


Wine Quality (Multiclass Classification)

LIBRARIES

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt


from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.inspection import permutation_importance
from sklearn.preprocessing import LabelEncoder, StandardScaler
from sklearn.model_selection import train_test_split
!pip install lime

import shap
from lime.lime_tabular import LimeTabularExplainer
```

 Requirement already satisfied: lime in /usr/local/lib/python3.12/dist-packages (0.2.0.1)
Requirement already satisfied: matplotlib in /usr/local/lib/python3.12/dist-packages (from lime) (3.10.0)
Requirement already satisfied: numpy in /usr/local/lib/python3.12/dist-packages (from lime) (2.0.2)
Requirement already satisfied: scipy in /usr/local/lib/python3.12/dist-packages (from lime) (1.16.1)
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Requirement already satisfied: tifffile>=2022.8.12 in /usr/local/lib/python3.12/dist-packages (from scikit-image>=0.12->lime) (2025.6.11)
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Requirement already satisfied: contourpy>=1.0.1 in /usr/local/lib/python3.12/dist-packages (from matplotlib->lime) (1.3.3)
Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.12/dist-packages (from matplotlib->lime) (0.12.1)
Requirement already satisfied: fonttools>=4.22.0 in /usr/local/lib/python3.12/dist-packages (from matplotlib->lime) (4.59.1)
Requirement already satisfied: kiwisolver>=1.3.1 in /usr/local/lib/python3.12/dist-packages (from matplotlib->lime) (1.4.9)
Requirement already satisfied: pyparsing>=2.3.1 in /usr/local/lib/python3.12/dist-packages (from matplotlib->lime) (3.2.3)
Requirement already satisfied: python-dateutil>=2.7 in /usr/local/lib/python3.12/dist-packages (from matplotlib->lime) (2.9.0.post0)
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.12/dist-packages (from python-dateutil>=2.7->matplotlib->lime) (1.17.0)

Load dataset

```
df = pd.read_csv("/content/wine_data.csv")
df.head()
```



	fixed_acidity	volatile_acidity	citric_acid	residual_sugar	chlorides	free_sulfur_dioxide	total_sulfur_dioxide	density	pH	sulphates	alcohol	qualit
0	11.6	0.580	0.66	2.20	0.074	10.0	47.0	1.00080	3.25	0.57	9.0	
1	10.4	0.610	0.49	2.10	0.200	5.0	16.0	0.99940	3.16	0.63	8.4	
2	7.4	1.185	0.00	4.25	0.097	5.0	14.0	0.99660	3.63	0.54	10.7	
3	10.4	0.440	0.42	1.50	0.145	34.0	48.0	0.99832	3.38	0.86	9.9	
4	8.3	1.020	0.02	3.40	0.084	6.0	11.0	0.99892	3.48	0.49	11.0	

Next steps:

[Generate code with df](#)

[View recommended plots](#)

[New interactive sheet](#)

Dropping lable & Scale features

```
X = df.drop(columns=["quality"])
y = df["quality"]

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

Train/test split

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

Encode categorical variables

```
X_encoded = X.copy()
for col in X_encoded.select_dtypes(include=['object']).columns:
    le = LabelEncoder()
    X_encoded[col] = le.fit_transform(X_encoded[col])
```

Train Logistic Regression

```
model = LogisticRegression(max_iter=500,multi_class="multinomial", solver="lbfgs", random_state=42)
model.fit(X_train_scaled, y_train)
```

```

/usr/local/lib/python3.12/dist-packages/sklearn/linear_model/_logistic.py:1247: FutureWarning: 'multi_class' was deprecated in version 1.5 and will be removed
warnings.warn(

LogisticRegression
LogisticRegression(max_iter=500, multi_class='multinomial', random_state=42)

```

Permutation Importance

```

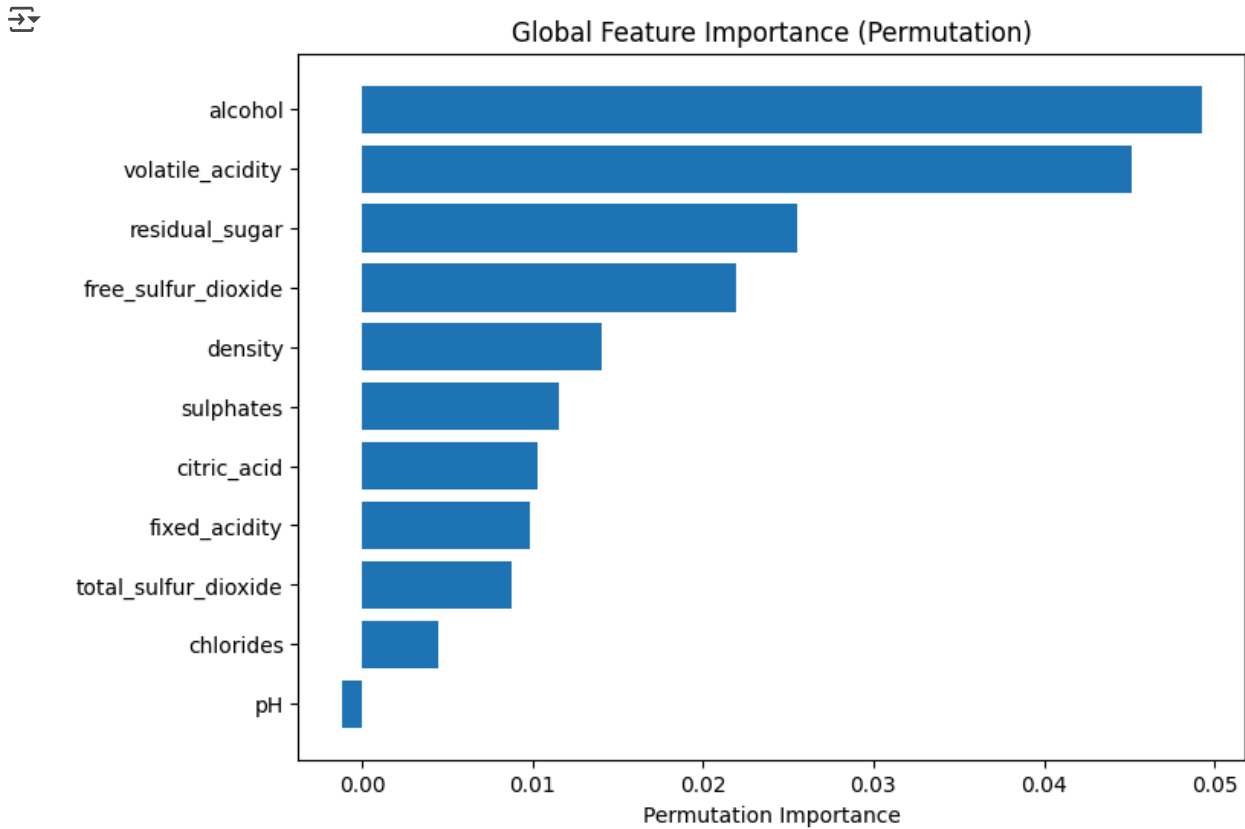
perm = permutation_importance(model, X_test_scaled, y_test, n_repeats=20, random_state=42)
sorted_idx = perm.importances_mean.argsort()

```

```

plt.figure(figsize=(8,6))
plt.barh(np.array(X.columns)[sorted_idx], perm.importances_mean[sorted_idx])
plt.xlabel("Permutation Importance")
plt.title("Global Feature Importance (Permutation)")
plt.show()

```



SHAP Explanations

```

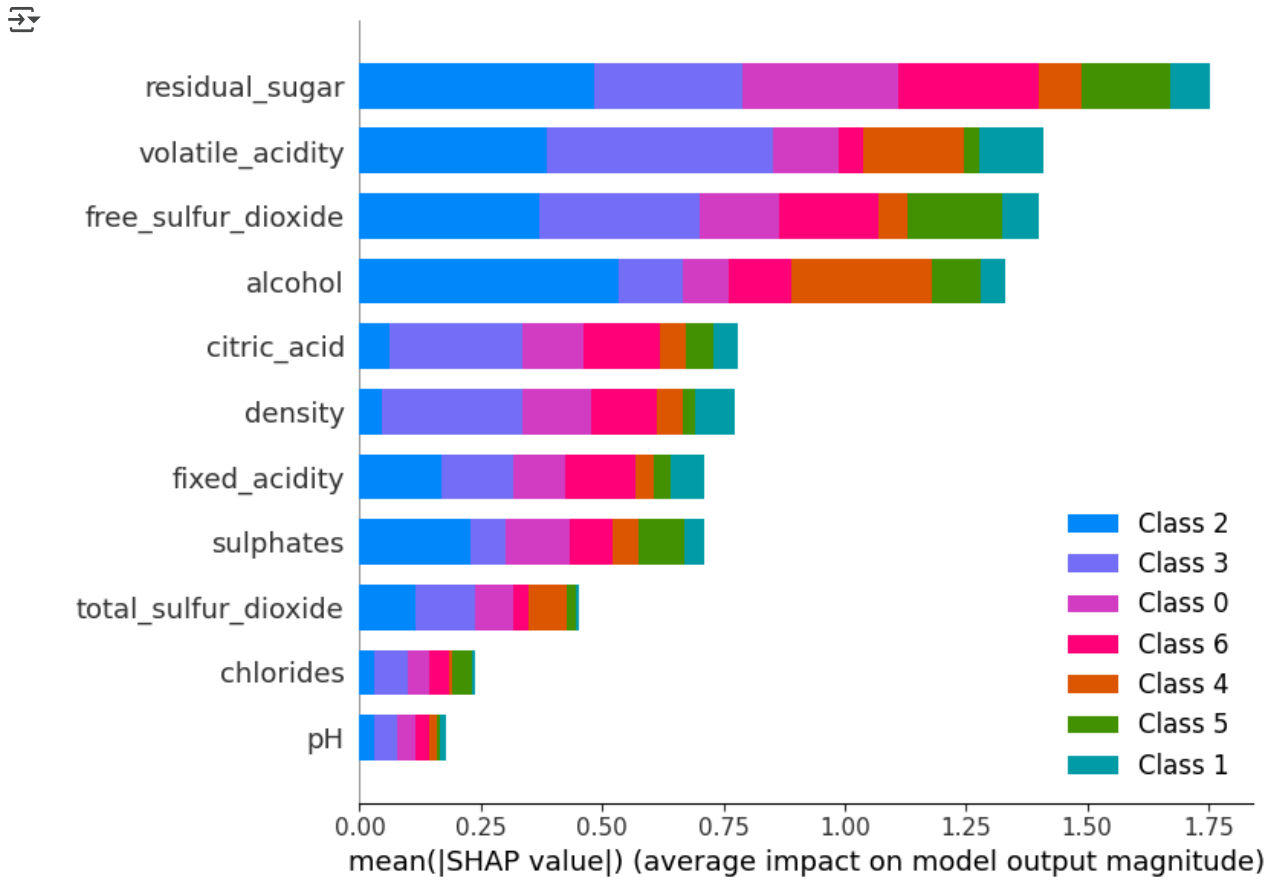
explainer = shap.LinearExplainer(model, X_train_scaled, feature_names=X.columns)
shap_values = explainer(X_test_scaled)

```

```

# Global summary plot
shap.summary_plot(shap_values, X_test, feature_names=X.columns)

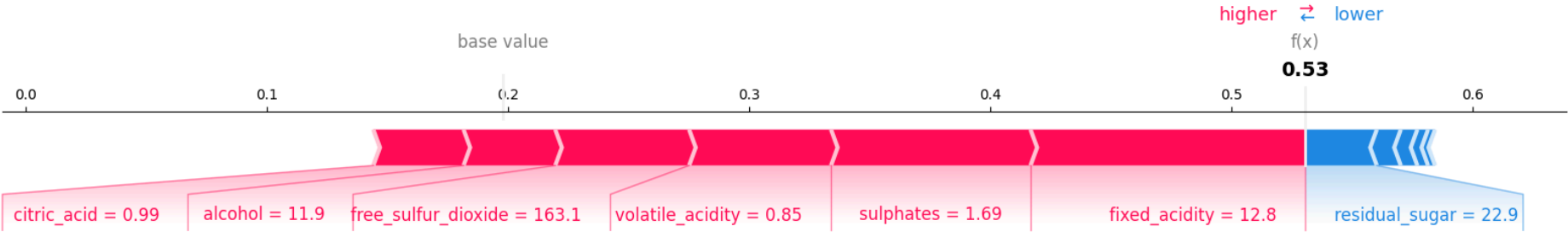
```



```

sample_idx = 0
class_idx = 1
shap.initjs()
shap.force_plot(
    explainer.expected_value[class_idx],
    shap_values.values[sample_idx, :, class_idx],
    X_test.iloc[sample_idx, :],
    feature_names=X.columns,
    matplotlib=True
)

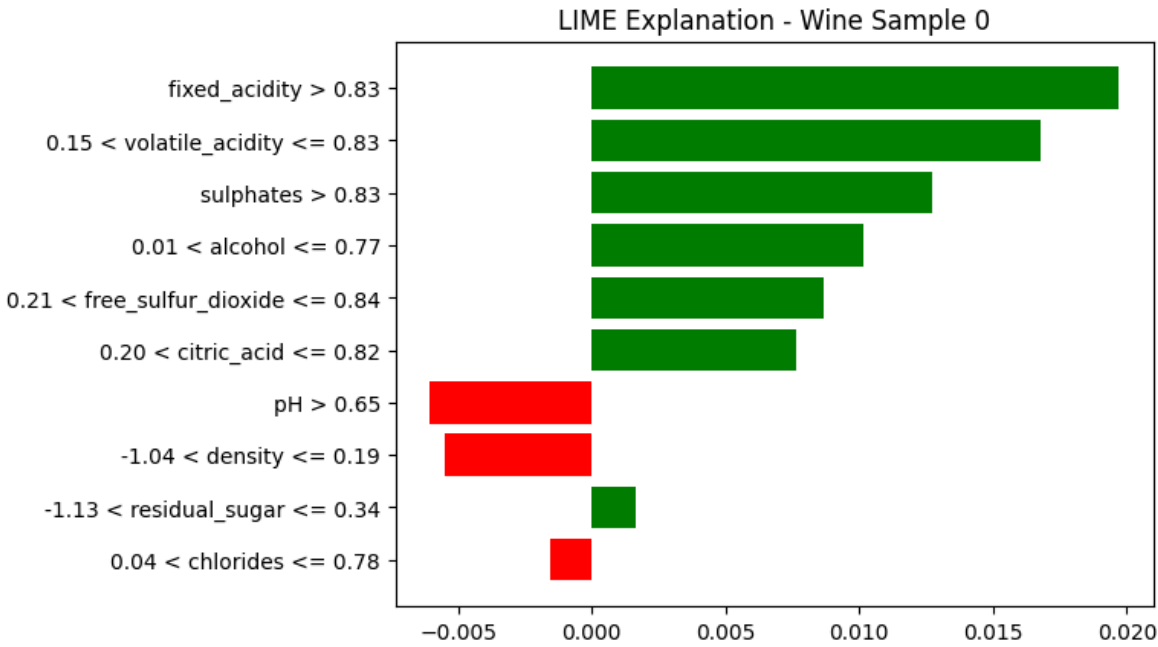
```



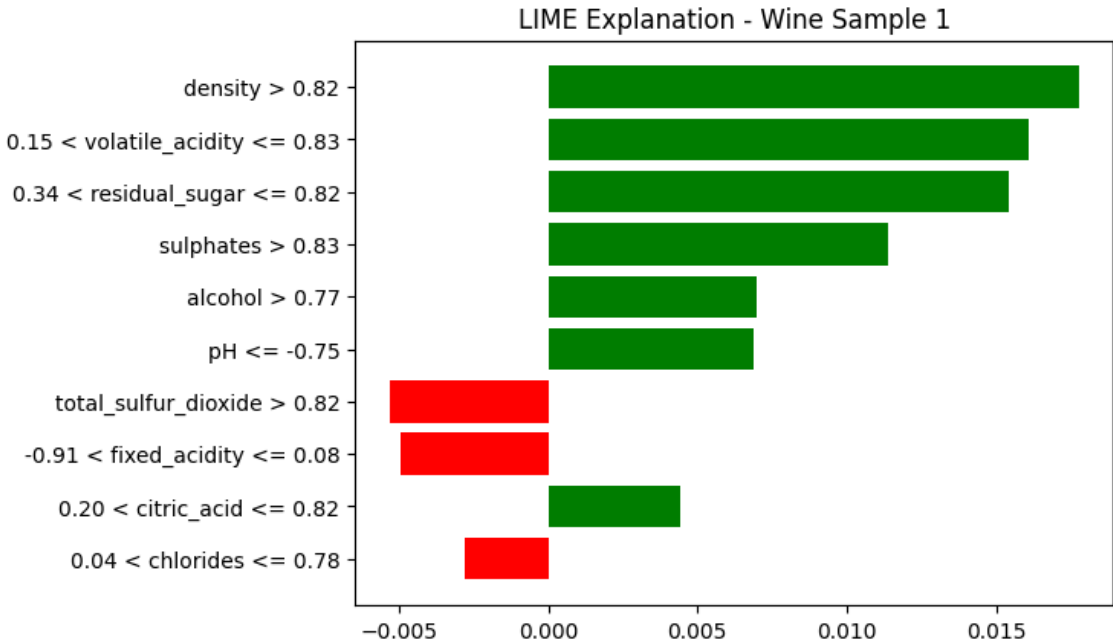
▼ LIME (Local Explanations)

```
lime_explainer = lime.lime_tabular.LimeTabularExplainer(  
    training_data=np.array(X_train_scaled),  
    feature_names=feature_names,  
    class_names=class_names,  
    mode="classification"  
)  
  
# Explain 2 wine samples  
wine_idx_1 = 0  
wine_idx_2 = 1  
  
exp1 = lime_explainer.explain_instance(  
    X_test_scaled[wine_idx_1],  
    model.predict_proba,  
    num_features=10  
)  
exp2 = lime_explainer.explain_instance(  
    X_test_scaled[wine_idx_2],  
    model.predict_proba,  
    num_features=10  
)  
  
exp1.as_pyplot_figure()  
print("LIME explanation for sample 0 (True Class: class_0)")  
plt.title(f"LIME Explanation - Wine Sample {wine_idx_1}")  
plt.show()  
  
exp2.as_pyplot_figure()  
print("LIME explanation for sample 1 (True Class: class_2)")  
plt.title(f"LIME Explanation - Wine Sample {wine_idx_2}")  
plt.show()
```

↗ ↘ LIME explanation for sample 0 (True Class: class_0)



LIME explanation for sample 1 (True Class: class_2)



Comparison

```
def clean_lime_feature_name(feats):
    return feats.split()[0]

# Sample 0
lime_scores_list_sample0 = exp1.as_list()
lime_scores_dict_sample0 = {clean_lime_feature_name(f): s for f, s in lime_scores_list_sample0}
lime_scores_sample0 = np.array([lime_scores_dict_sample0.get(f, 0) for f in X.columns[sorted_idx]])

# Sample 1
lime_scores_list_sample1 = exp2.as_list()
lime_scores_dict_sample1 = {clean_lime_feature_name(f): s for f, s in lime_scores_list_sample1}
lime_scores_sample1 = np.array([lime_scores_dict_sample1.get(f, 0) for f in X.columns[sorted_idx]])

# Comparison DataFrame
comparison = pd.DataFrame({
    "Permutation Importance": pi_scores,
    "SHAP (mean abs values)": shap_scores,
    "LIME (sample 0)": lime_scores_sample0,
    "LIME (sample 1)": lime_scores_sample1
}, index=X.columns[sorted_idx])

# Normalize
comparison_norm = comparison.apply(lambda x: (x - x.min()) / (x.max() - x.min()))

print("\n=== Comparative Feature Importance ===\n")
print(comparison_norm.sort_values("SHAP (mean abs values)", ascending=False).round(3))
```



=== Comparative Feature Importance ===

	Permutation Importance	SHAP (mean abs values) \
fixed_acidity	0.220	1.000
chlorides	0.112	0.781
sulphates	0.254	0.777
alcohol	1.000	0.733
total_sulfur_dioxide	0.198	0.382
free_sulfur_dioxide	0.459	0.378
pH	0.000	0.339
volatile_acidity	0.918	0.338
density	0.302	0.174
citric_acid	0.227	0.038
residual_sugar	0.530	0.000

	LIME (sample 0)	LIME (sample 1)
fixed_acidity	1.000	0.230
chlorides	0.235	0.230
sulphates	0.730	0.724
alcohol	0.235	0.533
total_sulfur_dioxide	0.235	0.000
free_sulfur_dioxide	0.235	0.230
pH	0.000	0.527
volatile_acidity	0.235	0.230
density	0.235	1.000
citric_acid	0.235	0.230
residual_sugar	0.235	0.230

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