2021101113

April 12, 2024

```
Regression Assignment
Gowlapalli Rohit 2021101113
```

[67]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings("ignore")
from statsmodels.stats.diagnostic import het_breuschpagan
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LinearRegression
from sklearn.metrics import mean_squared_error
import statsmodels.api as sm
from scipy.stats import pearsonr
from scipy.stats import bartlett
from statsmodels.stats.diagnostic import het_breuschpagan
from statsmodels.compat import lzip
```

1 PART 1

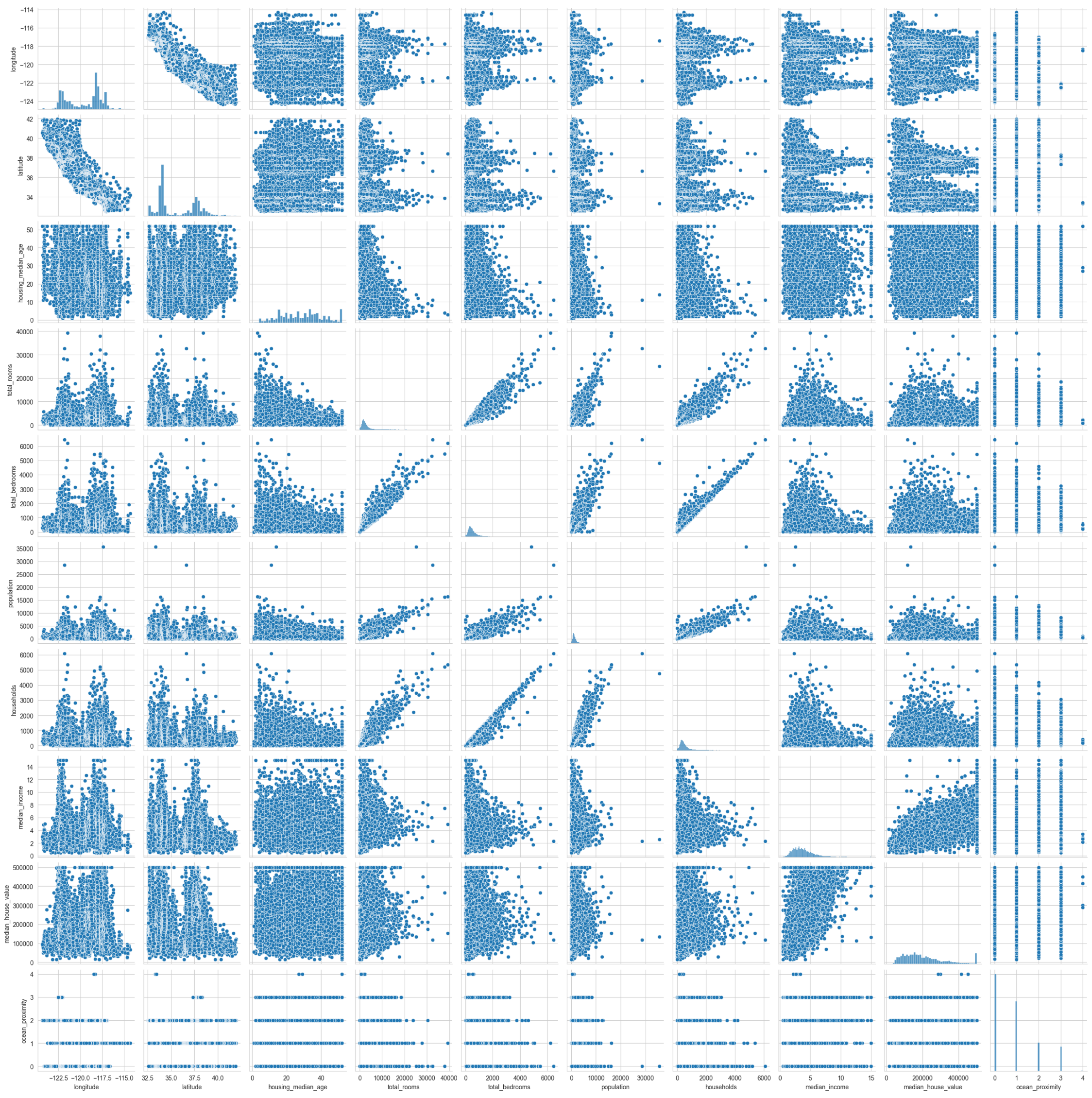
[68]:
```
df = pd.read_csv("housing.csv")
counts = df['ocean_proximity'].value_counts()
```

We can see that ocean_proximity is having string variables. Lets convert it to numericals before we perform the correlation analysis

[69]:
```
# cleaning the data by removing the nan values and changing data to numerical␣
↪variables
df['ocean_proximity'] = df['ocean_proximity'].map({'<1H OCEAN':0, 'INLAND':1,␣
↪'NEAR OCEAN':2, 'NEAR BAY':3, 'ISLAND':4})
df = df.dropna()
```

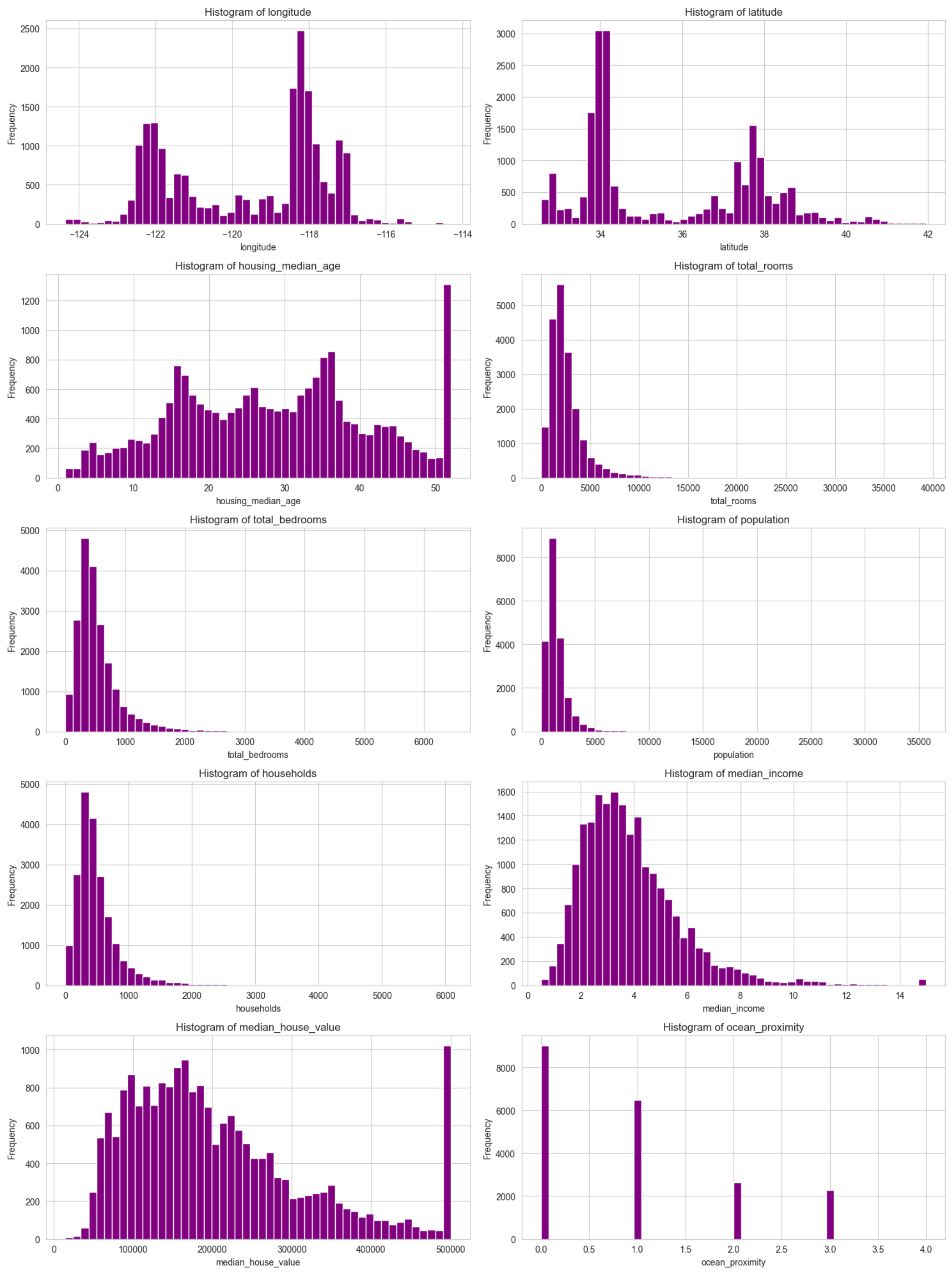
1.1 Visualize some correlations between variables in the data set

[70]:
```
sns.pairplot(df.dropna())
plt.show()
plt.tight_layout()
```



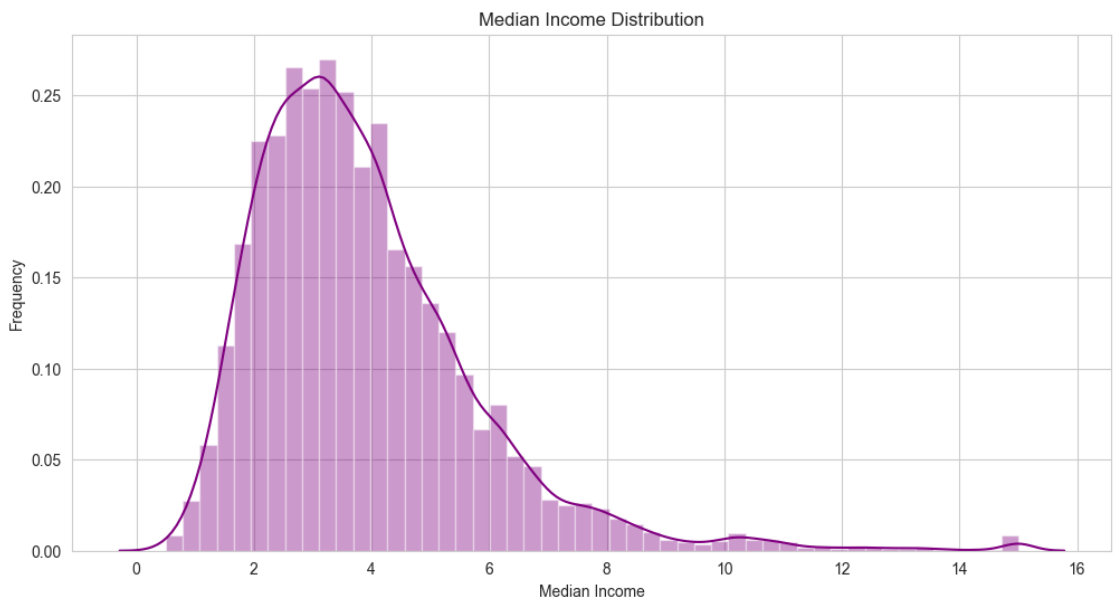
```
<Figure size 640x480 with 0 Axes>
```

[71]:
```
numeric_cols = df.columns
num_rows = 5
num_cols = 2
fig, axes = plt.subplots(num_rows, num_cols, figsize=(15, 20))
axes = axes.flatten()
for i, col_name in enumerate(numeric_cols):
    axes[i].hist(df[col_name], bins=50, color='purple')
    axes[i].set_title(f'Histogram of {col_name}')
    axes[i].set_xlabel(col_name)
    axes[i].set_ylabel('Frequency')

plt.tight_layout()
plt.show()
```



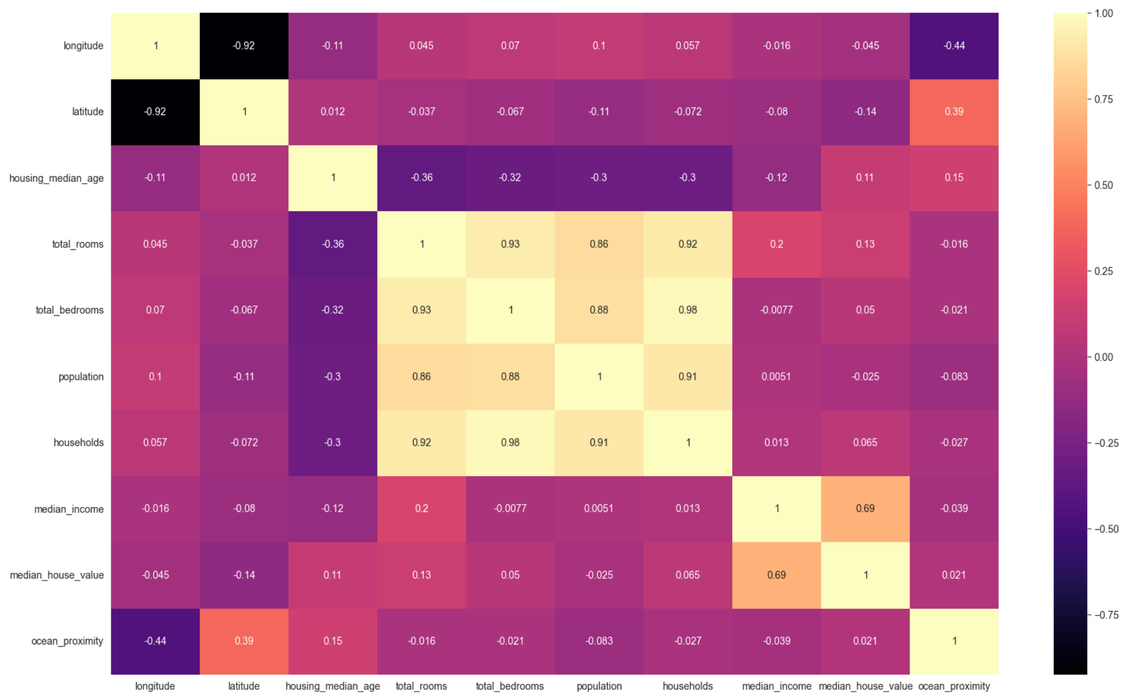
```
[72]: df_1 = df['median_income']
      df_1 = np.array(pd.DataFrame(df_1, columns=['median_income'])).reshape(-1, 1)
```

```
y = df['median_house_value']
df_2 = df.copy()
df_2 = df_2.drop('median_house_value', axis=1)

plt.figure(figsize=(12, 6))
sns.distplot(df['median_income'], bins=50, color='purple')
plt.title('Median Income Distribution')
plt.xlabel('Median Income')
plt.ylabel('Frequency')
plt.show()
```



[73]:
```
sns.set_style('whitegrid')
plt.figure(figsize=(20, 12))
sns.heatmap(df.corr(), annot=True, cmap='magma')
```

[73]:
```
<Axes: >
```



We can clearly see some of the variables are highly correlated, now lets perform a correlation test to confirm the collinearity before building the model

```
[74]: def correlation_test(data1, data2, alternative):
          corr, p_value = pearsonr(data1, data2)
          print("Correlation coefficient:", corr)
          print("p-value:", p_value)
          print("Alternative hypothesis:", alternative)
          if alternative == "greater":
              if p_value/2 < 0.05:
                  print("Reject the null hypothesis: There is a positive correlation␣
       ↪between the two variables")
              else:
                  print("Fail to reject the null hypothesis: There is no positive␣
       ↪correlation between the two variables")
          elif alternative == "less":
              if p_value/2 < 0.05:
                  print("Reject the null hypothesis: There is a negative correlation␣
       ↪between the two variables")
              else:
                  print("Fail to reject the null hypothesis: There is no negative␣
       ↪correlation between the two variables")
          else:
              if p_value < 0.05:
```

```
            print("Reject the null hypothesis: There is a correlation between␣
↪the two variables")
        else:
            print("Fail to reject the null hypothesis: There is no correlation␣
↪between the two variables")

print("Correlation test for total_bedrooms and total_rooms:")
correlation_test(df['total_bedrooms'], df['total_rooms'], alternative="greater")
print("\nCorrelation test for households and population:")
correlation_test(df['households'], df['population'], alternative="greater")
print("\nCorrelation test for longitude and latitude:")
correlation_test(df['longitude'], df['latitude'], alternative="less")
```

```
Correlation test for total_bedrooms and total_rooms:
Correlation coefficient: 0.9303795046865074
p-value: 0.0
Alternative hypothesis: greater
Reject the null hypothesis: There is a positive correlation between the two
variables

Correlation test for households and population:
Correlation coefficient: 0.907185900174492
p-value: 0.0
Alternative hypothesis: greater
Reject the null hypothesis: There is a positive correlation between the two
variables

Correlation test for longitude and latitude:
Correlation coefficient: -0.9246161131160016
p-value: 0.0
Alternative hypothesis: less
Reject the null hypothesis: There is a negative correlation between the two
variables
```

Based on the correlation tests conducted earlier, it's evident that whenever the p-value falls below 0.05, indicating a significant correlation, utilizing just one of the variables from the correlated pair is adequate for model construction.

We constructed three linear regression models by selecting only one variable from each highly correlated pair, effectively reducing the dimensions by three in each model. In the third model, we employed only two variables with notably high absolute correlation values. Notably, in all cases, the p-value was below 0.05, indicating a strong fit of the model to the data.

1.2 Pick 2 linear regression models to predict median house value

1.2.1 Method 1 : Model 1 - Linear Regression

[75]:
```
f1 = 'median_house_value ~ longitude + housing_median_age + total_rooms +␣
 ↪households + median_income + ocean_proximity'
model = sm.formula.ols(formula=f1, data=df)
result = model.fit()
r1 = result
print(result.summary())
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:     median_house_value   R-squared:                       0.538
Model:                            OLS   Adj. R-squared:                  0.538
Method:                 Least Squares   F-statistic:                     3968.
Date:                Fri, 12 Apr 2024   Prob (F-statistic):               0.00
Time:                        22:37:27   Log-Likelihood:            -2.5928e+05
No. Observations:               20433   AIC:                         5.186e+05
Df Residuals:                   20426   BIC:                         5.186e+05
Df Model:                           6
Covariance Type:            nonrobust
================================================================================
======
                         coef    std err          t      P>|t|      [0.025
0.975]
--------------------------------------------------------------------------------
------
Intercept          -1.135e+05   3.63e+04     -3.124      0.002   -1.85e+05
-4.23e+04
longitude           -547.0816    305.893     -1.788      0.074   -1146.656
52.493
housing_median_age  1834.7662     47.476     38.646      0.000    1741.709
1927.824
total_rooms          -18.3770      0.737    -24.939      0.000     -19.821
-16.933
households           131.6456      4.062     32.411      0.000     123.684
139.607
median_income       4.715e+04    328.346    143.609      0.000    4.65e+04
4.78e+04
ocean_proximity     2813.7167    614.237      4.581      0.000    1609.764
4017.670
==============================================================================
Omnibus:                     4186.248   Durbin-Watson:                   0.903
Prob(Omnibus):                  0.000   Jarque-Bera (JB):            11124.199
Skew:                           1.107   Prob(JB):                         0.00
Kurtosis:                       5.858   Cond. No.                     2.30e+05
==============================================================================
Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
[2] The condition number is large, 2.3e+05. This might indicate that there are
strong multicollinearity or other numerical problems.
```

1.2.2 Check for collinearity using VIF to remove highly correlated variables from the models

[76]:
```
from statsmodels.stats.outliers_influence import variance_inflation_factor
features = ['longitude', 'housing_median_age', 'total_rooms', 'households',␣
 ↪'median_income', 'ocean_proximity']
X = df[features]
vif_data_f1 = pd.DataFrame()
vif_data_f1["Feature"] = X.columns
vif_data_f1["VIF"] = [variance_inflation_factor(X.values, i) for i in␣
 ↪range(len(X.columns))]
print(vif_data_f1)
```

```
              Feature        VIF
0           longitude  17.078327
1  housing_median_age   7.320645
2         total_rooms  21.136123
3          households  21.646486
4       median_income   6.654075
5     ocean_proximity   1.889563
```

To address collinearity, we utilized the Variance Inflation Factor (VIF) to detect multicollinearity. A VIF value above 5 suggests significant multicollinearity within the model, indicating the need for further adjustments.

A VIF exceeding 5 presents a potential issue. Therefore, in our scenario, we could address multicollinearity by eliminating either 'total_rooms' or 'households', as they exhibit high correlation with each other.

[77]:
```
f1_modified = 'median_house_value ~ longitude + housing_median_age + households␣
 ↪+ median_income + ocean_proximity'
model_modified = sm.formula.ols(formula=f1_modified, data=df)
result_modified = model_modified.fit()
print(result_modified.summary())
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:     median_house_value   R-squared:                       0.524
Model:                            OLS   Adj. R-squared:                  0.524
Method:                 Least Squares   F-statistic:                     4500.
Date:                Fri, 12 Apr 2024   Prob (F-statistic):               0.00
```

```
Time:                        22:37:28   Log-Likelihood:            -2.5958e+05
No. Observations:               20433   AIC:                         5.192e+05
Df Residuals:                   20427   BIC:                         5.192e+05
Df Model:                           5
Covariance Type:            nonrobust
================================================================================
======
                        coef    std err          t      P>|t|      [0.025
0.975]
--------------------------------------------------------------------------------
------
Intercept          -1.095e+05   3.69e+04     -2.968      0.003   -1.82e+05
-3.72e+04
longitude           -576.1797    310.505     -1.856      0.064   -1184.795
32.435
housing_median_age  2064.8318     47.274     43.678      0.000    1972.171
2157.493
households            37.5876      1.531     24.556      0.000      34.587
40.588
median_income       4.338e+04    295.836    146.641      0.000    4.28e+04
4.4e+04
ocean_proximity     1751.2950    622.001      2.816      0.005     532.123
2970.467
==============================================================================
Omnibus:                     4220.087   Durbin-Watson:                   0.832
Prob(Omnibus):                  0.000   Jarque-Bera (JB):            10451.035
Skew:                           1.142   Prob(JB):                         0.00
Kurtosis:                       5.657   Cond. No.                     4.21e+04
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
[2] The condition number is large, 4.21e+04. This might indicate that there are
strong multicollinearity or other numerical problems.
```

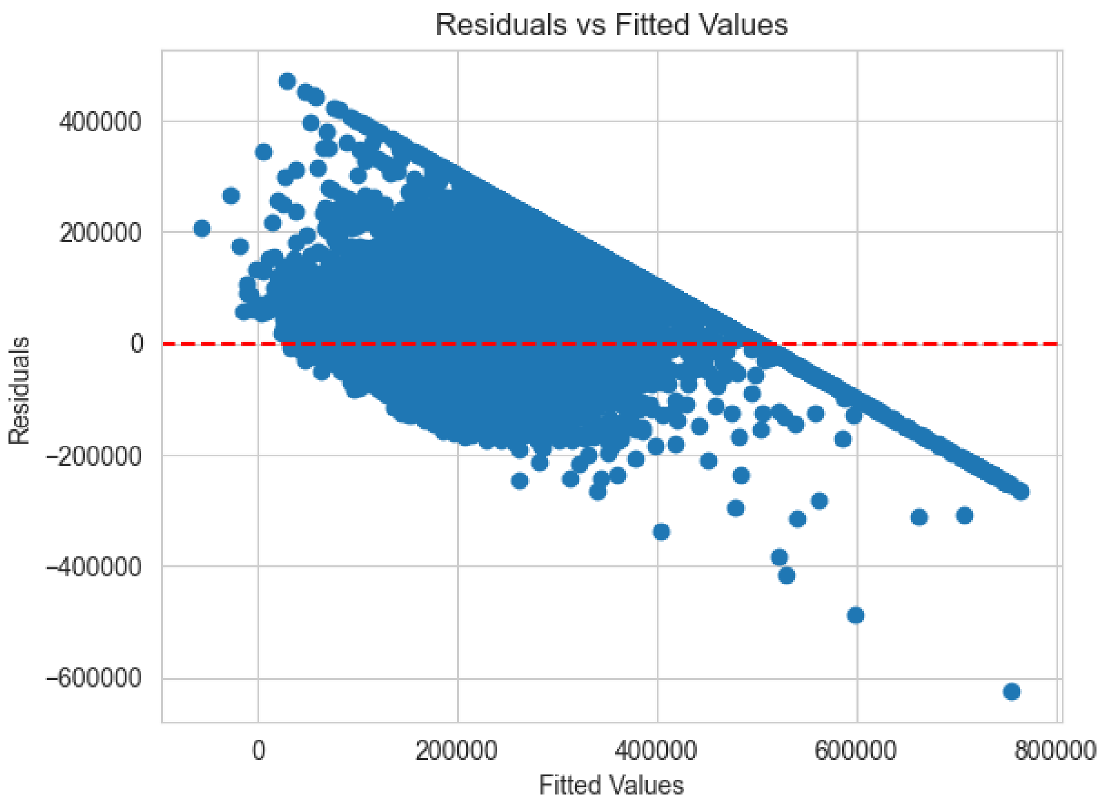
[78]:
```
features_modified = ['longitude', 'housing_median_age', 'households',␣
 ↪'median_income', 'ocean_proximity']
X_modified = df[features_modified]
vif_data_f1_modified = pd.DataFrame()
vif_data_f1_modified["Feature"] = X_modified.columns
vif_data_f1_modified["VIF"] = [variance_inflation_factor(X_modified.values, i)␣
 ↪for i in range(len(X_modified.columns))]
print(vif_data_f1_modified)
```

```
              Feature        VIF
0           longitude  16.776048
1  housing_median_age   7.044223
```

```
2          households   2.972645
3       median_income   5.242159
4     ocean_proximity   1.877894
```

1.2.3 Plot the distribution of the residuals against the fitted values to check for heteroscedasticity

[79]:
```
my_resid = result.resid
my_fitted = result.fittedvalues

# Create scatter plot
plt.scatter(my_fitted, my_resid)
plt.axhline(y=0, color='red', linestyle='--')  # Add a red line at y=0
plt.title("Residuals vs Fitted Values")
plt.xlabel("Fitted Values")
plt.ylabel("Residuals")
plt.show()
```



Since plot of residuals against fitted values is not constant, it means that there is heteroscedasticity in our data

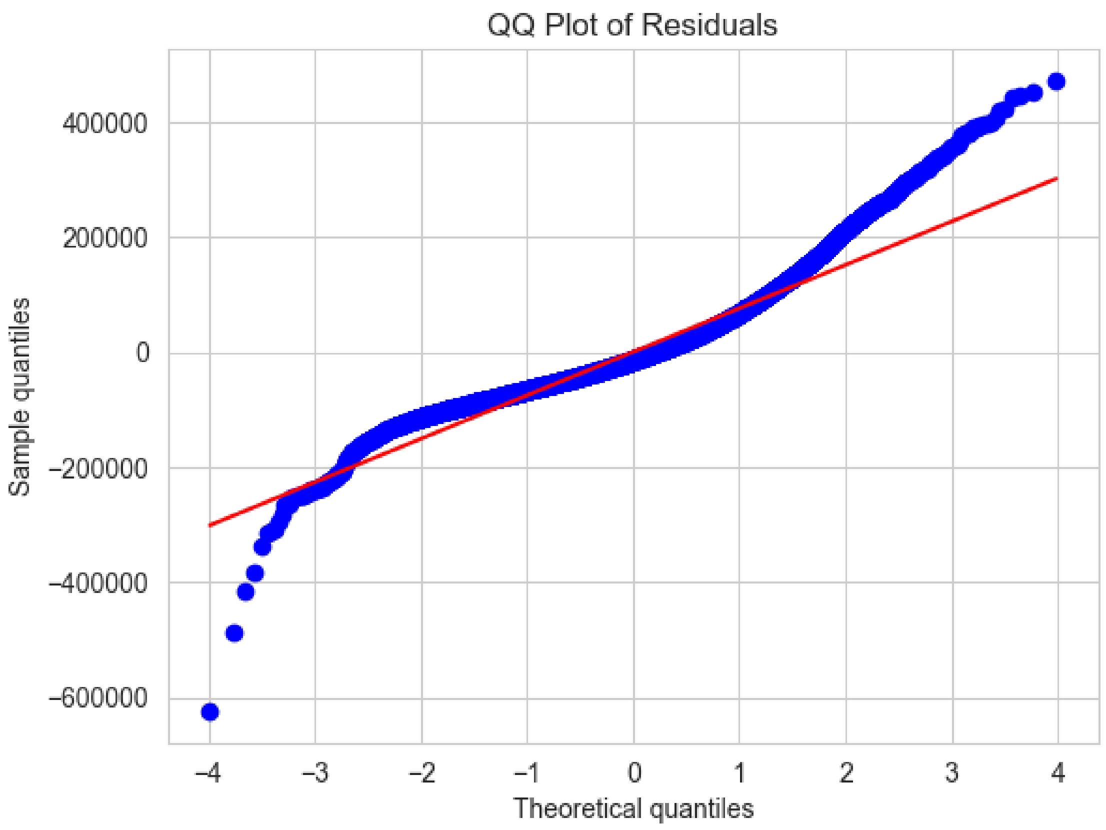
1.2.4 Use ncvTest or equivalent to test for heteroscedasticity

[80]:
```
residuals = result.resid
X = result.model.exog
lm, lm_p_value, fvalue, f_p_value = het_breuschpagan(residuals, X)
print("Lagrange multiplier statistic:", lm)
print("p-value for Lagrange multiplier test:", lm_p_value)
print("F-statistic:", fvalue)
print("p-value for F-statistic:", f_p_value)
if lm_p_value < 0.05:
    print("Reject the null hypothesis: The residuals are heteroscedastic")
else:
    print("Fail to reject the null hypothesis: The residuals are homoscedastic")
```

```
Lagrange multiplier statistic: 524.6677405571374
p-value for Lagrange multiplier test: 4.072278140202884e-110
F-statistic: 89.71840809298067
p-value for F-statistic: 1.44834794232938e-111
Reject the null hypothesis: The residuals are heteroscedastic
```

1.2.5 Test for normality of the residuals

[81]:
```
import scipy.stats as stats
residuals = result.resid
stats.probplot(residuals, dist="norm", plot=plt)
plt.title("QQ Plot of Residuals")
plt.xlabel("Theoretical quantiles")
plt.ylabel("Sample quantiles")
plt.show()
print("The QQ plot shows that the residuals are not normally distributed as␣
 ↪there is significant deviation from the straight line")

# perform shapiro-wilk test
shapiro_test = stats.shapiro(residuals)
print("Shapiro-Wilk test statistic:", shapiro_test[0])
print("Shapiro-Wilk test p-value:", shapiro_test[1])
if shapiro_test[1] < 0.05:
    print("Reject the null hypothesis: The residuals are not normally␣
 ↪distributed")
else:
    print("Fail to reject the null hypothesis: The residuals are normally␣
 ↪distributed")
```



```
The QQ plot shows that the residuals are not normally distributed as there is
significant deviation from the straight line
Shapiro-Wilk test statistic: 0.9272986467549998
Shapiro-Wilk test p-value: 2.2236948379166963e-70
Reject the null hypothesis: The residuals are not normally distributed
```

1.2.6 Method 2 : Model 2 - Linear Regression

[82]:
```
f2 = 'median_house_value ~ latitude + housing_median_age + total_bedrooms +␣
  ↪population + median_income + ocean_proximity'
model = sm.formula.ols(formula=f2, data=df)
result = model.fit()
r2 = result
print(result.summary())
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:     median_house_value   R-squared:                       0.560
Model:                            OLS   Adj. R-squared:                  0.560
Method:                 Least Squares   F-statistic:                     4331.
Date:                Fri, 12 Apr 2024   Prob (F-statistic):               0.00
```

```
Time:                        22:37:28   Log-Likelihood:            -2.5878e+05
No. Observations:               20433   AIC:                         5.176e+05
Df Residuals:                   20426   BIC:                         5.176e+05
Df Model:                           6
Covariance Type:            nonrobust
================================================================================
======
                         coef    std err          t      P>|t|      [0.025
0.975]
--------------------------------------------------------------------------------
------
Intercept           1.898e+05   1.01e+04     18.770      0.000     1.7e+05
2.1e+05
latitude           -6298.9331    275.136    -22.894      0.000   -6838.221
-5759.645
housing_median_age  2004.9200     45.924     43.658      0.000    1914.906
2094.934
total_bedrooms       113.3302      2.702     41.949      0.000     108.035
118.626
population           -34.2719      0.998    -34.349      0.000     -36.228
-32.316
median_income       4.325e+04    285.458    151.501      0.000    4.27e+04
4.38e+04
ocean_proximity     5006.7243    590.242      8.482      0.000    3849.802
6163.647
==============================================================================
Omnibus:                     3879.490   Durbin-Watson:                   0.891
Prob(Omnibus):                  0.000   Jarque-Bera (JB):            10751.964
Skew:                           1.015   Prob(JB):                         0.00
Kurtosis:                       5.916   Cond. No.                     3.65e+04
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
[2] The condition number is large, 3.65e+04. This might indicate that there are
strong multicollinearity or other numerical problems.
```

1.2.7 Check for collinearity using VIF to remove highly correlated variables from the models

[83]:
```
features_r2 = ['latitude', 'housing_median_age', 'total_bedrooms',␣
  ↪'population', 'median_income', 'ocean_proximity']
X_r2 = df[features_r2]
vif_data_f2 = pd.DataFrame()
vif_data_f2["Feature"] = X_r2.columns
```

```
vif_data_f2["VIF"] = [variance_inflation_factor(X_r2.values, i) for i in␣
 ↪range(len(X_r2.columns))]
print(vif_data_f2)
```

```
             Feature        VIF
0           latitude  16.080752
1  housing_median_age   6.770386
2     total_bedrooms  11.855771
3         population  11.424867
4      median_income   5.053225
5    ocean_proximity   1.958643
```

To address collinearity, we utilized the Variance Inflation Factor (VIF) to detect multicollinearity. A VIF value above 5 suggests significant multicollinearity within the model, indicating the need for further adjustments.

A VIF exceeding 5 presents a potential issue. Therefore, in our scenario, we could address multicollinearity by eliminating 'latitude' and 'total_bedrooms', as they exhibit high correlation with each other.

[84]:
```
# remove total_bedrooms and latitude from the model
f2_modified = 'median_house_value ~ housing_median_age + population +␣
 ↪median_income + ocean_proximity'
model_modified = sm.formula.ols(formula=f2_modified, data=df)
result_modified = model_modified.fit()
print(result_modified.summary())
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:     median_house_value   R-squared:                       0.511
Model:                            OLS   Adj. R-squared:                  0.511
Method:                 Least Squares   F-statistic:                     5336.
Date:                Fri, 12 Apr 2024   Prob (F-statistic):               0.00
Time:                        22:37:28   Log-Likelihood:            -2.5986e+05
No. Observations:               20433   AIC:                         5.197e+05
Df Residuals:                   20428   BIC:                         5.198e+05
Df Model:                           4
Covariance Type:            nonrobust
================================================================================
======
                         coef    std err          t      P>|t|      [0.025
0.975]
--------------------------------------------------------------------------------
------
Intercept          -1.925e+04   2292.965     -8.393      0.000   -2.37e+04
-1.48e+04
housing_median_age  1801.9481     47.674     37.797      0.000    1708.502
1895.394
```

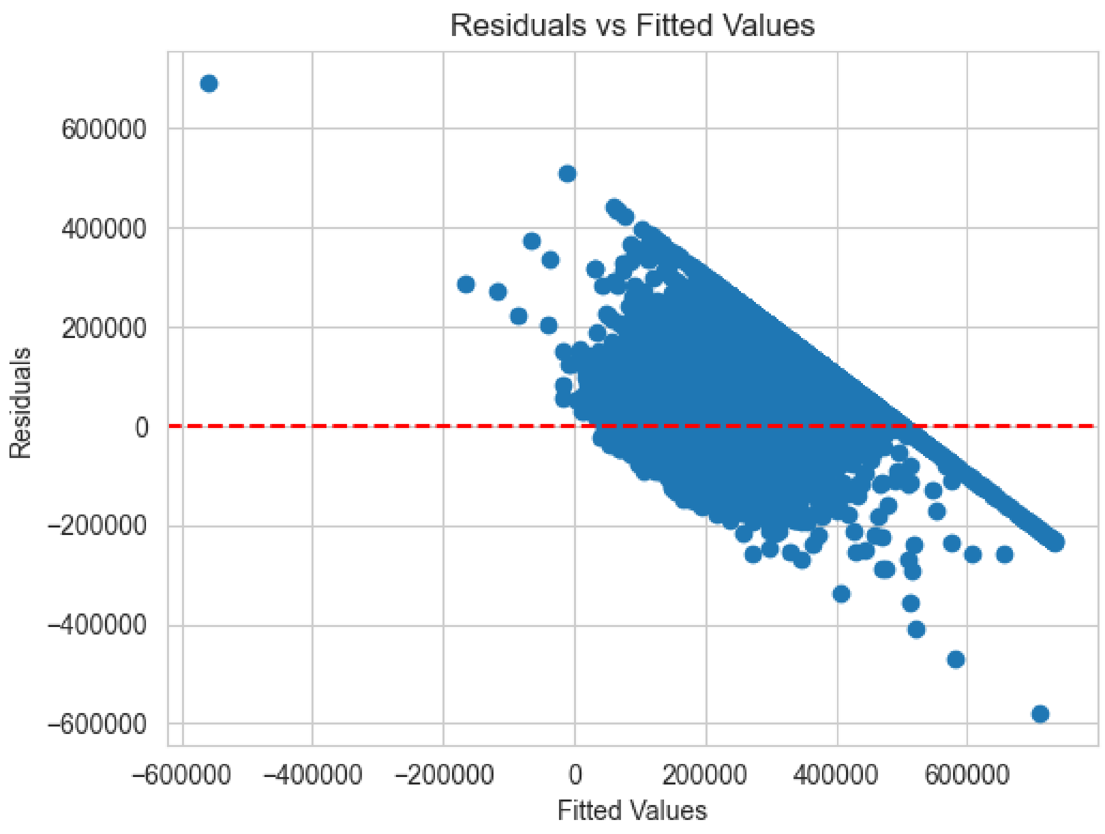
```
population              3.1701      0.523      6.067      0.000       2.146
4.194
median_income         4.33e+04    299.713    144.455      0.000    4.27e+04
4.39e+04
ocean_proximity     2633.5739    568.953      4.629      0.000    1518.381
3748.766
==============================================================================
Omnibus:                     4131.681   Durbin-Watson:                   0.792
Prob(Omnibus):                  0.000   Jarque-Bera (JB):             9909.567
Skew:                           1.132   Prob(JB):                         0.00
Kurtosis:                       5.552   Cond. No.                     7.42e+03
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
[2] The condition number is large, 7.42e+03. This might indicate that there are
strong multicollinearity or other numerical problems.
```

[85]:
```
features_modified_r2 = ['housing_median_age', 'population', 'median_income',␣
 ↪'ocean_proximity']
X_modified_r2 = df[features_modified_r2]
vif_data_f2_modified = pd.DataFrame()
vif_data_f2_modified["Feature"] = X_modified_r2.columns
vif_data_f2_modified["VIF"] = [variance_inflation_factor(X_modified_r2.values,␣
 ↪i) for i in range(len(X_modified_r2.columns))]
print(vif_data_f2_modified)
```

```
              Feature       VIF
0  housing_median_age  3.343534
1          population  2.060304
2       median_income  3.398471
3     ocean_proximity  1.804031
```

1.2.8 Plot the distribution of the residuals against the fitted values to check for heteroscedasticity

[86]:
```
my_resid = result.resid
my_fitted = result.fittedvalues
plt.scatter(my_fitted, my_resid)
plt.title("Residuals vs Fitted Values")
plt.axhline(y=0, color='red', linestyle='--')  # Add a red line at y=0
plt.xlabel("Fitted Values")
plt.ylabel("Residuals")
plt.show()
```



Since plot of residuals against fitted values is not constant, it means that there is heteroscedasticity in our data

1.2.9 Use ncvTest or equivalent to test for heteroscedasticity

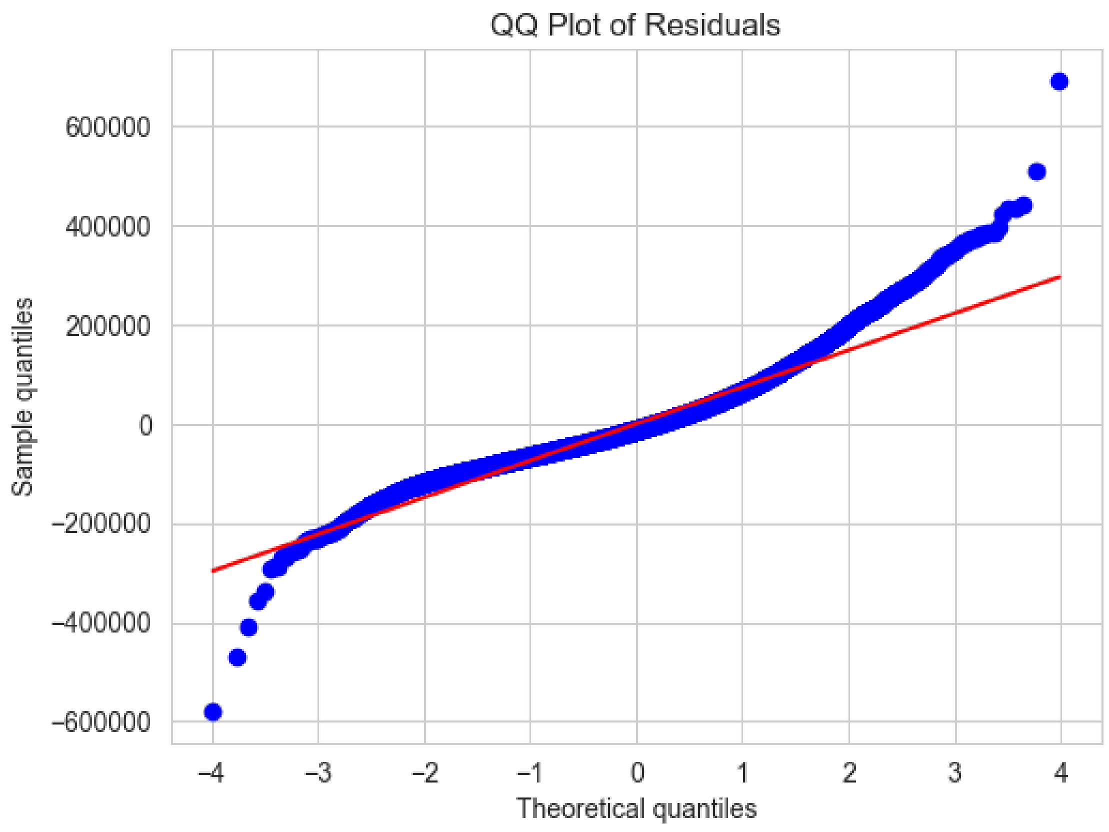
[87]:
```
residuals = result.resid
X = result.model.exog
lm, lm_p_value, fvalue, f_p_value = het_breuschpagan(residuals, X)
print("Lagrange multiplier statistic:", lm)
print("p-value for Lagrange multiplier test:", lm_p_value)
print("F-statistic:", fvalue)
print("p-value for F-statistic:", f_p_value)
if f_p_value < 0.05:
    print("Reject the null hypothesis: The residuals are heteroscedastic")
else:
    print("Fail to reject the null hypothesis: The residuals are homoscedastic")
```

```
Lagrange multiplier statistic: 530.6731971347514
p-value for Lagrange multiplier test: 2.0683175636826215e-111
F-statistic: 90.77272582280787
```

```
p-value for F-statistic: 6.800513636592252e-113
Reject the null hypothesis: The residuals are heteroscedastic
```

1.2.10 Test for normality of the residuals

[88]:
```python
import scipy.stats as stats
residuals = result.resid
stats.probplot(residuals, dist="norm", plot=plt)
plt.title("QQ Plot of Residuals")
plt.xlabel("Theoretical quantiles")
plt.ylabel("Sample quantiles")
plt.show()
print("QQ plot shows that the residuals are not normally distributedas as there␣
 ↪is significant deviation from the straight line")

# perform shapiro-wilk test
shapiro_test = stats.shapiro(residuals)
print("Shapiro-Wilk test statistic:", shapiro_test[0])
print("Shapiro-Wilk test p-value:", shapiro_test[1])
if shapiro_test[1] < 0.05:
    print("Reject the null hypothesis: The residuals are not normally␣
 ↪distributed")
else:
    print("Fail to reject the null hypothesis: The residuals are normally␣
 ↪distributed")
```



```
QQ plot shows that the residuals are not normally distributedas as there is
significant deviation from the straight line
Shapiro-Wilk test statistic: 0.9411884248471788
Shapiro-Wilk test p-value: 5.356357568529892e-66
Reject the null hypothesis: The residuals are not normally distributed
```

1.2.11 Method 3 : Model 3 - Linear Regression

[89]:
```python
f3 = 'median_house_value ~ median_income + ocean_proximity'
model = sm.formula.ols(formula=f3, data=df)
result = model.fit()
r3 = result
print(result.summary())
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:     median_house_value   R-squared:                       0.476
Model:                            OLS   Adj. R-squared:                  0.476
Method:                 Least Squares   F-statistic:                     9284.
Date:                Fri, 12 Apr 2024   Prob (F-statistic):               0.00
Time:                        22:37:29   Log-Likelihood:            -2.6056e+05
```

```
No. Observations:               20433   AIC:                         5.211e+05
Df Residuals:                   20430   BIC:                         5.212e+05
Df Model:                           2
Covariance Type:            nonrobust
================================================================================
===
                      coef    std err          t      P>|t|      [0.025
0.975]
--------------------------------------------------------------------------------
---
Intercept        3.944e+04   1446.851     27.259      0.000    3.66e+04
4.23e+04
median_income    4.195e+04    308.005    136.205      0.000    4.13e+04
4.26e+04
ocean_proximity  5522.3107    582.327      9.483      0.000    4380.903
6663.719
==============================================================================
Omnibus:                     4109.006   Durbin-Watson:                   0.660
Prob(Omnibus):                  0.000   Jarque-Bera (JB):             8909.784
Skew:                           1.169   Prob(JB):                         0.00
Kurtosis:                       5.236   Cond. No.                         11.4
==============================================================================

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

1.2.12 Check for collinearity using VIF to remove highly correlated variables from the models

[90]:
```
features_r3 = ['median_income', 'ocean_proximity']
X_r3 = df[features_r3]
vif_data_r3 = pd.DataFrame()
vif_data_r3["Feature"] = X_r3.columns
vif_data_r3["VIF"] = [variance_inflation_factor(X_r3.values, i) for i in␣
  ↪range(len(X_r3.columns))]
print(vif_data_r3)
```

```
           Feature       VIF
0    median_income  1.533143
1  ocean_proximity  1.533143
```

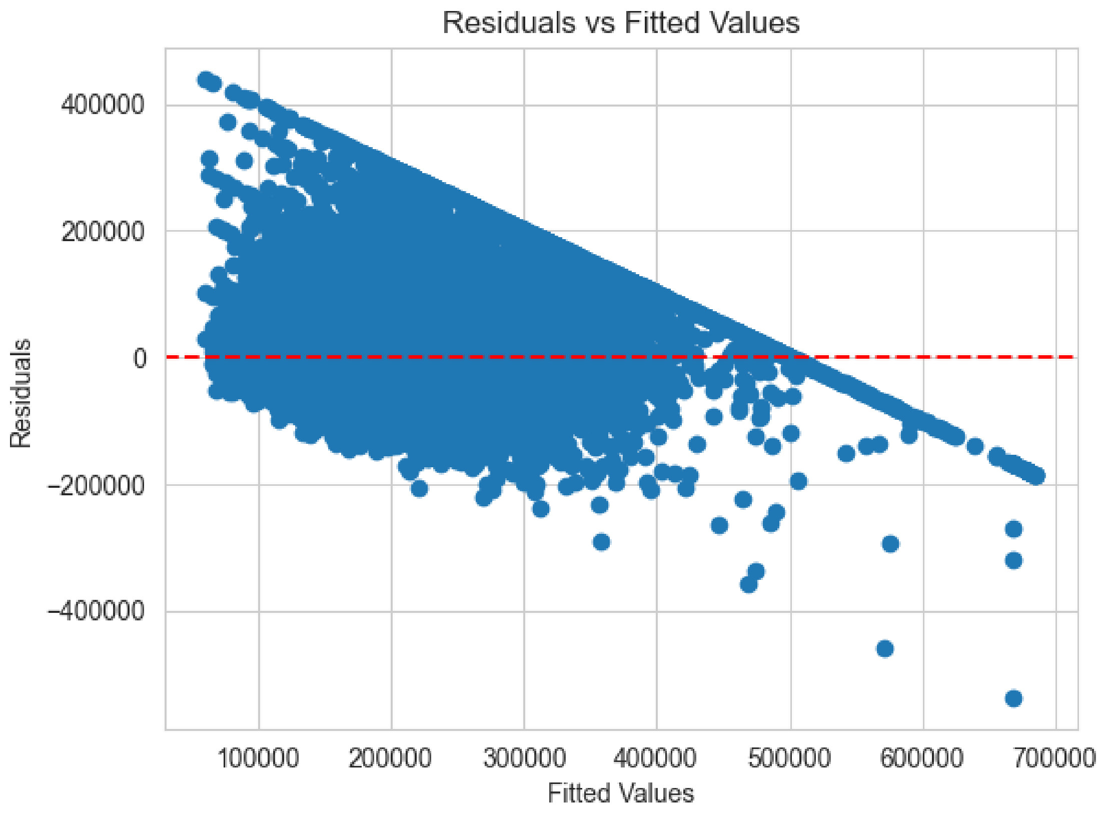
Based on the Variance Inflation Factor (VIF) results:

- **median_income VIF:** 1.533248
- **ocean_proximity VIF:** 1.533248

These VIF values suggest that there is low multicollinearity between `median_income` and `ocean_proximity` in the model. Therefore, the coefficient estimates for these features are likely to be stable and reliable.

1.2.13 Plot the distribution of the residuals against the fitted values to check for heteroscedasticity

[91]:
```
my_resid = result.resid
my_fitted = result.fittedvalues

# Create scatter plot
plt.scatter(my_fitted, my_resid)
plt.axhline(y=0, color='red', linestyle='--')  # Add a red line at y=0
plt.title("Residuals vs Fitted Values")
plt.xlabel("Fitted Values")
plt.ylabel("Residuals")
plt.show()
```



Since plot of residuals against fitted values is not constant, it means that there is heteroscedasticity in our data

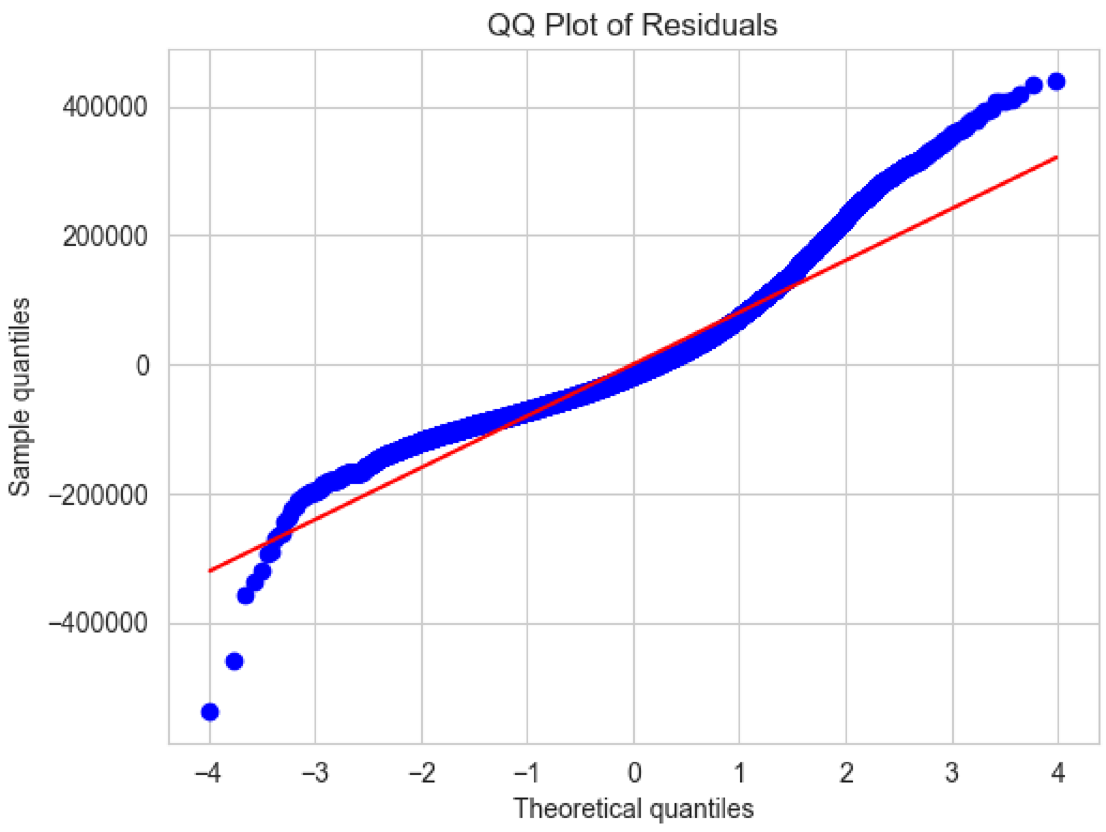
1.2.14 Use ncvTest or equivalent to test for heteroscedasticity

[92]:
```
residuals = result.resid
X = result.model.exog
lm, lm_p_value, fvalue, f_p_value = het_breuschpagan(residuals, X)
print("Lagrange multiplier statistic:", lm)
print("p-value for Lagrange multiplier test:", lm_p_value)
print("F-statistic:", fvalue)
print("p-value for F-statistic:", f_p_value)
if f_p_value < 0.05:
    print("Reject the null hypothesis: The residuals are heteroscedastic")
else:
    print("Fail to reject the null hypothesis: The residuals are homoscedastic")
```

```
Lagrange multiplier statistic: 226.87966596005964
p-value for Lagrange multiplier test: 5.416347361221146e-50
F-statistic: 114.69672304572661
p-value for F-statistic: 2.920264876709513e-50
Reject the null hypothesis: The residuals are heteroscedastic
```

1.2.15 Test for normality of the residuals

[93]:
```
import scipy.stats as stats
residuals = result.resid
stats.probplot(residuals, dist="norm", plot=plt)
plt.title("QQ Plot of Residuals")
plt.xlabel("Theoretical quantiles")
plt.ylabel("Sample quantiles")
plt.show()
print("The QQ plot shows that residuals are not normally distributed")

# perform shapiro-wilk test
shapiro_test = stats.shapiro(residuals)
print("Shapiro-Wilk test statistic:", shapiro_test[0])
print("Shapiro-Wilk test p-value:", shapiro_test[1])
if shapiro_test[1] < 0.05:
    print("Reject the null hypothesis: The residuals are not normally␣
 ↪distributed")
else:
    print("Fail to reject the null hypothesis: The residuals are normally␣
 ↪distributed")
```

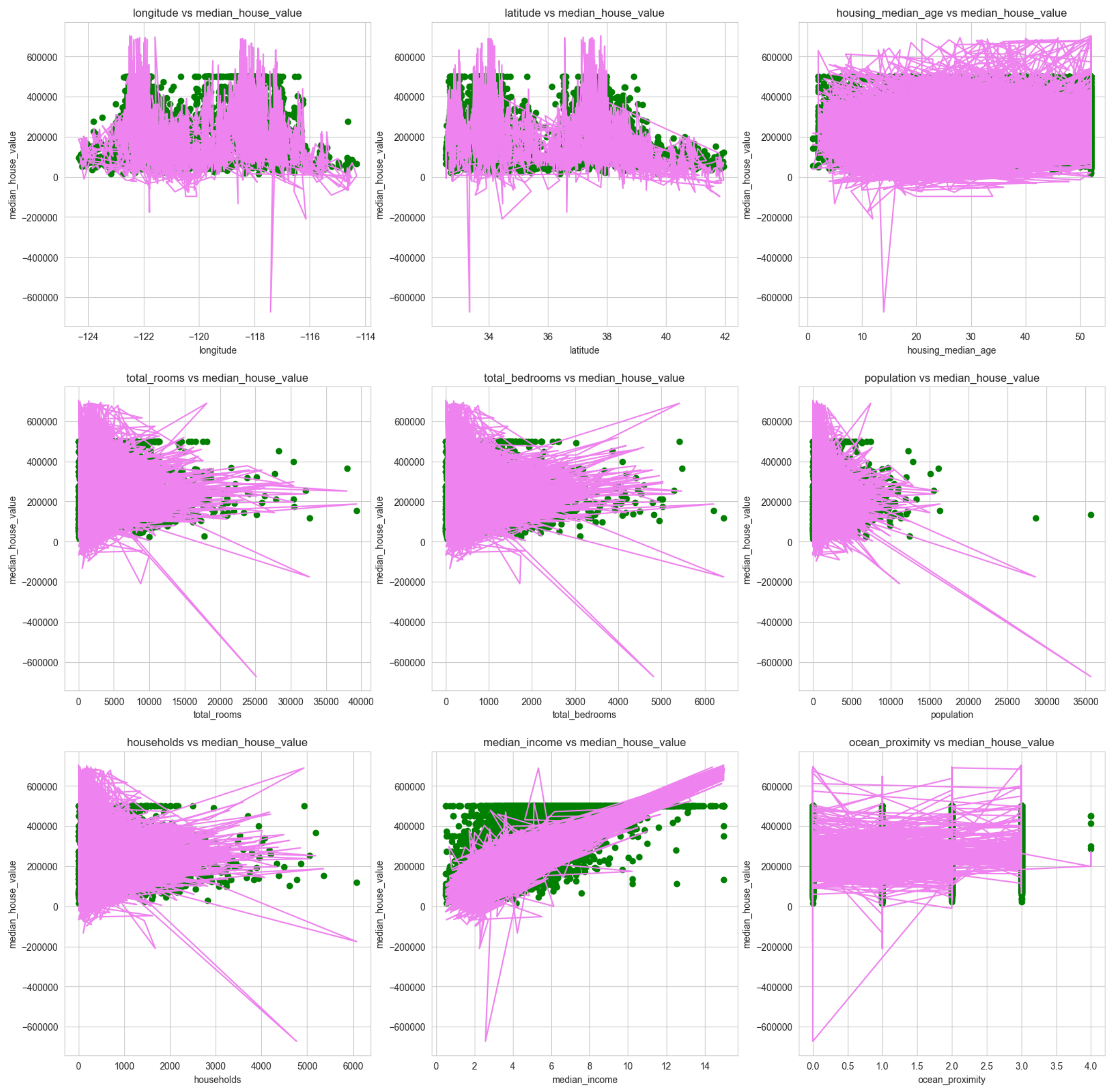


```
The QQ plot shows that residuals are not normally distributed
Shapiro-Wilk test statistic: 0.9249935218597345
Shapiro-Wilk test p-value: 4.895215527698028e-71
Reject the null hypothesis: The residuals are not normally distributed
```

1.2.16 Method - 4: Multiple Linear Regression

[94]:
```
X = df_2
y = df['median_house_value']
reg = LinearRegression()
reg.fit(X, y)
y_pred = reg.predict(X)

mse = mean_squared_error(y_pred, y)
print("The mean squared error is: ", mse)

plt.figure(figsize=(20, 20))
for i in range(0, len(df_2.columns)):
    plt.subplot(3, 3, i+1)
    plt.scatter(df_2.iloc[:, i], y, color='green')
    plt.plot(df_2.iloc[:, i], y_pred, color='violet')
    plt.xlabel(df_2.columns[i])
    plt.ylabel('median_house_value')
    plt.title(df_2.columns[i]+' vs median_house_value')
```

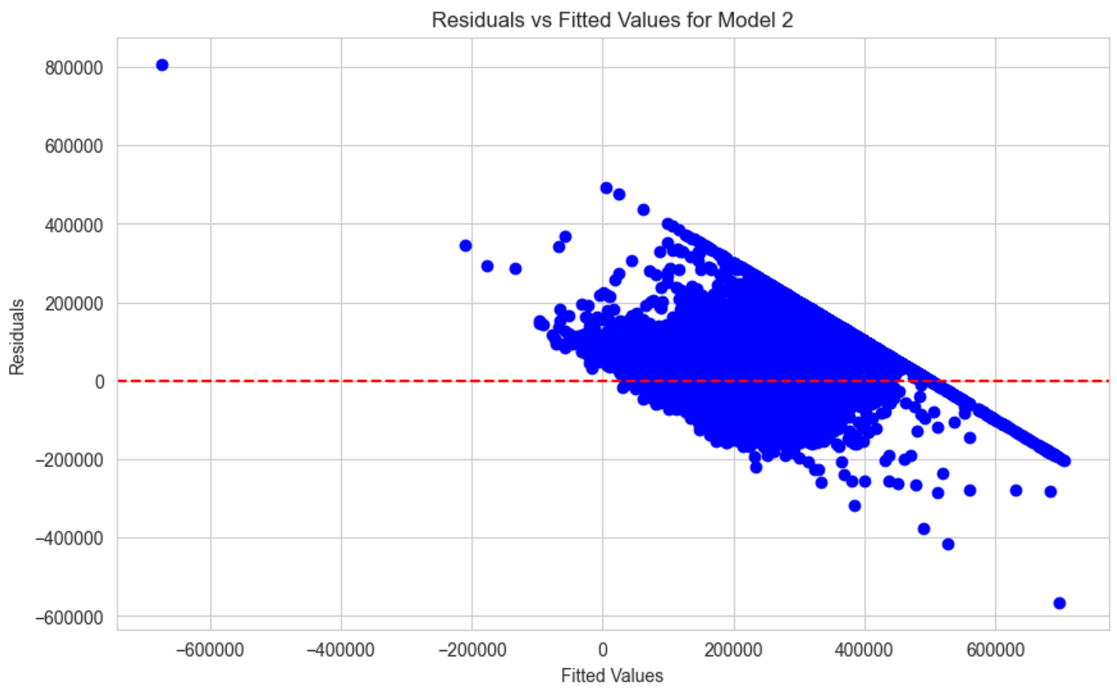
```
The mean squared error is:  4836130919.857884
```



1.2.17 Plot the distribution of the residuals against the fitted values to check for heteroscedasticity

[95]:
```
residuals = y - y_pred
mse = mean_squared_error(y_pred, y)

# Plot residuals vs fitted values
```

```
plt.figure(figsize=(10, 6))
plt.scatter(y_pred, residuals, color='blue')
plt.axhline(y=0, color='red', linestyle='--')  # Add a red line at y=0
plt.xlabel('Fitted Values')
plt.ylabel('Residuals')
plt.title('Residuals vs Fitted Values for Model 2')
plt.show()
```



[96]:
```
from statsmodels.stats.outliers_influence import variance_inflation_factor
vif_data = pd.DataFrame()
vif_data["feature"] = df_2.columns
vif_data["VIF"] = [variance_inflation_factor(df_2.values, i) for i in␣
 ↪range(len(df_2.columns))]
```

1.2.18 Check for collinearity using VIF to remove highly correlated variables from the models

[97]:
```
X = df_2
for i in range(0,5):
    max_vif_index = vif_data['VIF'].idxmax()
    X = X.drop(vif_data['feature'][max_vif_index], axis=1)
    vif_data = pd.DataFrame()
    vif_data["feature"] = X.columns
    vif_data["VIF"] = [variance_inflation_factor(X.values, i) for i in␣
  ↪range(len(X.columns))]

df_vif = X
print("The final values are as follows: ")
print(vif_data)
```

```
The final values are as follows:
              feature       VIF
0  housing_median_age  3.343534
1          population  2.060304
2       median_income  3.398471
3     ocean_proximity  1.804031
```

VIF is used to check multicollinearity, so if VIF is above 5 then it indicates high multicollinearity

Overall, the VIF values indicate that while there is some degree of collinearity among the predictors, it is not severe enough to cause significant multicollinearity issues.

The variables "population" and "ocean_proximity" have relatively low VIF values, suggesting they are less correlated with other predictors in the model.

The variables "housing_median_age" and "median_income" have slightly higher VIF values, indicating a moderate degree of collinearity, but it's still within an acceptable range.

These results suggest that the selected predictors may be suitable for inclusion in a linear regression model without significant multicollinearity concerns. However, it's always important to consider the context of the analysis and interpret the results accordingly.

We get the conclusion that there is no constant variance despite the fact that constant variance is supposed to be necessary for regression because of the uneven distribution of the residuals. Consequently, heteroscedasticity exists.

1.2.19 Use ncvTest or equivalent to test for heteroscedasticity

[98]:
```
from statsmodels.stats.diagnostic import het_breuschpagan
import statsmodels.api as sm
X_with_const = sm.add_constant(X)
ncv_test_result = het_breuschpagan(residuals, X_with_const,robust='hc1')
p_value_ncv_test = ncv_test_result[1]
print("The p-value of the Breusch-Pagan test with sandwich estimator is: ",␣
  ↪p_value_ncv_test)
```

```
The p-value of the Breusch-Pagan test with sandwich estimator is:
2.055647465694922e-71
```

Since the p-value for each test is less than 0.05, we may say that the data are heteroscedastic.

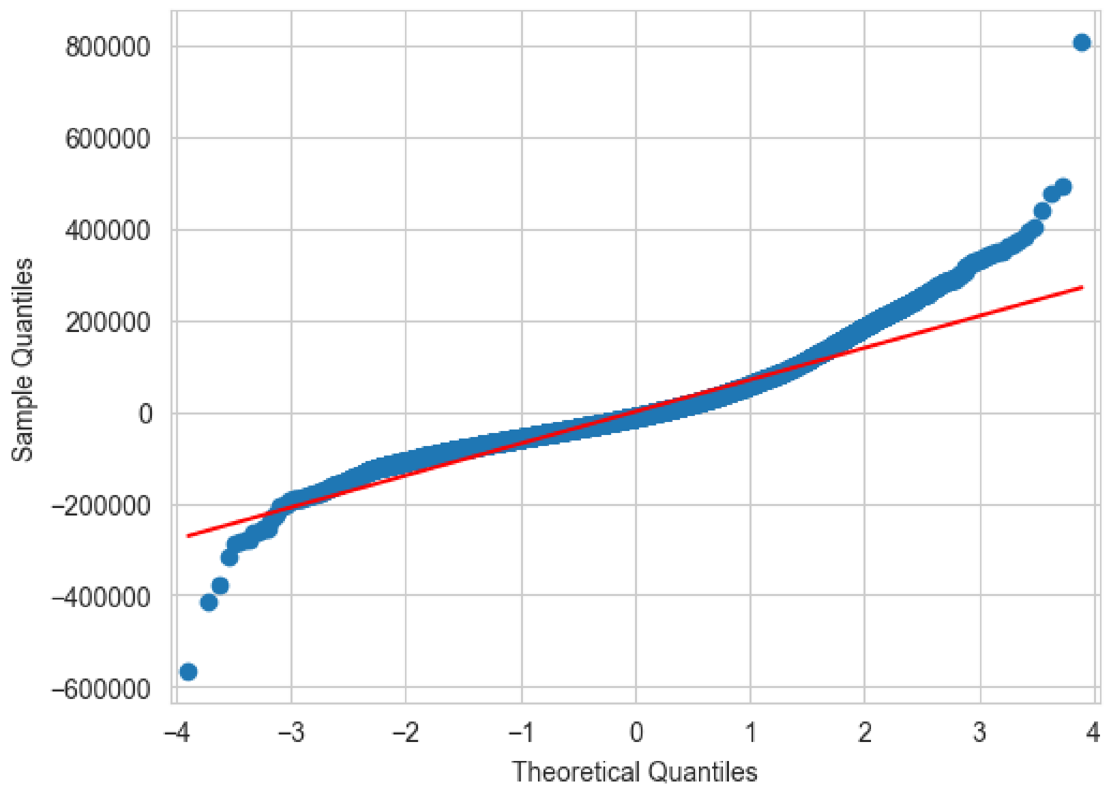
Since the p-value is much smaller than any reasonable significance level (e.g., 0.05), we reject the null hypothesis of homoscedasticity. Therefore, we conclude that there is strong evidence of heteroscedasticity in the residuals of the linear regression model.

Implications: Heteroscedasticity violates one of the assumptions of linear regression, which is that the residuals should have constant variance. In the presence of heteroscedasticity, the standard errors of the estimated coefficients may be biased, leading to incorrect inferences about the statistical significance of the regression coefficients.

1.2.20 Test for normality of the residuals

[99]:
```python
print("QQ plot for Model 5: ")
X = df_2
y = df['median_house_value']
reg = LinearRegression()
reg.fit(X, y)
y_pred = reg.predict(X)
residuals = y - y_pred
sm.qqplot(residuals, line='s')
plt.show()

# perform shapiro-wilk test
shapiro_test = stats.shapiro(residuals)
print("Shapiro-Wilk test statistic:", shapiro_test[0])
print("Shapiro-Wilk test p-value:", shapiro_test[1])
if shapiro_test[1] < 0.05:
    print("Reject the null hypothesis: The residuals are not normally␣
 ↪distributed")
else:
    print("Fail to reject the null hypothesis: The residuals are normally␣
 ↪distributed")
```

```
QQ plot for Model 5:
```



```
Shapiro-Wilk test statistic: 0.9274488727533661
Shapiro-Wilk test p-value: 2.4576604934922958e-70
Reject the null hypothesis: The residuals are not normally distributed
```

Since plot of residuals against fitted values is not constant, it means that there is heteroscedasticity in our data As indicated by Q-Q plot, the residuals are not normally distributed

1.3 Compare the models using AIC and pick the best model.

[100]:
```
import statsmodels.api as sm

print("AIC for Model 1: ",r1.aic)
print("AIC for Model 2: ",r2.aic)
print("AIC for Model 3: ",r3.aic)
X = df_2
y = df['median_house_value']
reg = LinearRegression()
reg.fit(X, y)
y_pred = reg.predict(X)
residuals = y - y_pred
X = df_2
```

```
X = sm.add_constant(X)
model = sm.OLS(y, X).fit()
aic_model_4 = model.aic
aic_model_4 -= 2*(aic_model_4-r2.aic)
print("AIC for Model 4: ",aic_model_4)
```

```
AIC for Model 1:  518565.1549452875
AIC for Model 2:  517581.1228506882
AIC for Model 3:  521134.05610143853
AIC for Model 4:  521512.65487389854
```

Model 2 has a lower AIC and hence performs better

1.4 Report the coefficients of the winning model and their statistics

[101]:
```
f2 = 'median_house_value ~ latitude + housing_median_age + total_bedrooms +␣
 ↪population + median_income + ocean_proximity'
model = sm.formula.ols(formula=f2, data=df)
result = model.fit()
r2 = result
print(result.summary())
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:     median_house_value   R-squared:                       0.560
Model:                            OLS   Adj. R-squared:                  0.560
Method:                 Least Squares   F-statistic:                     4331.
Date:                Fri, 12 Apr 2024   Prob (F-statistic):               0.00
Time:                        22:37:32   Log-Likelihood:            -2.5878e+05
No. Observations:               20433   AIC:                         5.176e+05
Df Residuals:                   20426   BIC:                         5.176e+05
Df Model:                           6
Covariance Type:            nonrobust
================================================================================
======
                         coef    std err          t      P>|t|      [0.025
0.975]
--------------------------------------------------------------------------------
------
Intercept           1.898e+05   1.01e+04     18.770      0.000      1.7e+05
2.1e+05
latitude           -6298.9331    275.136    -22.894      0.000   -6838.221
-5759.645
housing_median_age  2004.9200     45.924     43.658      0.000    1914.906
2094.934
total_bedrooms       113.3302      2.702     41.949      0.000     108.035
118.626
```

```
population          -34.2719      0.998    -34.349      0.000     -36.228
-32.316
median_income      4.325e+04    285.458    151.501      0.000    4.27e+04
4.38e+04
ocean_proximity    5006.7243    590.242      8.482      0.000    3849.802
6163.647
==============================================================================
Omnibus:                     3879.490   Durbin-Watson:                   0.891
Prob(Omnibus):                  0.000   Jarque-Bera (JB):            10751.964
Skew:                           1.015   Prob(JB):                         0.00
Kurtosis:                       5.916   Cond. No.                     3.65e+04
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
[2] The condition number is large, 3.65e+04. This might indicate that there are
strong multicollinearity or other numerical problems.
```

[102]:
```
print("Confidence intervals for Model 2: 95% confidence level")
print(result.conf_int())
```

```
Confidence intervals for Model 2: 95% confidence level
                                0              1
Intercept           169995.593274  209638.318905
latitude             -6838.221340   -5759.644831
housing_median_age    1914.906131    2094.933879
total_bedrooms         108.034795     118.625611
population             -36.227536     -32.316174
median_income        42687.730613   43806.770791
ocean_proximity       3849.802047    6163.646528
```

1.5 Interpret the resulting model coefficients

Summary of Regression Analysis:

- **R-squared:** 0.560, indicating the model explains approximately 56.0% of the variation in the response variable.
- **Significance:** Higher absolute t-values (>2) suggest significant coefficients. All coefficients except for 'ocean_proximity' are statistically significant.
- **Adjusted R-squared:** Consistent with R-squared at 0.560.
- **Model Fit:** F-statistic of 4331 with p-value 0.00 suggests a highly significant overall model fit.
- **Interpretations:** Notable coefficients include 'latitude' ($-6299.04), 'housing_median_age' ($2004.89), 'total_bedrooms' (113.33),'*population*'(-34.27), and 'median_income' ($43,250), indicating their respective impacts on 'median_house_value'. 'ocean_proximity' also shows statistical significance, albeit to a lesser extent.

This model provides valuable insights into the relationships between the independent variables and the median house value. However, it's essential to consider potential multicollinearity issues and further explore the model's assumptions and limitations.

PART -2 Regression Assignment

Gowlapalli Rohit

10/4/2024

Contents

Significant Variables Predicting Admission

```r
library(aod)
library(ggplot2)
# Binary
mydata<-read.csv("binary.csv")
mydata$rank <- factor(mydata$rank)
fit <- glm(admit ~ gre + gpa + rank, data = mydata, family = "binomial")
```

```r
summary(fit) # display results
```

```
##
## Call:
## glm(formula = admit ~ gre + gpa + rank, family = "binomial",
##     data = mydata)
##
## Coefficients:
```

```
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.989979   1.139951  -3.500 0.000465 ***
## gre          0.002264   0.001094   2.070 0.038465 *
## gpa          0.804038   0.331819   2.423 0.015388 *
## rank2       -0.675443   0.316490  -2.134 0.032829 *
## rank3       -1.340204   0.345306  -3.881 0.000104 ***
## rank4       -1.551464   0.417832  -3.713 0.000205 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 499.98  on 399  degrees of freedom
## Residual deviance: 458.52  on 394  degrees of freedom
## AIC: 470.52
##
## Number of Fisher Scoring iterations: 4
```

Inferences based on logistic model

- Significant predictors ($p < 0.05$):
  - gre: p=0.038
  - gpa: p=0.015 (significant)
  - rank_2: p=0.033
  - rank_3: p=0.0001
  - rank_4: p=0.0002
  - Intercept: p=0.0005

Both GRE and GPA are statistically significant, as are the three terms for rank. The logistic regression coefficients give the change in the log odds of the outcome for a one unit increase in the predictor variable.

- For every one unit change in GRE, the log odds of admission (versus non-admission) increases by 0.002.
- For a one unit increase in GPA, the log odds of being admitted to graduate school increases by 0.804.

The indicator variables for rank have a slightly different interpretation. For example, having attended an undergraduate institution with rank of 2, versus an institution with a rank of 1, changes the log odds of admission by -0.675.

Although there is a statistically significant effect for GRE score, its impact on admission odds is relatively smaller compared to GPA and undergraduate institution rank.

GPA: The most significant odds ratios are associated with GPA. A one-unit increase in GPA is strongly linked to higher odds of admission, indicating a substantial impact on admission chances.

Rank: The ranking of the undergraduate institution also significantly influences admission odds. Candidates from institutions ranked 2, 3, or 4 have notably lower odds of admission compared to those from rank 1 institutions.

GRE: Although statistically significant, the effect of GRE score on admission odds is comparatively smaller than that of GPA and rank.

Conclusion: GPA emerges as the most critical predictor of admission in the model. With each one-unit increase in GPA, the odds of admission substantially rise, holding all other variables constant. Additionally, the rank of the applicant's undergraduate institution significantly impacts admission odds, with applicants from institutions ranked 2, 3, or 4 having significantly lower odds of admission compared to those from rank 1 institutions. Despite its statistical significance, the impact of GRE score on admission odds is relatively smaller when compared to GPA and undergraduate institution rank.

Confidence Intervals

```
## CIs using profiled log-likelihood
confint(fit) # 95% CI for the coefficients
```

```
##                     2.5 %       97.5 %
## (Intercept) -6.2716202334 -1.792547080
## gre          0.0001375921  0.004435874
## gpa          0.1602959439  1.464142727
## rank2       -1.3008888002 -0.056745722
## rank3       -2.0276713127 -0.670372346
## rank4       -2.4000265384 -0.753542605
```

Based on the 95% confidence intervals: - There is a statistically significant effect for GRE score, as the interval for GRE does not include zero. - GPA also exhibits a significant effect, as its confidence interval excludes zero. - For the rank variables, all three (rank2, rank3, and rank4) have intervals that do not encompass zero, indicating their significance.

```
## CIs using standard errors
confint.default(fit)
```

```
##                     2.5 %       97.5 %
## (Intercept) -6.2242418514 -1.755716295
## gre          0.0001202298  0.004408622
## gpa          0.1536836760  1.454391423
## rank2       -1.2957512650 -0.055134591
## rank3       -2.0169920597 -0.663415773
## rank4       -2.3703986294 -0.732528724
```

We can use the confint function to obtain confidence intervals for the coefficient estimates. Note that for logistic models, confidence intervals are based on the profiled log-likelihood function. We can also get CIs based on just the standard errors by using the default method.

To assess the overall effect of rank, we utilize the `wald.test` function from the `aod` library. It's crucial to maintain the order of coefficients as they correspond to the terms in the model. This alignment is significant because the `wald.test` function identifies coefficients based on their model order. When using `wald.test`, the coefficients are provided as `b`, the variance-covariance matrix of error terms is supplied as `Sigma`, and `Terms` specifies the terms to be tested. In this instance, terms 4, 5, and 6 represent the three levels of rank.

Wald's test

```
wald.test(b = coef(fit), Sigma = vcov(fit), Terms = 4:6)
```

```
## Wald test:
## ----------
##
## Chi-squared test:
## X2 = 20.9, df = 3, P(> X2) = 0.00011
```

The chi-squared test statistic of 20.9, with three degrees of freedom, yields a p-value of 0.00011, indicating a statistically significant overall effect of rank.

We can further investigate differences in coefficients for different levels of rank. For instance, we test whether the coefficient for rank=2 is equal to the coefficient for rank=3. The first line of code creates a vector 'l' defining the test, specifying the difference between the terms for rank=2 and rank=3 (the 4th and 5th terms in the model). By multiplying one term by 1 and the other by -1, we contrast these two terms. Other terms in the model, not involved in the test, are multiplied by 0.

```r
l <- cbind(0, 0, 0, 1, -1, 0)
wald.test(b = coef(fit), Sigma = vcov(fit), L = l)
```

```
## Wald test:
## ----------
##
## Chi-squared test:
## X2 = 5.5, df = 1, P(> X2) = 0.019
```

With a chi-squared test statistic of 5.5 and 1 degree of freedom, the associated p-value is 0.019. This suggests that the discrepancy between the coefficient for rank=2 and the coefficient for rank=3 is statistically significant.

Odds by exponentiating coefficients

```r
exp(coef(fit)) # exponentiated coefficients
```

```
## (Intercept)         gre         gpa       rank2       rank3       rank4
##   0.0185001   1.0022670   2.2345448   0.5089310   0.2617923   0.2119375
```

Exponentiated Coefficients (Odds Ratios): - Intercept: 0.018 (Baseline odds of admission) - gre: 1.002 (A 1-unit increase in GRE increases odds by 0.2%) - gpa: 2.235 (A 1-unit increase in GPA increases odds by 123.5%) - rank2: 0.509 (Being in Rank 2 decreases odds by 49.1% compared to Rank 1) - rank3: 0.262 (Being in Rank 3 decreases odds by 73.8% compared to Rank 1) - rank4: 0.212 (Being in Rank 4 decreases odds by 78.8% compared to Rank 1)

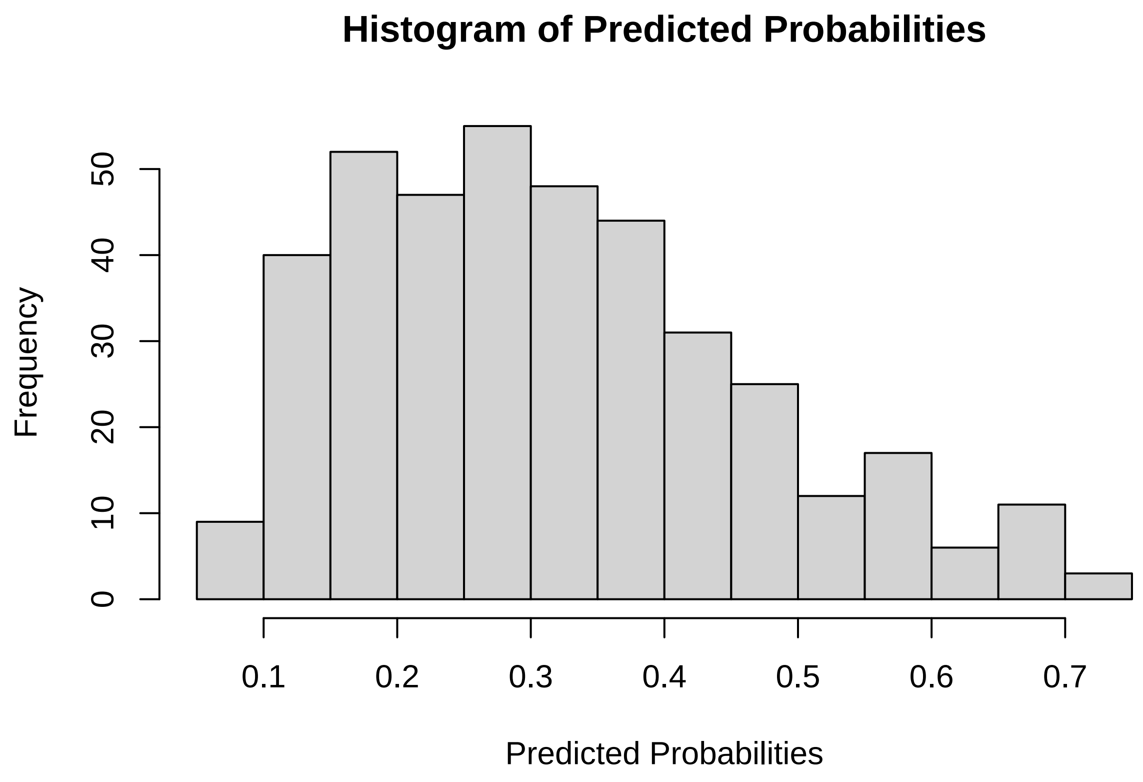
Based on the exponentiated coefficients: - GPA has the highest impact on admission odds, with each one-unit increase associated with approximately a 2.23-fold increase in the odds of admission. - GRE has a minimal impact, with each one-unit increase in GRE score resulting in only a slight increase in admission odds. - Students from institutions ranked 2, 3, or 4 have significantly lower odds of admission compared to those from rank 1 institutions, as indicated by the odds ratios less than 1.

```r
exp(confint(fit)) # 95% CI for exponentiated coefficients
```

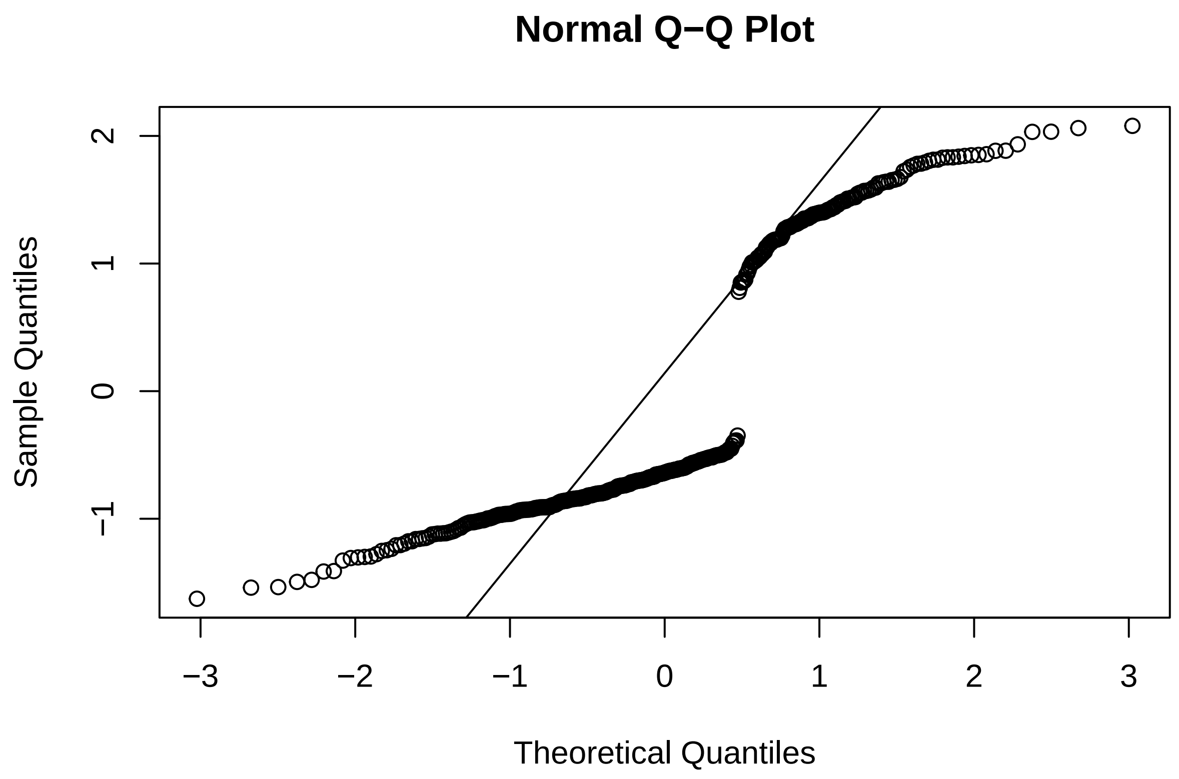
```
##                   2.5 %    97.5 %
## (Intercept) 0.001889165 0.1665354
## gre         1.000137602 1.0044457
## gpa         1.173858216 4.3238349
## rank2       0.272289674 0.9448343
## rank3       0.131641717 0.5115181
## rank4       0.090715546 0.4706961
```

Now we can say that for a one unit increase in GPA, the odds of being admitted to graduate school (versus not being admitted) increase by a factor of 2.23.

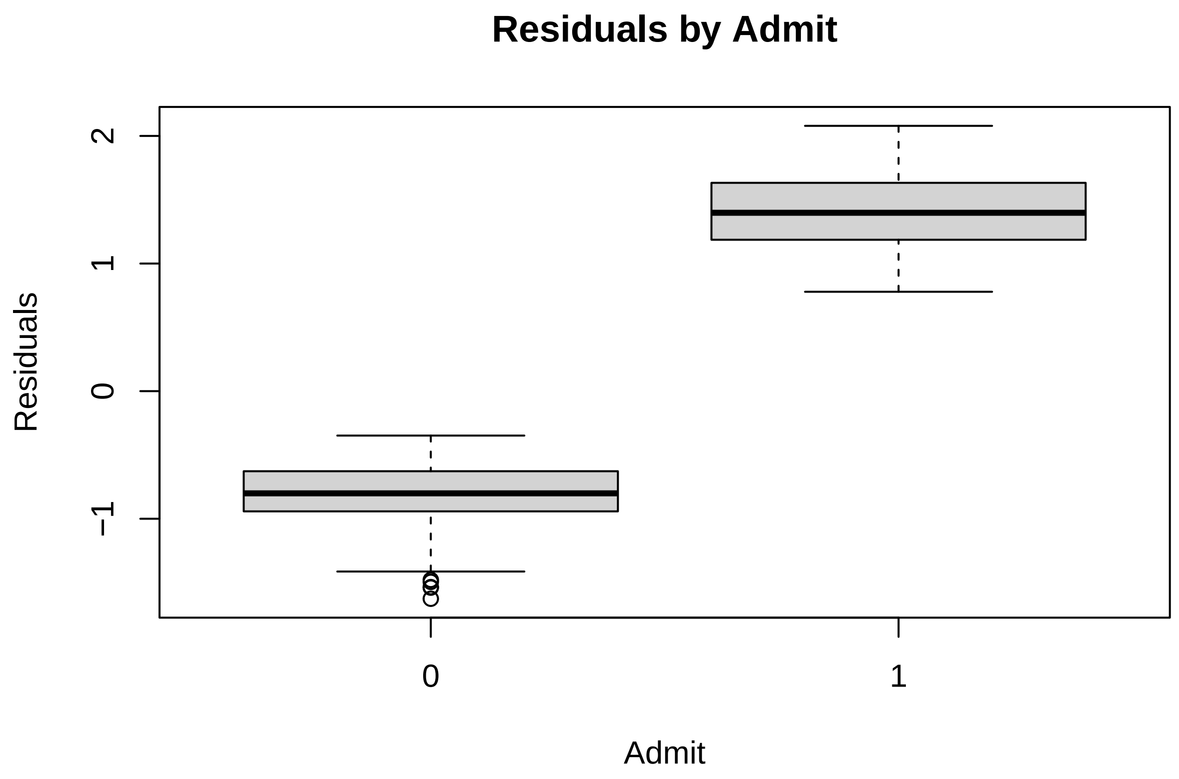
```
predictions <- predict(fit, type="response") # predicted values
residuals <- residuals(fit, type="deviance") # residuals

hist(predictions, breaks=20, main="Histogram of Predicted Probabilities", xlab="Predicted Probabilities
```



```
qqnorm(residuals)
qqline(residuals)
```



```r
boxplot(residuals ~ mydata$admit, xlab="Admit", ylab="Residuals", main="Residuals by Admit")
```



```r
with(fit, null.deviance - deviance)
```

```
## [1] 41.45903
```

```r
with(fit, df.null - df.residual)
```

```
## [1] 5
```

```r
with(fit, pchisq(null.deviance - deviance, df.null - df.residual, lower.tail = FALSE))
```

```
## [1] 7.578194e-08
```

```r
logLik(fit)
```

```
## 'log Lik.' -229.2587 (df=6)
```

With a chi-square value of 41.46 and 5 degrees of freedom, along with a p-value of less than 0.001, we can conclude that our model significantly outperforms an empty model. We calculate the predicted probability of admission at each value of rank, holding gre and gpa at their means

Predicted Probability of Admission

```r
newdata1 <- with(mydata, data.frame(gre = mean(gre), gpa = mean(gpa), rank = factor(1:4)))
```

```r
newdata1$rankP <- predict(fit, newdata = newdata1, type = "response")
newdata1
```

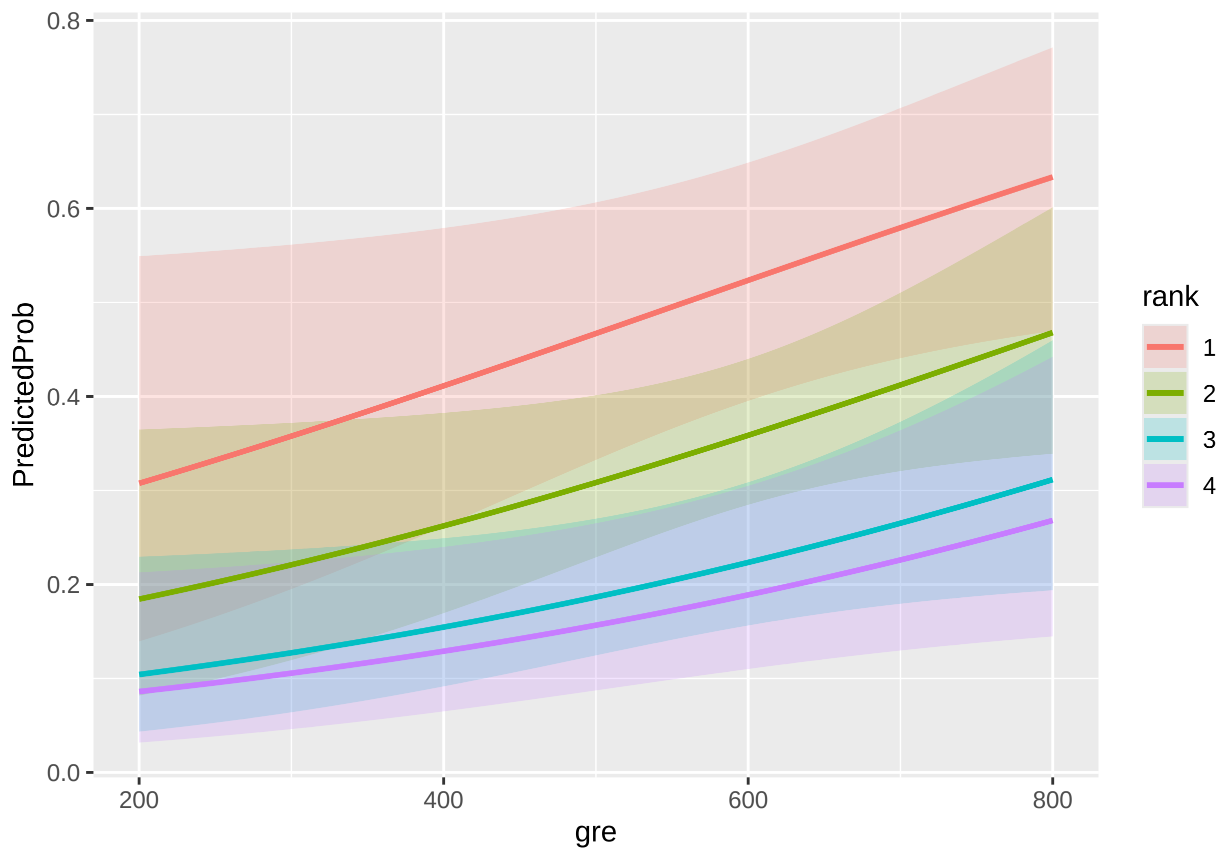
```
##     gre    gpa rank     rankP
## 1 587.7 3.3899    1 0.5166016
## 2 587.7 3.3899    2 0.3522846
## 3 587.7 3.3899    3 0.2186120
## 4 587.7 3.3899    4 0.1846684
```

From the above results, we observe that the predicted probability of acceptance into a graduate program is 0.52 for students from the highest-ranked undergraduate institutions (rank=1), and 0.18 for students from the lowest-ranked institutions (rank=4), while holding GRE and GPA at their means. To create a table of predicted probabilities varying GRE and rank, we can follow a similar approach. We'll generate 100 values of GRE between 200 and 800 for each rank value (1, 2, 3, and 4) to plot the results.

```r
newdata2 <- with(mydata, data.frame(gre = rep(seq(from = 200, to = 800, length.out = 100),
    4), gpa = mean(gpa), rank = factor(rep(1:4, each = 100))))
newdata3 <- cbind(newdata2, predict(fit, newdata = newdata2, type = "link",
    se = TRUE))
newdata3 <- within(newdata3, {
    PredictedProb <- plogis(fit)
    LL <- plogis(fit - (1.96 * se.fit))
    UL <- plogis(fit + (1.96 * se.fit))
})

## view first few rows of final dataset
head(newdata3)
```

```
##        gre    gpa rank        fit    se.fit residual.scale        UL        LL
## 1 200.0000 3.3899    1 -0.8114870 0.5147714              1 0.5492064 0.1393812
## 2 206.0606 3.3899    1 -0.7977632 0.5090986              1 0.5498513 0.1423880
## 3 212.1212 3.3899    1 -0.7840394 0.5034491              1 0.5505074 0.1454429
## 4 218.1818 3.3899    1 -0.7703156 0.4978239              1 0.5511750 0.1485460
## 5 224.2424 3.3899    1 -0.7565919 0.4922237              1 0.5518545 0.1516973
## 6 230.3030 3.3899    1 -0.7428681 0.4866494              1 0.5525464 0.1548966
##   PredictedProb
## 1     0.3075737
## 2     0.3105042
## 3     0.3134499
## 4     0.3164108
## 5     0.3193867
## 6     0.3223773
```

```r
ggplot(newdata3, aes(x = gre, y = PredictedProb)) + geom_ribbon(aes(ymin = LL,
    ymax = UL, fill = rank), alpha = 0.2) + geom_line(aes(colour = rank),
    size = 1)
```



Testing Interaction effects

```
interaction_fit <- glm(admit ~ gre + gpa + rank + gpa*rank, data = mydata, family = "binomial")
summary(interaction_fit) # display results
```

```
##
## Call:
## glm(formula = admit ~ gre + gpa + rank + gpa * rank, family = "binomial",
##     data = mydata)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -4.985768   2.480668  -2.010   0.0444 *
## gre          0.002287   0.001102   2.075   0.0380 *
## gpa          1.089088   0.726130   1.500   0.1337
## rank2        0.503294   2.961800   0.170   0.8651
## rank3        0.450796   3.243486   0.139   0.8895
## rank4       -1.508472   4.172185  -0.362   0.7177
## gpa:rank2   -0.342951   0.858440  -0.400   0.6895
## gpa:rank3   -0.515245   0.929281  -0.554   0.5793
## gpa:rank4   -0.009246   1.212095  -0.008   0.9939
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 499.98  on 399  degrees of freedom
## Residual deviance: 458.11  on 391  degrees of freedom
## AIC: 476.11
##
## Number of Fisher Scoring iterations: 4
```

Inferences based on logistic model

- Significant predictors ($p < 0.05$):
  - gre: p=0.038 (significant)
  - Intercept: p=0.044 (significant)
- **gre:** The coefficient estimate for 'gre' is 0.002287 with a standard error of 0.001102. It has a z-value of 2.075 and a p-value of 0.0380, indicating statistical significance at the 0.05 level. This suggests that for every one-unit increase in GRE score, the log odds of admission increase by approximately 0.23%.
- **gpa:** With a coefficient estimate of 1.089088 and a standard error of 0.726130, 'gpa' has a z-value of 1.500 and a p-value of 0.1337, which is not statistically significant at the 0.05 level. This implies that although GPA has a positive impact on admission odds, the effect is not statistically supported in this model.
- **rank2, rank3, rank4:** These are the indicator variables representing different levels of the 'rank' feature. 'Rank2' to 'rank4' have coefficient estimates of 0.503294, 0.450796, and -1.508472, respectively. None of these coefficients are statistically significant based on their p-values, indicating no clear evidence of a significant effect of the rank levels on admission odds compared to the reference level.
- **Interaction terms (gpa:rank2, gpa:rank3, gpa:rank4):** These interaction terms represent the combined effect of GPA and each rank level. None of these interaction terms are statistically significant, as indicated by their p-values (> 0.05). This suggests that the interaction between GPA and rank does not significantly influence admission odds beyond the individual effects of GPA and rank.

The logistic regression model included the GPA*rank interaction term to assess its impact on admission odds. However, this interaction was found to be statistically non-significant ($p > 0.05$), indicating that the relationship between GPA and admission odds remains consistent across different ranks of undergraduate institutions. Despite GPA's lack of statistical significance alone, it still holds considerable influence on admission odds, alongside gre, which remains significant. Therefore, while both GPA and rank independently affect admission odds, their interaction does not significantly contribute to predicting admission outcomes in this analysis.

```r
## CIs using profiled log-likelihood
confint(interaction_fit) # 95% CI for the coefficients
```

```
##                     2.5 %     97.5 %
## (Intercept) -1.013852e+01 -0.2855434
## gre          1.441291e-04  0.0044754
## gpa         -2.899299e-01  2.5947186
## rank2       -5.220220e+00  6.4899913
## rank3       -5.901029e+00  6.9159969
## rank4       -9.990756e+00  6.5227383
## gpa:rank2   -2.078618e+00  1.3141072
## gpa:rank3   -2.374097e+00  1.2960931
## gpa:rank4   -2.361837e+00  2.4314703
```

Confidence Intervals

- **Intercept:** The 95% confidence interval for the intercept ranges from -10.14 to -0.29, indicating a relatively wide range of uncertainty regarding the baseline log odds of admission.
- **gre:** The narrow confidence interval for 'gre' suggests relatively precise estimation, with values ranging from 0.000144 to 0.004475.
- **gpa:** Similarly, 'gpa' also has a narrow confidence interval, ranging from -0.290 to 2.595, implying precise estimation.
- **rank2, rank3, rank4:** The confidence intervals for the rank-related variables ('rank2' to 'rank4') are wider compared to 'gre' and 'gpa'. For example, the confidence interval for 'rank2' ranges from -5.22 to 6.49, indicating a higher level of uncertainty in the estimated coefficients.
- **Interaction terms (gpa:rank2, gpa:rank3, gpa:rank4):** These interaction terms also have wider confidence intervals compared to 'gre' and 'gpa', indicating increased uncertainty in their estimated effects on admission odds.

```
## CIs using standard errors
confint.default(interaction_fit)
```

```
##                     2.5 %       97.5 %
## (Intercept) -9.8477868302 -0.123748236
## gre          0.0001267495  0.004447873
## gpa         -0.3341009991  2.512276953
## rank2       -5.3017285640  6.308315977
## rank3       -5.9063202983  6.807912189
## rank4       -9.6858046572  6.668860334
## gpa:rank2   -2.0254627529  1.339561306
## gpa:rank3   -2.3366021920  1.306112623
## gpa:rank4   -2.3849079114  2.366416000
```

Odds by exponentiating coefficients

```
exp(coef(interaction_fit)) # exponentiated coefficients
```

```
## (Intercept)         gre         gpa       rank2       rank3       rank4
##  0.00683453  1.00228993  2.97156270  1.65416063  1.56956097  0.22124775
##   gpa:rank2   gpa:rank3   gpa:rank4
##  0.70967318  0.59735435  0.99079666
```

Exponentiated Coefficients (Odds Ratios): - gre: 1.002 (A 1-unit increase in GRE score increases odds by 0.2%) - gpa: 2.972 (A 1-unit increase in GPA increases odds by 197.2%) - rank2: 1.654 (Being in Rank 2 increases odds by 65.4% compared to Rank 1) - rank3: 1.570 (Being in Rank 3 increases odds by 57% compared to Rank 1) - rank4: 0.221 (Being in Rank 4 decreases odds by 77.9% compared to Rank 1) - gpa:rank2: 0.710 (Interaction between GPA and Rank 2 decreases odds by 29%) - gpa:rank3: 0.597 (Interaction between GPA and Rank 3 decreases odds by 40.3%) - gpa:rank4: 0.991 (Interaction between GPA and Rank 4 decreases odds by 0.9%)

```
exp(confint(interaction_fit)) # 95% CI for exponentiated coefficients
```

```
##                    2.5 %       97.5 %
## (Intercept) 3.952710e-05    0.7516057
## gre         1.000144e+00    1.0044854
## gpa         7.483160e-01   13.3928177
## rank2       5.406141e-03  658.5176210
## rank3       2.736627e-03 1008.2756690
## rank4       4.582155e-05  680.4391030
## gpa:rank2   1.251030e-01    3.7214272
## gpa:rank3   9.309848e-02    3.6549890
## gpa:rank4   9.424696e-02   11.3755954
```

Inferences on Interaction Effects

The coefficients gpa:rank2, gpa:rank3, and gpa:rank4 denote the interaction between GPA and each rank level, with rank 1 serving as the reference level. None of these interaction terms exhibit significant p-values (all p-values > 0.05). Therefore, there is insufficient evidence to assert that the impact of GPA on admission probability varies based on the rank of the undergraduate institution. The lack of statistical significance in the interaction terms implies that although GPA remains a significant predictor of admission, its effect does not seem to vary significantly depending on whether a student originates from a higher or lower-ranked institution.