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November 13, 2025

1 Insurance Charges Dataset

[46]:
```
import pandas as pd

# Load the CSV file into a pandas DataFrame
df = pd.read_csv('/content/insurance[1].csv')
# Display the first 5 rows of the DataFrame to inspect the data
df.head()
```

[46]:
```
   age     sex     bmi  children smoker     region      charges
0   19  female  27.900         0    yes  southwest  16884.92400
1   18    male  33.770         1     no  southeast   1725.55230
2   28    male  33.000         3     no  southeast   4449.46200
3   33    male  22.705         0     no  northwest  21984.47061
4   32    male  28.880         0     no  northwest   3866.85520
```

[47]:
```
df.duplicated().sum()
```

[47]:
```
np.int64(1)
```

[48]:
```
print("DataFrame Info:")
df.info()

print("\nMissing Values:")
print(df.isnull().sum())

print("\nDescriptive Statistics:")
print(df.describe())
```

```
DataFrame Info:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1338 entries, 0 to 1337
Data columns (total 7 columns):
 #   Column    Non-Null Count  Dtype
---  ------    --------------  -----
 0   age       1338 non-null   int64
 1   sex       1338 non-null   object
 2   bmi       1338 non-null   float64
```

```
 3   children  1338 non-null   int64
 4   smoker    1338 non-null   object
 5   region    1338 non-null   object
 6   charges   1338 non-null   float64
dtypes: float64(2), int64(2), object(3)
memory usage: 73.3+ KB

Missing Values:
age         0
sex         0
bmi         0
children    0
smoker      0
region      0
charges     0
dtype: int64

Descriptive Statistics:
               age          bmi     children       charges
count  1338.000000  1338.000000  1338.000000   1338.000000
mean     39.207025    30.663397     1.094918  13270.422265
std      14.049960     6.098187     1.205493  12110.011237
min      18.000000    15.960000     0.000000   1121.873900
25%      27.000000    26.296250     0.000000   4740.287150
50%      39.000000    30.400000     1.000000   9382.033000
75%      51.000000    34.693750     2.000000  16639.912515
max      64.000000    53.130000     5.000000  63770.428010
```

[49]:

```python
# Remove duplicate rows
df.drop_duplicates(inplace=True)

# Verify that duplicates have been removed
print(f"Number of duplicate rows after removal: {df.duplicated().sum()}")
print(f"New shape of the DataFrame: {df.shape}")
```

```
Number of duplicate rows after removal: 0
New shape of the DataFrame: (1337, 7)
```

[50]:

```python
# Select 'age' as the independent variable (X) and reshape it for scikit-learn
X = df['age'].values.reshape(-1, 1)
# Select 'charges' as the dependent variable (y)
y = df['charges'].values

from sklearn.model_selection import train_test_split

# Split the data into training and testing sets (80% train, 20% test)
```

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

# Print the shapes of the resulting datasets to verify the split
print("Shape of X_train:", X_train.shape)
print("Shape of X_test:", X_test.shape)
print("Shape of y_train:", y_train.shape)
print("Shape of y_test:", y_test.shape)
```

```
Shape of X_train: (1069, 1)
Shape of X_test: (268, 1)
Shape of y_train: (1069,)
Shape of y_test: (268,)
```

[51]:

```
# Get the total number of rows in the original DataFrame
total_rows_df = df.shape[0]
print(f"Total rows in original DataFrame: {total_rows_df}")

# Get the number of rows in the training and testing sets
total_rows_train = X_train.shape[0]
total_rows_test = X_test.shape[0]
print(f"Rows in training set: {total_rows_train}")
print(f"Rows in testing set: {total_rows_test}")

# Sum the rows from training and testing sets
combined_rows = total_rows_train + total_rows_test
print(f"Combined rows (training + testing): {combined_rows}")

# Verify if the combined rows match the original DataFrame rows
if total_rows_df == combined_rows:
    print("All data from the original dataset has been used in the training and␣
↪testing sets.")
else:
    print("There is a mismatch in the number of rows.")
```

```
Total rows in original DataFrame: 1337
Rows in training set: 1069
Rows in testing set: 268
Combined rows (training + testing): 1337
All data from the original dataset has been used in the training and testing
sets.
```

[52]:

```
from sklearn.linear_model import LinearRegression

# Initialize the Linear Regression model
model = LinearRegression()
# Train the model using the training data
```

```
model.fit(X_train, y_train)

print("Linear Regression model trained successfully.")
```

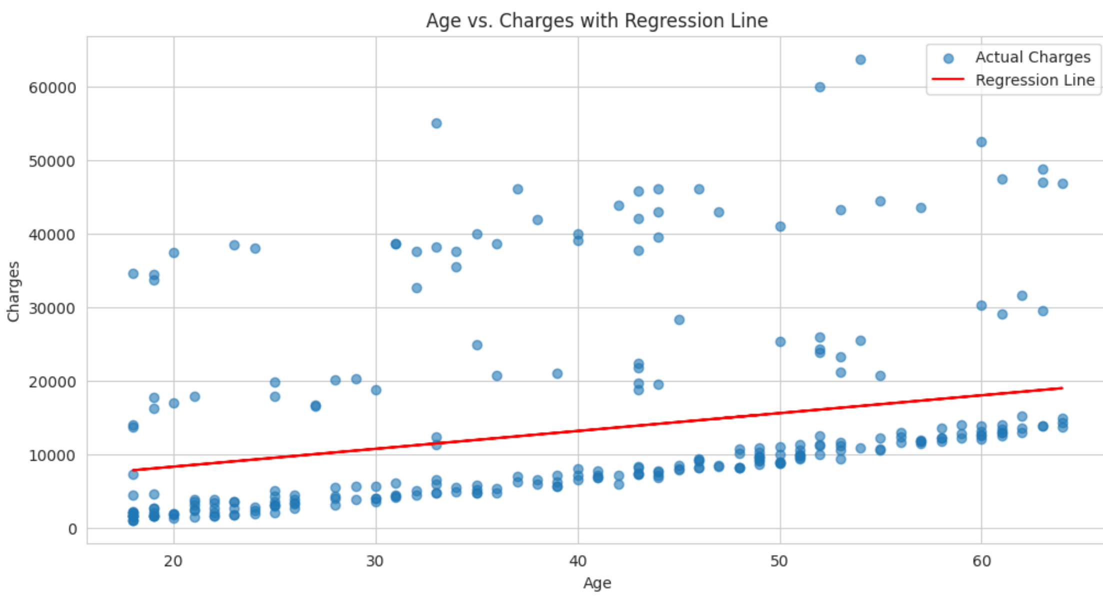
```
Linear Regression model trained successfully.
```

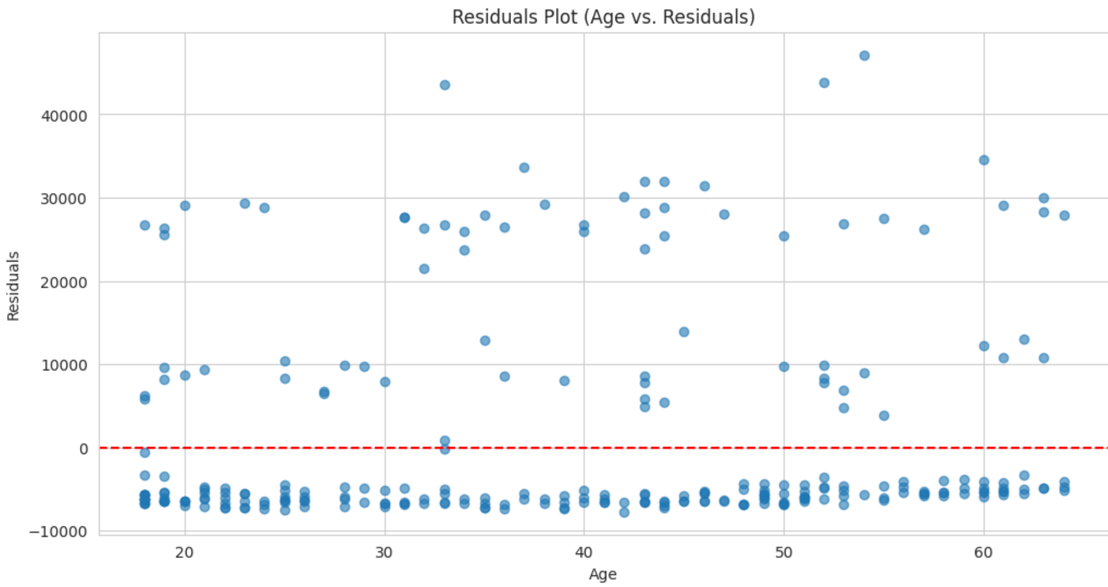
[53]:
```
# Make predictions on the test set using the trained model
y_pred = model.predict(X_test)

from sklearn.metrics import r2_score, mean_absolute_error, mean_squared_error

# Calculate R-squared, Mean Absolute Error (MAE), and Mean Squared Error (MSE)
r2 = r2_score(y_test, y_pred)
mae = mean_absolute_error(y_test, y_pred)
mse = mean_squared_error(y_test, y_pred)

# Print the evaluation metrics
print(f"R-squared: {r2:.4f}")
print(f"Mean Absolute Error (MAE): {mae:.2f}")
print(f"Mean Squared Error (MSE): {mse:.2f}")
```

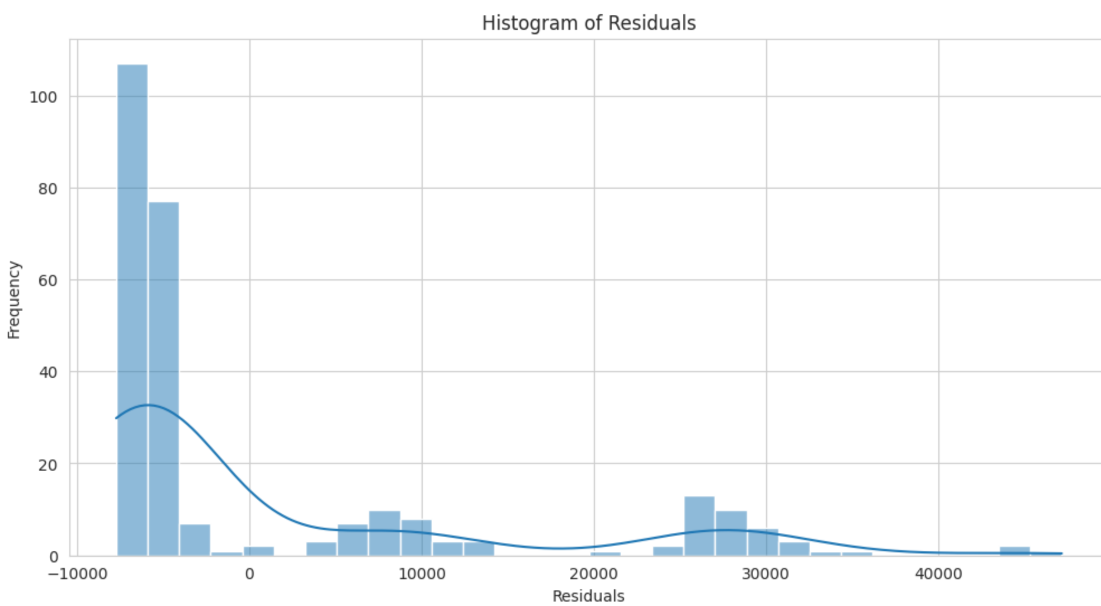
```
R-squared: 0.0951
Mean Absolute Error (MAE): 9657.79
Mean Squared Error (MSE): 166275348.23
```

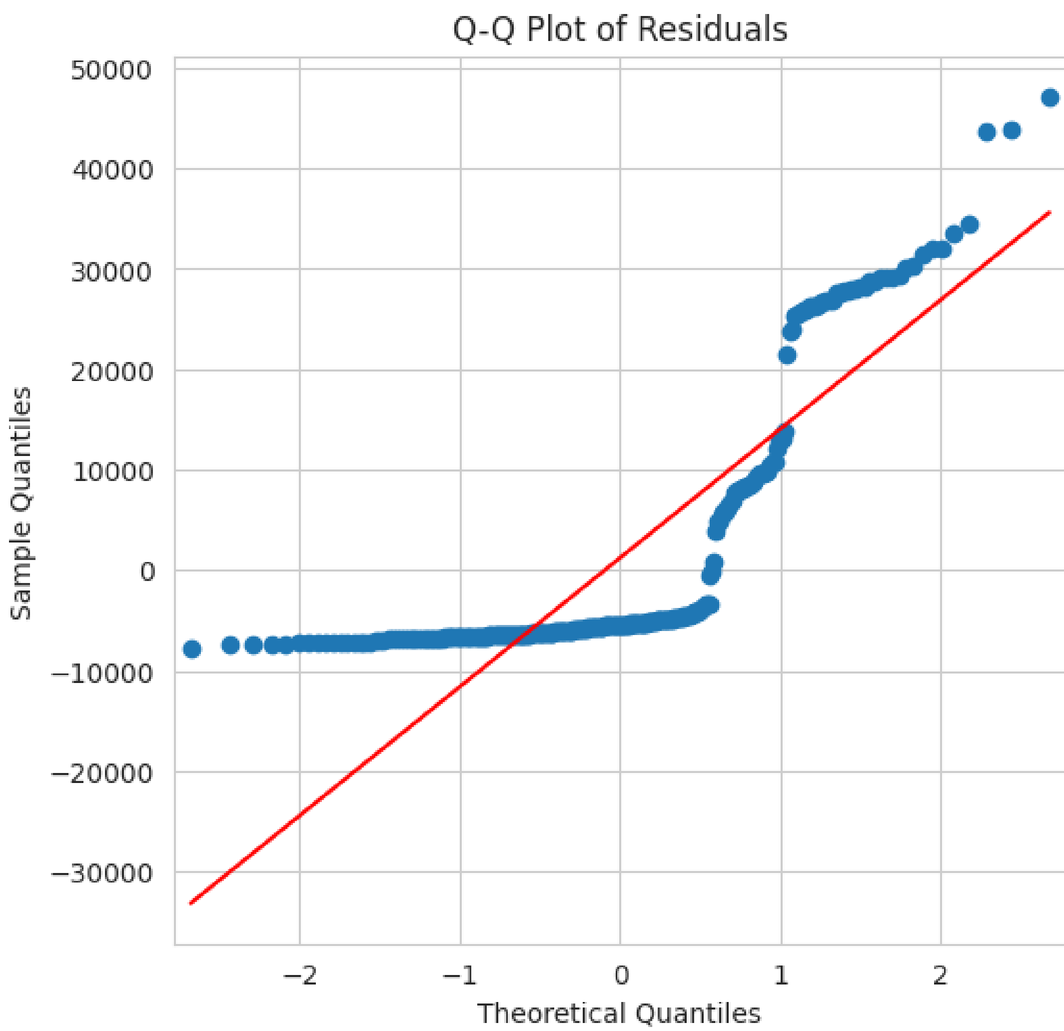
[54]:
```
import matplotlib.pyplot as plt
import seaborn as sns
import statsmodels.api as sm

# Set up plot style for better aesthetics
sns.set_style("whitegrid")

# 1. Scatter plot of data with regression line
plt.figure(figsize=(12, 6))
# Plot actual charges against age
plt.scatter(X_test, y_test, alpha=0.6, label='Actual Charges')
# Plot the regression line (predicted charges against age)
plt.plot(X_test, y_pred, color='red', label='Regression Line')
plt.xlabel('Age')
plt.ylabel('Charges')
plt.title('Age vs. Charges with Regression Line')
plt.legend()
plt.show()

# 2. Residuals plot
# Calculate the residuals (actual values - predicted values)
residuals = y_test - y_pred
```

```
plt.figure(figsize=(12, 6))
# Plot residuals against the independent variable (age)
plt.scatter(X_test, residuals, alpha=0.6)
# Draw a horizontal line at y=0 to easily visualize deviations
plt.axhline(y=0, color='red', linestyle='--')
plt.xlabel('Age')
plt.ylabel('Residuals')
plt.title('Residuals Plot (Age vs. Residuals)')
plt.show()

# 3. Histogram of residuals
plt.figure(figsize=(12, 6))
# Plot a histogram of the residuals to check their distribution
sns.histplot(residuals, kde=True, bins=30)
plt.xlabel('Residuals')
plt.ylabel('Frequency')
plt.title('Histogram of Residuals')
plt.show()

# 4. Q-Q plot of residuals
plt.figure(figsize=(6, 6))
# Create a Q-Q plot to assess if residuals are normally distributed
sm.qqplot(residuals, line='s', ax=plt.gca())
plt.title('Q-Q Plot of Residuals')
plt.show()

print("Visualization of linear regression results completed.")
```




Residuals Plot (Age vs. Residuals)
Residuals
Age
40000
30000
20000
10000
0
−10000
20
30
40
50
60


Histogram of Residuals
Frequency
Residuals
100
80
60
40
20
0
−10000
0
10000
20000
30000
40000




```
Visualization of linear regression results completed.
```

1.1 Feature Engineering and Selection

[55]:
```python
import pandas as pd

# Select the specified features from the DataFrame
X_features = df[['age', 'bmi', 'children', 'sex', 'smoker', 'region']].copy()

# Apply one-hot encoding to categorical columns and drop the original columns
X_features = pd.get_dummies(X_features, columns=['sex', 'smoker', 'region'],␣
↪drop_first=False)

# Display the first few rows of the encoded DataFrame and its info to verify
print("First 5 rows of X_features after encoding:")
```

```
print(X_features.head())
print("\nDataFrame Info for X_features:")
X_features.info()
```

```
First 5 rows of X_features after encoding:
   age     bmi  children  sex_female  sex_male  smoker_no  smoker_yes  \
0   19  27.900         0        True     False      False        True
1   18  33.770         1       False      True       True       False
2   28  33.000         3       False      True       True       False
3   33  22.705         0       False      True       True       False
4   32  28.880         0       False      True       True       False

   region_northeast  region_northwest  region_southeast  region_southwest
0             False             False             False              True
1             False             False              True             False
2             False             False              True             False
3             False              True             False             False
4             False              True             False             False

DataFrame Info for X_features:
<class 'pandas.core.frame.DataFrame'>
Index: 1337 entries, 0 to 1337
Data columns (total 11 columns):
 #   Column            Non-Null Count  Dtype
---  ------            --------------  -----
 0   age               1337 non-null   int64
 1   bmi               1337 non-null   float64
 2   children          1337 non-null   int64
 3   sex_female        1337 non-null   bool
 4   sex_male          1337 non-null   bool
 5   smoker_no         1337 non-null   bool
 6   smoker_yes        1337 non-null   bool
 7   region_northeast  1337 non-null   bool
 8   region_northwest  1337 non-null   bool
 9   region_southeast  1337 non-null   bool
 10  region_southwest  1337 non-null   bool
dtypes: bool(8), float64(1), int64(2)
memory usage: 52.2 KB
```

[56]:

```
from sklearn.model_selection import train_test_split

y = df['charges']

# Split the encoded data into training and testing sets (80% train, 20% test)
X_train_multi, X_test_multi, y_train_multi, y_test_multi =␣
 ↪train_test_split(X_features, y, test_size=0.2, random_state=42)
```

```
# Print the shapes of the resulting datasets to verify the split
print("Shape of X_train_multi:", X_train_multi.shape)
print("Shape of X_test_multi:", X_test_multi.shape)
print("Shape of y_train_multi:", y_train_multi.shape)
print("Shape of y_test_multi:", y_test_multi.shape)
```

```
Shape of X_train_multi: (1069, 11)
Shape of X_test_multi: (268, 11)
Shape of y_train_multi: (1069,)
Shape of y_test_multi: (268,)
```

1.2 Train Multiple Linear Regression Model

[57]:
```
from sklearn.linear_model import LinearRegression

# Initialize the Linear Regression model for multiple features
model_multi = LinearRegression()

# Train the model using the prepared training data
model_multi.fit(X_train_multi, y_train_multi)

print("Multiple Linear Regression model trained successfully.")
```

```
Multiple Linear Regression model trained successfully.
```

1.3 Evaluate Multiple Linear Regression Model

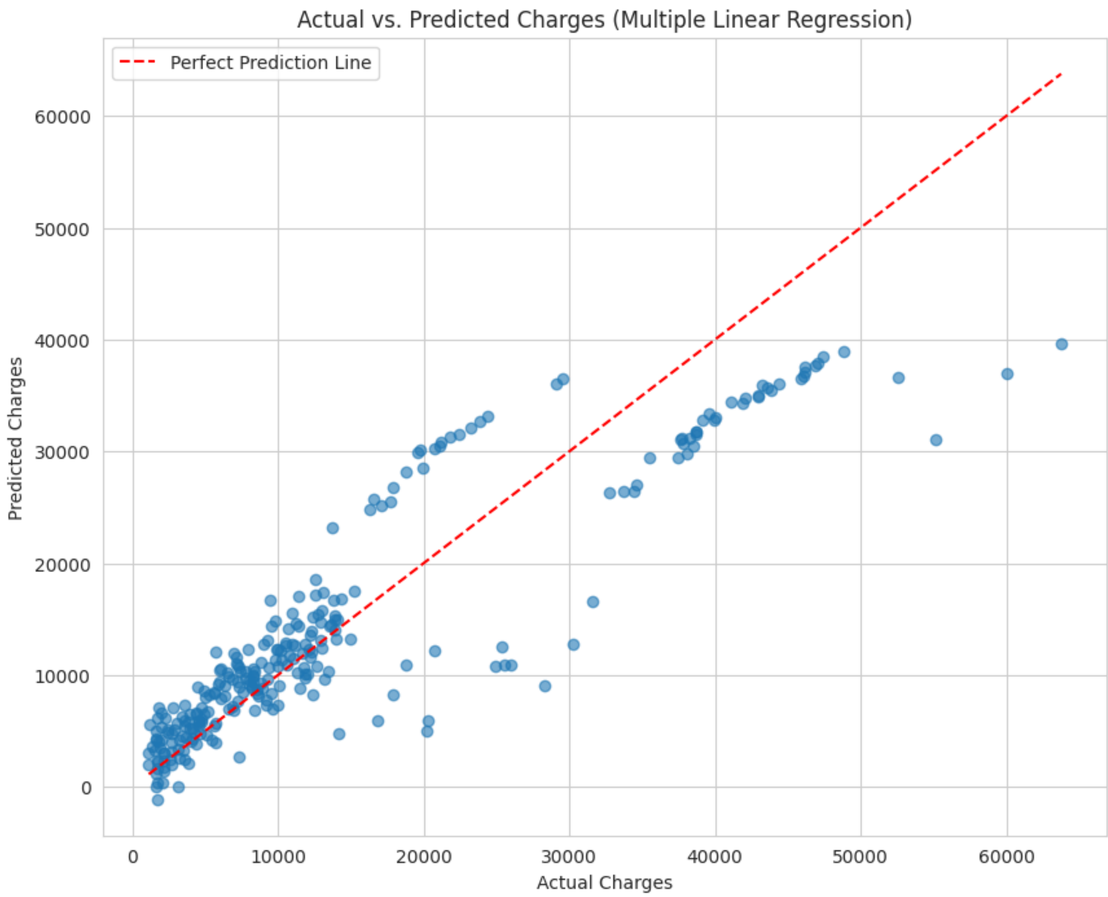
[58]:
```
from sklearn.metrics import r2_score, mean_absolute_error, mean_squared_error

# Make predictions on the test set using the trained multiple linear regression␣
↪model
y_pred_multi = model_multi.predict(X_test_multi)

# Calculate R-squared, Mean Absolute Error (MAE), and Mean Squared Error (MSE)
r2_multi = r2_score(y_test_multi, y_pred_multi)
mae_multi = mean_absolute_error(y_test_multi, y_pred_multi)
mse_multi = mean_squared_error(y_test_multi, y_pred_multi)

# Print the evaluation metrics
print(f"R-squared (Multiple Linear Regression): {r2_multi:.4f}")
print(f"Mean Absolute Error (MAE) (Multiple Linear Regression): {mae_multi:.
↪2f}")
print(f"Mean Squared Error (MSE) (Multiple Linear Regression): {mse_multi:.2f}")
```

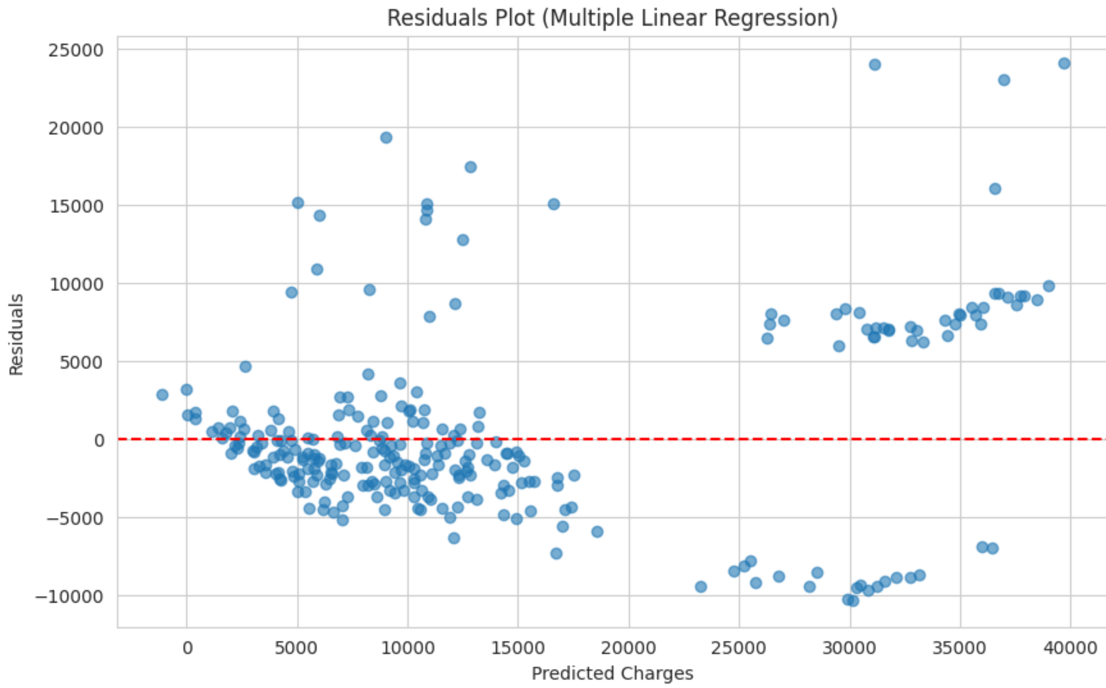
```
R-squared (Multiple Linear Regression): 0.8069
Mean Absolute Error (MAE) (Multiple Linear Regression): 4177.05
Mean Squared Error (MSE) (Multiple Linear Regression): 35478020.68
```

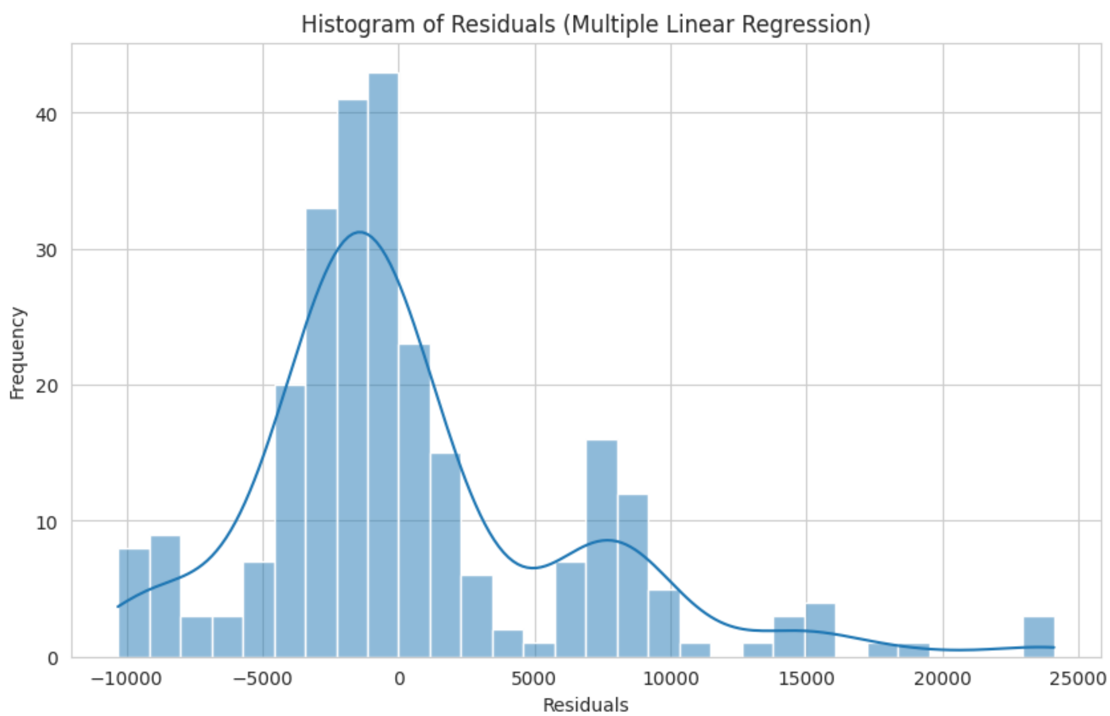
1.4 Visualize Multiple Linear Regression Results

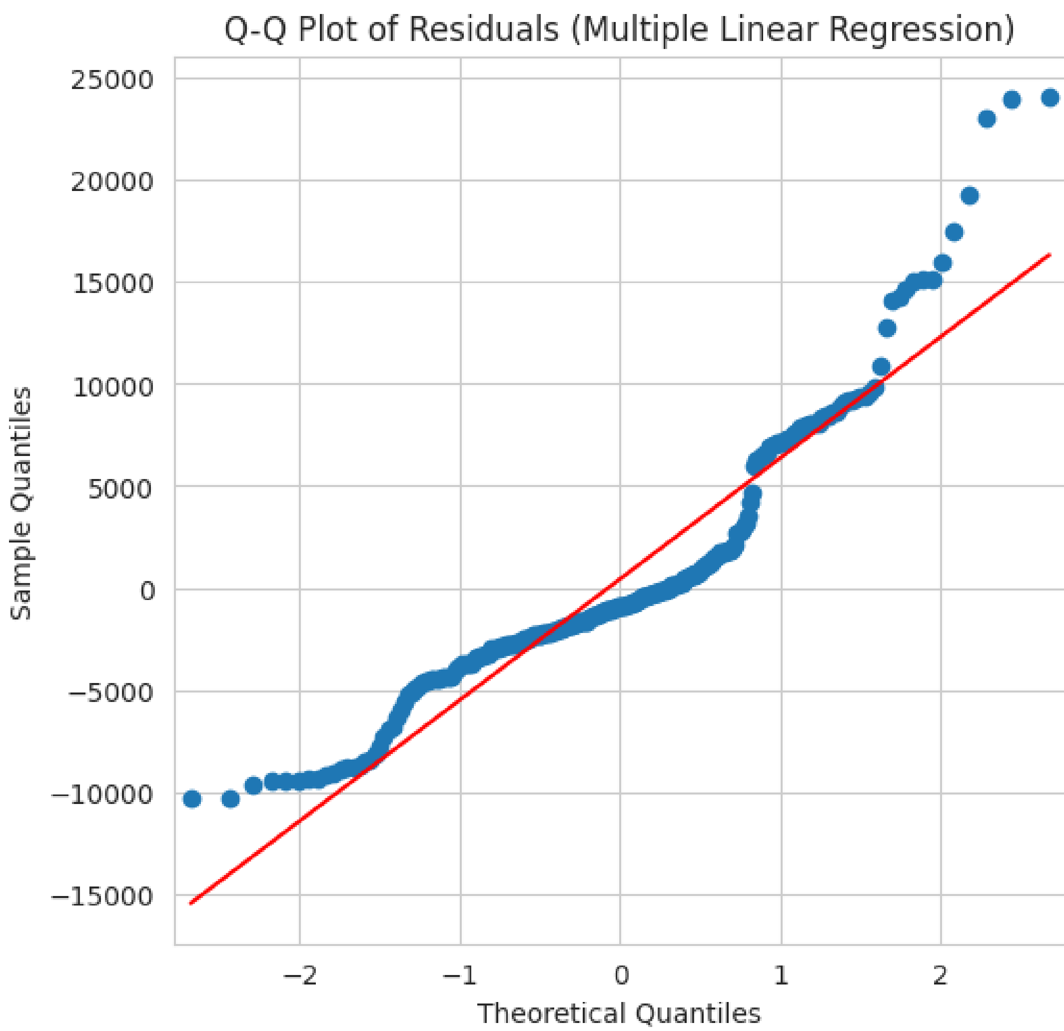
[59]:
```
import matplotlib.pyplot as plt
import seaborn as sns
import statsmodels.api as sm

# Set up plot style for better aesthetics
sns.set_style("whitegrid")

# 1. Scatter plot of actual vs. predicted charges
plt.figure(figsize=(10, 8))
plt.scatter(y_test_multi, y_pred_multi, alpha=0.6)
plt.plot([min(y_test_multi), max(y_test_multi)], [min(y_test_multi),␣
 ↪max(y_test_multi)], 'r--', label='Perfect Prediction Line')
plt.xlabel('Actual Charges')
plt.ylabel('Predicted Charges')
plt.title('Actual vs. Predicted Charges (Multiple Linear Regression)')
plt.legend()
plt.show()

# 2. Residuals plot
# Calculate the residuals (actual values - predicted values)
residuals_multi = y_test_multi - y_pred_multi

plt.figure(figsize=(10, 6))
# Plot predicted values against residuals
plt.scatter(y_pred_multi, residuals_multi, alpha=0.6)
# Draw a horizontal line at y=0 to easily visualize deviations
plt.axhline(y=0, color='red', linestyle='--')
plt.xlabel('Predicted Charges')
plt.ylabel('Residuals')
plt.title('Residuals Plot (Multiple Linear Regression)')
plt.show()

# 3. Histogram of residuals
plt.figure(figsize=(10, 6))
# Plot a histogram of the residuals to check their distribution
sns.histplot(residuals_multi, kde=True, bins=30)
plt.xlabel('Residuals')
plt.ylabel('Frequency')
plt.title('Histogram of Residuals (Multiple Linear Regression)')
plt.show()

# 4. Q-Q plot of residuals
plt.figure(figsize=(6, 6))
# Create a Q-Q plot to assess if residuals are normally distributed
sm.qqplot(residuals_multi, line='s', ax=plt.gca())
```

```python
plt.title('Q-Q Plot of Residuals (Multiple Linear Regression)')
plt.show()

print("Visualization of multiple linear regression results completed.")
```




Residuals Plot (Multiple Linear Regression)
Residuals
Predicted Charges
25000
20000
15000
10000
5000
0
−5000
−10000
0
5000
10000
15000
20000
25000
30000
35000
40000


Histogram of Residuals (Multiple Linear Regression)
Frequency
Residuals
40
30
20
10
0
−10000
−5000
0
5000
10000
15000
20000
25000



Visualization of multiple linear regression results completed.

1.5 Data Transformation

[60]:
```
import numpy as np

# Apply a natural logarithm transformation to the 'charges' column
df['charges_log'] = np.log(df['charges'])

# Display the first few rows of the DataFrame to verify the new 'charges_log'␣
↪column
print("DataFrame with 'charges_log' column:")
df.head()
```

DataFrame with 'charges_log' column:

[60]:
```
   age     sex     bmi  children smoker     region      charges  charges_log
0   19  female  27.900         0    yes  southwest  16884.92400     9.734176
1   18    male  33.770         1     no  southeast   1725.55230     7.453302
2   28    male  33.000         3     no  southeast   4449.46200     8.400538
3   33    male  22.705         0     no  northwest  21984.47061     9.998092
4   32    male  28.880         0     no  northwest   3866.85520     8.260197
```

1.6 Advanced Feature Engineering

[61]:
```
X_features['smoker_age_interaction'] = X_features['age'] *␣
  ↪X_features['smoker_yes']
X_features['smoker_bmi_interaction'] = X_features['bmi'] *␣
  ↪X_features['smoker_yes']

# Display the first few rows of the updated DataFrame to verify the new columns
print("X_features DataFrame with interaction terms:")
print(X_features.head())

print("\nDataFrame Info for X_features after adding interaction terms:")
X_features.info()
```

```
X_features DataFrame with interaction terms:
   age     bmi  children  sex_female  sex_male  smoker_no  smoker_yes  \
0   19  27.900         0        True     False      False        True
1   18  33.770         1       False      True       True       False
2   28  33.000         3       False      True       True       False
3   33  22.705         0       False      True       True       False
4   32  28.880         0       False      True       True       False

   region_northeast  region_northwest  region_southeast  region_southwest  \
0             False             False             False              True
1             False             False              True             False
2             False             False              True             False
3             False              True             False             False
4             False              True             False             False

   smoker_age_interaction  smoker_bmi_interaction
0                      19                    27.9
1                       0                     0.0
2                       0                     0.0
3                       0                     0.0
4                       0                     0.0

DataFrame Info for X_features after adding interaction terms:
<class 'pandas.core.frame.DataFrame'>
Index: 1337 entries, 0 to 1337
Data columns (total 13 columns):
```

```
 #   Column                  Non-Null Count  Dtype
---  ------                  --------------  -----
 0   age                     1337 non-null   int64
 1   bmi                     1337 non-null   float64
 2   children                1337 non-null   int64
 3   sex_female              1337 non-null   bool
 4   sex_male                1337 non-null   bool
 5   smoker_no               1337 non-null   bool
 6   smoker_yes              1337 non-null   bool
 7   region_northeast        1337 non-null   bool
 8   region_northwest        1337 non-null   bool
 9   region_southeast        1337 non-null   bool
 10  region_southwest        1337 non-null   bool
 11  smoker_age_interaction  1337 non-null   int64
 12  smoker_bmi_interaction  1337 non-null   float64
dtypes: bool(8), float64(2), int64(3)
memory usage: 73.1 KB
```

1.7 Prepare Transformed Data

[62]:
```python
from sklearn.model_selection import train_test_split

# 1. Set the independent variables X_enhanced to the X_features DataFrame
X_enhanced = X_features

# 2. Set the dependent variable y_log to the charges_log column from the␣
↪original df DataFrame
y_log = df['charges_log']

# 3. Split X_enhanced and y_log into training and testing sets
X_train_enhanced, X_test_enhanced, y_train_log, y_test_log =␣
↪train_test_split(X_enhanced, y_log, test_size=0.2, random_state=42)

# 4. Print the shapes of the new training and testing sets
print("Shape of X_train_enhanced:", X_train_enhanced.shape)
print("Shape of X_test_enhanced:", X_test_enhanced.shape)
print("Shape of y_train_log:", y_train_log.shape)
print("Shape of y_test_log:", y_test_log.shape)
```

```
Shape of X_train_enhanced: (1069, 13)
Shape of X_test_enhanced: (268, 13)
Shape of y_train_log: (1069,)
Shape of y_test_log: (268,)
```

1.8 Train and Evaluate Enhanced Linear Regression Model

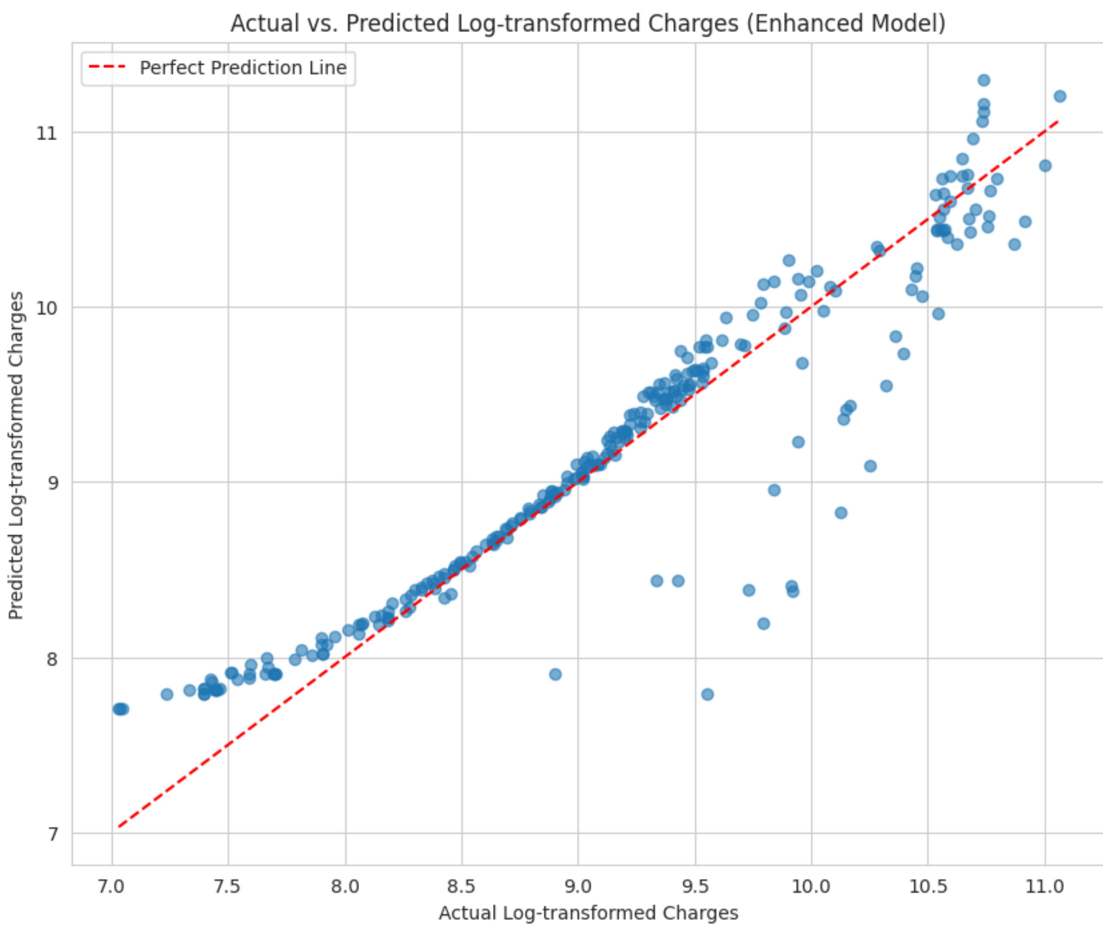
[63]:
```
from sklearn.linear_model import LinearRegression
from sklearn.metrics import r2_score, mean_absolute_error, mean_squared_error
import numpy as np

# Initialize the Linear Regression model for enhanced features and␣
↪log-transformed target
model_enhanced = LinearRegression()

# Train the model using the prepared training data
model_enhanced.fit(X_train_enhanced, y_train_log)

# Make predictions on the test set
y_pred_enhanced = model_enhanced.predict(X_test_enhanced)

# Calculate evaluation metrics
r2_enhanced = r2_score(y_test_log, y_pred_enhanced)
mae_enhanced = mean_absolute_error(y_test_log, y_pred_enhanced)
mse_enhanced = mean_squared_error(y_test_log, y_pred_enhanced)

# Print the evaluation metrics
print(f"R-squared (Enhanced Model with Log-transformed Target): {r2_enhanced:.
↪4f}")
print(f"Mean Absolute Error (MAE) (Enhanced Model with Log-transformed Target):␣
↪{mae_enhanced:.4f}")
print(f"Mean Squared Error (MSE) (Enhanced Model with Log-transformed Target):␣
↪{mse_enhanced:.4f}")

# Optionally, transform back to original scale for MAE/MSE if comparison is␣
↪needed with original model
# Note: This is an approximation as np.exp(E[log(y)]) != E[y]
y_pred_original_scale = np.exp(y_pred_enhanced)
y_test_original_scale = np.exp(y_test_log)

mae_original_scale = mean_absolute_error(y_test_original_scale,␣
↪y_pred_original_scale)
mse_original_scale = mean_squared_error(y_test_original_scale,␣
↪y_pred_original_scale)

print(f"\nMean Absolute Error (MAE) (Original Scale, for comparison):␣
↪{mae_original_scale:.2f}")
print(f"Mean Squared Error (MSE) (Original Scale, for comparison):␣
↪{mse_original_scale:.2f}")
```

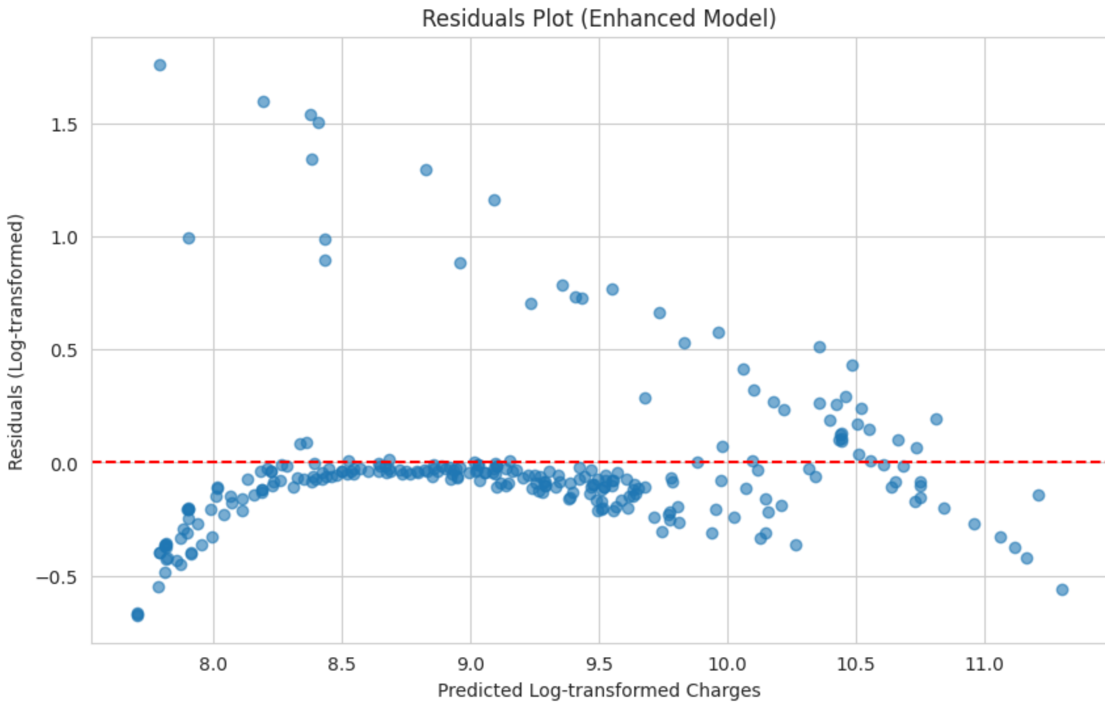
```
R-squared (Enhanced Model with Log-transformed Target): 0.8709
Mean Absolute Error (MAE) (Enhanced Model with Log-transformed Target): 0.2055
```

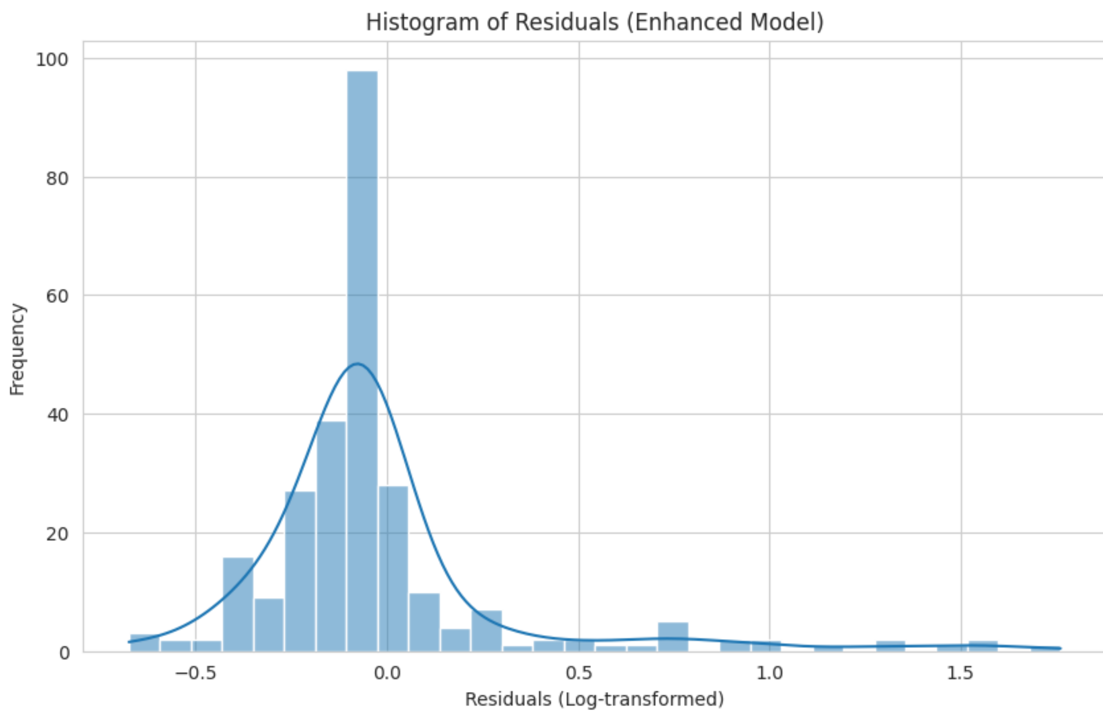
```
Mean Squared Error (MSE) (Enhanced Model with Log-transformed Target): 0.1198

Mean Absolute Error (MAE) (Original Scale, for comparison): 3023.94
Mean Squared Error (MSE) (Original Scale, for comparison): 34328892.68
```

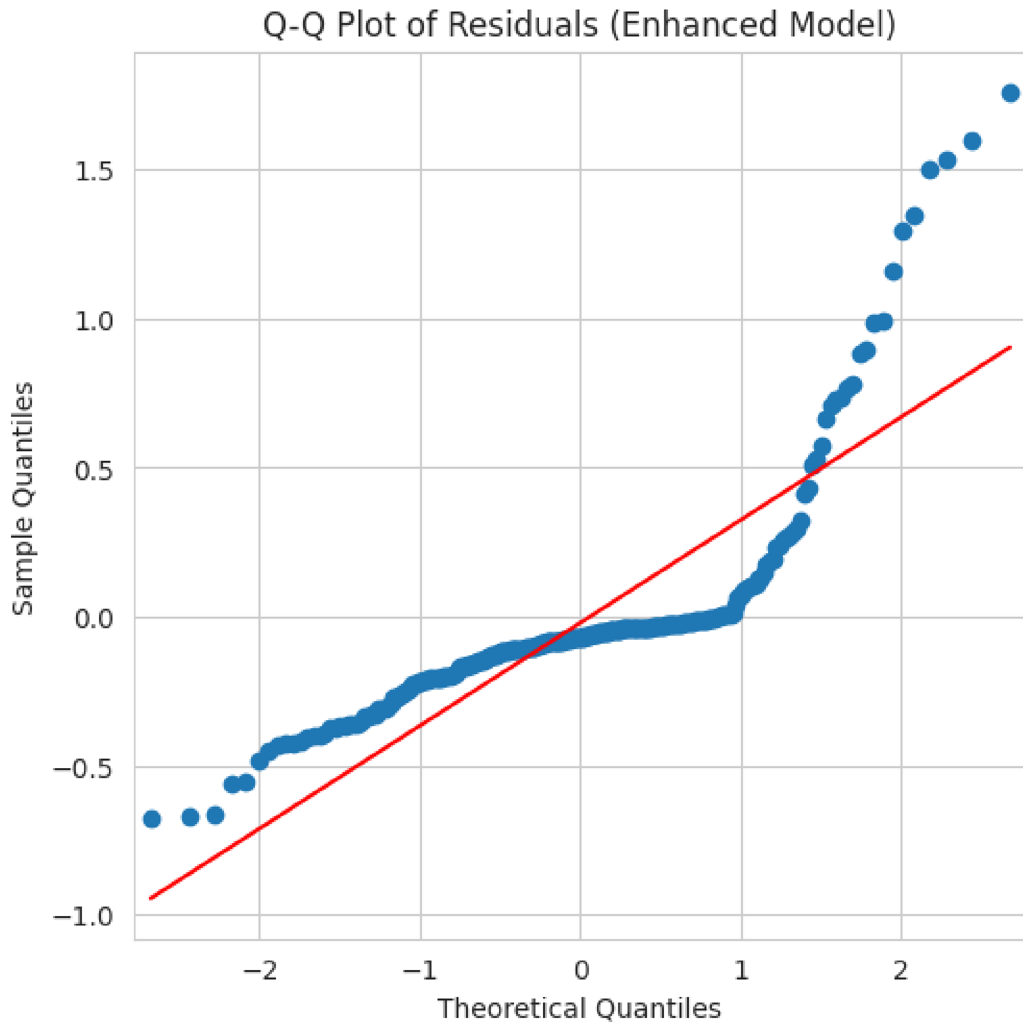
[64]:
```python
import matplotlib.pyplot as plt
import seaborn as sns
import statsmodels.api as sm

# Set up plot style for better aesthetics
sns.set_style("whitegrid")

# 1. Scatter plot of actual vs. predicted charges (on log scale)
plt.figure(figsize=(10, 8))
plt.scatter(y_test_log, y_pred_enhanced, alpha=0.6)
plt.plot([min(y_test_log), max(y_test_log)], [min(y_test_log),␣
 ↪max(y_test_log)], 'r--', label='Perfect Prediction Line')
plt.xlabel('Actual Log-transformed Charges')
plt.ylabel('Predicted Log-transformed Charges')
plt.title('Actual vs. Predicted Log-transformed Charges (Enhanced Model)')
plt.legend()
plt.show()

# 2. Residuals plot
# Calculate the residuals (actual values - predicted values)
residuals_enhanced = y_test_log - y_pred_enhanced

plt.figure(figsize=(10, 6))
# Plot predicted values against residuals
plt.scatter(y_pred_enhanced, residuals_enhanced, alpha=0.6)
# Draw a horizontal line at y=0 to easily visualize deviations
plt.axhline(y=0, color='red', linestyle='--')
plt.xlabel('Predicted Log-transformed Charges')
plt.ylabel('Residuals (Log-transformed)')
plt.title('Residuals Plot (Enhanced Model)')
plt.show()

# 3. Histogram of residuals
plt.figure(figsize=(10, 6))
# Plot a histogram of the residuals to check their distribution
sns.histplot(residuals_enhanced, kde=True, bins=30)
plt.xlabel('Residuals (Log-transformed)')
plt.ylabel('Frequency')
plt.title('Histogram of Residuals (Enhanced Model)')
plt.show()

# 4. Q-Q plot of residuals
```

```python
plt.figure(figsize=(6, 6))
# Create a Q-Q plot to assess if residuals are normally distributed
sm.qqplot(residuals_enhanced, line='s', ax=plt.gca())
plt.title('Q-Q Plot of Residuals (Enhanced Model)')
plt.show()

print("Visualization of enhanced linear regression results completed.")
```




Residuals Plot (Enhanced Model)
Residuals (Log-transformed)
Predicted Log-transformed Charges
1.5
1.0
0.5
0.0
−0.5
8.0
8.5
9.0
9.5
10.0
10.5
11.0


Histogram of Residuals (Enhanced Model)
Frequency
Residuals (Log-transformed)
100
80
60
40
20
0
−0.5
0.0
0.5
1.0
1.5




```
Visualization of enhanced linear regression results completed.
```

charges

Data Type: Float (float64) Description: Individual medical costs billed by health insurance (the target variable). Range: $1121.87 to $63770.43. Average: Approximately $13270.42. Standard Deviation: $12110.01. Insight: The wide range and high standard deviation indicate a highly skewed distribution (many low costs, a few very high costs), making direct prediction challenging without transformations.

Data Quality Missing Values: There are no missing values in any of the columns. Duplicate Entries: One duplicate row was identified and successfully removed, ensuring data uniqueness.

[ ]: