
std	0.811827	1.117146	0.274344	3.339564	14.282484
min	11.030000	0.740000	1.360000	10.600000	70.000000
25%	12.362500	1.602500	2.210000	17.200000	88.000000
50%	13.050000	1.865000	2.360000	19.500000	98.000000
75%	13.677500	3.082500	2.557500	21.500000	107.000000
max	14.830000	5.800000	3.230000	30.000000	162.000000

	total_phenols	flavanoids	nonflavanoid_phenols	proanthocyanins
count	178.000000	178.000000	178.000000	178.000000
mean	2.295112	2.029270	0.361854	1.590899
std	0.625851	0.998859	0.124453	0.572359
min	0.980000	0.340000	0.130000	0.410000
25%	1.742500	1.205000	0.270000	1.250000
50%	2.355000	2.135000	0.340000	1.555000
75%	2.800000	2.875000	0.437500	1.950000
max	3.880000	5.080000	0.660000	3.580000

	color_intensity	hue	od280/od315_of_diluted_wines	proline
count	178.000000	178.000000	178.000000	178.000000
mean	5.058090	0.957449	2.611685	746.893258
std	2.318286	0.228572	0.709990	314.907474
min	1.280000	0.480000	1.270000	278.000000
25%	3.220000	0.782500	1.937500	500.500000
50%	4.690000	0.965000	2.780000	673.500000
75%	6.200000	1.120000	3.170000	985.000000
max	13.000000	1.710000	4.000000	1680.000000

	TARGET
count	178.000000
mean	0.938202
std	0.775035
min	0.000000
25%	0.000000
50%	1.000000
75%	2.000000
max	2.000000

[6]:
```
corr_matrix = data.corr()
```

[7]:
```
corr_matrix['TARGET']
```

[7]:
```
alcohol                        -0.328222
malic_acid                      0.437776
ash                            -0.049643
alcalinity_of_ash               0.517859
magnesium                      -0.209179
total_phenols                  -0.719163
flavanoids                     -0.847498
nonflavanoid_phenols            0.489109
proanthocyanins                -0.499130
color_intensity                 0.265668
hue                            -0.617369
od280/od315_of_diluted_wines   -0.788230
proline                        -0.633717
TARGET                          1.000000
Name: TARGET, dtype: float64
```

[8]:
```
corr_matrix_kendall = data.corr(method='kendall')
corr_matrix_kendall['TARGET']
```

[8]:
```
alcohol                        -0.238984
malic_acid                      0.247494
ash                            -0.038085
alcalinity_of_ash               0.449402
magnesium                      -0.184992
total_phenols                  -0.590404
flavanoids                     -0.725255
nonflavanoid_phenols            0.379234
proanthocyanins                -0.450225
color_intensity                 0.065124
hue                            -0.479229
od280/od315_of_diluted_wines   -0.607572
proline                        -0.406260
TARGET                          1.000000
Name: TARGET, dtype: float64
```

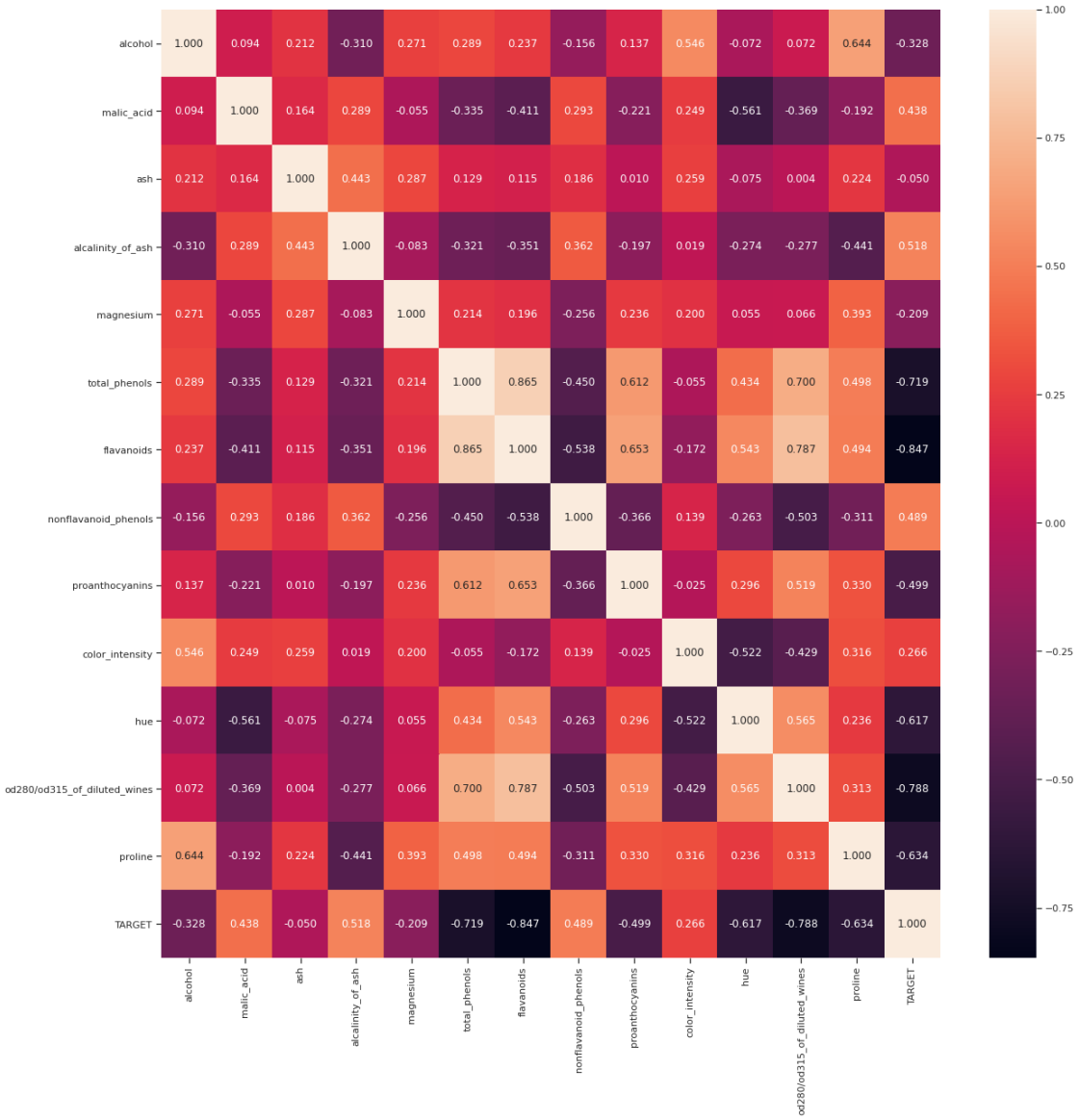
[9]:
```
corr_matrix_spearman = data.corr(method='spearman')
corr_matrix_spearman['TARGET']
```

[9]:
```
alcohol                        -0.354167
malic_acid                      0.346913
ash                            -0.053988
alcalinity_of_ash               0.569792
magnesium                      -0.250498
```

```
total_phenols                  -0.726544
flavanoids                     -0.854908
nonflavanoid_phenols            0.474205
proanthocyanins                -0.570648
color_intensity                 0.131170
hue                            -0.616570
od280/od315_of_diluted_wines   -0.743787
proline                        -0.576383
TARGET                          1.000000
Name: TARGET, dtype: float64
```

[10]:
```
plt.figure(figsize=(20,20))
sns.heatmap(corr_matrix, annot=True, fmt='.3f')
```

[10]:
```
<AxesSubplot:>
```



3.0.2

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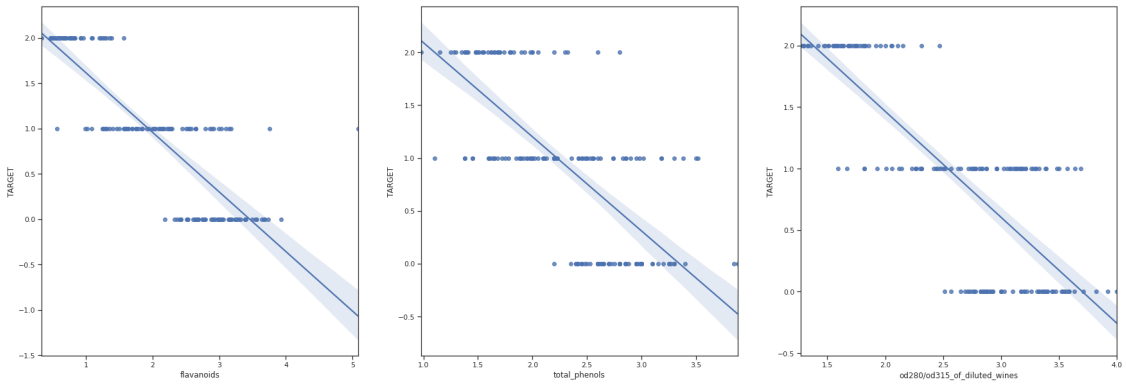
- flavanoids
- od280….
- total_phenols

[11]:
```
fig, axs = plt.subplots(ncols=3, figsize=(30,10))
sns.regplot(x=data['flavanoids'], y=data['TARGET'], ax = axs[0])
sns.regplot(x=data['total_phenols'], y=data['TARGET'], ax = axs[1])
```

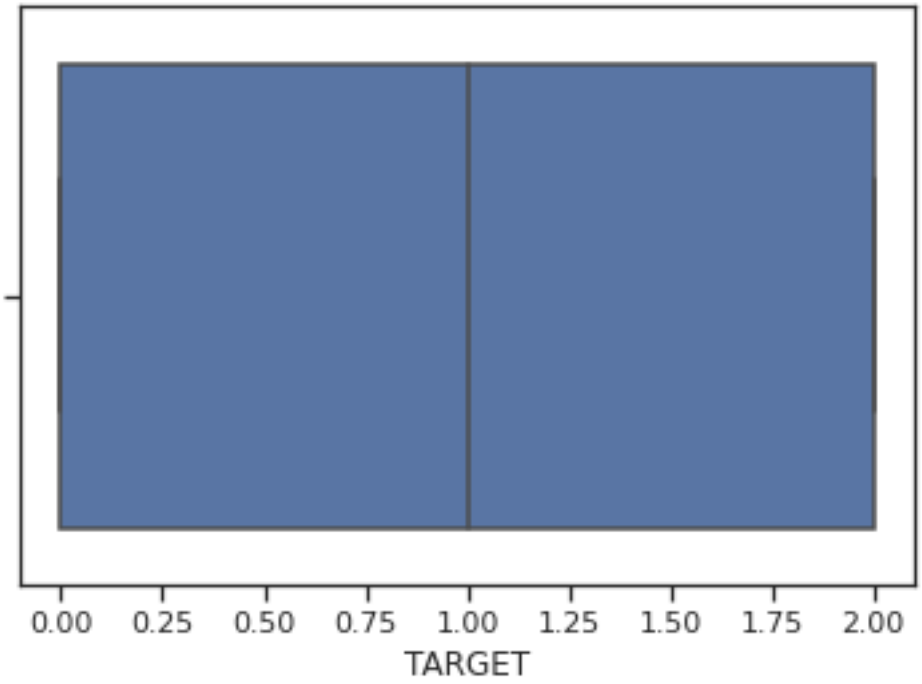
```
sns.regplot(x=data['od280/od315_of_diluted_wines'], y=data['TARGET'], ax =
↪axs[2])
```

[11]: <AxesSubplot:xlabel='od280/od315_of_diluted_wines', ylabel='TARGET'>



[12]: `sns.boxplot(x=data['TARGET'])`

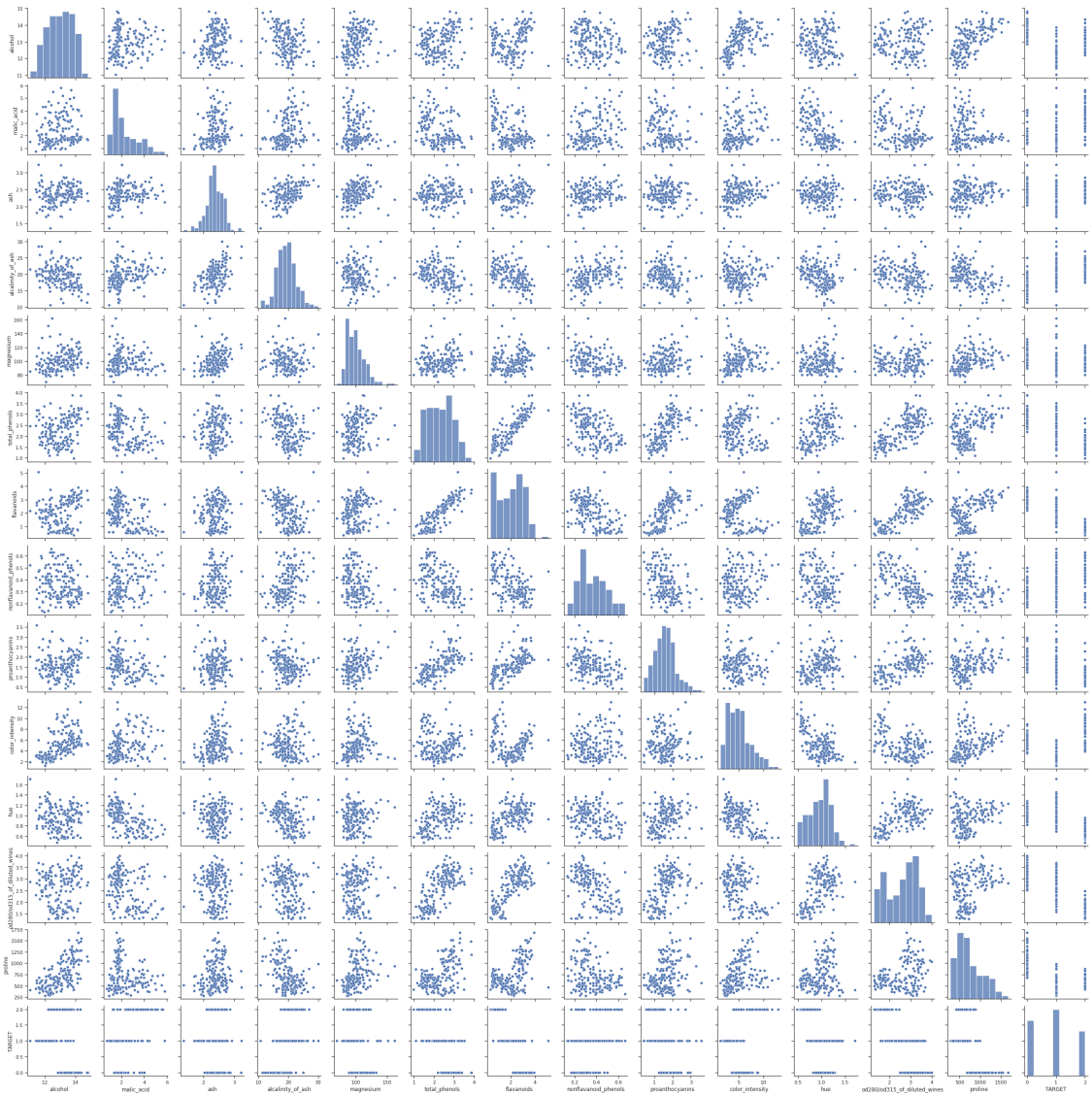
[12]: <AxesSubplot:xlabel='TARGET'>



[13]:
```
plt.figure(figsize=(12,6))
sns.pairplot(data)
```

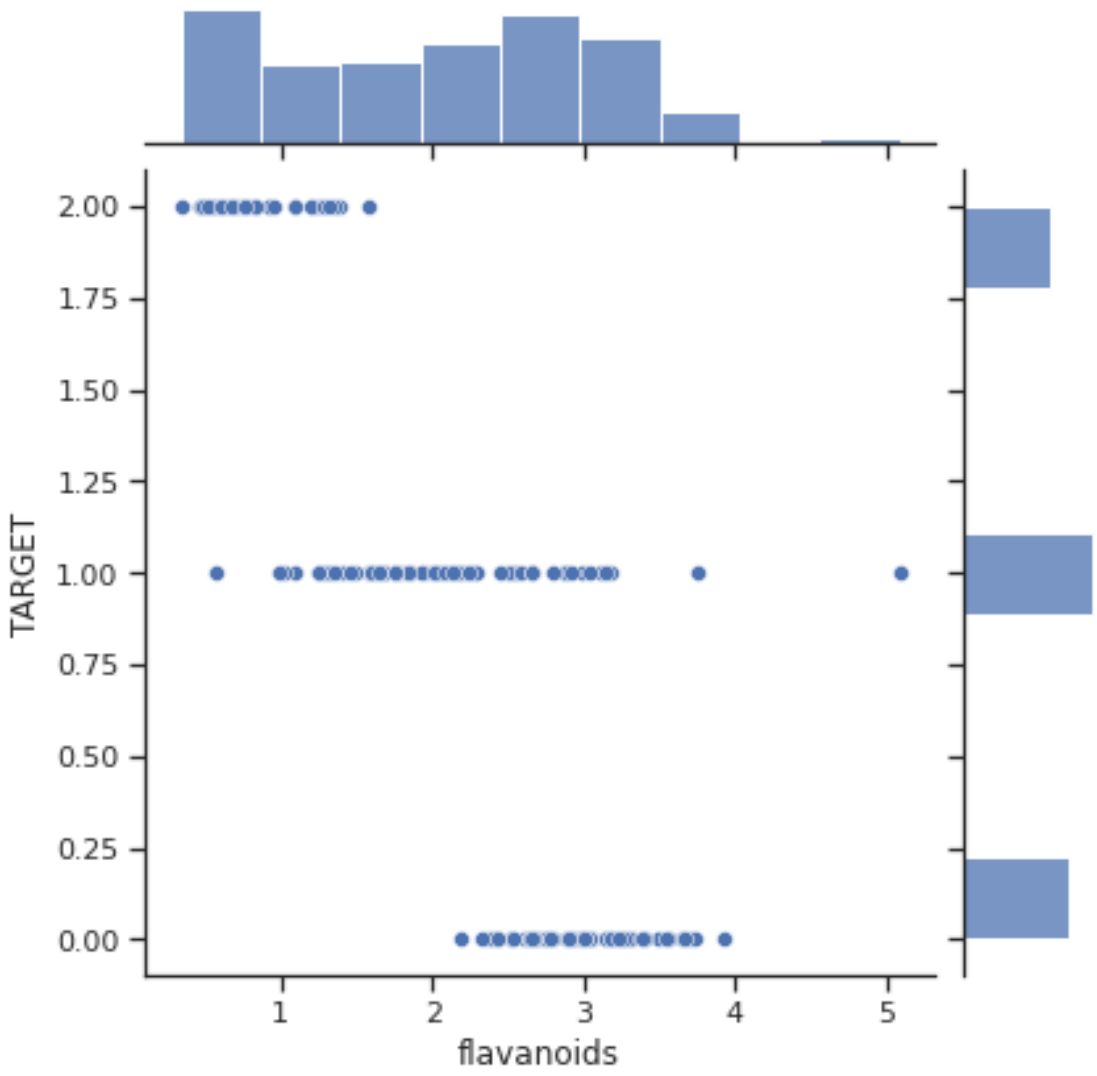
[13]: <seaborn.axisgrid.PairGrid at 0x7fa0de9cf760>

<Figure size 864x432 with 0 Axes>



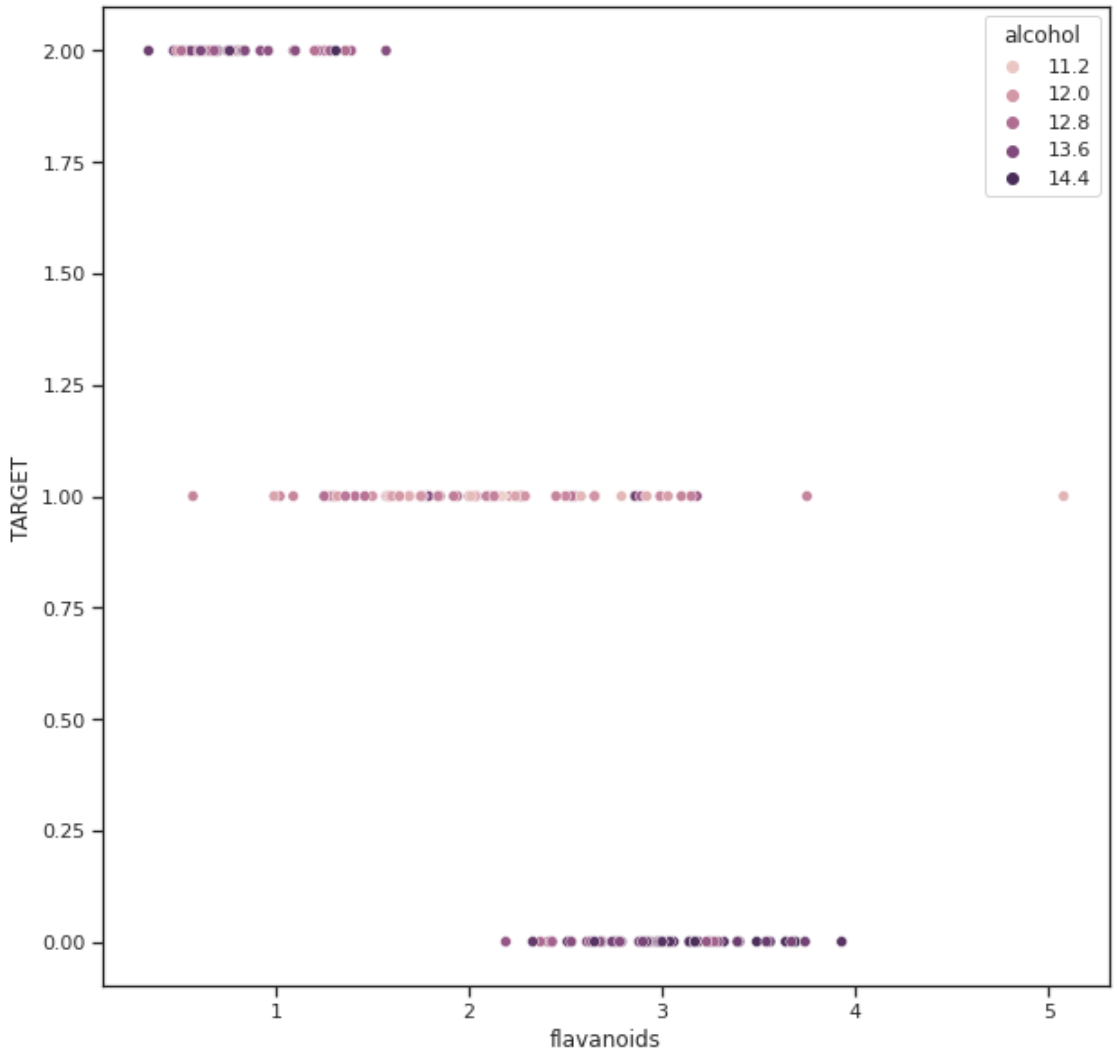
[14]:
```
sns.jointplot(x = "flavanoids", y = "TARGET", kind="scatter", data = data)
```

[14]: <seaborn.axisgrid.JointGrid at 0x7fa0b98c8e80>



[15]:
```
fig, ax = plt.subplots(figsize=(10,10))
sns.scatterplot(ax=ax, x='flavanoids', y='TARGET', data=data, hue='alcohol')
```

[15]: <AxesSubplot:xlabel='flavanoids', ylabel='TARGET'>



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flavanoids total_phenols , .

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ash color_intensity, .

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