Data Set Information:

The two datasets are related to red and white variants of the Portuguese "Vinho Verde" wine. For more details, consult: [Web Link] or the reference [Cortez et al., 2009]. Due to privacy and logistic issues, only physicochemical (inputs) and sensory (the output) variables are available (e.g. there is no data about grape types, wine brand, wine selling price, etc.).

These datasets can be viewed as classification or regression tasks. The classes are ordered and not balanced (e.g. there are many more normal wines than excellent or poor ones). Outlier detection algorithms could be used to detect the few excellent or poor wines. Also, we are not sure if all input variables are relevant. So it could be interesting to test feature selection methods.

Attribute Information:

For more information, read [Cortez et al., 2009]. Input variables (based on physicochemical tests): 1 - fixed acidity 2 - volatile acidity 3 - citric acid 4 - residual sugar 5 - chlorides 6 - free sulfur dioxide 7 - total sulfur dioxide 8 - density 9 - pH 10 - sulphates 11 - alcohol Output variable (based on sensory data): 12 - quality (score between 0 and 10)

Link for the dataset: https://archive.ics.uci.edu/ml/datasets/wine+quality

Import necessary Libraries

In [1]:

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import warnings
%matplotlib inline
warnings.filterwarnings('ignore')
```

Import the dataset

In [2]:

```
df = pd.read_csv('winequalityN.csv')
df.head()
```

Out[2]:

	type	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
0	white	7.0	0.27	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.8	6
1	white	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.5	6
2	white	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.1	6
3	white	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.9	6
4	white	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.9	6

In [3]:

```
# statistical info
df.describe()
```

Out[3]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH
count	6487.000000	6489.000000	6494.000000	6495.000000	6495.000000	6497.000000	6497.000000	6497.000000	6488.000000
mean	7.216579	0.339691	0.318722	5.444326	0.056042	30.525319	115.744574	0.994697	3.218395
std	1.296750	0.164649	0.145265	4.758125	0.035036	17.749400	56.521855	0.002999	0.160748
min	3.800000	0.080000	0.000000	0.600000	0.009000	1.000000	6.000000	0.987110	2.720000
25%	6.400000	0.230000	0.250000	1.800000	0.038000	17.000000	77.000000	0.992340	3.110000
50%	7.000000	0.290000	0.310000	3.000000	0.047000	29.000000	118.000000	0.994890	3.210000
75%	7.700000	0.400000	0.390000	8.100000	0.065000	41.000000	156.000000	0.996990	3.320000
max	15.900000	1.580000	1.660000	65.800000	0.611000	289.000000	440.000000	1.038980	4.010000

In [4]:

```
df.describe().T
```

Out[4]:

	count	mean	std	min	25%	50%	75%	max
fixed acidity	6487.0	7.216579	1.296750	3.80000	6.40000	7.00000	7.70000	15.90000
volatile acidity	6489.0	0.339691	0.164649	0.08000	0.23000	0.29000	0.40000	1.58000
citric acid	6494.0	0.318722	0.145265	0.00000	0.25000	0.31000	0.39000	1.66000
residual sugar	6495.0	5.444326	4.758125	0.60000	1.80000	3.00000	8.10000	65.80000
chlorides	6495.0	0.056042	0.035036	0.00900	0.03800	0.04700	0.06500	0.61100
...	...	...	...	...	...	...	...	...
density	6497.0	0.994697	0.002999	0.98711	0.99234	0.99489	0.99699	1.03898
pH	6488.0	3.218395	0.160748	2.72000	3.11000	3.21000	3.32000	4.01000
sulphates	6493.0	0.531215	0.148814	0.22000	0.43000	0.51000	0.60000	2.00000
alcohol	6497.0	10.491801	1.192712	8.00000	9.50000	10.30000	11.30000	14.90000
quality	6497.0	5.818378	0.873255	3.00000	5.00000	6.00000	6.00000	9.00000

In [5]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 6497 entries, 0 to 6496
Data columns (total 13 columns):
 #   Column                Non-Null Count  Dtype  
---  ------                --------------  -----  
 0   type                  6497 non-null   object 
 1   fixed acidity         6487 non-null   float64
 2   volatile acidity      6489 non-null   float64
 3   citric acid           6494 non-null   float64
 4   residual sugar        6495 non-null   float64
 5   chlorides             6495 non-null   float64
 6   free sulfur dioxide   6497 non-null   float64
 7   total sulfur dioxide  6497 non-null   float64
 8   density               6497 non-null   float64
 9   pH                    6488 non-null   float64
 10  sulphates             6493 non-null   float64
 11  alcohol               6497 non-null   float64
 12  quality               6497 non-null   int64  
dtypes: float64(11), int64(1), object(1)
memory usage: 660.0+ KB
```

In [6]:

```
df.dtypes
```

Out[6]:

```
type                     object
fixed acidity           float64
volatile acidity        float64
citric acid             float64
residual sugar          float64
chlorides               float64
free sulfur dioxide     float64
total sulfur dioxide    float64
density                 float64
pH                      float64
sulphates               float64
alcohol                 float64
quality                   int64
dtype: object
```

In [7]:

```
df.isnull().sum()
```

Out[7]:

```
type                     0
fixed acidity           10
volatile acidity         8
citric acid              3
residual sugar           2
chlorides                2
free sulfur dioxide      0
total sulfur dioxide     0
density                  0
pH                       9
sulphates                4
alcohol                  0
quality                  0
dtype: int64
```

In [8]:

```
# fill the missing values
for col, value in df.items():
    if col != 'type':
        df[col] = df[col].fillna(df[col].mean())
```

In [9]:

```
df.isnull().sum()
```

Out[9]:

```
type                    0
fixed acidity           0
volatile acidity        0
citric acid             0
residual sugar          0
chlorides               0
free sulfur dioxide     0
total sulfur dioxide    0
density                 0
pH                      0
sulphates               0
alcohol                 0
quality                 0
dtype: int64
```

In [10]:

```
df.describe().T
```

Out[10]:

	count	mean	std	min	25%	50%	75%	max

	count	mean	std	min	25%	50%	75%	max
fixed acidity	6497.0	7.216579	1.296751	3.80000	6.40000	7.00000	7.70000	15.90000
volatile acidity	6497.0	0.339691	0.164548	0.08000	0.23000	0.29000	0.40000	1.58000
citric acid	6497.0	0.318722	0.145231	0.00000	0.25000	0.31000	0.39000	1.66000
residual sugar	6497.0	5.444326	4.757392	0.60000	1.80000	3.00000	8.10000	65.80000
chlorides	6497.0	0.056042	0.035031	0.00900	0.03800	0.04700	0.06500	0.61100
...	...	...	...	...	...	...	...	...
density	6497.0	0.994697	0.002999	0.98711	0.99234	0.99489	0.99699	1.03898
pH	6497.0	3.218395	0.160637	2.72000	3.11000	3.21000	3.32000	4.01000
sulphates	6497.0	0.531215	0.148768	0.22000	0.43000	0.51000	0.60000	2.00000
alcohol	6497.0	10.491801	1.192712	8.00000	9.50000	10.30000	11.30000	14.90000
quality	6497.0	5.818378	0.873255	3.00000	5.00000	6.00000	6.00000	9.00000

In [11]:

```
df.corr()
```

Out[11]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	q
fixed acidity	1.000000	0.219918	0.323349	-0.112219	0.298282	-0.283237	-0.329409	0.458941	-0.251683	0.300225	-0.095560	0.0
volatile acidity	0.219918	1.000000	-0.377759	-0.196578	0.377122	-0.353055	-0.414706	0.271107	0.260283	0.225313	-0.038215	0.2
citric acid	0.323349	-0.377759	1.000000	0.142451	0.039310	0.133426	0.195148	0.096307	-0.328354	0.057564	-0.010431	0.0
residual sugar	-0.112219	-0.196578	0.142451	1.000000	-0.128887	0.403242	0.495704	0.552487	-0.266717	-0.185716	-0.359656	0.0
chlorides	0.298282	0.377122	0.039310	-0.128887	1.000000	-0.194978	-0.279547	0.362580	0.044754	0.395073	-0.256844	0.2
...	...	...	...	...	...	...	...	...	...	...	...	
density	0.458941	0.271107	0.096307	0.552487	0.362580	0.025717	0.032395	1.000000	0.011913	0.259432	-0.686745	0.3
pH	-0.251683	0.260283	-0.328354	-0.266717	0.044754	-0.145116	-0.237523	0.011913	1.000000	0.191075	0.120939	0.0
sulphates	0.300225	0.225313	0.057564	-0.185716	0.395073	-0.188471	-0.275291	0.259432	0.191075	1.000000	-0.003261	0.0
alcohol	-0.095560	-0.038215	-0.010431	-0.359656	-0.256844	-0.179838	-0.265740	-0.686745	0.120939	-0.003261	1.000000	0.4
quality	-0.076967	-0.265838	0.085699	-0.036819	-0.200818	0.055463	-0.041385	-0.305858	0.019356	0.038713	0.444319	1.0

In [12]:

```
df.shape
```

Out[12]:

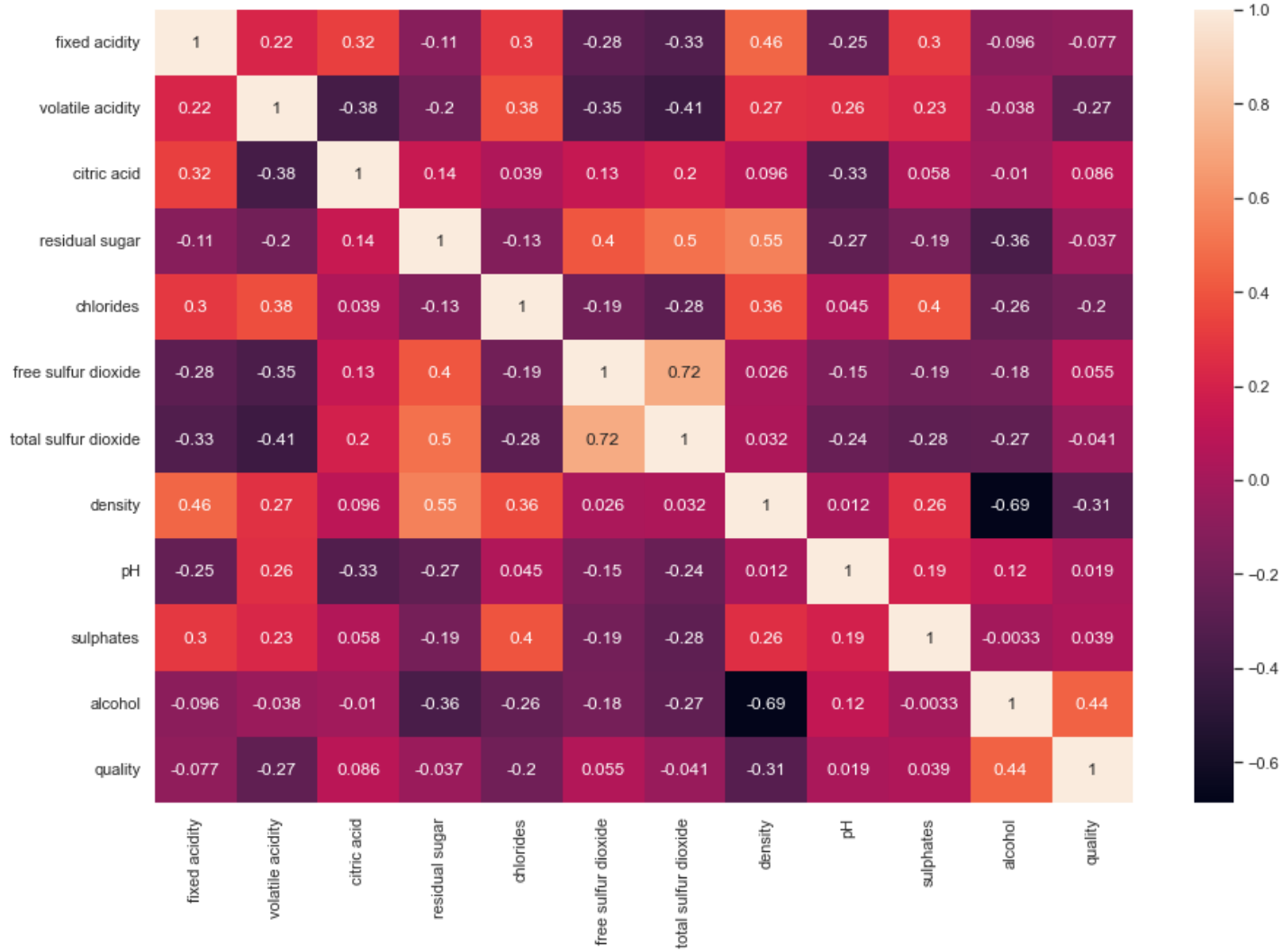
```
(6497, 13)
```

In [13]:

```
sns.set(rc={'figure.figsize':(15,10)})
sns.heatmap(df.corr(),annot=True)
```

Out[13]:

<AxesSubplot:>



Correlation

IMPORTANT NOTE! There is 'multicollinearity' problem

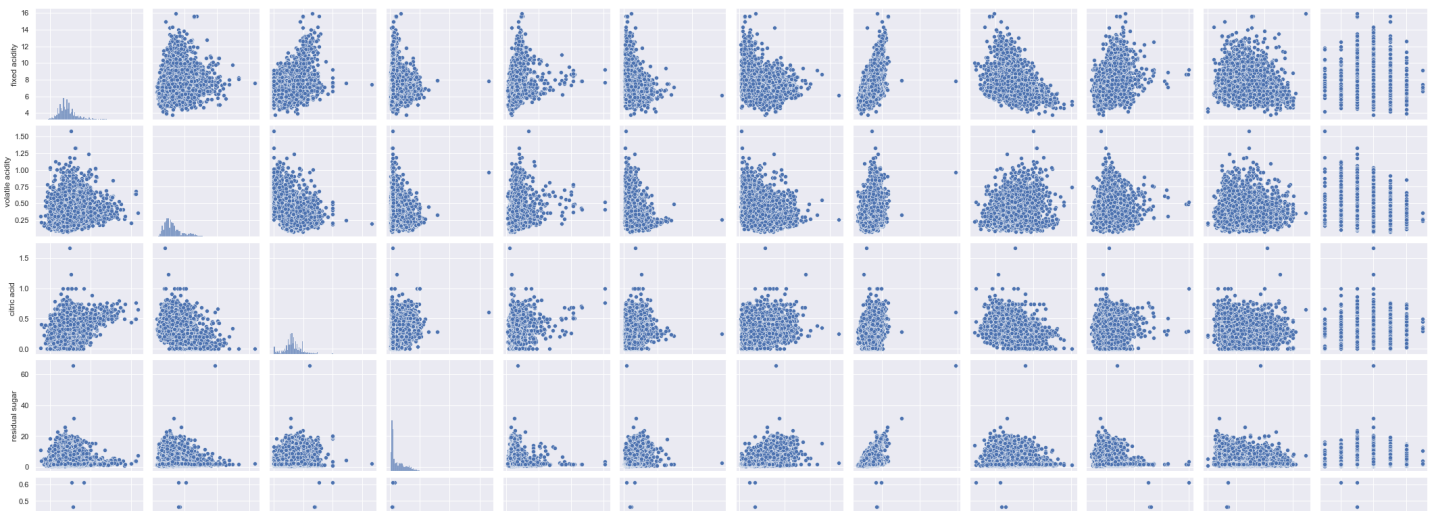
Here we see that there is relatively high (0.67, positive) correlation between 'free sulfur dioxide' and 'total_sulfur_dioxide' variables. There is relatively high (-0.68, negative) correlation between "pH" and "fixed_acidity" variables. And there is about 0.5 correlation between some of other variables. That's why we must consider when build Machine Learning models.

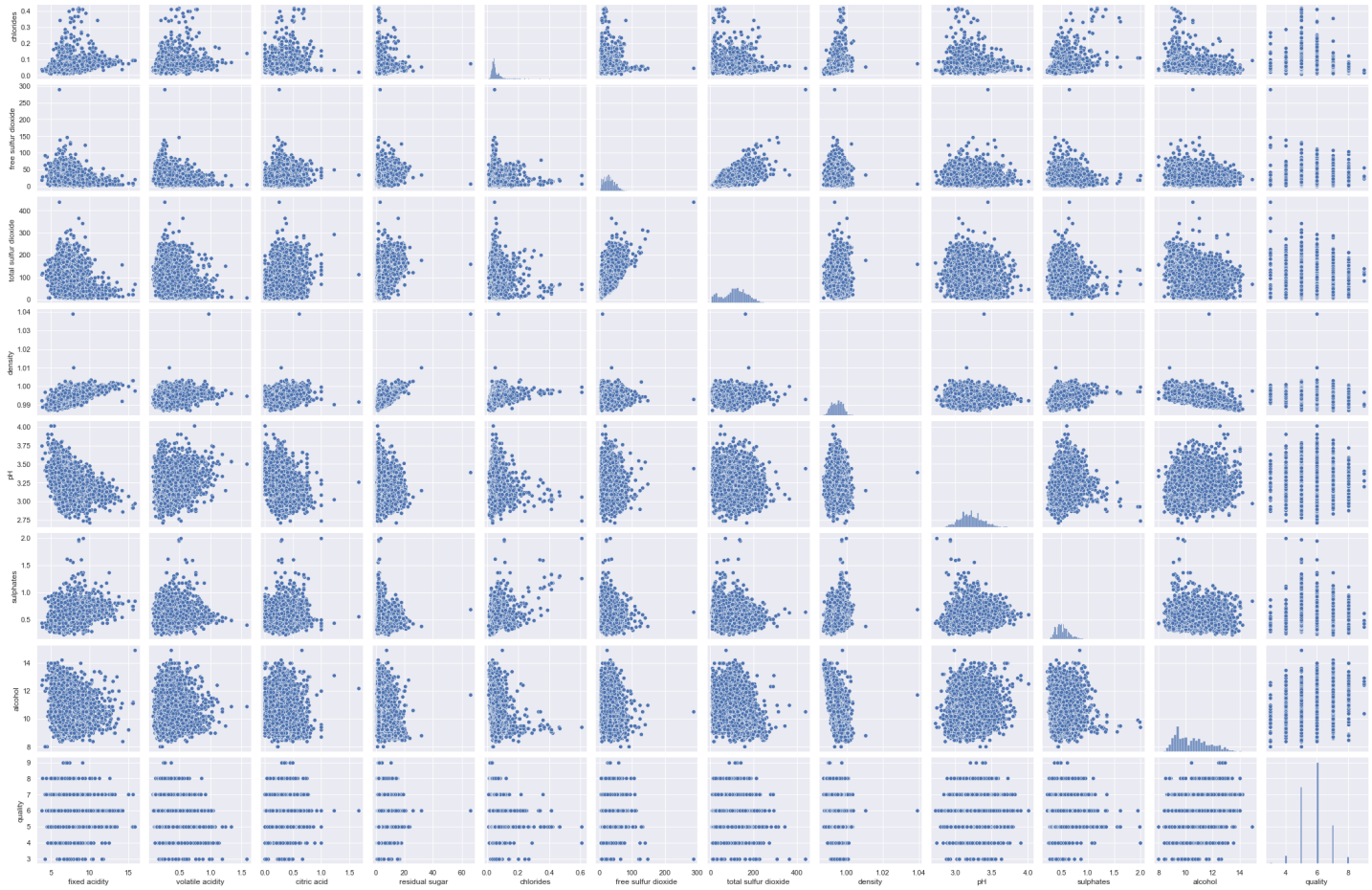
In [14]:

```
sns.pairplot(df)
```

Out[14]:

<seaborn.axisgrid.PairGrid at 0x19053e3b340>



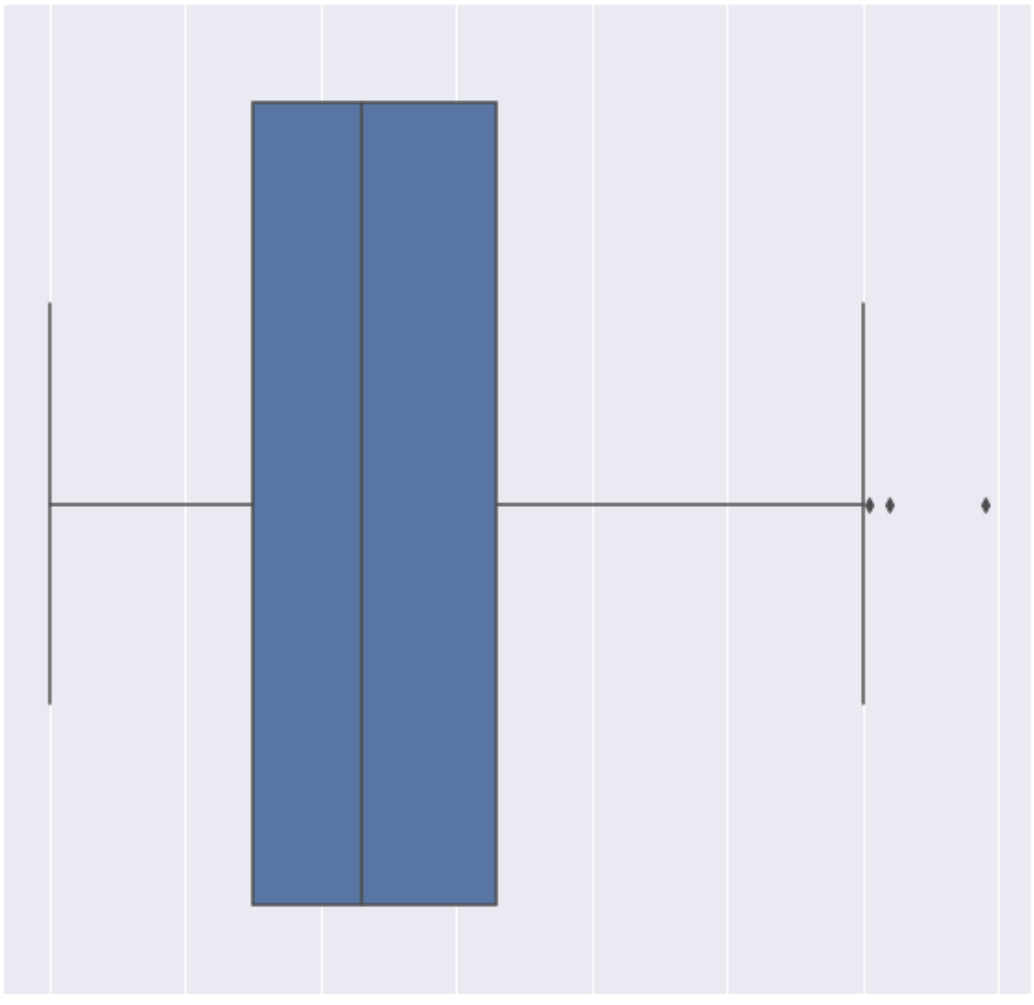


In [15]:

```
sns.set(rc={'figure.figsize':(10,10)})
sns.boxplot(df['alcohol'])
```

Out[15]:

```
<AxesSubplot:xlabel='alcohol'>
```

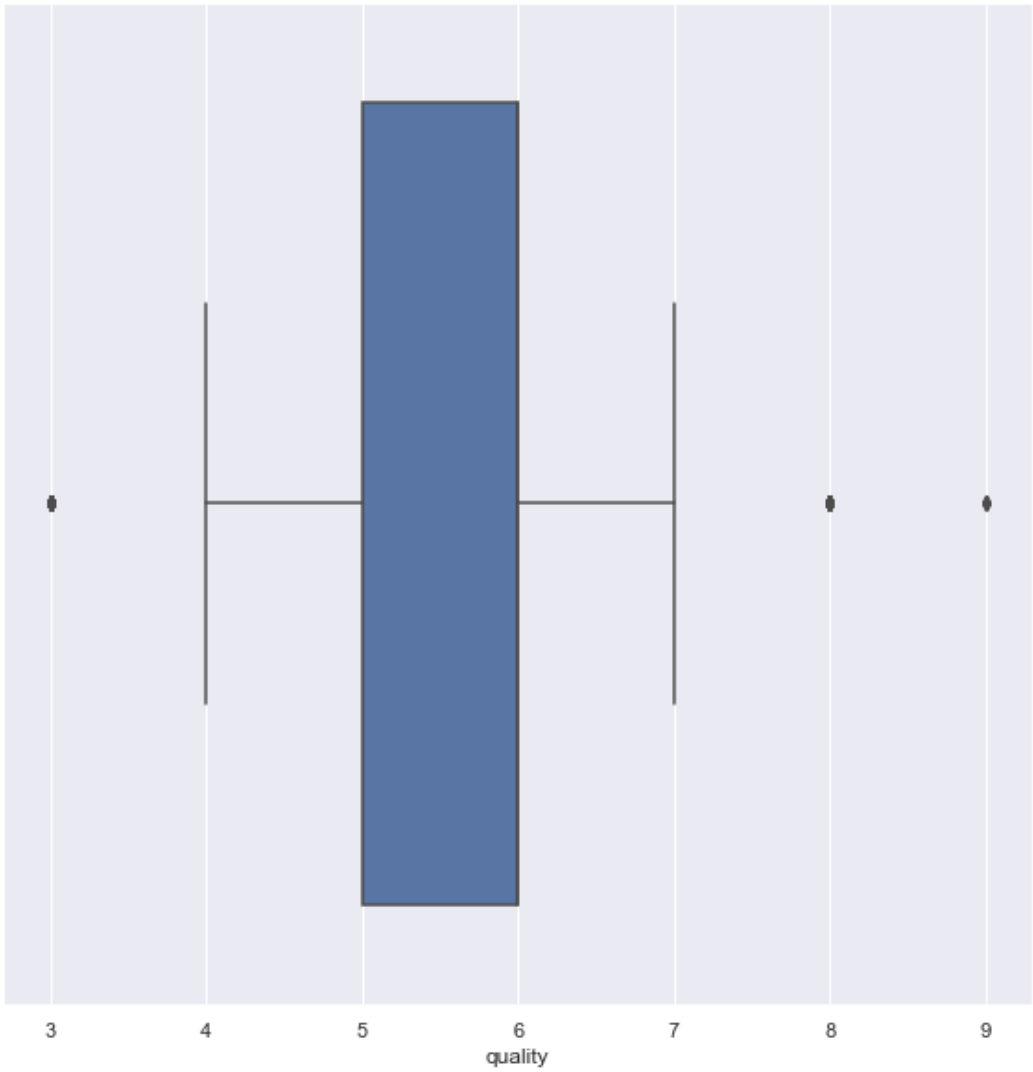


In [16]:

```
sns.set(rc={'figure.figsize':(10,10)})
sns.boxplot(df['quality'])
```

Out[16]:

```
<AxesSubplot:xlabel='quality'>
```

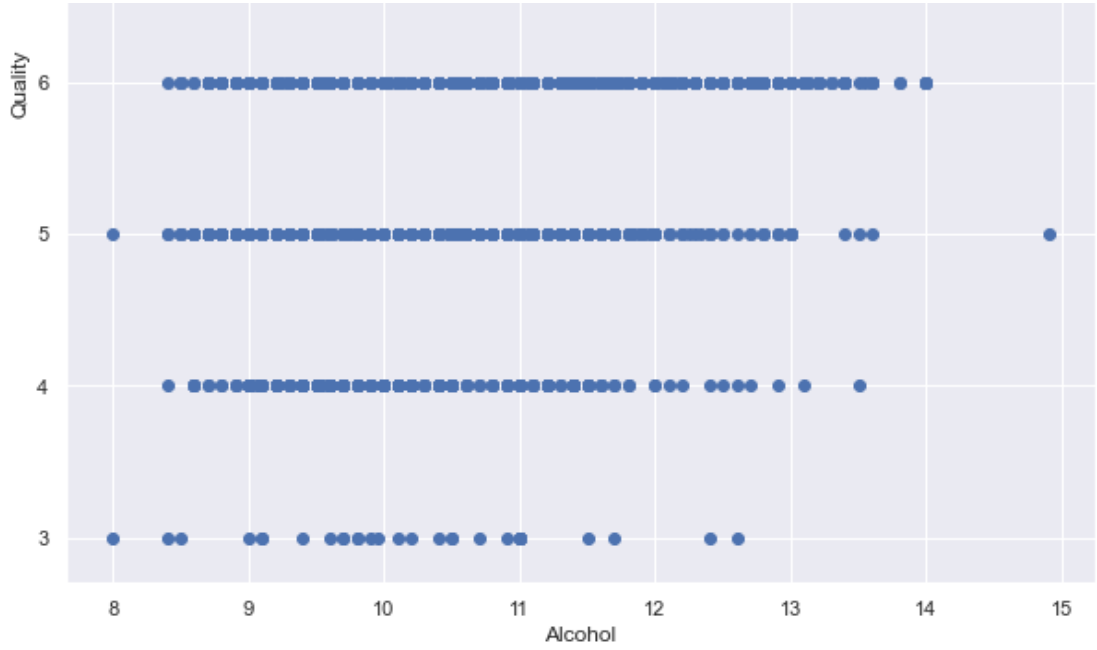


In [17]:

```
plt.scatter(df['alcohol'],df['quality'])
plt.xlabel("Alcohol")
plt.ylabel("Quality")
```

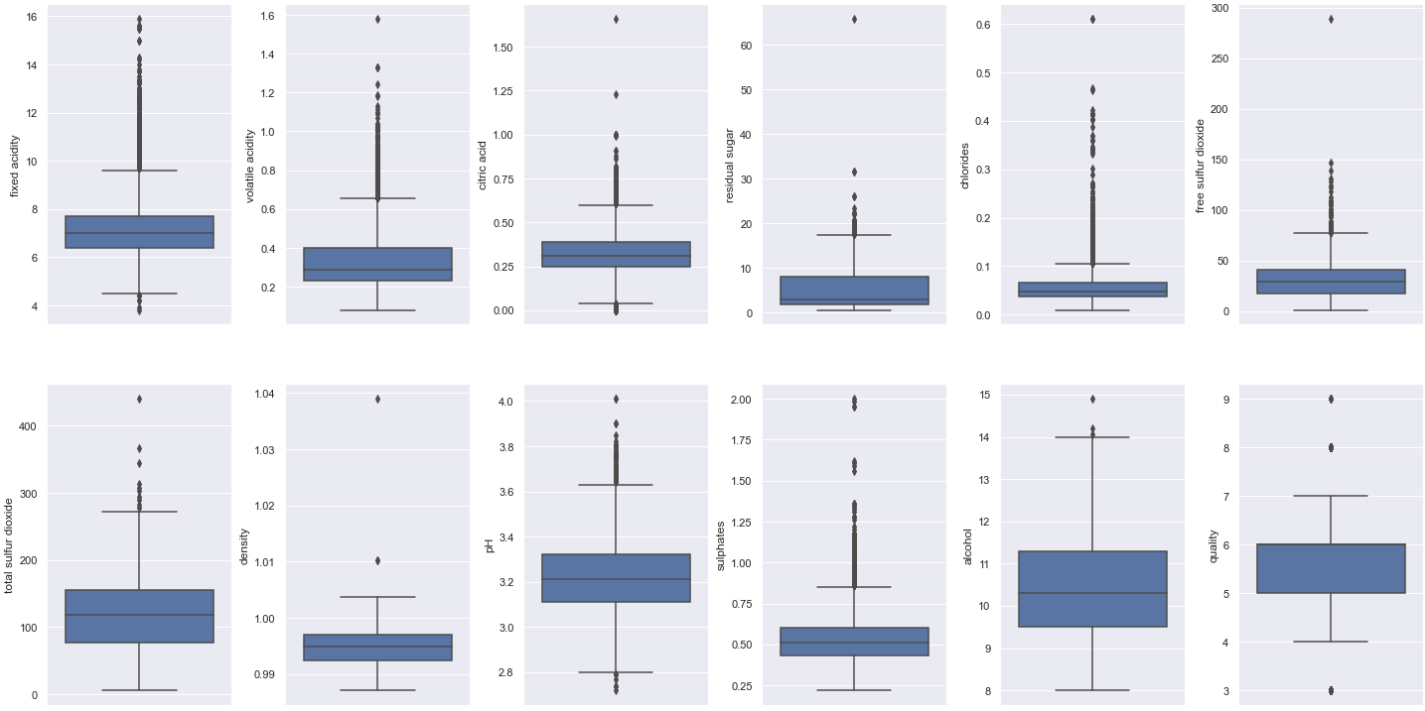
Out[17]:

```
Text(0, 0.5, 'Quality')
```



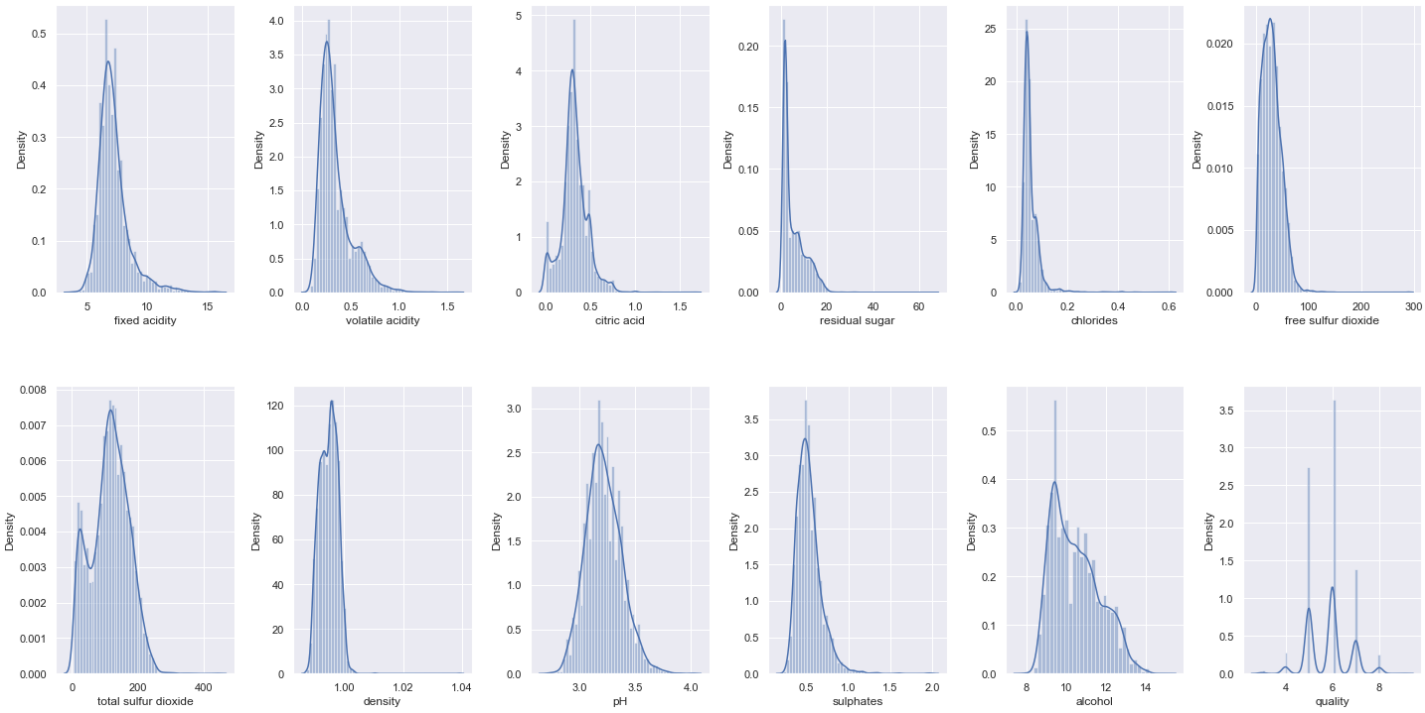
In [18]:

```
# create box plots
fig, ax = plt.subplots(ncols=6, nrows=2, figsize=(20,10))
index = 0
ax = ax.flatten()

for col, value in df.items():
    if col != 'type':
        sns.boxplot(y=col, data=df, ax=ax[index])
        index += 1
plt.tight_layout(pad=0.5, w_pad=0.7, h_pad=5.0)
```



In [19]:

```
# create dist plot
fig, ax = plt.subplots(ncols=6, nrows=2, figsize=(20,10))
index = 0
ax = ax.flatten()

for col, value in df.items():
    if col != 'type':
        sns.distplot(value, ax=ax[index])
        index += 1
plt.tight_layout(pad=0.5, w_pad=0.7, h_pad=5.0)
```



In [20]:

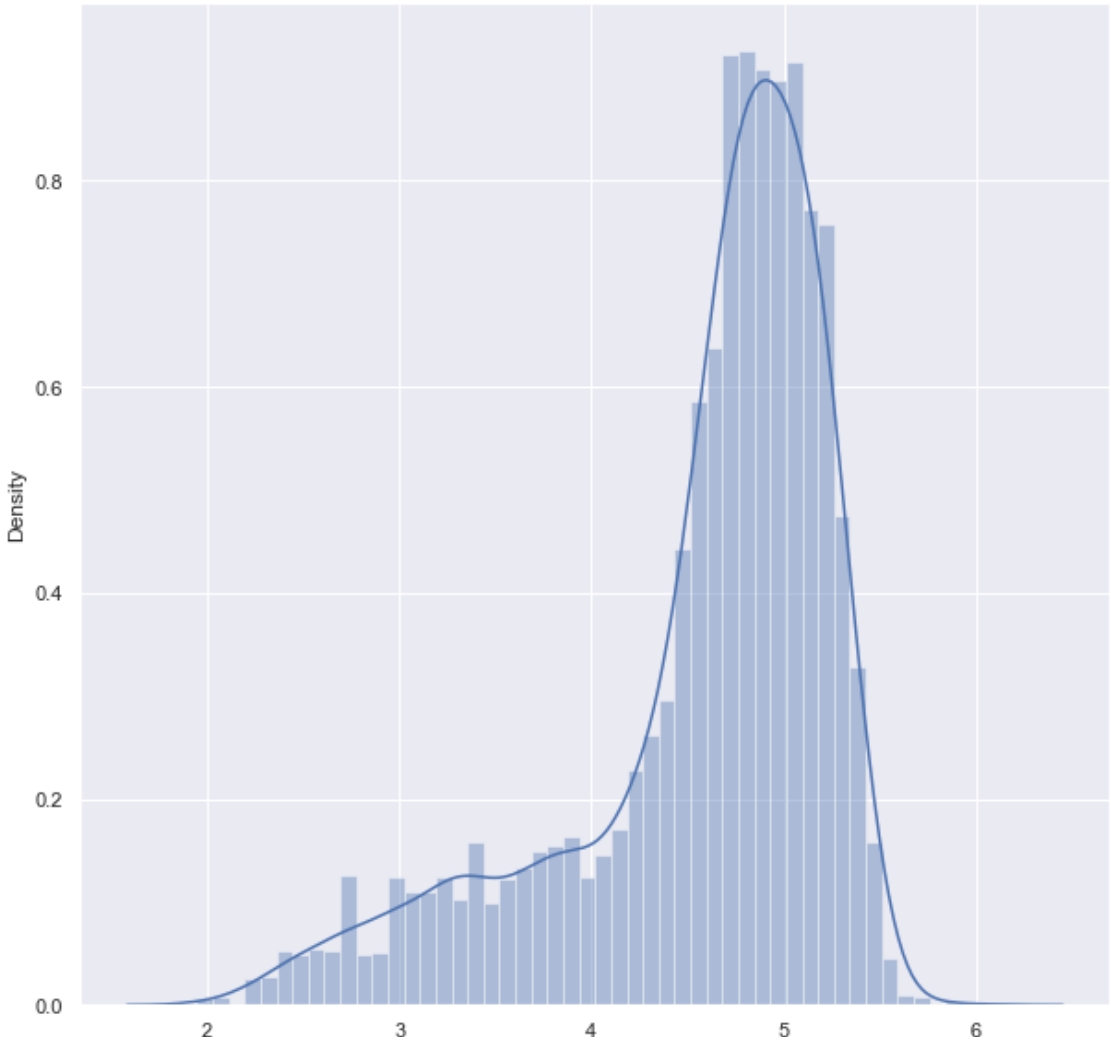
```
# log transformation Log transformation helps to make the highly skewed distribution to l
ess skewed.
df['total sulfur dioxide'] = np.log(1 + df['total sulfur dioxide'])
```

In [21]:

```
sns.distplot(df['total sulfur dioxide'])
```

Out[21]:

```
<AxesSubplot:xlabel='total sulfur dioxide', ylabel='Density'>
```



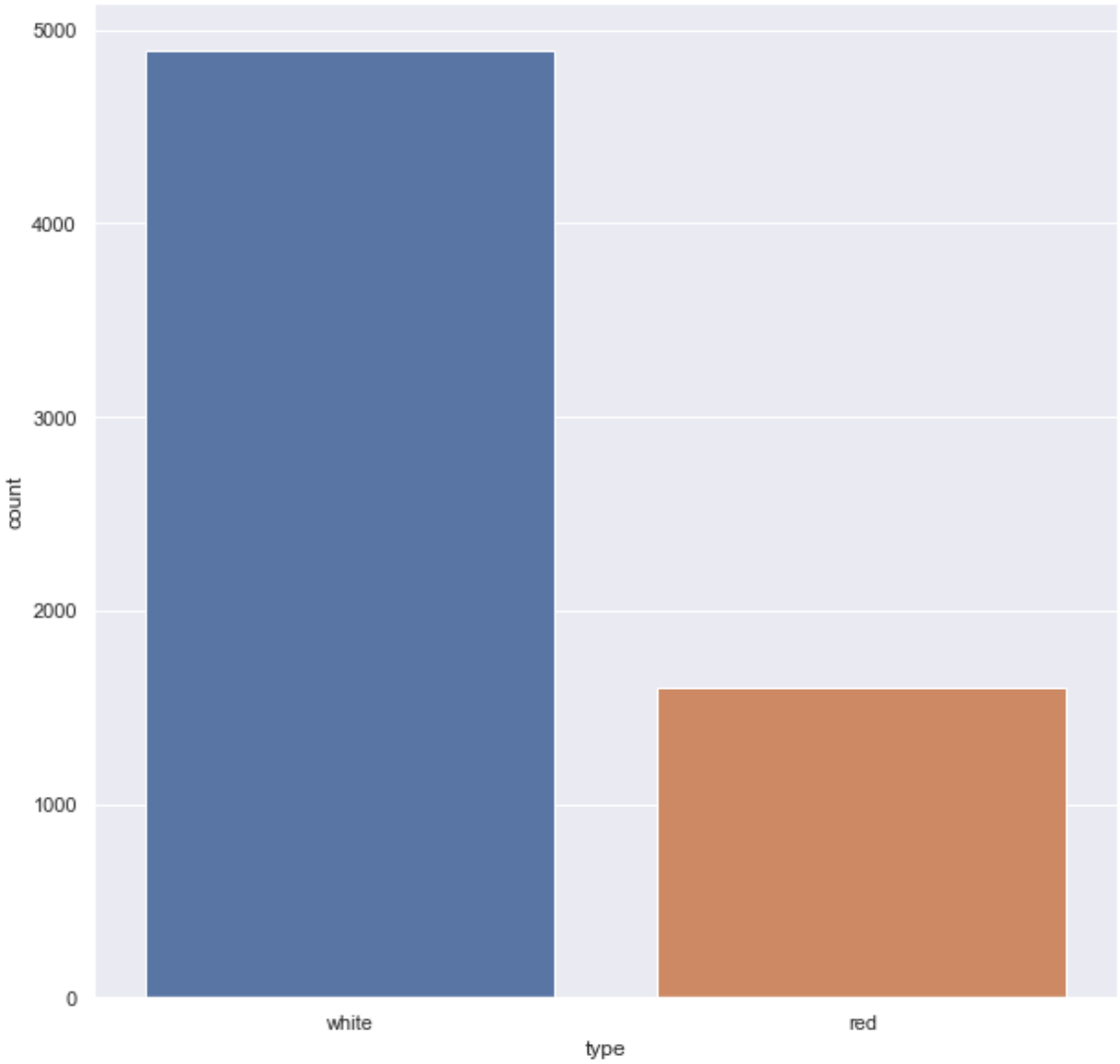
total sulfur dioxide

In [22]:

```
sns.countplot(df['type'])
```

Out[22]:

```
<AxesSubplot:xlabel='type', ylabel='count'>
```

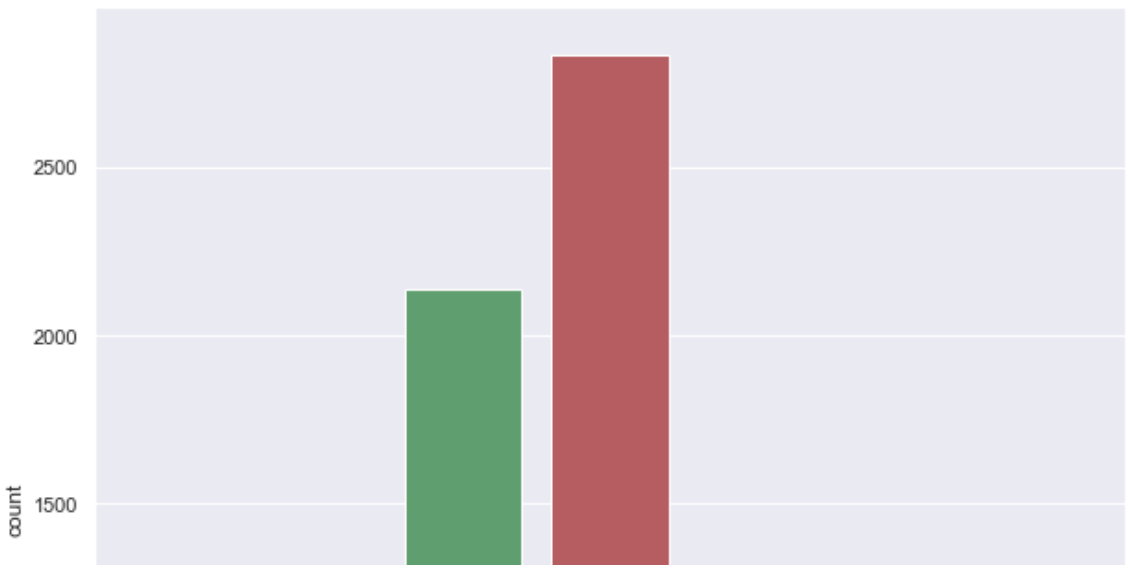


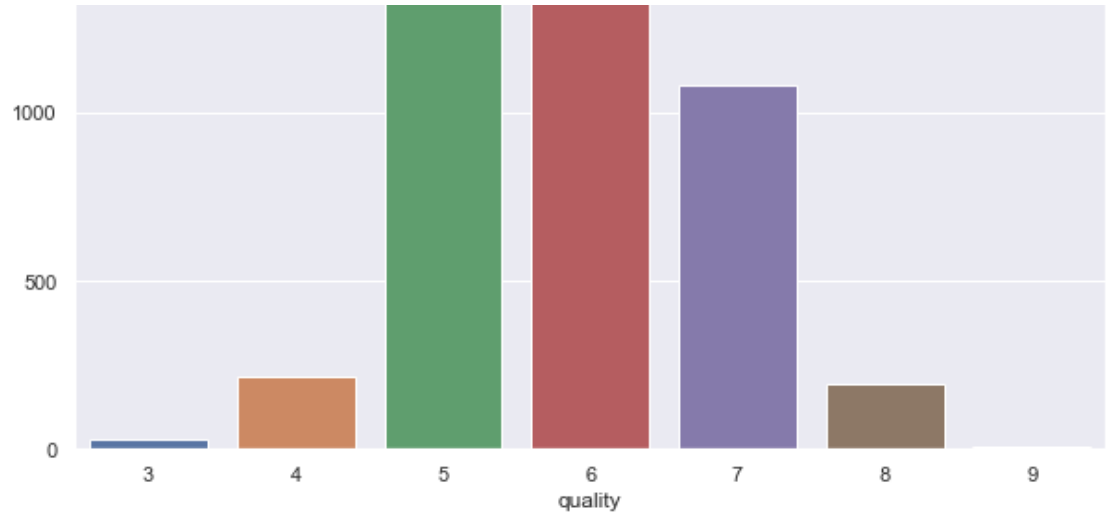
In [23]:

```
sns.countplot(df['quality'])
```

Out[23]:

```
<AxesSubplot:xlabel='quality', ylabel='count'>
```





Making binary classificaion for the response variable.

Dividing wine as good and bad by giving the limit for the quality

In [24]:

```
bins = (2, 6.5, 8)
group_names = ['bad', 'good']
df['quality'] = pd.cut(df['quality'], bins = bins, labels = group_names)
```

In [25]:

```
X = df.drop(['quality','type'],axis=1)
Y = df['quality']
```

In [26]:

```
# Encoding our dependent variable:Quality column
from sklearn.preprocessing import LabelEncoder
labelencoder_y = LabelEncoder()
Y = labelencoder_y.fit_transform(Y)
Y
```

Out[26]:

```
array([0, 0, 0, ..., 0, 0, 0])
```

Splitting the dataset into the Training set and Test set.%20 of dataset for test set,%80 for training set.

In [27]:

```
from sklearn.model_selection import train_test_split, GridSearchCV, cross_val_score
X_train, X_test, y_train, y_test = train_test_split(X, Y, test_size = 0.25, random_state
= 42)
```

In [28]:

```
X_train
```

Out[28]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol
1539	7.3	0.26	0.49	5.0	0.028	32.0	4.682131	0.99360	3.24	0.54	10.8
1109	9.2	0.22	0.40	2.4	0.054	18.0	5.023881	0.99520	3.04	0.46	9.3
100	7.4	0.25	0.37	13.5	0.060	52.0	5.262690	0.99750	3.00	0.44	9.1
5477	10.6	0.31	0.49	2.2	0.063	18.0	3.713572	0.99760	3.14	0.51	9.8
6416	7.4	0.47	0.46	2.2	0.114	7.0	3.044522	0.99647	3.32	0.63	10.5

...	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol
3772	6.3	0.24	0.29	13.7	0.035	53.0	4.905275	0.99567	3.17	0.38	10.6
5191	6.9	0.36	0.25	2.4	0.098	5.0	2.833213	0.99640	3.41	0.60	10.1
5226	13.4	0.27	0.62	2.6	0.082	6.0	3.091042	1.00020	3.16	0.67	9.7
5390	8.9	0.40	0.51	2.6	0.052	13.0	3.332205	0.99500	3.32	0.90	13.4
860	8.1	0.27	0.35	1.7	0.030	38.0	4.644391	0.99255	3.22	0.63	10.4

In [29]:

```
y_train
```

Out[29]:

```
array([0, 0, 0, ..., 0, 1, 1])
```

In [30]:

```
X_test
```

Out[30]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol
3103	7.0	0.25	0.45	2.3	0.045	40.0	4.779123	0.99064	3.16	0.48	11.9
1419	7.6	0.14	0.74	1.6	0.040	27.0	4.644391	0.99160	3.07	0.40	10.8
4761	6.2	0.15	0.27	11.0	0.035	46.0	4.762174	0.99602	3.12	0.38	9.1
4690	6.7	0.16	0.32	12.5	0.035	18.0	5.056246	0.99666	2.88	0.36	9.0
4032	6.8	0.27	0.22	17.8	0.034	16.0	4.762174	0.99890	3.07	0.53	9.2
...	...	...	...	...	...	...	...	...	...	...	...
4509	6.7	0.23	0.17	1.3	0.061	14.0	4.615121	0.99250	3.07	0.55	9.5
3350	7.2	0.22	0.28	7.2	0.060	41.0	4.890349	0.99350	3.08	0.59	11.3
1730	9.2	0.23	0.30	1.1	0.031	40.0	4.605170	0.99290	2.94	0.30	10.4
2225	7.6	0.23	0.26	15.3	0.067	32.0	5.117994	0.99860	3.03	0.44	9.2
5230	8.0	0.58	0.28	3.2	0.066	21.0	4.744932	0.99730	3.22	0.54	9.4

In [31]:

```
y_test
```

Out[31]:

```
array([1, 1, 0, ..., 0, 0, 0])
```

Scaling the data using StandardScaler to bring the data points closer to the best fit line

In [32]:

```
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
```

In [33]:

```
X_train_scaled = scaler.fit_transform(X_train)
```

In [34]:

```
X_test_scaled = scaler.fit_transform(X_test)
```

In [35]:

```
X_train_scaled
```

Out[35]:

```
array([[ 0.05774648, -0.48603987,  1.17497687, ...,  0.13174139,
         0.04025317,  0.25267266],
       [ 1.50939876, -0.72679705,  0.55539336, ..., -1.11293313,
        -0.48733115, -1.00093862],
       [ 0.13414923, -0.54622916,  0.34886553, ..., -1.36186804,
        -0.61922723, -1.16808679],
       ...,
       [ 4.71831433, -0.42585057,  2.06993083, ..., -0.36612842,
         0.8975777 , -0.66664228],
       [ 1.28019051,  0.35661028,  1.31266209, ...,  0.6296112 ,
         2.41438262,  2.42559889],
       [ 0.6689685 , -0.42585057,  0.2111803 , ...,  0.00727394,
         0.63378553, -0.08162368]])
```

In [36]:

```
X_test_scaled
```

Out[36]:

```
array([[-0.15385272, -0.54212657,  0.91725851, ..., -0.35583504,
        -0.30958735,  1.20767302],
       [ 0.32425573, -1.23145329,  2.91603552, ..., -0.91680168,
        -0.88320424,  0.27594721],
       [-0.79133065, -1.16878722, -0.32336171, ..., -0.60515355,
        -1.02660846, -1.16399267],
       ...,
       [ 1.5992116 , -0.6674587 , -0.11659167, ..., -1.72708682,
        -1.60022535, -0.06286217],
       [ 0.32425573, -0.6674587 , -0.39228505, ..., -1.16612019,
        -0.59639579, -1.07929033],
       [ 0.6429947 ,  1.52585358, -0.25443836, ...,  0.01814272,
         0.12062532, -0.90988563]])
```

In [37]:

```
from sklearn.svm import SVC
from sklearn.svm import LinearSVC,SVC
from sklearn.pipeline import make_pipeline
clf = SVC()
```

In [38]:

```
clf = clf.fit(X_train,y_train)
```

In [39]:

```
y_pred = clf.predict(X_test)
```

In [40]:

```
# #Finding best parameters for our SVC model
# param = {
#     'C': [0.1,0.8,0.9,1,1.1,1.2,1.3,1.4],
#     'kernel':['linear', 'rbf'],
#     'gamma' :[0.1,0.8,0.9,1,1.1,1.2,1.3,1.4]
# }
# grid_svc = GridSearchCV(clf, param_grid=param, scoring='accuracy', cv=10)
```

In [41]:

```
# grid_svc.fit(X_train, y_train)
```

In [42]:

```
from sklearn.metrics import accuracy_score
```

```
print("Accuracy: %.2f%%" % (accuracy_score(y_pred,y_test) * 100.0))
```

```
Accuracy: 81.05%
```

Classification Report for the unscaled Data

In [51]:

```
from sklearn.metrics import confusion_matrix, classification_report
print(classification_report(y_test, y_pred))
```

```
              precision    recall  f1-score   support

           0       0.81      1.00      0.90      1317
           1       0.00      0.00      0.00       308

    accuracy                           0.81      1625
   macro avg       0.41      0.50      0.45      1625
weighted avg       0.66      0.81      0.73      1625
```

In [43]:

```
clf_scaled = clf.fit(X_train_scaled,y_train)
```

In [44]:

```
y_pred_scaled = clf_scaled.predict(X_test_scaled)
```

In [45]:

```
print("Accuracy: %.2f%%" % (accuracy_score(y_pred_scaled,y_test) * 100.0))
```

```
Accuracy: 83.45%
```

Classification Report for the Scaled Data

In [50]:

```
from sklearn.metrics import confusion_matrix, classification_report
print(classification_report(y_test, y_pred_scaled))
```

```
              precision    recall  f1-score   support

           0       0.85      0.96      0.90      1317
           1       0.65      0.28      0.39       308

    accuracy                           0.83      1625
   macro avg       0.75      0.62      0.65      1625
weighted avg       0.81      0.83      0.81      1625
```

In [47]:

```
#k-Fold cross validation for improving our model
from sklearn.model_selection import cross_val_score
accuracy_cv = cross_val_score(estimator = clf, X = X_train,y = y_train, cv = 20)
#we can see model's average accuracy
accuracy_cv.mean()
```

Out[47]:

```
0.8011106051406596
```

In [48]:

```
#k-Fold cross validation for improving our model
from sklearn.model_selection import cross_val_score
accuracy_cv = cross_val_score(estimator = clf, X = X_train_scaled,y = y_train, cv = 20)
```

```
#we can see model's average accuracy
accuracy_cv.mean()
```

Out[48]:

```
0.8327152060986306
```

Improving the Accuracy using best params

In [52]:

```
svc2 = SVC(C = 1.2, gamma =  0.9, kernel= 'rbf')
svc2.fit(X_train, y_train)
pred_svc2 = svc2.predict(X_test)
print(classification_report(y_test, pred_svc2))
```

```
              precision    recall  f1-score   support

           0       0.86      0.97      0.91      1317
           1       0.71      0.35      0.47       308

    accuracy                           0.85      1625
   macro avg       0.79      0.66      0.69      1625
weighted avg       0.84      0.85      0.83      1625
```

In [56]:

```
svc2 = SVC(C = 1.2, gamma =  0.9, kernel= 'rbf')
svc2.fit(X_train_scaled, y_train)
pred_svc2_scaled = svc2.predict(X_test_scaled)
print(classification_report(y_test, pred_svc2_scaled))
```

```
              precision    recall  f1-score   support

           0       0.88      0.96      0.92      1317
           1       0.71      0.42      0.53       308

    accuracy                           0.86      1625
   macro avg       0.80      0.69      0.72      1625
weighted avg       0.85      0.86      0.84      1625
```

In [ ]:

```

```