

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

```
↳ /usr/local/lib/python3.6/dist-packages/statsmodels/tools/_testing.py:19: FutureWarning:
    import pandas.util.testing as tm
```

```
from sklearn.datasets import load_wine
```

```
raw_data = load_wine()
features = pd.DataFrame(data=raw_data['data'], columns=raw_data['feature_names'])
data = features
data['target'] = raw_data['target']
data['class'] = data['target'].map(lambda ind: raw_data['target_names'][ind])
data.head()
```

```
↳
```

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phenols	flava
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	

```
data.describe()
```

```
↳
```

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phe
count	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000
mean	13.000618	2.336348	2.366517	19.494944	99.741573	2.296191
std	0.811827	1.117146	0.274344	3.339564	14.282484	0.625191
min	11.030000	0.740000	1.360000	10.600000	70.000000	0.984865
25%	12.362500	1.602500	2.210000	17.200000	88.000000	1.742454
50%	13.050000	1.865000	2.360000	19.500000	98.000000	2.335451
75%	13.677500	3.082500	2.557500	21.500000	107.000000	2.801848
max	14.830000	5.800000	3.230000	30.000000	162.000000	3.861279

```
data.shape
```

```
↳ (178, 15)
```

Датасет включает в себя 13 атрибутов:

Alcohol

Malic acid

Ash

Alcalinity of ash

Magnesium

Total phenols

Flavanoids

Nonflavanoid phenols

Proanthocyanins

Color intensity

Hue

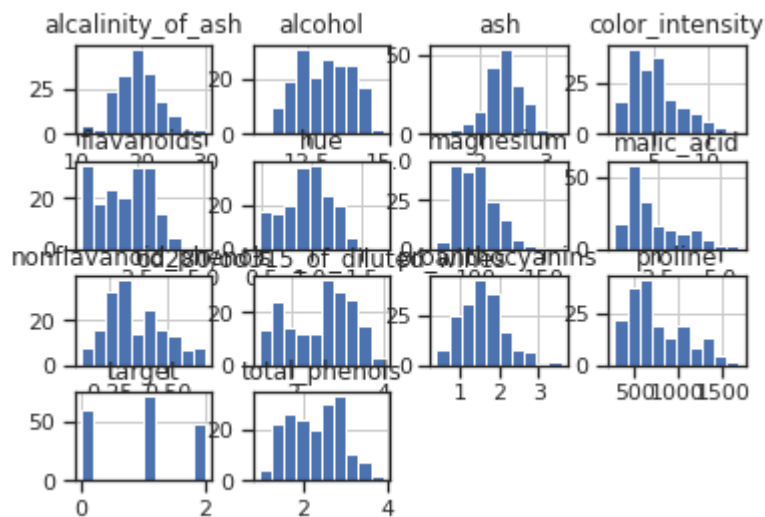
OD280/OD315 of diluted wines

Proline

```
data.hist()
```

```
↳
```

```
array([[<matplotlib.axes._subplots.AxesSubplot object at 0x7f9de315cb38>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de3134358>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de30df9b0>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de308ffd0>],
      [<matplotlib.axes._subplots.AxesSubplot object at 0x7f9de30476a0>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de3074cf8>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de302c390>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de2fd89b0>],
      [<matplotlib.axes._subplots.AxesSubplot object at 0x7f9de2fd8a20>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de2fbe6d8>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de2f6fd30>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de2f2d3c8>],
      [<matplotlib.axes._subplots.AxesSubplot object at 0x7f9de2edda20>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de2e9a0b8>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de2e49710>,
      <matplotlib.axes._subplots.AxesSubplot object at 0x7f9de2e79d68>]],
      dtype=object)
```

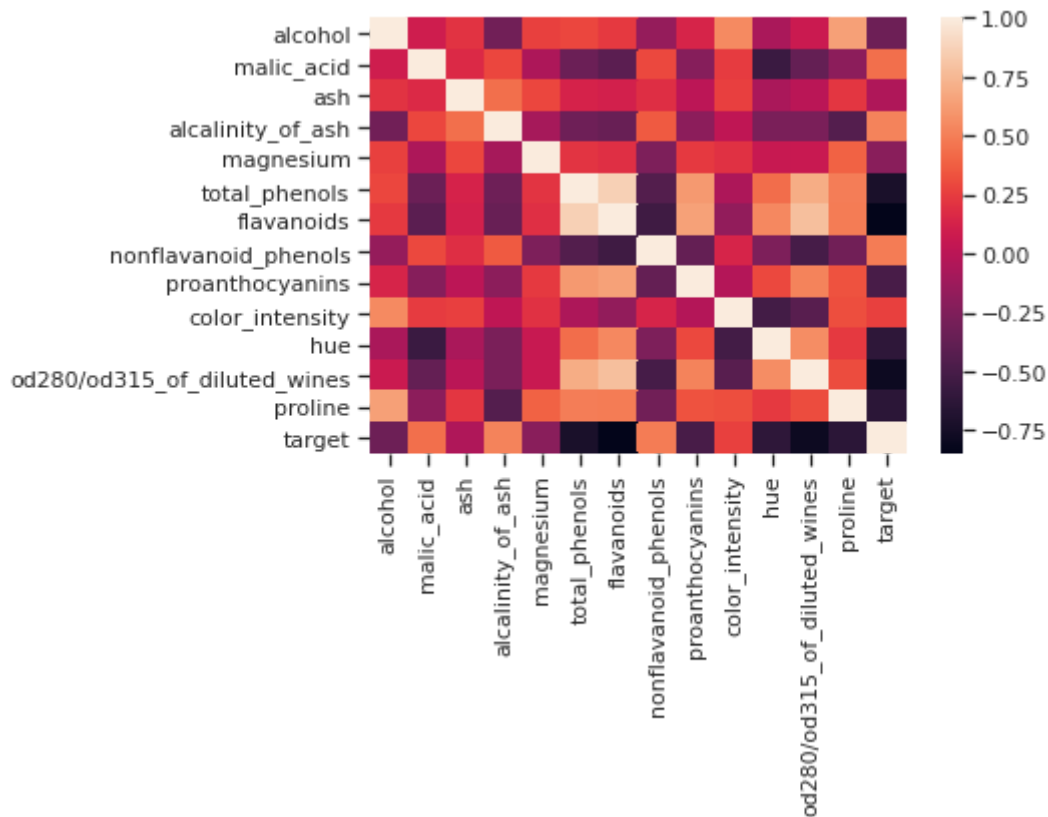


```
corr = data.corr()
```

```
sns.heatmap(corr,
             xticklabels=corr.columns,
             yticklabels=corr.columns)
```



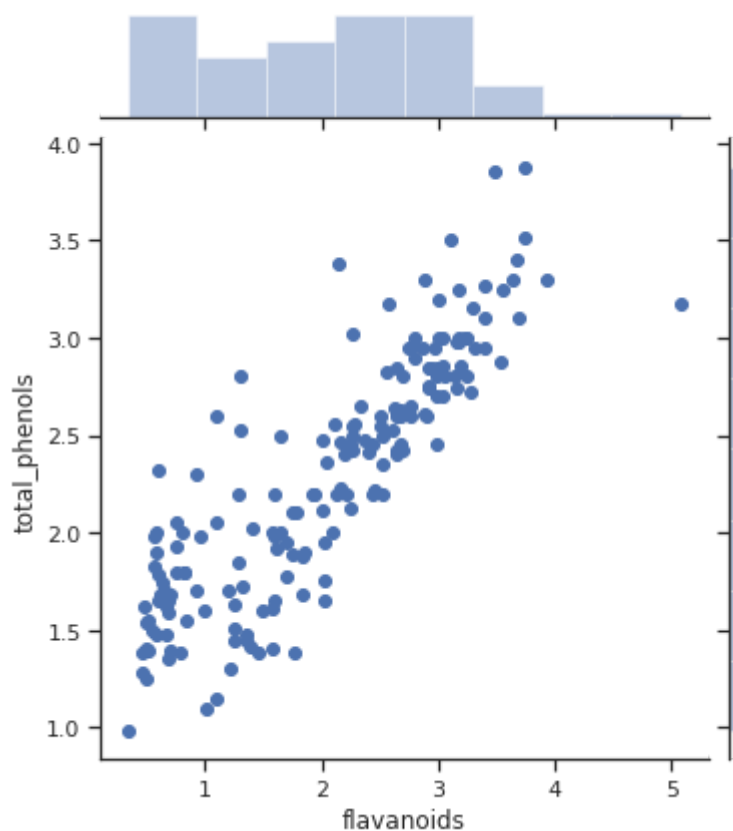
<matplotlib.axes._subplots.AxesSubplot at 0x7f9de26f9cf8>



Видим наибольшую корреляцию между *flavanoids* и *total_phenols*

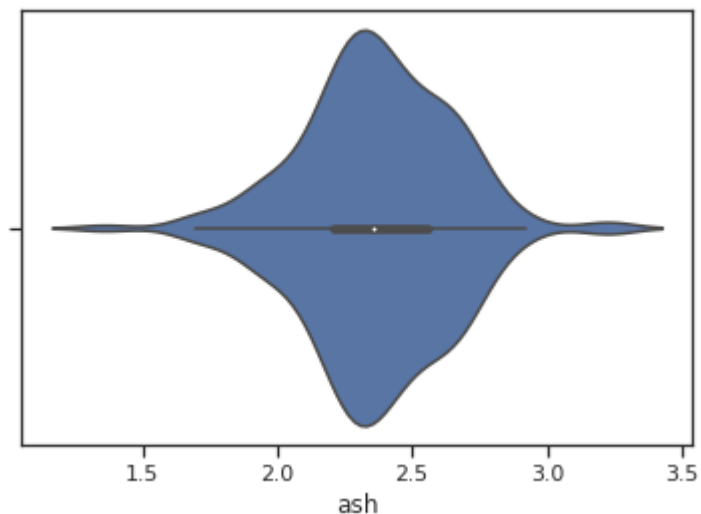
```
sns.jointplot(x='flavanoids', y='total_phenols', data=data)
```

↗ <seaborn.axisgrid.JointGrid at 0x7f9de13b5cc0>



```
sns.violinplot(x=data['ash'])
```

↪ <matplotlib.axes._subplots.AxesSubplot at 0x7f9ddd8fc0b8>



```
for i in data.target.unique():  
    sns.distplot(data['alcohol'][data.target==i],  
                  kde=1, label='{}'.format(i))
```

```
plt.legend()
```

↪ <matplotlib.legend.Legend at 0x7f9ddaf33cf8>

