linear-regression-1

February 6, 2024

[7]:
```
pip install matplotlib numpy pandas seaborn shap
```

```
Requirement already satisfied: matplotlib in /opt/conda/lib/python3.11/site-
packages (3.8.2)
Requirement already satisfied: numpy in /opt/conda/lib/python3.11/site-packages
(1.26.2)
Requirement already satisfied: pandas in /opt/conda/lib/python3.11/site-packages
(2.0.3)
Requirement already satisfied: seaborn in /opt/conda/lib/python3.11/site-
packages (0.13.2)
Collecting shap
  Downloading shap-0.44.1-cp311-cp311-manylinux_2_12_x86_64.manylinux2010_x86_64
.manylinux_2_17_x86_64.manylinux2014_x86_64.whl.metadata (24 kB)
Requirement already satisfied: contourpy>=1.0.1 in
/opt/conda/lib/python3.11/site-packages (from matplotlib) (1.2.0)
Requirement already satisfied: cycler>=0.10 in /opt/conda/lib/python3.11/site-
packages (from matplotlib) (0.12.1)
Requirement already satisfied: fonttools>=4.22.0 in
/opt/conda/lib/python3.11/site-packages (from matplotlib) (4.47.2)
Requirement already satisfied: kiwisolver>=1.3.1 in
/opt/conda/lib/python3.11/site-packages (from matplotlib) (1.4.5)
Requirement already satisfied: packaging>=20.0 in
/opt/conda/lib/python3.11/site-packages (from matplotlib) (23.2)
Requirement already satisfied: pillow>=8 in /opt/conda/lib/python3.11/site-
packages (from matplotlib) (10.2.0)
Requirement already satisfied: pyparsing>=2.3.1 in
/opt/conda/lib/python3.11/site-packages (from matplotlib) (3.1.1)
Requirement already satisfied: python-dateutil>=2.7 in
/opt/conda/lib/python3.11/site-packages (from matplotlib) (2.8.2)
Requirement already satisfied: pytz>=2020.1 in /opt/conda/lib/python3.11/site-
packages (from pandas) (2023.3.post1)
Requirement already satisfied: tzdata>=2022.1 in /opt/conda/lib/python3.11/site-
packages (from pandas) (2023.4)
Requirement already satisfied: scipy in /opt/conda/lib/python3.11/site-packages
(from shap) (1.12.0)
Requirement already satisfied: scikit-learn in /opt/conda/lib/python3.11/site-
packages (from shap) (1.4.0)
Requirement already satisfied: tqdm>=4.27.0 in /opt/conda/lib/python3.11/site-
```

```
packages (from shap) (4.66.1)
Collecting slicer==0.0.7 (from shap)
  Downloading slicer-0.0.7-py3-none-any.whl (14 kB)
Collecting numba (from shap)
  Downloading
numba-0.58.1-cp311-cp311-manylinux2014_x86_64.manylinux_2_17_x86_64.whl.metadata
(2.7 kB)
Collecting cloudpickle (from shap)
  Downloading cloudpickle-3.0.0-py3-none-any.whl.metadata (7.0 kB)
Requirement already satisfied: six>=1.5 in /opt/conda/lib/python3.11/site-
packages (from python-dateutil>=2.7->matplotlib) (1.16.0)
Collecting llvmlite<0.42,>=0.41.0dev0 (from numba->shap)
  Downloading llvmlite-0.41.1-cp311-cp311-manylinux_2_17_x86_64.manylinux2014_x8
6_64.whl.metadata (4.8 kB)
Requirement already satisfied: joblib>=1.2.0 in /opt/conda/lib/python3.11/site-
packages (from scikit-learn->shap) (1.3.2)
Requirement already satisfied: threadpoolctl>=2.0.0 in
/opt/conda/lib/python3.11/site-packages (from scikit-learn->shap) (3.2.0)
Downloading shap-0.44.1-cp311-cp311-manylinux_2_12_x86_64.manylinux2010_x86_64.m
anylinux_2_17_x86_64.manylinux2014_x86_64.whl (535 kB)
                         535.8/535.8 kB
42.2 MB/s eta 0:00:00
Downloading cloudpickle-3.0.0-py3-none-any.whl (20 kB)
Downloading
numba-0.58.1-cp311-cp311-manylinux2014_x86_64.manylinux_2_17_x86_64.whl (3.6 MB)
                         3.6/3.6 MB
84.9 MB/s eta 0:00:00:00:01
Downloading
llvmlite-0.41.1-cp311-cp311-manylinux_2_17_x86_64.manylinux2014_x86_64.whl (43.6
MB)
                         43.6/43.6 MB
43.4 MB/s eta 0:00:00:00:0100:01
Installing collected packages: slicer, llvmlite, cloudpickle, numba, shap
Successfully installed cloudpickle-3.0.0 llvmlite-0.41.1 numba-0.58.1
shap-0.44.1 slicer-0.0.7
Note: you may need to restart the kernel to use updated packages.
```

[8]:
```python
import pandas as pd

github_url = 'https://raw.githubusercontent.com/aniruddhachoudhury/
 ↪Red-Wine-Quality/master/winequality-red.csv'
wine_data = pd.read_csv(github_url)
print('Wine Quality Dataset:')
print(wine_data.head())
```

```
Wine Quality Dataset:
   fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0            7.4              0.70         0.00             1.9      0.076
```

```
1            7.8              0.88         0.00              2.6      0.098
2            7.8              0.76         0.04              2.3      0.092
3           11.2              0.28         0.56              1.9      0.075
4            7.4              0.70         0.00              1.9      0.076

   free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0                 11.0                  34.0   0.9978  3.51       0.56
1                 25.0                  67.0   0.9968  3.20       0.68
2                 15.0                  54.0   0.9970  3.26       0.65
3                 17.0                  60.0   0.9980  3.16       0.58
4                 11.0                  34.0   0.9978  3.51       0.56

   alcohol  quality
0      9.4        5
1      9.8        5
2      9.8        5
3      9.8        6
4      9.4        5
```

[9]:

```
# Assuming 'wine_data' is your DataFrame
column_name_mapping = {
    'fixed acidity': 'fixed_acidity',
    'volatile acidity': 'volatile_acidity',
    'citric acid': 'citric_acid',
    'residual sugar': 'residual_sugar',
    'free sulfur dioxide': 'free_sulfur_dioxide',
    'total sulfur dioxide': 'total_sulfur_dioxide',
    'density': 'density',
    'pH': 'pH',
    'sulphates': 'sulphates',
    'alcohol': 'alcohol',
    'quality': 'quality',
}

# Rename the columns
wine_data = wine_data.rename(columns=column_name_mapping)
```

[10]:

```
pip install statsmodels
```

```
Collecting statsmodels
  Downloading statsmodels-0.14.1-cp311-cp311-manylinux_2_17_x86_64.manylinux2014
_x86_64.whl.metadata (9.5 kB)
Requirement already satisfied: numpy<2,>=1.18 in /opt/conda/lib/python3.11/site-
packages (from statsmodels) (1.26.2)
Requirement already satisfied: scipy!=1.9.2,>=1.4 in
/opt/conda/lib/python3.11/site-packages (from statsmodels) (1.12.0)
Requirement already satisfied: pandas!=2.1.0,>=1.0 in
/opt/conda/lib/python3.11/site-packages (from statsmodels) (2.0.3)
```

```
Collecting patsy>=0.5.4 (from statsmodels)
  Downloading patsy-0.5.6-py2.py3-none-any.whl.metadata (3.5 kB)
Requirement already satisfied: packaging>=21.3 in
/opt/conda/lib/python3.11/site-packages (from statsmodels) (23.2)
Requirement already satisfied: python-dateutil>=2.8.2 in
/opt/conda/lib/python3.11/site-packages (from pandas!=2.1.0,>=1.0->statsmodels)
(2.8.2)
Requirement already satisfied: pytz>=2020.1 in /opt/conda/lib/python3.11/site-
packages (from pandas!=2.1.0,>=1.0->statsmodels) (2023.3.post1)
Requirement already satisfied: tzdata>=2022.1 in /opt/conda/lib/python3.11/site-
packages (from pandas!=2.1.0,>=1.0->statsmodels) (2023.4)
Requirement already satisfied: six in /opt/conda/lib/python3.11/site-packages
(from patsy>=0.5.4->statsmodels) (1.16.0)
Downloading
statsmodels-0.14.1-cp311-cp311-manylinux_2_17_x86_64.manylinux2014_x86_64.whl
(10.8 MB)
                         10.8/10.8 MB
78.8 MB/s eta 0:00:00:00:010:01
Downloading patsy-0.5.6-py2.py3-none-any.whl (233 kB)
                         233.9/233.9 kB
43.5 MB/s eta 0:00:00
Installing collected packages: patsy, statsmodels
Successfully installed patsy-0.5.6 statsmodels-0.14.1
Note: you may need to restart the kernel to use updated packages.
```

[11]:

```python
import statsmodels.api as sm

# Original formula
original_formula = 'quality ~ fixed_acidity + volatile_acidity + citric_acid + residual_sugar + chlorides + free_sulfur_dioxide + total_sulfur_dioxide + density + pH + sulphates + alcohol'

# Create the original model
original_model = sm.OLS.from_formula(original_formula, data=wine_data).fit()

# Print summaries
original_model.summary()
```

[11]:

Dep. Variable:	quality	**R-squared:**	0.361
Model:	OLS	**Adj. R-squared:**	0.356
Method:	Least Squares	**F-statistic:**	81.35
Date:	Tue, 30 Jan 2024	**Prob (F-statistic):**	1.79e-145
Time:	01:28:08	**Log-Likelihood:**	-1569.1
No. Observations:	1599	**AIC:**	3162.
Df Residuals:	1587	**BIC:**	3227.
Df Model:	11		
Covariance Type:	nonrobust		

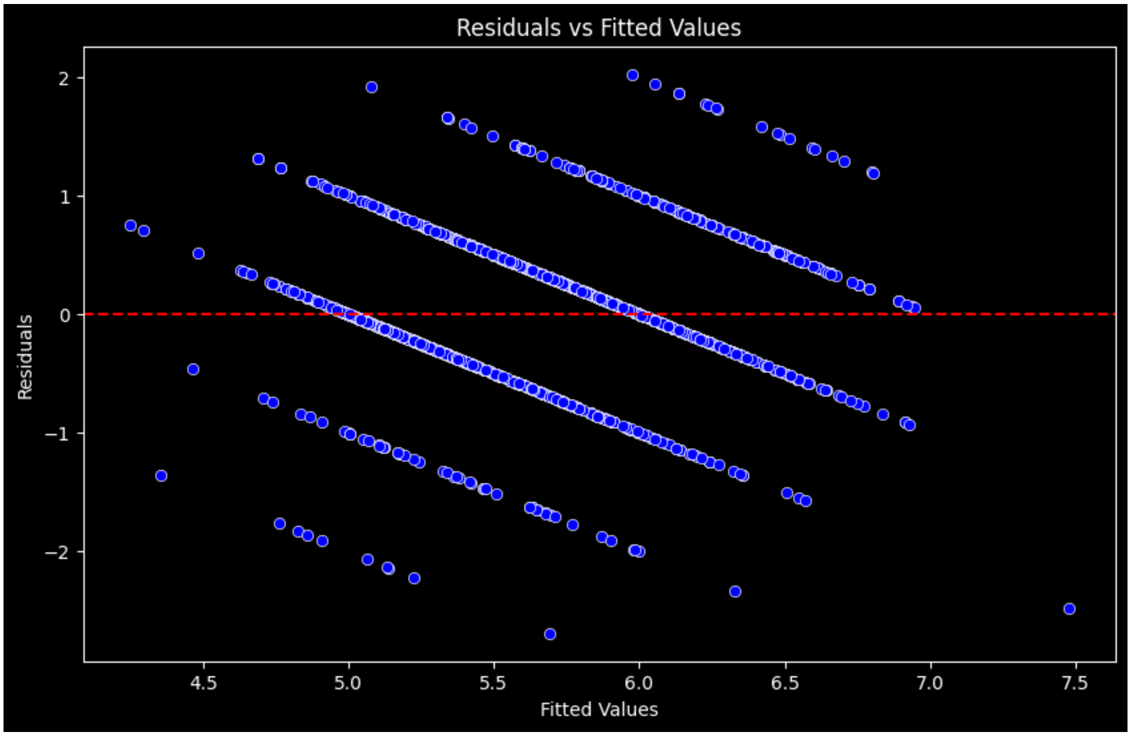
	coef	std err	t	P>|t|	[0.025	0.975]
Intercept	21.9652	21.195	1.036	0.300	-19.607	63.538
fixed_acidity	0.0250	0.026	0.963	0.336	-0.026	0.076
volatile_acidity	-1.0836	0.121	-8.948	0.000	-1.321	-0.846
citric_acid	-0.1826	0.147	-1.240	0.215	-0.471	0.106
residual_sugar	0.0163	0.015	1.089	0.276	-0.013	0.046
chlorides	-1.8742	0.419	-4.470	0.000	-2.697	-1.052
free_sulfur_dioxide	0.0044	0.002	2.009	0.045	0.000	0.009
total_sulfur_dioxide	-0.0033	0.001	-4.480	0.000	-0.005	-0.002
density	-17.8812	21.633	-0.827	0.409	-60.314	24.551
pH	-0.4137	0.192	-2.159	0.031	-0.789	-0.038
sulphates	0.9163	0.114	8.014	0.000	0.692	1.141
alcohol	0.2762	0.026	10.429	0.000	0.224	0.328

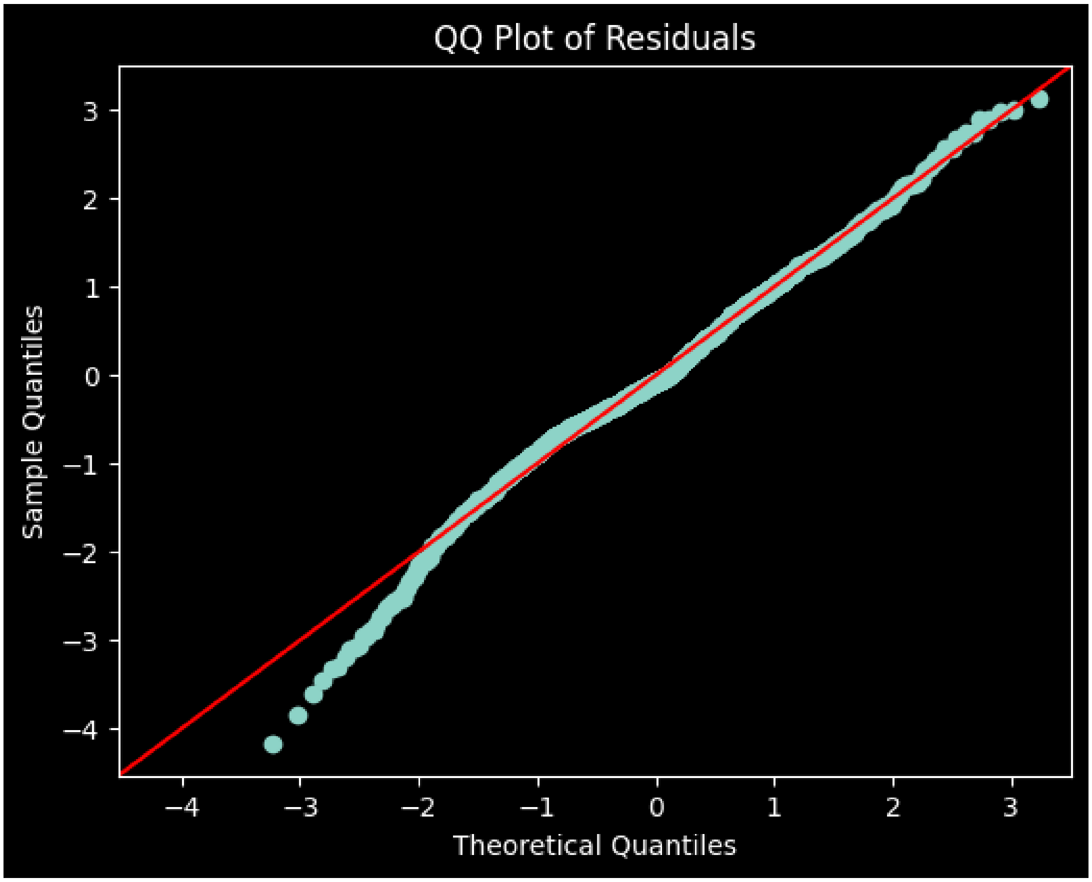
Omnibus:	27.376	**Durbin-Watson:**	1.757
Prob(Omnibus):	0.000	**Jarque-Bera (JB):**	40.965
Skew:	-0.168	**Prob(JB):**	1.27e-09
Kurtosis:	3.708	**Cond. No.**	1.13e+05

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
[2] The condition number is large, 1.13e+05. This might indicate that there are
strong multicollinearity or other numerical problems.

[169]:
```python
import statsmodels.api as sm
import matplotlib.pyplot as plt
import seaborn as sns

# Original formula
original_formula = 'quality ~ fixed_acidity + volatile_acidity + citric_acid +␣
↪residual_sugar + chlorides + free_sulfur_dioxide + total_sulfur_dioxide +␣
↪density + pH + sulphates + alcohol'

# Create the original model
original_model = sm.OLS.from_formula(original_formula, data=wine_data).fit()

# Residuals vs Fitted Values Plot
plt.figure(figsize=(10, 6))
sns.scatterplot(x=original_model.fittedvalues, y=original_model.resid,␣
↪color='blue')
plt.title('Residuals vs Fitted Values')
plt.xlabel('Fitted Values')
plt.ylabel('Residuals')
plt.axhline(y=0, color='red', linestyle='--')
plt.show()

# QQ Plot (Normality Check)
sm.qqplot(original_model.resid, line='45', fit=True)
```

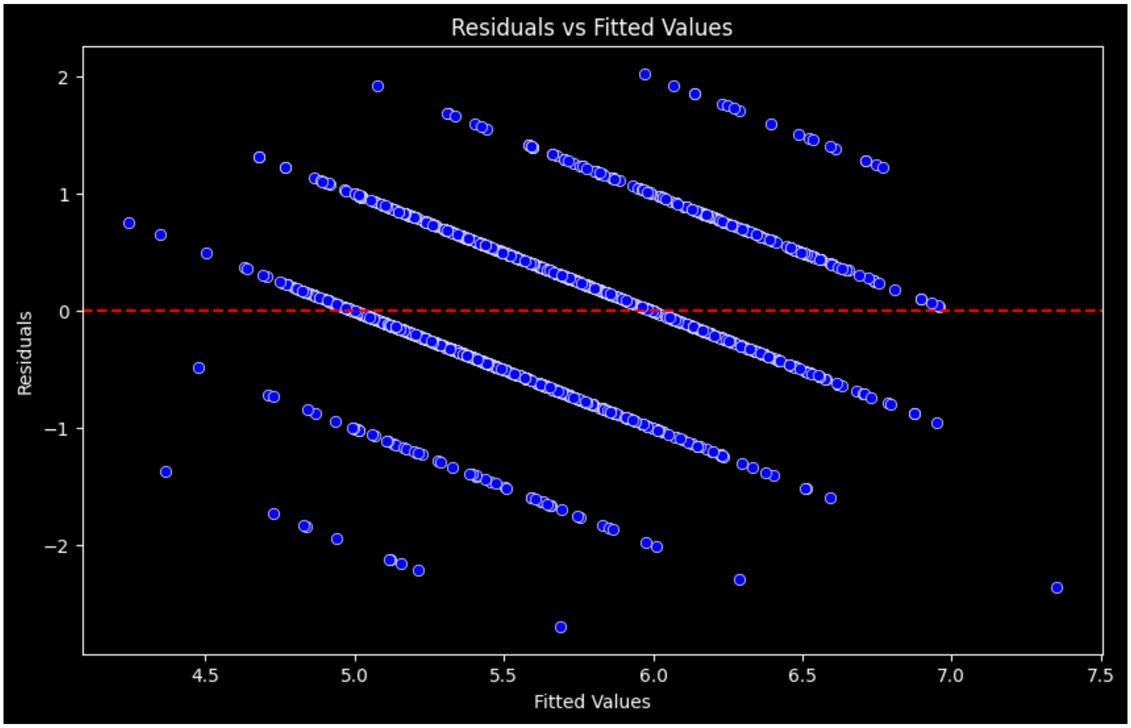
```
plt.title('QQ Plot of Residuals')
plt.show()
```

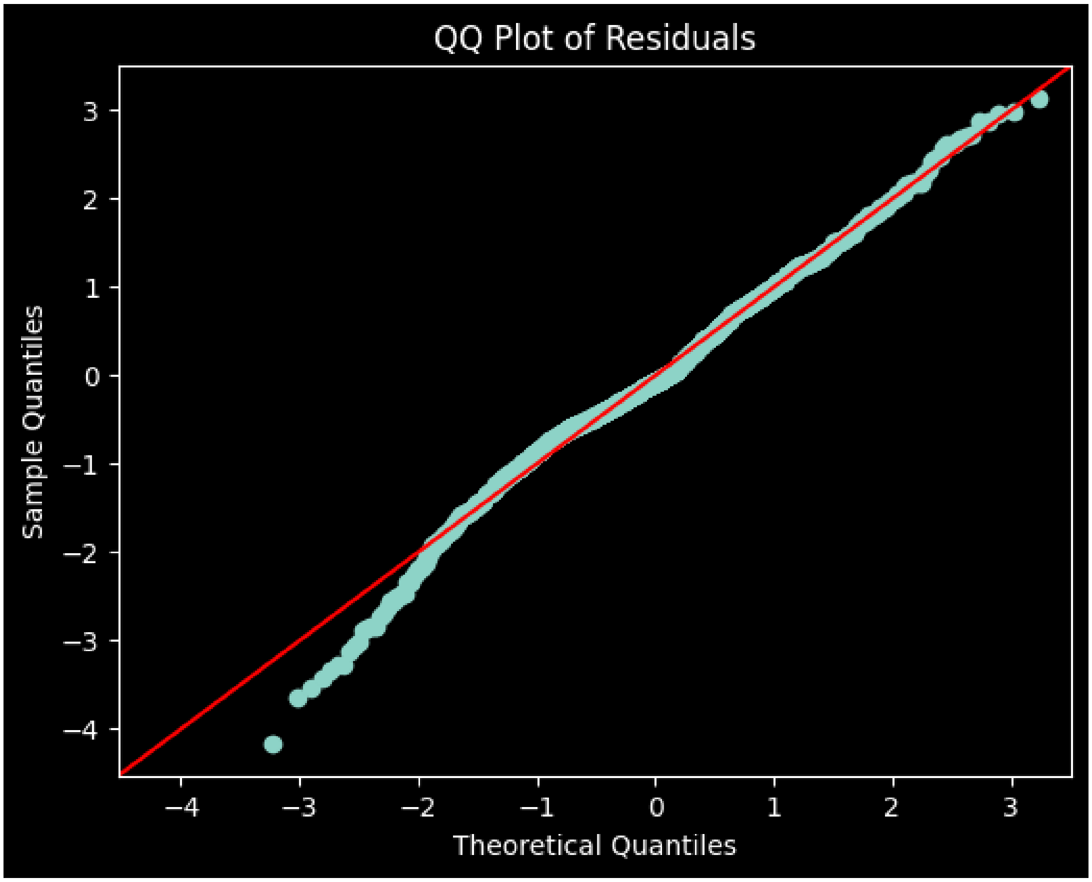




[14]:
```
import statsmodels.api as sm
import statsmodels.formula.api as smf
import matplotlib.pyplot as plt
import seaborn as sns

# Assuming 'wine_data' is a pandas DataFrame with the same structure as in R
# Correct the variable names by enclosing them in backticks
red_model1_formula = 'quality ~ free_sulfur_dioxide + pH + total_sulfur_dioxide␣
↪+ chlorides + sulphates + volatile_acidity + alcohol'
red_model1 = smf.ols(red_model1_formula, data=wine_data).fit()

# Residuals vs Fitted Values Plot
plt.figure(figsize=(10, 6))
sns.scatterplot(x=red_model1.fittedvalues, y=red_model1.resid, color='blue')
plt.title('Residuals vs Fitted Values')
plt.xlabel('Fitted Values')
plt.ylabel('Residuals')
plt.axhline(y=0, color='red', linestyle='--')
plt.show()
```

```python
# QQ Plot (Normality Check)
sm.qqplot(red_model1.resid, line='45', fit=True)
plt.title('QQ Plot of Residuals')
plt.show()
```





[13]:
```
import statsmodels.api as sm
import statsmodels.formula.api as smf

# Assuming 'wine_data' is a pandas DataFrame with the same structure as in R
# Check the column names in 'wine_data'
print(wine_data.columns)

# Assuming 'wine_data' is a pandas DataFrame with the same structure as in R
# Correct the variable names by enclosing them in backticks
red_model1_formula = 'quality ~ free_sulfur_dioxide + pH + total_sulfur_dioxide␣
↪+ chlorides + sulphates + volatile_acidity + alcohol'
red_model1 = smf.ols(red_model1_formula, data=wine_data).fit()
red_model1.summary()
```

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

[13]:

Dep. Variable:	quality	**R-squared:**	0.359
Model:	OLS	**Adj. R-squared:**	0.357
Method:	Least Squares	**F-statistic:**	127.6
Date:	Tue, 30 Jan 2024	**Prob (F-statistic):**	5.32e-149
Time:	01:28:09	**Log-Likelihood:**	-1570.5
No. Observations:	1599	**AIC:**	3157.
Df Residuals:	1591	**BIC:**	3200.
Df Model:	7		
Covariance Type:	nonrobust		

	coef	**std err**	**t**	**P> |t|**	**[0.025**	**0.975]**
Intercept	4.4301	0.403	10.995	0.000	3.640	5.220
free_sulfur_dioxide	0.0051	0.002	2.389	0.017	0.001	0.009
pH	-0.4827	0.118	-4.106	0.000	-0.713	-0.252
total_sulfur_dioxide	-0.0035	0.001	-5.070	0.000	-0.005	-0.002
chlorides	-2.0178	0.398	-5.076	0.000	-2.798	-1.238
sulphates	0.8827	0.110	8.031	0.000	0.667	1.098
volatile_acidity	-1.0128	0.101	-10.043	0.000	-1.211	-0.815
alcohol	0.2893	0.017	17.225	0.000	0.256	0.322

Omnibus:	24.204	**Durbin-Watson:**	1.750
Prob(Omnibus):	0.000	**Jarque-Bera (JB):**	35.245
Skew:	-0.156	**Prob(JB):**	2.22e-08
Kurtosis:	3.657	**Cond. No.**	1.71e+03

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
[2] The condition number is large, 1.71e+03. This might indicate that there are
strong multicollinearity or other numerical problems.

[15]:
```
import statsmodels.api as sm
from statsmodels.stats.anova import anova_lm
anova_lm(red_model1, original_model)
```

[15]:

	df_resid	ssr	df_diff	ss_diff	F	Pr(>F)
0	1591.0	667.537059	0.0	NaN	NaN	NaN
1	1587.0	666.410700	4.0	1.126359	0.670582	0.612412

[16]:
```
import numpy as np
import pandas as pd
import statsmodels.api as sm
from scipy.stats import boxcox

# Assuming redWine is a pandas DataFrame with the necessary columns
# and 'quality' is a column in redWine DataFrame

# Apply Box-Cox transformation to multiple columns
# Since powerTransform is not directly available in Python, we use boxcox from␣
↪scipy.stats
```

```
# Note: boxcox requires positive data for all values
# If any of the columns contain non-positive values, a shift may be necessary

# Define the columns to transform
columns_to_transform = ['free_sulfur_dioxide', 'pH', 'total_sulfur_dioxide',
                        'chlorides', 'sulphates', 'volatile_acidity', 'alcohol']

# Apply Box-Cox transformation to each column and store in a new DataFrame
transformed_data = pd.DataFrame()
for col in columns_to_transform:
    transformed_data[col], _ = boxcox(wine_data[col] + 1)  # Adding 1 to avoid␣
 ↪zero or negative values

# Linear regression model
# Prepare the independent variables with transformations
wine_data['log_pH'] = np.log(wine_data['pH'])
wine_data['log_total_sulfur_dioxide'] = np.
 ↪log(wine_data['total_sulfur_dioxide'])
wine_data['inv_sqrt_chlorides'] = 1 / np.sqrt(wine_data['chlorides'])
wine_data['inv_sulphates'] = 1 / wine_data['sulphates']
wine_data['volatile_acidity_cbrt'] = wine_data['volatile_acidity'] ** (1/3)
wine_data['inv_alcohol_cbrt'] = 1 / (wine_data['alcohol'] ** (1/3))

# Define the dependent variable
wine_data['quality_transformed'] = wine_data['quality'] ** 3.62

# Define the independent variables
X = wine_data[['log_pH', 'log_total_sulfur_dioxide', 'inv_sqrt_chlorides',␣
 ↪'sulphates',
             'inv_sulphates', 'volatile_acidity_cbrt', 'inv_alcohol_cbrt']]
X = sm.add_constant(X)  # Adds a constant term to the predictor

# Fit the model
model = sm.OLS(wine_data['quality_transformed'], X).fit()
model.summary()
```

[16]:

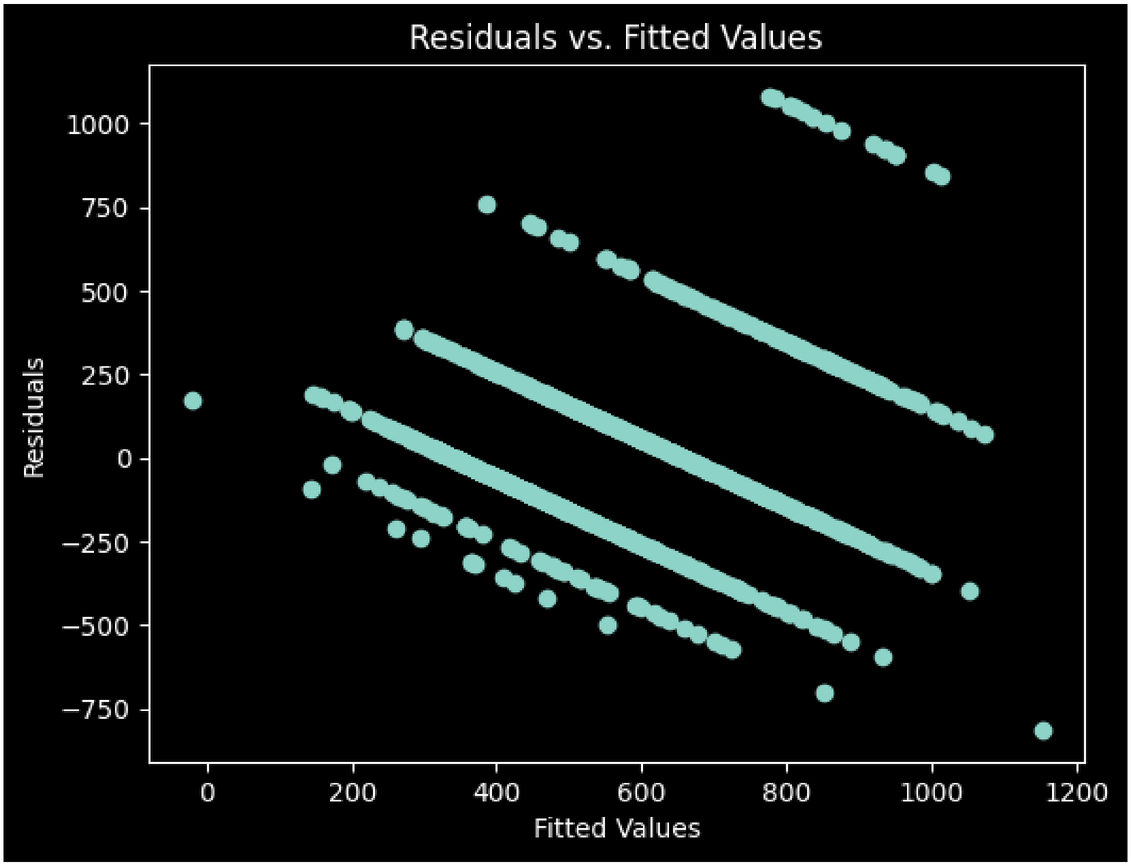
Dep. Variable:	quality_transformed	**R-squared:**	0.378
Model:	OLS	**Adj. R-squared:**	0.376
Method:	Least Squares	**F-statistic:**	138.4
Date:	Tue, 30 Jan 2024	**Prob (F-statistic):**	2.35e-159
Time:	01:28:09	**Log-Likelihood:**	-11036.
No. Observations:	1599	**AIC:**	2.209e+04
Df Residuals:	1591	**BIC:**	2.213e+04
Df Model:	7		
Covariance Type:	nonrobust		

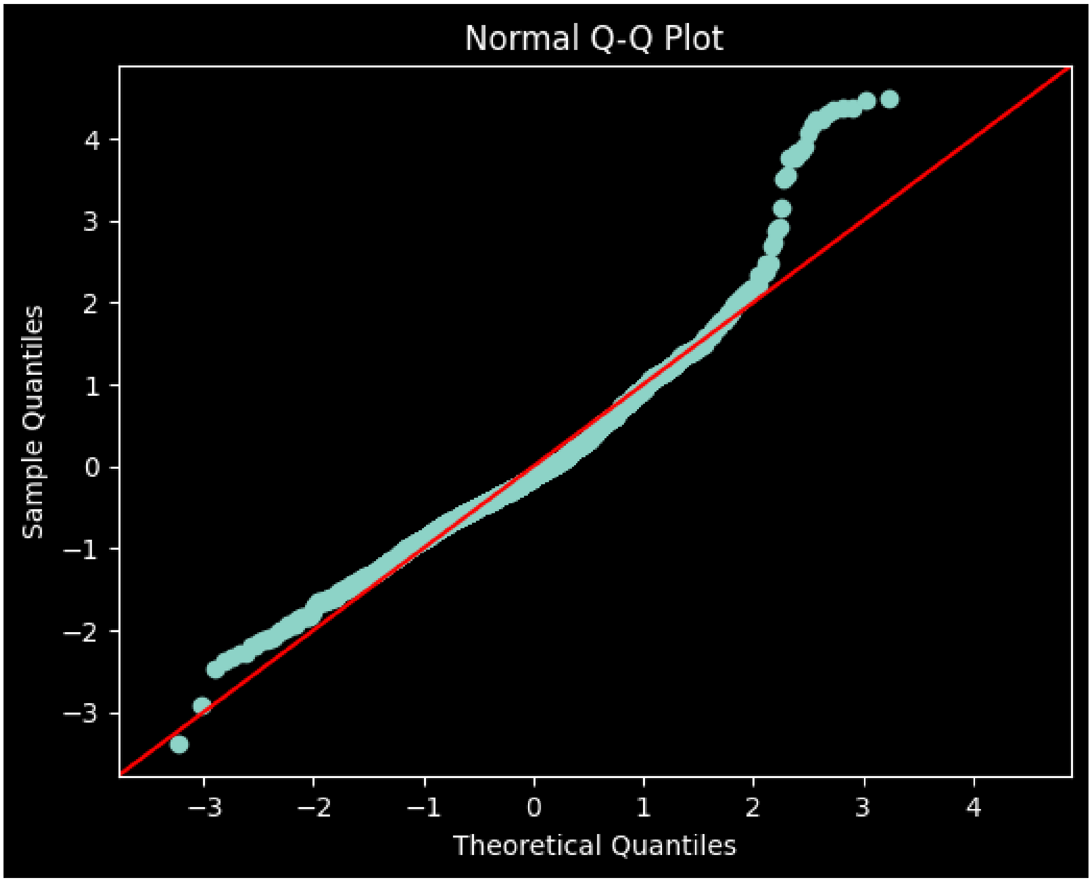
	coef	std err	t	P> |t|	[0.025	0.975]
const	6267.1127	326.168	19.214	0.000	5627.348	6906.877
log__pH	-762.6941	146.519	-5.205	0.000	-1050.085	-475.303
log__total__sulfur__dioxide	-36.9420	8.887	-4.157	0.000	-54.374	-19.511
inv__sqrt__chlorides	59.1809	12.830	4.613	0.000	34.016	84.345
sulphates	-382.3325	95.231	-4.015	0.000	-569.125	-195.540
inv__sulphates	-390.0515	49.183	-7.931	0.000	-486.521	-293.582
volatile__acidity__cbrt	-535.2796	74.843	-7.152	0.000	-682.080	-388.479
inv__alcohol__cbrt	-7747.3220	463.260	-16.723	0.000	-8655.987	-6838.657

Omnibus:	244.917	**Durbin-Watson:**	1.756
Prob(Omnibus):	0.000	**Jarque-Bera (JB):**	547.104
Skew:	0.876	**Prob(JB):**	1.58e-119
Kurtosis:	5.268	**Cond. No.**	499.

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.

[22]:
```
# Residuals vs. Fitted Values Plot
plt.scatter(model.fittedvalues, model.resid)
plt.title('Residuals vs. Fitted Values')
plt.xlabel('Fitted Values')
plt.ylabel('Residuals')
plt.show()

# Normal Q-Q Plot
sm.qqplot(model.resid, line = '45', fit = 'true')
plt.title('Normal Q-Q Plot')
plt.show()
```


Residuals vs. Fitted Values
Residuals
Fitted Values
1000
750
500
250
0
−250
−500
−750
0
200
400
600
800
1000
1200


Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
4
3
2
1
0
−1
−2
−3
−3
−2
−1
0
1
2
3
4

```
[ ]:
```