In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

red_wine = pd.read_csv('winequality-red.csv', sep=';')
white_wine = pd.read_csv('winequality-white.csv', sep=';')

red_wine['type'] = 'red'
white_wine['type'] = 'white'

wine = pd.concat([red_wine, white_wine])

wine.head()
```

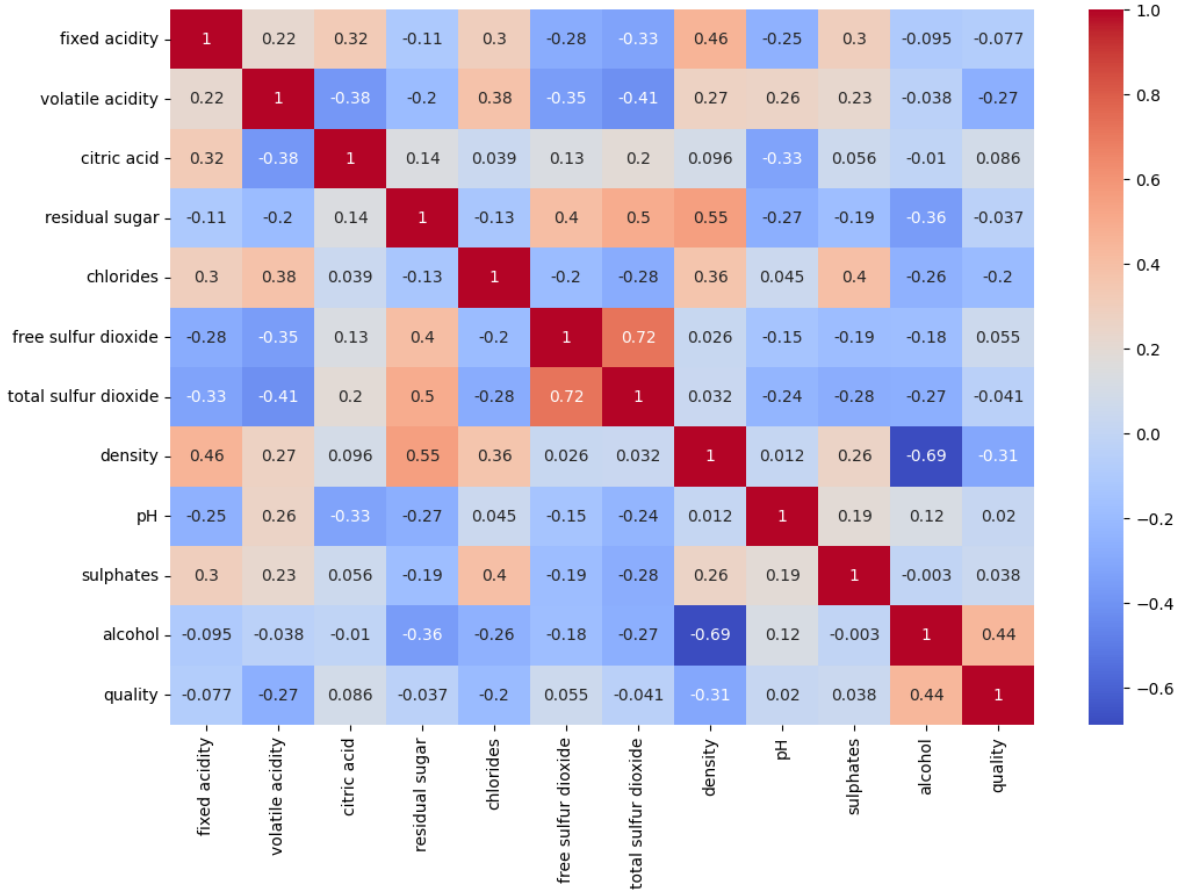
Out[1]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality	type
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5	red
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	5	red
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	5	red
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	6	red
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5	red

In [2]:
```
def quality_to_category(quality):
    if quality <= 4:
        return 'low'
    elif quality <= 6:
        return 'medium'
    else:
        return 'high'

wine['quality_category'] = wine['quality'].apply(quality_to_category)
```

In [3]:
```
plt.figure(figsize=(12, 8))
sns.heatmap(wine.corr(), annot=True, cmap='coolwarm')
plt.show()
```

```
C:\Users\deanm\AppData\Local\Temp\ipykernel_4132\914103240.py:2: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a futur
e version, it will default to False. Select only valid columns or specify the value of numeric_only to silence this warning.
  sns.heatmap(wine.corr(), annot=True, cmap='coolwarm')
```



In [4]:
```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, LabelEncoder

X = wine.drop(['quality', 'quality_category'], axis=1)
```

```
X = pd.get_dummies(X)
y = wine['quality_category']

label_encoder = LabelEncoder()
y = label_encoder.fit_transform(y)

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

In [5]:
```
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, accuracy_score

clf = RandomForestClassifier(random_state=42)
clf.fit(X_train, y_train)

y_pred = clf.predict(X_test)

print("Accuracy:", accuracy_score(y_test, y_pred))
print("\nClassification Report:\n", classification_report(y_test, y_pred, target_names=label_encoder.classes_))
```

```
Accuracy: 0.8546153846153847

Classification Report:
               precision    recall  f1-score   support

        high       0.79      0.59      0.67       252
         low       0.83      0.10      0.18        49
      medium       0.87      0.96      0.91       999

    accuracy                           0.85      1300
   macro avg       0.83      0.55      0.59      1300
weighted avg       0.85      0.85      0.84      1300
```

In [6]:
```
from sklearn.svm import SVC

svm_clf = SVC(kernel='linear', random_state=42)
svm_clf.fit(X_train, y_train)

svm_y_pred = svm_clf.predict(X_test)

svm_accuracy = accuracy_score(y_test, svm_y_pred)
svm_classification_rep = classification_report(y_test, svm_y_pred, target_names=label_encoder.classes_)

svm_accuracy, svm_classification_rep
```

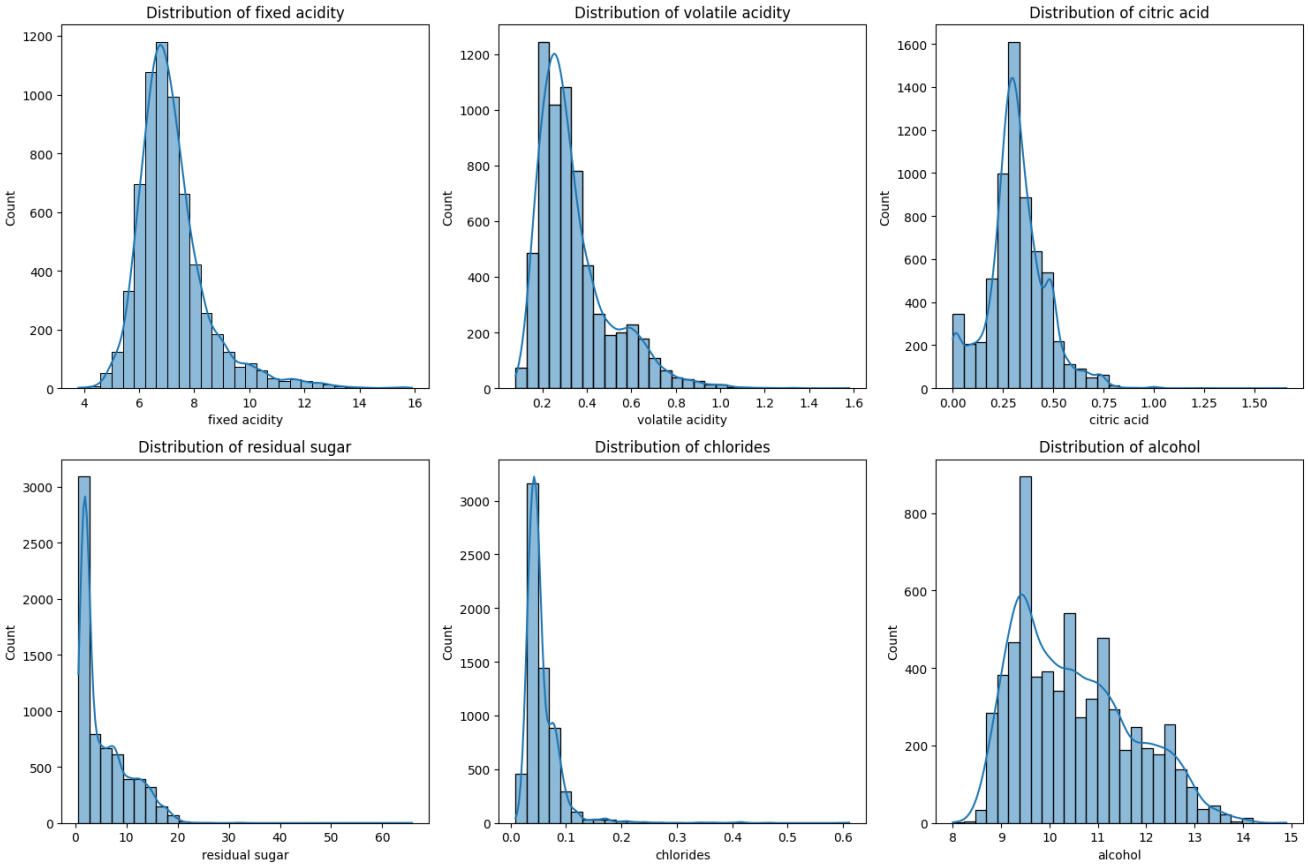
```
C:\Users\deanm\AppData\Roaming\Python\Python38\site-packages\sklearn\metrics\_classification.py:1344: UndefinedMetricWarning: Precision and F-score are ill-d
efined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
C:\Users\deanm\AppData\Roaming\Python\Python38\site-packages\sklearn\metrics\_classification.py:1344: UndefinedMetricWarning: Precision and F-score are ill-d
efined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
C:\Users\deanm\AppData\Roaming\Python\Python38\site-packages\sklearn\metrics\_classification.py:1344: UndefinedMetricWarning: Precision and F-score are ill-d
efined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```

Out[6]:
```
(0.7684615384615384,
 '              precision    recall  f1-score   support\n\n        high       0.00      0.00      0.00       252\n         low       0.00      0.00      0.0
0        49\n      medium       0.77      1.00      0.87       999\n\n    accuracy                           0.77      1300\n   macro avg       0.26      0.
33      0.29      1300\nweighted avg       0.59      0.77      0.67      1300\n')
```

In [7]:
```
from sklearn.ensemble import GradientBoostingClassifier

gbm_clf = GradientBoostingClassifier(random_state=42)
gbm_clf.fit(X_train, y_train)

gbm_y_pred = gbm_clf.predict(X_test)

gbm_accuracy = accuracy_score(y_test, gbm_y_pred)
gbm_classification_rep = classification_report(y_test, gbm_y_pred, target_names=label_encoder.classes_)

gbm_accuracy, gbm_classification_rep
```

Out[7]:
```
(0.81,
 '              precision    recall  f1-score   support\n\n        high       0.68      0.40      0.50       252\n         low       0.50      0.10      0.1
7        49\n      medium       0.83      0.95      0.89       999\n\n    accuracy                           0.81      1300\n   macro avg       0.67      0.
48      0.52      1300\nweighted avg       0.79      0.81      0.78      1300\n')
```

In [8]:
```
features_to_plot = ['fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar', 'chlorides', 'alcohol']

plt.figure(figsize=(15, 10))
for i, feature in enumerate(features_to_plot, 1):
    plt.subplot(2, 3, i)
    sns.histplot(wine[feature], bins=30, kde=True)
    plt.title(f'Distribution of {feature}')
    plt.tight_layout()

plt.show()
```



In [9]:
```
wine['fixed_acidity_bin'] = pd.qcut(wine['fixed acidity'], q=3, labels=['low', 'medium', 'high'])
wine['volatile_acidity_bin'] = pd.qcut(wine['volatile acidity'], q=3, labels=['low', 'medium', 'high'])
wine['citric_acid_bin'] = pd.qcut(wine['citric acid'], q=3, labels=['low', 'medium', 'high'])
wine['residual_sugar_bin'] = pd.qcut(wine['residual sugar'], q=3, labels=['low', 'medium', 'high'])
wine['chlorides_bin'] = pd.qcut(wine['chlorides'], q=3, labels=['low', 'medium', 'high'])
wine['alcohol_bin'] = pd.qcut(wine['alcohol'], q=3, labels=['low', 'medium', 'high'])
wine['fixed_acidity_citric_acid'] = wine['fixed acidity'] * wine['citric acid']
wine['volatile_acidity_chlorides'] = wine['volatile acidity'] * wine['chlorides']
wine['fixed_acidity_squared'] = wine['fixed acidity'] ** 2
wine['volatile_acidity_squared'] = wine['volatile acidity'] ** 2

wine.head()
```

Out[9]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	...	fixed_acidity_bin	volatile_acidity_bin	citric_acid_bin	residual_sugar_bin	chlori
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	...	medium	high	low	low	
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	...	high	high	low	medium	
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	...	high	high	low	medium	
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	...	high	medium	high	low	
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	...	medium	high	low	low	

5 rows × 24 columns

In [10]:
```
wine_low = wine[wine['quality_category'] == 'low']
wine_medium = wine[wine['quality_category'] == 'medium']
wine_high = wine[wine['quality_category'] == 'high']

wine_low_oversampled = wine_low.sample(len(wine_medium), replace=True, random_state=42)

wine_oversampled = pd.concat([wine_low_oversampled, wine_medium, wine_high])

X_oversampled = wine_oversampled.drop(['quality', 'quality_category'], axis=1)
X_oversampled = pd.get_dummies(X_oversampled)

y_oversampled = label_encoder.transform(wine_oversampled['quality_category'])

X_train_over, X_test_over, y_train_over, y_test_over = train_test_split(X_oversampled, y_oversampled, test_size=0.2, random_state=42)

rf_over = RandomForestClassifier(random_state=42)
rf_over.fit(X_train_over, y_train_over)

rf_y_pred_over = rf_over.predict(X_test_over)

rf_accuracy_over = accuracy_score(y_test_over, rf_y_pred_over)
```

```
rf_classification_rep_over = classification_report(y_test_over, rf_y_pred_over, target_names=label_encoder.classes_)

gbm_over = GradientBoostingClassifier(random_state=42)
gbm_over.fit(X_train_over, y_train_over)

gbm_y_pred_over = gbm_over.predict(X_test_over)

gbm_accuracy_over = accuracy_score(y_test_over, gbm_y_pred_over)
gbm_classification_rep_over = classification_report(y_test_over, gbm_y_pred_over, target_names=label_encoder.classes_)

rf_accuracy_over, rf_classification_rep_over, gbm_accuracy_over, gbm_classification_rep_over
```

Out[10]:

```
(0.9389755011135857,
 '              precision    recall  f1-score   support\n\n        high       0.83      0.57      0.68       246\n         low       1.00      1.00      1.0
0      1035\n      medium       0.90      0.97      0.93       964\n\n    accuracy                           0.94      2245\n   macro avg       0.91      0.
85      0.87      2245\nweighted avg       0.94      0.94      0.93      2245\n',
 0.84543429844098,
 '              precision    recall  f1-score   support\n\n        high       0.67      0.46      0.54       246\n         low       0.89      0.95      0.9
2      1035\n      medium       0.82      0.83      0.83       964\n\n    accuracy                           0.85      2245\n   macro avg       0.80      0.
75      0.76      2245\nweighted avg       0.84      0.85      0.84      2245\n')
```

Accuracy for random forest: 94%