In [1]:
```
from ucimlrepo import fetch_ucirepo

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import OneHotEncoder
```

In [147…
```
sns.set_style('whitegrid')
sns.set_palette("deep")
sns.color_palette("deep", n_colors=11)

sns.set_theme(style='whitegrid')
```

In [148…
```
wine_quality = fetch_ucirepo(id=186)
X = wine_quality.data.original
```

A peak of the top 10 rows of the data.

In [149…
```
display(X.head(10))
```

	fixed_acidity	volatile_acidity	citric_acid	residual_sugar	chlorides	free_sulfur_dioxide	tot
0	7.4	0.70	0.00	1.9	0.076	11.0	
1	7.8	0.88	0.00	2.6	0.098	25.0	
2	7.8	0.76	0.04	2.3	0.092	15.0	
3	11.2	0.28	0.56	1.9	0.075	17.0	
4	7.4	0.70	0.00	1.9	0.076	11.0	
5	7.4	0.66	0.00	1.8	0.075	13.0	
6	7.9	0.60	0.06	1.6	0.069	15.0	
7	7.3	0.65	0.00	1.2	0.065	15.0	
8	7.8	0.58	0.02	2.0	0.073	9.0	
9	7.5	0.50	0.36	6.1	0.071	17.0	

Checking the column names of the data. This includes possible features and target for machine learning.

In [150…
```
print(f'Columns: \n{X.columns}\n')
print(f'Shape: {X.shape}\n')
print(f'Info: \n{X.info()}\n')
```

```
Columns:
Index(['fixed_acidity', 'volatile_acidity', 'citric_acid', 'residual_sugar',
       'chlorides', 'free_sulfur_dioxide', 'total_sulfur_dioxide', 'density',
       'pH', 'sulphates', 'alcohol', 'quality', 'color'],
      dtype='object')

Shape: (6497, 13)

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 6497 entries, 0 to 6496
Data columns (total 13 columns):
 #   Column                Non-Null Count  Dtype  
---  ------                --------------  -----  
 0   fixed_acidity         6497 non-null   float64
 1   volatile_acidity      6497 non-null   float64
 2   citric_acid           6497 non-null   float64
 3   residual_sugar        6497 non-null   float64
 4   chlorides             6497 non-null   float64
 5   free_sulfur_dioxide   6497 non-null   float64
 6   total_sulfur_dioxide  6497 non-null   float64
 7   density               6497 non-null   float64
 8   pH                    6497 non-null   float64
 9   sulphates             6497 non-null   float64
 10  alcohol               6497 non-null   float64
 11  quality               6497 non-null   int64  
 12  color                 6497 non-null   object 
dtypes: float64(11), int64(1), object(1)
memory usage: 660.0+ KB
Info:
None
```

Quick checking of statistics of data. Adding parameter include='all' to also see statistics for color -- which is a categorical data.

In [151…

```
X.describe(include='all').T
```

Out[151…

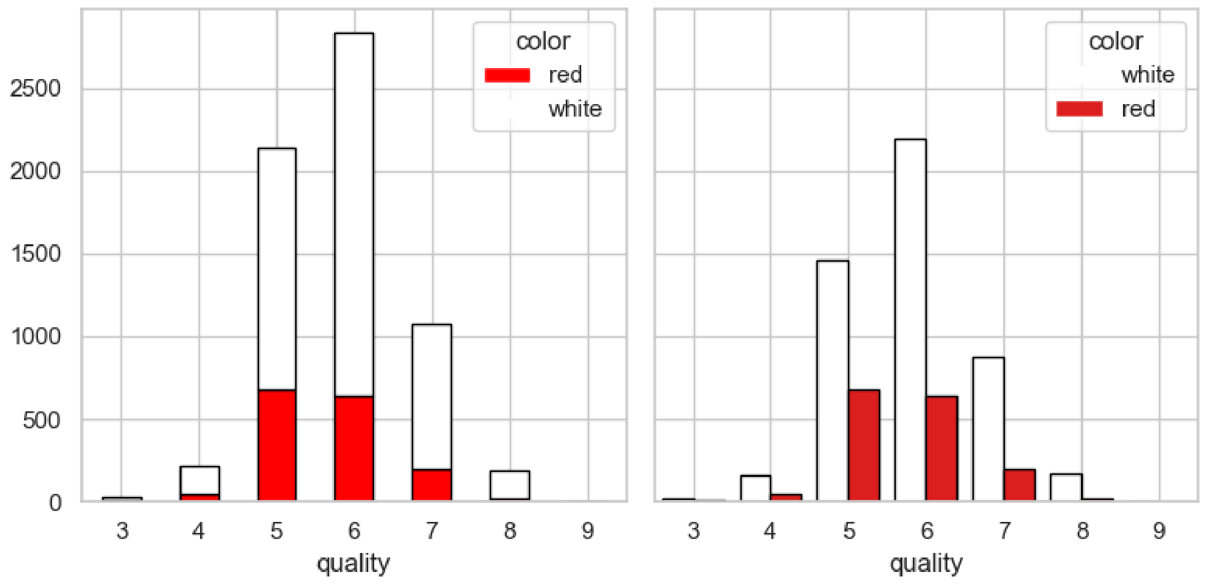
	count	unique	top	freq	mean	std	min	25%
fixed_acidity	6497.0	NaN	NaN	NaN	7.215307	1.296434	3.8	6.4
volatile_acidity	6497.0	NaN	NaN	NaN	0.339666	0.164636	0.08	0.23
citric_acid	6497.0	NaN	NaN	NaN	0.318633	0.145318	0.0	0.25
residual_sugar	6497.0	NaN	NaN	NaN	5.443235	4.757804	0.6	1.8
chlorides	6497.0	NaN	NaN	NaN	0.056034	0.035034	0.009	0.038
free_sulfur_dioxide	6497.0	NaN	NaN	NaN	30.525319	17.7494	1.0	17.0
total_sulfur_dioxide	6497.0	NaN	NaN	NaN	115.744574	56.521855	6.0	77.0
density	6497.0	NaN	NaN	NaN	0.994697	0.002999	0.98711	0.99234
pH	6497.0	NaN	NaN	NaN	3.218501	0.160787	2.72	3.11
sulphates	6497.0	NaN	NaN	NaN	0.531268	0.148806	0.22	0.43
alcohol	6497.0	NaN	NaN	NaN	10.491801	1.192712	8.0	9.5
quality	6497.0	NaN	NaN	NaN	5.818378	0.873255	3.0	5.0
color	6497	2	white	4898	NaN	NaN	NaN	NaN

It can be observed that the scales vary for each feature. *chlorides* ranges from ~0.009-0.611 while *total_sulfur_dioxide* ranges from 6.0-440.0. It is obvious that proper scaling should be used later if we want to compare and visualize the data.

Visualizing the proportion of the count of the different quality. Note that using bar graph over pie chart to visualize proportions is a preference. Here, it is observed that the majority of the quality score is centered on 6.0.

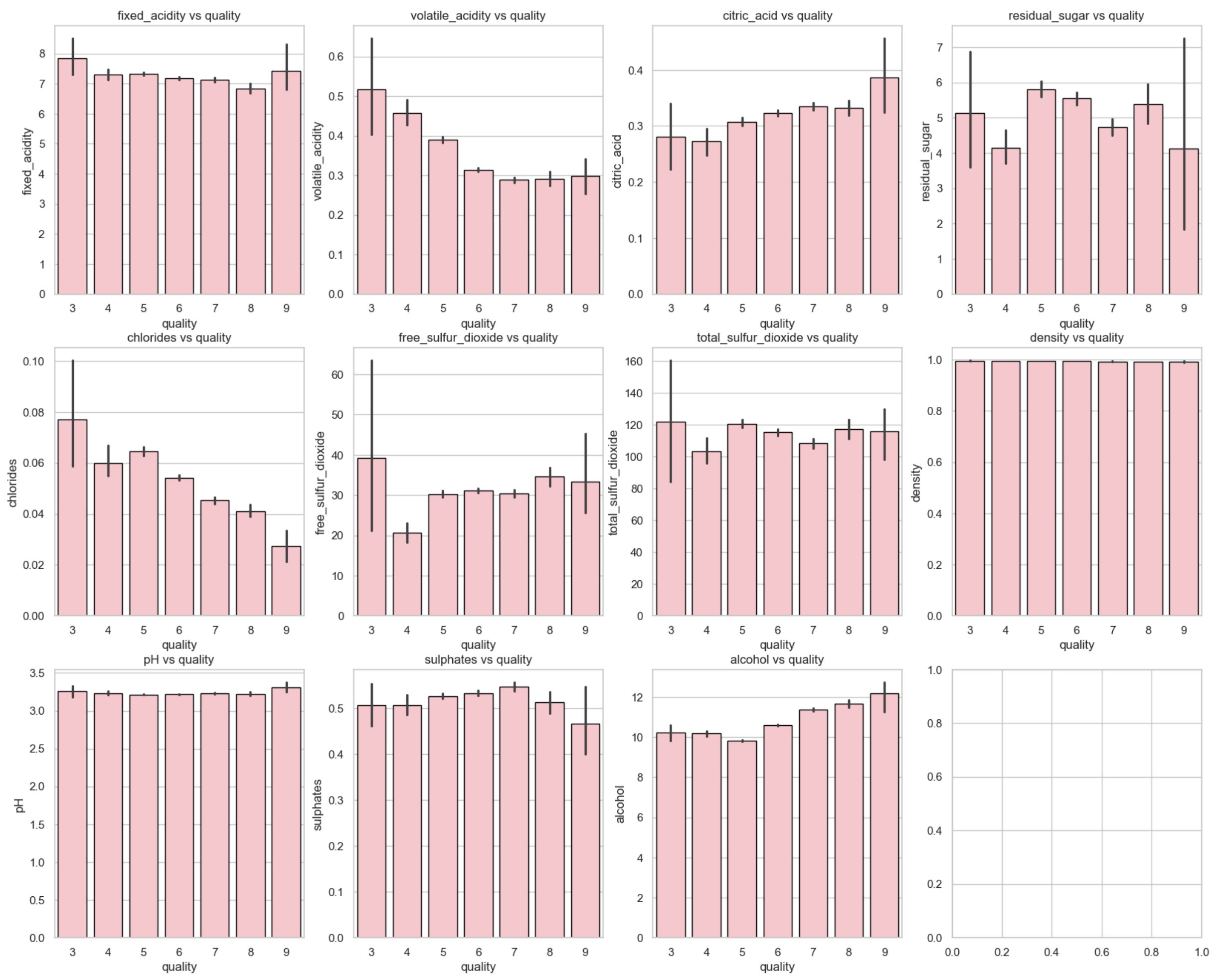
In [160…

```python
fig, ax = plt.subplots(1, 2, figsize=(8, 4), sharey=True)

color_palette = {'red': 'red', 'white': 'white'}
df_to_view = X[['quality', 'color']].value_counts().reset_index()

(
    df_to_view
    .pivot(index='quality', columns='color', values='count')
    .plot(kind='bar', stacked=True, ax=ax[0],
          color=[color_palette['red'], color_palette['white']])
)
ax[0].set_xticklabels(ax[0].get_xticklabels(), rotation=0)
plt.grid()

sns.barplot(
    data=df_to_view,
    x='quality',
    y='count',
    hue='color',
    ax=ax[1],
    palette=[color_palette['white'], color_palette['red']]
)
plt.grid()

for patch in ax[0].patches:
    patch.set_edgecolor('black')
    patch.set_linewidth(1)

for patch in ax[1].patches:
    patch.set_edgecolor('black')
    patch.set_linewidth(1)

plt.tight_layout()
```



In [162…

```
fig, ax = plt.subplots(3, 4, figsize=(20, 16))

for i, col_name in enumerate(X.columns[:-2]):
    row = i // 4
    col = i % 4
    sns.barplot(X, x='quality', y=col_name, ax=ax[row, col], color='pink')
    ax[row, col].set_title(f'{col_name} vs quality')

    for patch in ax[row, col].patches:
        patch.set_edgecolor('black')
        patch.set_linewidth(1)
```

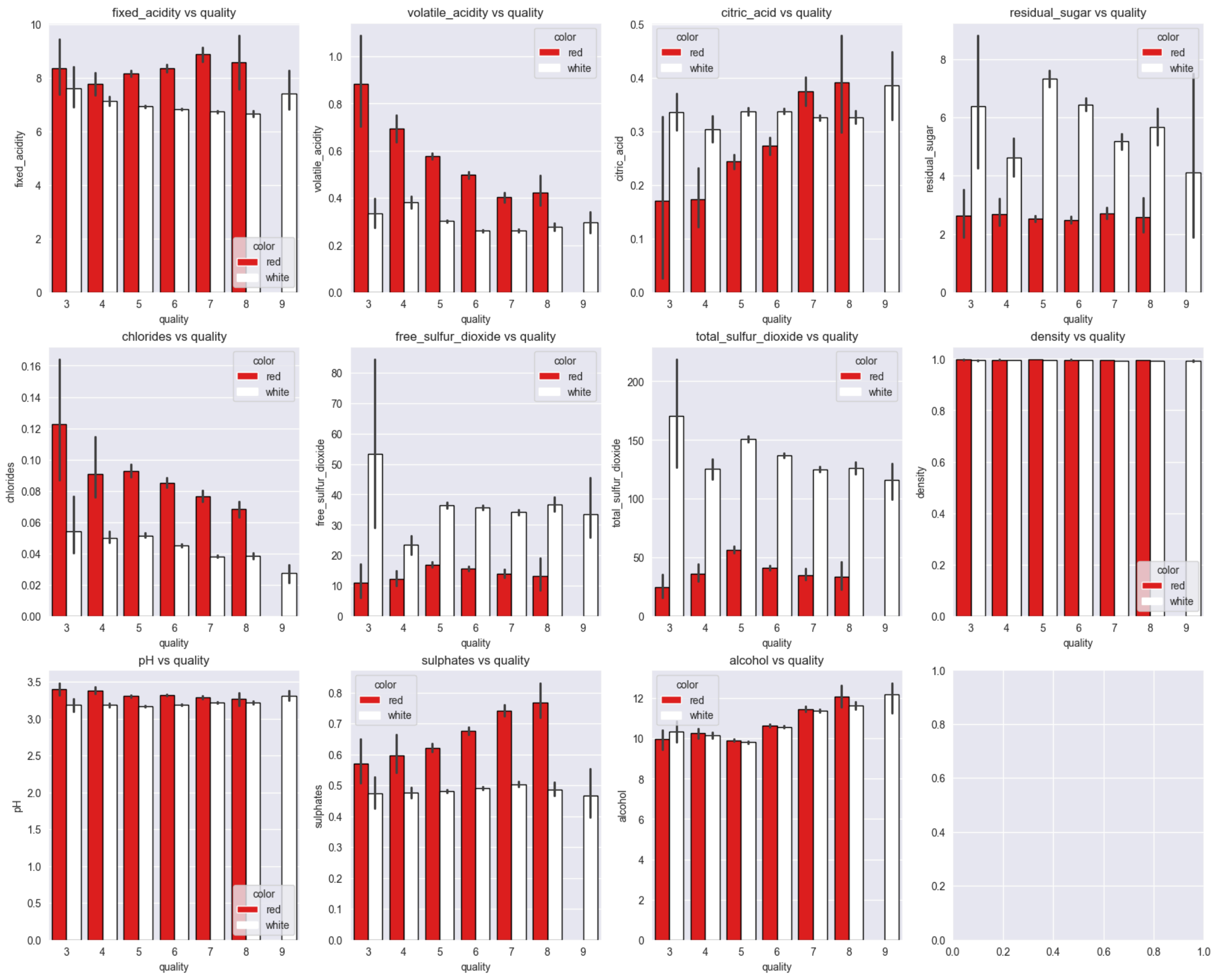


Above shows the mean with the error bar (the black wick) which represents the 95% confidence interval of the 11 features against the quality. Some initial insights that can be observed based on plots are the following:

feature	if_feature	target	then_target
volatile_acidity	↑	quality	↓
citric_acid	↑	quality	↑
chlorides	↑	quality	↓
alcohol	↑	quality	↑

In [146…

```
fig, ax = plt.subplots(3, 4, figsize=(20, 16))

for i, col_name in enumerate(X.columns[:-2]):
    row = i // 4
    col = i % 4
    sns.barplot(
        X,
        x='quality',
        y=col_name,
        hue='color',
        ax=ax[row, col],
        palette=[color_palette['red'], color_palette['white']]
    )
    for patch in ax[row, col].patches:
        patch.set_edgecolor('black')
        patch.set_linewidth(1)

    ax[row, col].set_title(f'{col_name} vs quality')
```



This shows the same plots but now show distinction for each color (red or white).

These observations are based from above but now with an added note. | feature | if_feature | target | then_target | notes | | - | :- | :-: | -: | -: | | volatile_acidity | ↑ | quality | ↓ | Trend seems to only apply for color=red | | citric_acid | ↑ | quality | ↑ | Trend seems to only apply for color=red | | chlorides | ↑ | quality | ↓ | Trend applies to both colors | | alcohol | ↑ | quality | ↑ | Trend applies to both colors |

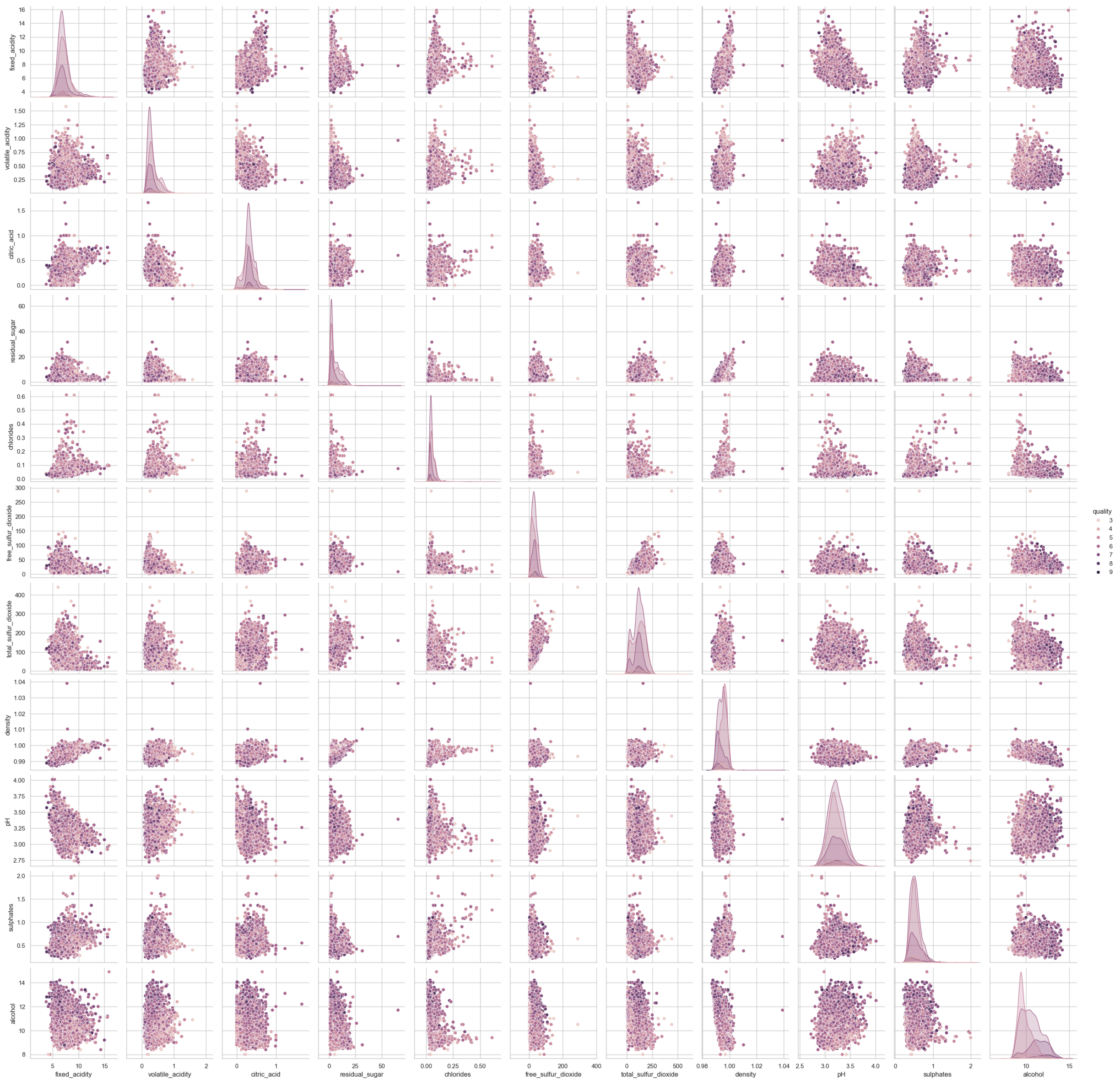
Although the purpose of the plot was to view different features against quality, obvious observations can be argued such as: | feature | observation | | - | :- | | volatile_acidity | red > white | | residual_sugar | white > red | | chlorides | red > white | | free_sulfur_dioxide | white > red | | total_sulfur_dioxide | white > red | | sulphates | red > white |

An interesting observation here is that no color=red exists for quality=9. This is unsure if this is just due to lack of data (given the fact that quality=9 already has a low count).

In [163…
```
plt.figure(figsize=(10, 10))
sns.pairplot(X.drop('color', axis=1), hue='quality')
```

Out[163…
```
<seaborn.axisgrid.PairGrid at 0x1458e51eb90>
```

```
<Figure size 1000x1000 with 0 Axes>
```



For each pair of features shown on a scatter plot, there seems to be little distinction for wines per quality score. But this could be somewhat misleading since it is know that majority of the wines have a score of {5, 6, 7}.

In [186…
```
scaler = StandardScaler()
X2 = X.drop(['color', 'quality'], axis=1).copy()
X_scaled = scaler.fit_transform(X2)
X_scaled = pd.DataFrame(X_scaled, columns=X2.columns)
display(X_scaled)
```

	fixed_acidity	volatile_acidity	citric_acid	residual_sugar	chlorides	free_sulfur_dioxide
0	0.142473	2.188833	-2.192833	-0.744778	0.569958	-1.100140
1	0.451036	3.282235	-2.192833	-0.597640	1.197975	-0.311320
2	0.451036	2.553300	-1.917553	-0.660699	1.026697	-0.874763
3	3.073817	-0.362438	1.661085	-0.744778	0.541412	-0.762074
4	0.142473	2.188833	-2.192833	-0.744778	0.569958	-1.100140
...	...	...	...	...	...	...
6492	-0.783214	-0.787650	-0.197054	-0.807837	-0.486252	-0.367664
6493	-0.474652	-0.119460	0.284686	0.537425	-0.257883	1.491697
6494	-0.551792	-0.605417	-0.885253	-0.891916	-0.429160	-0.029599
6495	-1.323198	-0.301694	-0.128234	-0.912936	-0.971538	-0.593041
6496	-0.937495	-0.787650	0.422326	-0.975995	-1.028631	-0.480353

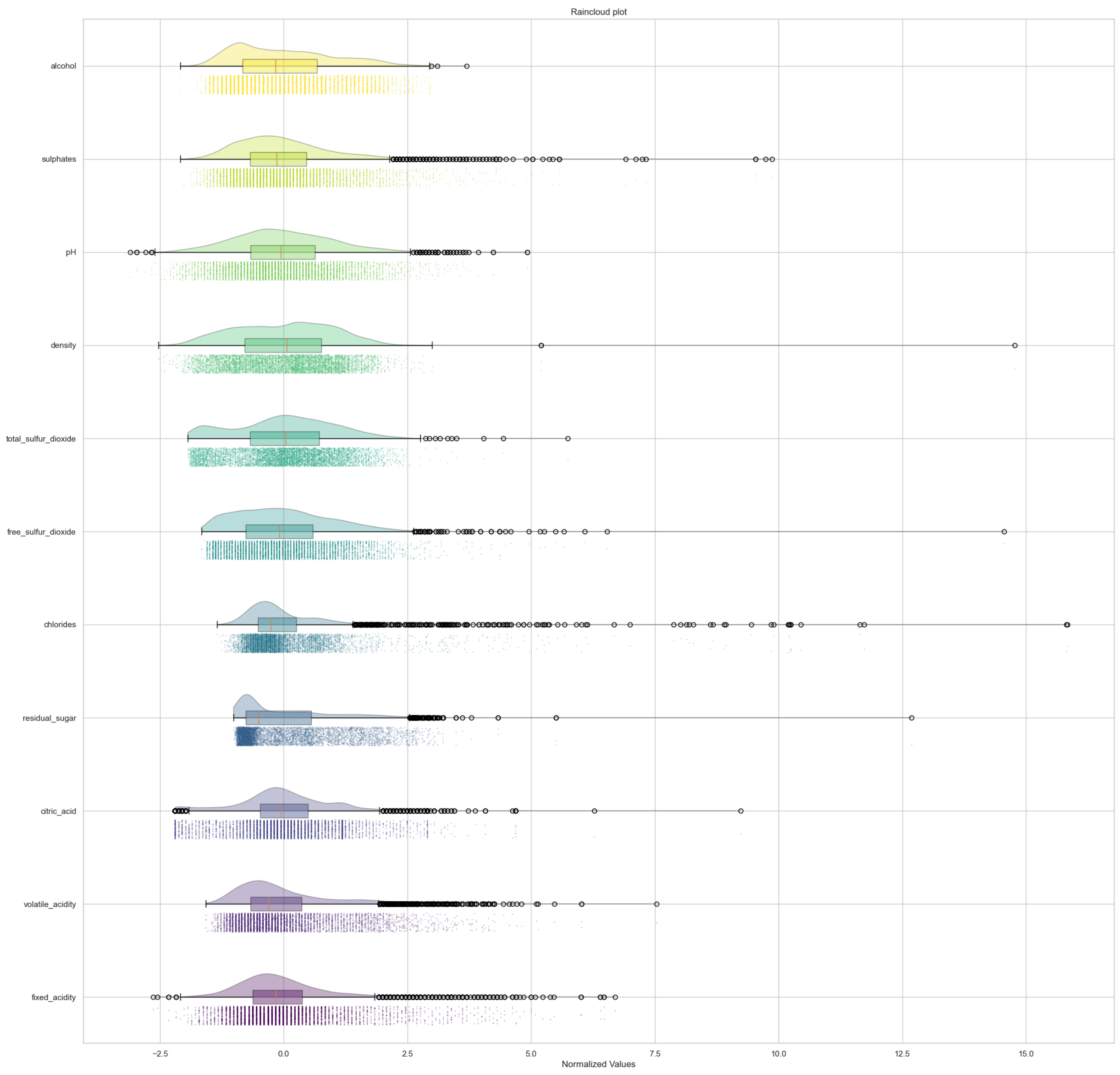
6497 rows × 11 columns

In [184…

```python
def generate_colors(n_colors, colormap_name='viridis'):
    cmap = plt.get_cmap(colormap_name)  # Choose a colormap
    colors = [cmap(i) for i in np.linspace(0, 1, n_colors)]  # Generate colors dyna
    return colors


def raincloud_plot(dataframe, figsize=(25, 25)):
    fig, ax = plt.subplots(figsize=figsize)

    nrows = dataframe.shape[1]

    boxplots_colors = generate_colors(nrows)
    violin_colors = generate_colors(nrows)
    scatter_colors = generate_colors(nrows)

    # Boxplot
    bp = ax.boxplot(
        dataframe,
        patch_artist=True,
        vert=False,
        widths=.15
    )

    # Change to the desired color and add transparency
    for patch, color in zip(bp['boxes'], boxplots_colors):
        patch.set_facecolor(color)
        patch.set_alpha(0.4)

    # Violinplot
    vp = ax.violinplot(
        dataframe,
        points=500,
        showmeans=False,
        showextrema=False,
        showmedians=False,
        vert=False,
        side='high'
    )

    for idx, b in enumerate(vp['bodies']):
        b.set_color(violin_colors[idx])
        b.set_edgecolor('black')



    # Scatterplot
    for idx, features in enumerate(dataframe):
        # Add jitter effect so the features do not overlap on the y-axis
        y = np.full(len(dataframe[features]), idx + .8)
        idxs = np.arange(len(y))
        out = y.astype(float)
        out.flat[idxs] += np.random.uniform(low=-.1, high=.1, size=len(idxs))
        y = out
        plt.scatter(dataframe[features], y, s=.3, color=scatter_colors[idx],
                    alpha=0.3)

    plt.yticks(np.arange(1,nrows+1,1), dataframe.columns.to_list())
    plt.xlabel('Normalized Values')
    plt.title("Raincloud plot")
    plt.show()
```

In [187…

```
raincloud_plot(X_scaled)
```

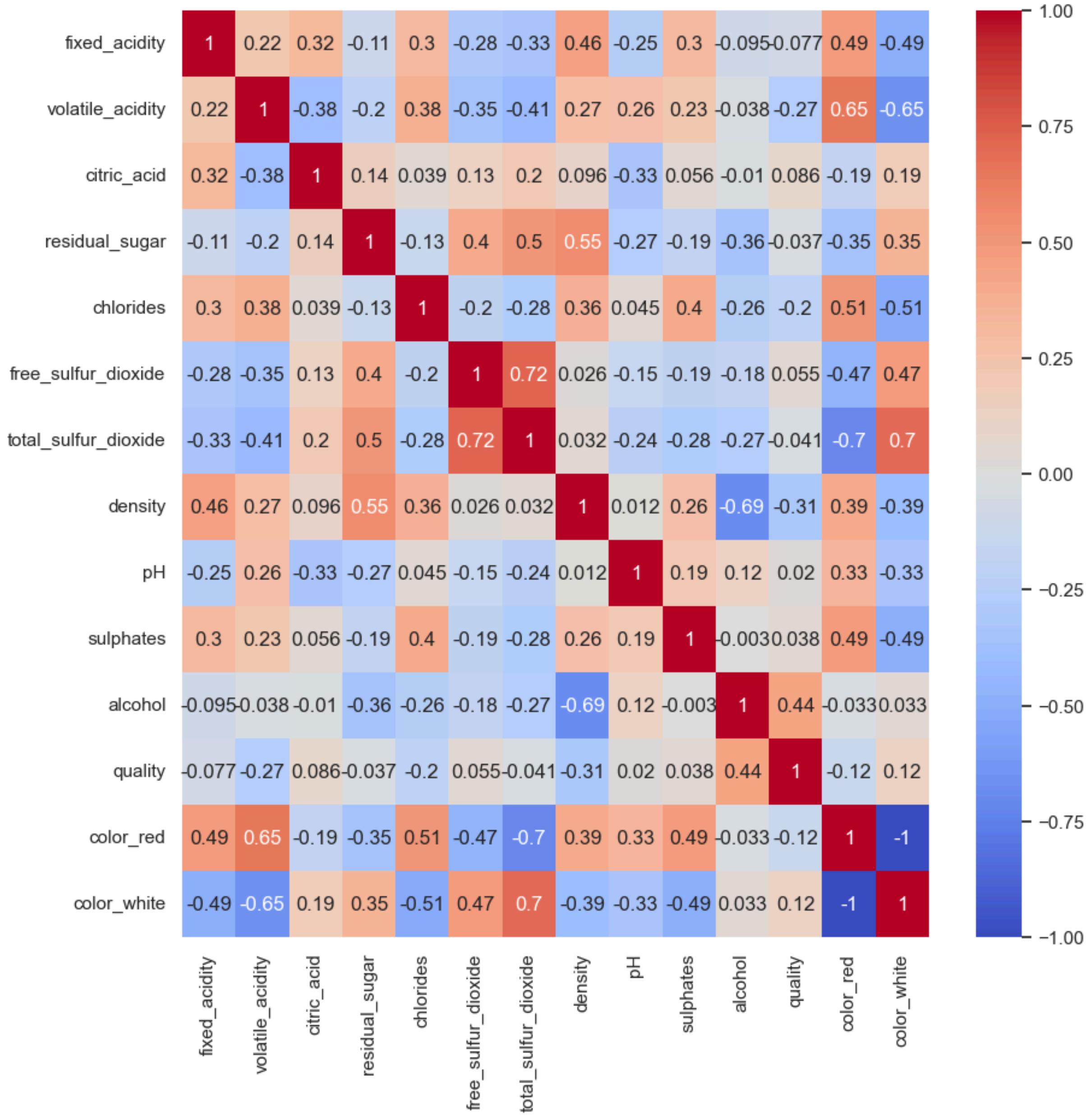


Shown is a raincloud plot (a combination of top-side violin plot, box plot, and strip plot which appears as a rain cloud). This plot was chosen to visualize distribution together with the standard percentiles.

In [188…
```
onehotencoder = OneHotEncoder(sparse_output=False)

ohe = onehotencoder.fit_transform(X[['color']])
ohe = pd.DataFrame(ohe, columns=onehotencoder.get_feature_names_out())
X1 = pd.concat([X, ohe], axis=1).drop(['color'], axis=1)
```

In [189…
```
plt.figure(figsize=(10, 10))
sns.heatmap(X1.corr(), annot=True, cmap='coolwarm')
```

Out[189…
```
<Axes: >
```



Shown is a heatmap of the correlation of the different features of the dataset to each other. Note here that normalized data does not affect correlation score since the standard deviations just cancel out each other. Pairs with noticeable correlation scores are total_sulfur_dioxide & free_sulfur_dioxide (positive correlation) and alcohol & density (negative correlation).

In [172…

```
X_scaled['quality'] = X['quality']
melted_X = pd.melt(
    X_scaled,
    id_vars='quality',
    value_vars=X_scaled.columns
)
melted_X
```

Out[172…

	quality	variable	value
0	5	fixed_acidity	0.142473
1	5	fixed_acidity	0.451036
2	5	fixed_acidity	0.451036
3	6	fixed_acidity	3.073817
4	5	fixed_acidity	0.142473
...	...	...	...
71462	6	alcohol	0.593818
71463	5	alcohol	-0.747766
71464	6	alcohol	-0.915464
71465	7	alcohol	1.935402
71466	6	alcohol	1.096912

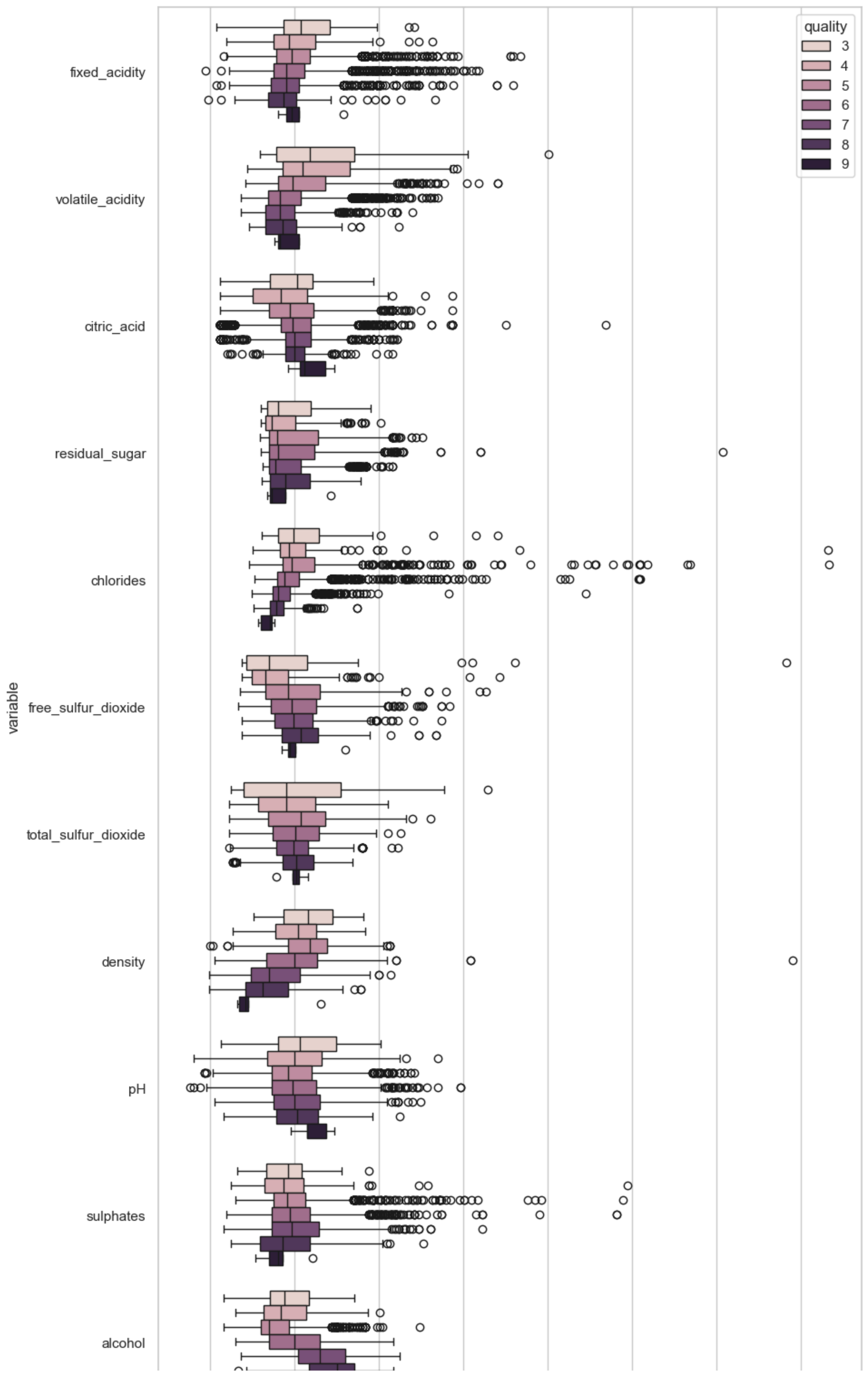
71467 rows × 3 columns

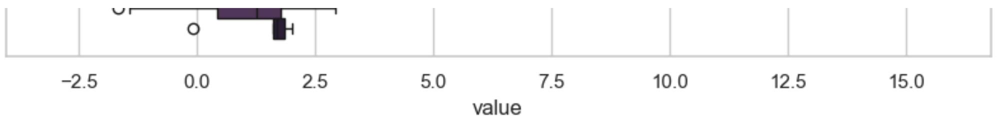
In [173…

```
plt.figure(figsize=(10, 20))
sns.boxplot(
    data=melted_X,
    width=0.8,
    orient='h',
    x='value',
    y='variable',
    hue='quality'
)
```

Out[173…

```
<Axes: xlabel='value', ylabel='variable'>
```


quality
3
4
5
6
7
8
9
variable
fixed_acidity
volatile_acidity
citric_acid
residual_sugar
chlorides
free_sulfur_dioxide
total_sulfur_dioxide
density
pH
sulphates
alcohol



```
In [ ]:
```