# Stroke_and_Life_Expectancy

[1]:
```python
# Stroke and Life Expectancy Qualitative and Quantitative Analysis
### Author: Scott Eugley
### Date: 12/15/2023
```

[2]:
```python
# Load in datasets and libraries

import pandas as pd
import numpy as np
import os
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression, LinearRegression, Lasso,␣
↪Ridge, LassoCV, RidgeCV
from sklearn.metrics import confusion_matrix, mean_squared_error,␣
↪accuracy_score, mean_absolute_error, roc_curve,␣
↪roc_auc_score,precision_recall_curve, auc
from sklearn.decomposition import PCA
from sklearn.cross_decomposition import PLSRegression
from sklearn.pipeline import Pipeline
import statsmodels.api as sm
from sklearn.neighbors import KNeighborsClassifier
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis,␣
↪QuadraticDiscriminantAnalysis
from sklearn.tree import DecisionTreeClassifier, plot_tree, DecisionTreeRegressor
from sklearn.ensemble import BaggingRegressor, RandomForestClassifier,␣
↪GradientBoostingRegressor, RandomForestRegressor
from sklearn.model_selection import GridSearchCV, KFold
from scipy.stats import zscore
import itertools
from sklearn.preprocessing import StandardScaler
from sklearn.cross_decomposition import PLSRegression
from sklearn.model_selection import cross_val_score
from sklearn.tree import export_text
import math
from matplotlib.colors import ListedColormap
from sklearn.neighbors import KNeighborsClassifier
```

```python
# Set working directory
directory_path = '/Users/seugley/Desktop/GitHub/Machine_Learning/
↪Stroke_and_Life_Expectancy'
os.chdir(directory_path)

# Load the Stroke.csv dataset (Qualitative)
stroke = pd.read_csv('Stroke.csv')

# Use the features of the dataset to build models for predicting whether an␣
↪individual is at high risk of having a stroke or not

# Load the Life Expectancy.csv dataset (Quantitative)
life_expectancy = pd.read_csv('Life Expectancy.csv')

# Use the features of the dataset to build models for predicting life expectancy
```

[3]:
```python
# Qualitative Analysis

# Stroke Data Dictionary

# id: Unique identifier
# gender: Male = 0, Female = 1
# age: Age of the patient
# hypertension: 0 if the patient doesn't have hypertension, 1 if the patient has␣
↪hypertension
# heart_disease: 0 if the patient doesn't have any heart diseases, 1 if the␣
↪patient has a heart disease
# ever_married: Yes = 1 and No = 0
# work_type: Never_worked = 0, Self-employed = 1, Private = 2, Govt_job = 3,␣
↪children = 4
# Residence_type: Rural = 0 and Urban = 1
# avg_glucose_level: average glucose level in blood
# bmi: body mass index
# smoking_status: never smoked = 0, smokes = 1, formerly smoked = 2
# stroke: 1 if the patient had a stroke or 0 if not
```

[4]:
```python
# Clean Stroke Dataset

# Drop null values
stroke_cleaned = stroke.dropna()

# Drop 'Unknown' values in the 'smoking_status' column
stroke_cleaned = stroke_cleaned[stroke_cleaned['smoking_status'] != 'Unknown']

# Drop the 'id' column
stroke_cleaned = stroke_cleaned.drop('id', axis=1)
```

```python
# Count the number of 'Other' ocurrences in the 'gender' column
other_gender_count = stroke_cleaned['gender'].value_counts().get('Other', 0)

print(f"Number of 'Other' in gender column: {other_gender_count}")

# Since there is only 1 'Other' value in the gender column, I will remove this␣
↪value to avoid unneccessary encoding
stroke_cleaned = stroke_cleaned[stroke_cleaned['gender'] != 'Other']

# Reset index after dropping rows
stroke_cleaned = stroke_cleaned.reset_index(drop=True)
```

```
Number of 'Other' in gender column: 1
```

[5]:

```python
# Variable Encoding

# Encoding for the 'gender' column
gender_mapping = {'Male': 0, 'Female': 1}
stroke_cleaned['gender'] = stroke_cleaned['gender'].replace(gender_mapping)

# Encoding for the 'ever_married' column
married_mapping = {'Yes': 1, 'No': 0}
stroke_cleaned['ever_married'] = stroke_cleaned['ever_married'].
↪replace(married_mapping)

# Encoding for the 'work_type' column
work_mapping = {'children': 4, 'Govt_job': 3, 'Never_worked': 0, 'Private': 2,␣
↪'Self-employed': 1}
stroke_cleaned['work_type'] = stroke_cleaned['work_type'].replace(work_mapping)

# Encoding for the 'Residence_type' column
residence_mapping = {'Rural': 0, 'Urban': 1}
stroke_cleaned['Residence_type'] = stroke_cleaned['Residence_type'].
↪replace(residence_mapping)

# Encoding for the 'smoking_status' column
smoking_mapping = {'formerly smoked': 2, 'never smoked': 0, 'smokes': 1}
stroke_cleaned['smoking_status'] = stroke_cleaned['smoking_status'].
↪replace(smoking_mapping)

# Rename cleaned dataset to working dataframe for modeling
stroke_df = stroke_cleaned
```

[6]:

```python
# Use bootstrapping on dataset to increase observations. Total observations in␣
↪original dataset = 3425. However, the original cleaned dataset only includes␣
↪206 individuals with heart disease, 68 individuals that are a stay-at-home␣
↪parent as a job, 14 individuals who never worked, and 180 individuals who had␣
↪a stroke. I'd like to create more data-points in these variables to make them␣
↪more robust for modeling

def bootstrap_category(df, column, category, target_size):
    category_data = df[df[column] == category]
    replication_factor = int(np.ceil(target_size / len(category_data)))
    bootstrapped_data = pd.concat([category_data] * replication_factor,␣
↪ignore_index=True)
    bootstrapped_data = bootstrapped_data.head(target_size)

    return bootstrapped_data

# Set target sizes for each category
target_size_heart_disease = 500
target_size_stay_at_home = 500
target_size_never_worked = 500
target_size_stroke = 500

# Apply bootstrapping to each category
bootstrapped_heart_disease = bootstrap_category(stroke_df, 'heart_disease', 1,␣
↪target_size_heart_disease)
bootstrapped_stay_at_home = bootstrap_category(stroke_df, 'work_type', 0,␣
↪target_size_stay_at_home)
bootstrapped_never_worked = bootstrap_category(stroke_df, 'work_type', 4,␣
↪target_size_never_worked)
bootstrapped_stroke = bootstrap_category(stroke_df, 'stroke', 1,␣
↪target_size_stroke)

# Concatenate the bootstrapped data with the original cleaned data
bootstrapped_df = pd.concat([stroke_df, bootstrapped_heart_disease,␣
↪bootstrapped_stay_at_home, bootstrapped_never_worked, bootstrapped_stroke],␣
↪ignore_index=True)

# Shuffle the dataset to mix original and bootstrapped data
bootstrapped_df = bootstrapped_df.sample(frac=1, random_state=42).
↪reset_index(drop=True)

# Rename bootstrapped data to working dataset for modeling
stroke_df = bootstrapped_df
```

[7]:
```python
# Stroke Data Summary
```

```
# Total number of observations
num_observations = stroke_df.shape[0]
print(f"Total Number of Observations in the Dataset: {num_observations}")

# Print the number of males and females in the dataset
gender_counts = stroke_df['gender'].value_counts()

num_males = gender_counts.get(0, 0)
num_females = gender_counts.get(1, 0)

print(f"Number of males in the dataset: {num_males}")
print(f"Number of females in the dataset: {num_females}")

# Print the number of individuals with and without hypertension
hypertension_counts = stroke_df['hypertension'].value_counts()

num_without_hypertension = hypertension_counts.get(0, 0)
num_with_hypertension = hypertension_counts.get(1, 0)

print(f"Number of Individuals With Hypertension: {num_with_hypertension}")
print(f"Number of Individuals Without Hypertension: {num_without_hypertension}")

# Print the number of individuals with and without heart disease
heart_disease_counts = stroke_df['heart_disease'].value_counts()

num_without_heart_disease = heart_disease_counts.get(0, 0)
num_with_heart_disease = heart_disease_counts.get(1, 0)

print(f"Number of Individuals With Heart Disease: {num_with_heart_disease}")
print(f"Number of Individuals Without Heart Disease:␣
↪{num_without_heart_disease}")

# Print the number of individuals who are and are not ever married
ever_married_counts = stroke_df['ever_married'].value_counts()

num_not_ever_married = ever_married_counts.get(0, 0)
num_ever_married = ever_married_counts.get(1, 0)

print(f"Number of Individuals Ever Married: {num_ever_married}")
print(f"Number of Individuals Not Ever Married: {num_not_ever_married}")

# Print the number of individuals in each work type
work_type_counts = stroke_df['work_type'].value_counts()

print("Number of Individuals in Each Work Type (Never_worked = 0, Self-employed␣
↪= 1, Private = 2, Govt_job = 3, children = 4):")
print(work_type_counts)
```

```
# Print the number of individuals in each residence type
residence_type_counts = stroke_df['Residence_type'].value_counts()

print("Number of Individuals in Each Residence Type (0 = Rural 1 = Urban):")
print(residence_type_counts)

# Print the number of individuals in each smoking status category
smoking_status_counts = stroke_df['smoking_status'].value_counts()

print("Number of Individuals in Each Smoking Status Category (never smoked = 0,␣
 ↪smokes = 1, formerly smoked = 2):")
print(smoking_status_counts)

# Print the number of individuals who have and have not had a stroke
stroke_counts = stroke_df['stroke'].value_counts()

num_no_stroke = stroke_counts.get(0, 0)
num_yes_stroke = stroke_counts.get(1, 0)

print(f"Number of Individuals Who Have Had a Stroke: {num_yes_stroke}")
print(f"Number of Individuals Who Have Not Had a Stroke: {num_no_stroke}")

# Numerical summary of the age, avg_glucose_level, and bmi variables
selected_columns = ['age', 'avg_glucose_level', 'bmi']
stroke_numerical_summary = stroke_df[selected_columns].describe()

# Print the summary
print(stroke_numerical_summary)
```

```
Total Number of Observations in the Dataset: 5425
Number of males in the dataset: 2271
Number of females in the dataset: 3154
Number of Individuals With Hypertension: 703
Number of Individuals Without Hypertension: 4722
Number of Individuals With Heart Disease: 807
Number of Individuals Without Heart Disease: 4618
Number of Individuals Ever Married: 3488
Number of Individuals Not Ever Married: 1937
Number of Individuals in Each Work Type (Never_worked = 0, Self-employed = 1,
Private = 2, Govt_job = 3, children = 4):
2    2812
1     885
3     646
4     568
0     514
Name: work_type, dtype: int64
Number of Individuals in Each Residence Type (0 = Rural 1 = Urban):
```

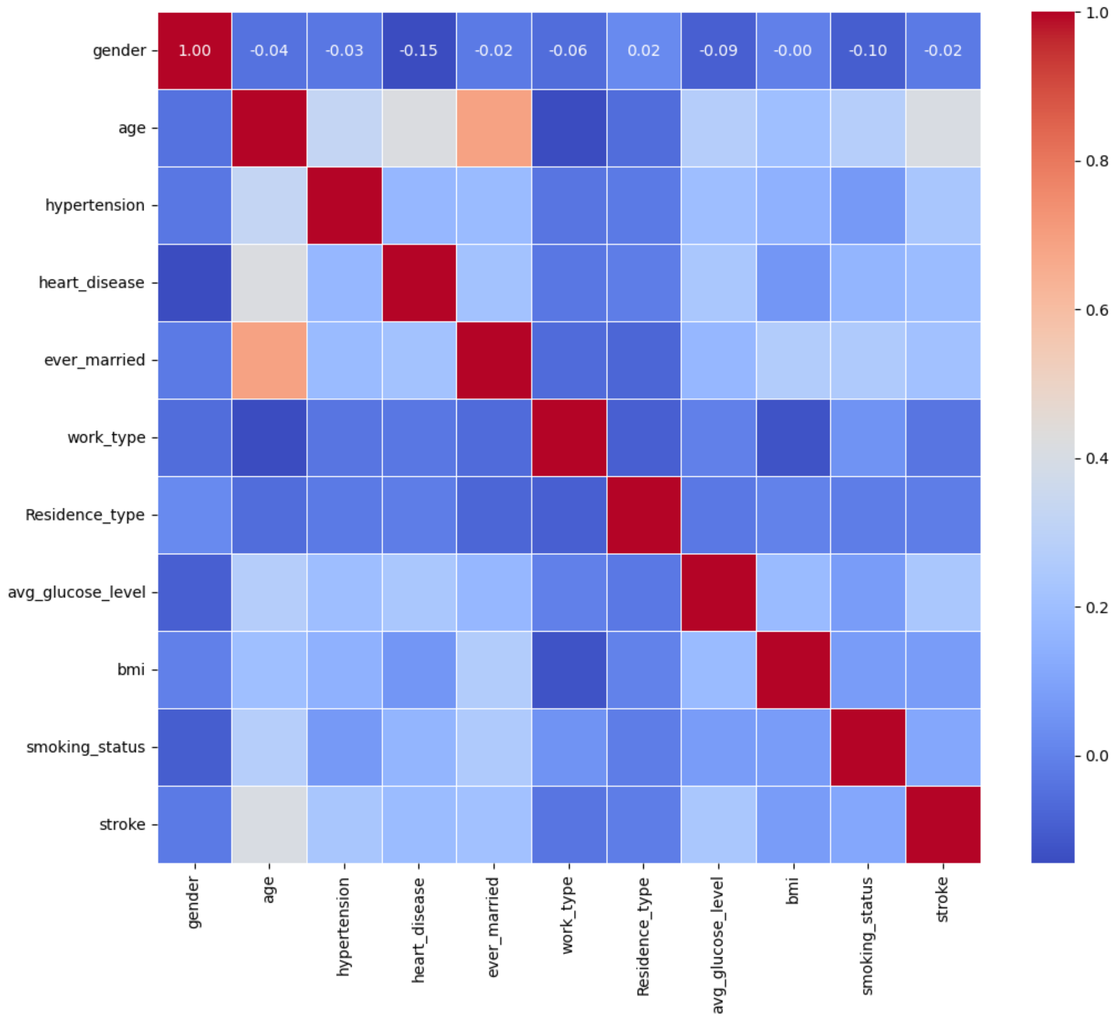
```
1    2929
0    2496
Name: Residence_type, dtype: int64
Number of Individuals in Each Smoking Status Category (never smoked = 0, smokes
= 1, formerly smoked = 2):
0    3175
2    1255
1     995
Name: smoking_status, dtype: int64
Number of Individuals Who Have Had a Stroke: 788
Number of Individuals Who Have Not Had a Stroke: 4637
               age  avg_glucose_level          bmi
count  5425.000000        5425.000000  5425.000000
mean     45.950783         112.148151    29.417954
std      22.954625          50.053917     7.262230
min      10.000000          55.120000    11.500000
25%      23.000000          78.080000    24.300000
50%      49.000000          94.040000    28.300000
75%      66.000000         125.260000    33.100000
max      82.000000         271.740000    92.000000
```

[8]:
```
# Correlation matrix and heatmap

# Create correlation matrix
correlation_matrix = stroke_df.corr()
print(correlation_matrix)

# Create a heatmap
plt.figure(figsize=(12, 10))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', fmt='.2f',␣
 ↪linewidths=0.5)
plt.show()
```

```
                     gender       age  hypertension  heart_disease  \
gender             1.000000 -0.043396     -0.031943      -0.145087
age               -0.043396  1.000000      0.327786       0.414061
hypertension      -0.031943  0.327786      1.000000       0.170318
heart_disease     -0.145087  0.414061      0.170318       1.000000
ever_married      -0.023288  0.691312      0.182147       0.214217
work_type         -0.056405 -0.143185     -0.035936      -0.030171
Residence_type     0.022589 -0.059843     -0.023737      -0.011127
avg_glucose_level -0.093555  0.273409      0.195963       0.238641
bmi               -0.004823  0.203616      0.146646       0.059430
smoking_status    -0.100098  0.279620      0.068522       0.159247
stroke            -0.021346  0.406154      0.235033       0.187853

                   ever_married  work_type  Residence_type  avg_glucose_level  \
gender                -0.023288  -0.056405        0.022589          -0.093555
```

| | | | | |
|---|---|---|---|---|
| age | 0.691312 | -0.143185 | -0.059843 | 0.273409 |
| hypertension | 0.182147 | -0.035936 | -0.023737 | 0.195963 |
| heart_disease | 0.214217 | -0.030171 | -0.011127 | 0.238641 |
| ever_married | 1.000000 | -0.061015 | -0.075800 | 0.171327 |
| work_type | -0.061015 | 1.000000 | -0.094787 | -0.004901 |
| Residence_type | -0.075800 | -0.094787 | 1.000000 | -0.025851 |
| avg_glucose_level | 0.171327 | -0.004901 | -0.025851 | 1.000000 |
| bmi | 0.265702 | -0.126559 | 0.000153 | 0.185230 |
| smoking_status | 0.256090 | 0.049641 | -0.012178 | 0.076596 |
| stroke | 0.212209 | -0.037247 | -0.015164 | 0.239070 |

| | bmi | smoking_status | stroke |
|---|---|---|---|
| gender | -0.004823 | -0.100098 | -0.021346 |
| age | 0.203616 | 0.279620 | 0.406154 |
| hypertension | 0.146646 | 0.068522 | 0.235033 |
| heart_disease | 0.059430 | 0.159247 | 0.187853 |
| ever_married | 0.265702 | 0.256090 | 0.212209 |
| work_type | -0.126559 | 0.049641 | -0.037247 |
| Residence_type | 0.000153 | -0.012178 | -0.015164 |
| avg_glucose_level | 0.185230 | 0.076596 | 0.239070 |
| bmi | 1.000000 | 0.074657 | 0.074330 |
| smoking_status | 0.074657 | 1.000000 | 0.113181 |
| stroke | 0.074330 | 0.113181 | 1.000000 |




[9]:
```
# Collinearity Evaluation

# Set correlation threshold
correlation_threshold = 0.65

# Find highly correlated feature pairs
highly_correlated_pairs = []

for i in range(len(correlation_matrix.columns)):
    for j in range(i+1, len(correlation_matrix.columns)):
        if abs(correlation_matrix.iloc[i, j]) > correlation_threshold:
            pair = (correlation_matrix.columns[i], correlation_matrix.
↪columns[j], correlation_matrix.iloc[i, j])
            highly_correlated_pairs.append(pair)
```

```
# Print highly correlated pairs excluding the target (stroke)
target_variable = 'stroke'
for pair in highly_correlated_pairs:
    if target_variable not in pair:
        print(f"Highly Correlated Pairs: {pair}")

# It appears as though age and ever_married are highly correlated, which makes␣
↪sense as people tend to have been or are married at older ages. This being the␣
↪only highly correlated pair is a good sign that there aren't issues with␣
↪collinearity
```

```
Highly Correlated Pairs: ('age', 'ever_married', 0.6913119458910274)
```

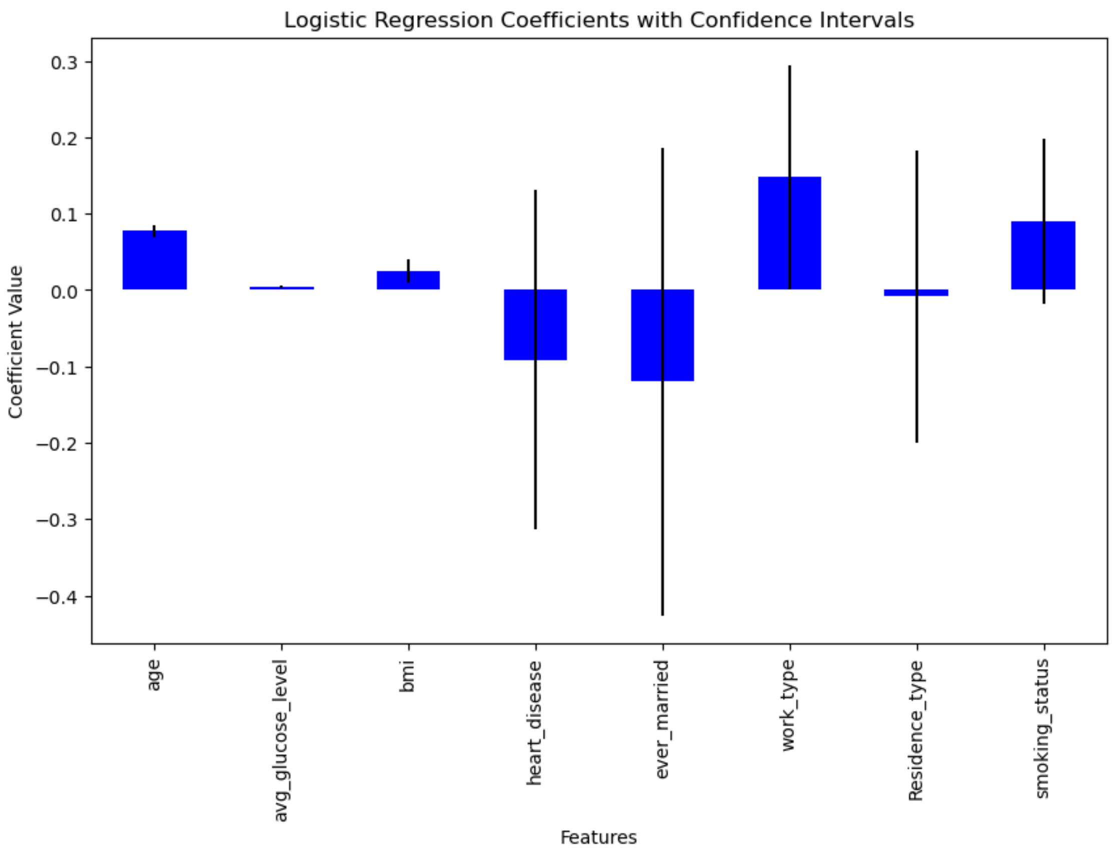
[10]:

```
# Logistic Regression Model

# Define features and target variable
features = ['age', 'avg_glucose_level', 'bmi', 'heart_disease', 'ever_married',␣
↪'work_type', 'Residence_type', 'smoking_status']
target = 'stroke'

# Separate features and target variable
X = stroke_df[features]
y = stroke_df[target]

# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state=42)

# Fit the logistic regression model
logreg_model = LogisticRegression(max_iter=1000)
logreg_model.fit(X_train, y_train)

# Predictions on the test set
y_pred = logreg_model.predict(X_test)

# Confusion Matrix
conf_matrix = confusion_matrix(y_test, y_pred)
conf_matrix_labels = pd.DataFrame(conf_matrix, index=['Actual 0', 'Actual 1'],␣
↪columns=['Predicted 0', 'Predicted 1'])
print("Confusion Matrix:")
print(conf_matrix_labels)

# Accuracy Score
accuracy = accuracy_score(y_test, y_pred)
print(f"\nAccuracy Score: {accuracy}")

# Coefficients and p-values
```

```
X_train_with_intercept = sm.add_constant(X_train)
logit_model = sm.Logit(y_train, X_train_with_intercept)
result = logit_model.fit()
print(result.summary())

# The most significant predictors using this model appear to be age,␣
↪avg_glucose_level, bmi, and work_type based on their p-values < 0.05

# Plot coefficients excluding 'const'
plt.figure(figsize=(10, 6))
ci = result.conf_int().drop('const')
coef = result.params.drop('const')
coef.plot(kind='bar', yerr=(ci[1]-ci[0])/2, color='blue')
plt.title('Logistic Regression Coefficients with Confidence Intervals')
plt.xlabel('Features')
plt.ylabel('Coefficient Value')
plt.show()
```

```
Confusion Matrix:
          Predicted 0  Predicted 1
Actual 0          901           33
Actual 1          124           27

Accuracy Score: 0.8552995391705069
Optimization terminated successfully.
         Current function value: 0.308275
         Iterations 8
                           Logit Regression Results
==============================================================================
Dep. Variable:                 stroke   No. Observations:                 4340
Model:                          Logit   Df Residuals:                     4331
Method:                           MLE   Df Model:                            8
Date:                Sat, 17 Aug 2024   Pseudo R-squ.:                  0.2609
Time:                        21:36:20   Log-Likelihood:                -1337.9
converged:                       True   LL-Null:                       -1810.1
Covariance Type:            nonrobust   LLR p-value:                 1.516e-198
================================================================================
=====
                        coef    std err          z      P>|z|      [0.025
0.975]
--------------------------------------------------------------------------------
-----
const                -7.8293      0.431    -18.148      0.000      -8.675
-6.984
age                   0.0778      0.004     19.776      0.000       0.070
0.086
avg_glucose_level     0.0047      0.001      5.628      0.000       0.003
0.006
```

```
bmi                      0.0248      0.008      3.159      0.002       0.009
0.040
heart_disease           -0.0918      0.113     -0.809      0.419      -0.314
0.131
ever_married            -0.1196      0.156     -0.764      0.445      -0.426
0.187
work_type                0.1478      0.075      1.971      0.049       0.001
0.295
Residence_type          -0.0080      0.098     -0.082      0.935      -0.199
0.183
smoking_status           0.0900      0.055      1.624      0.104      -0.019
0.199
================================================================================
=====
```




[11]:
```
# LDA, QDA, and KNN Models

# Re-define features including only the significant variables (age,␣
↪avg_glucose_level, bmi, and work_type)
features = ['age', 'avg_glucose_level', 'bmi','work_type']
```

```python
target = 'stroke'

# Separate features and target variable
X = stroke_df[features]
y = stroke_df[target]

# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state=42)


# Create function for model evaluation and accuracy score
def evaluate_model(model, model_name):

    # Fit the model
    model.fit(X_train, y_train)

    # Predictions on the test set
    y_pred = model.predict(X_test)

    # Confusion Matrix
    conf_matrix = confusion_matrix(y_test, y_pred)
    conf_matrix_labels = pd.DataFrame(conf_matrix, index=['Actual 0', 'Actual␣
↪1'], columns=['Predicted 0', 'Predicted 1'])
    print(f"\nConfusion Matrix for {model_name}:")
    print(conf_matrix_labels)

    # Accuracy Score
    accuracy = accuracy_score(y_test, y_pred)
    print(f"\nAccuracy Score for {model_name}: {accuracy}")

# LDA
lda_model = LinearDiscriminantAnalysis()
evaluate_model(lda_model, "LDA")

# QDA
qda_model = QuadraticDiscriminantAnalysis()
evaluate_model(qda_model, "QDA")

# KNN (K=1)
knn_model = KNeighborsClassifier(n_neighbors=1)
evaluate_model(knn_model, "KNN (K=1)")

# KNN (K=10)
knn_model = KNeighborsClassifier(n_neighbors=10)
evaluate_model(knn_model, "KNN (K=10)")
```

```python
# KNN (K=100)
knn_model = KNeighborsClassifier(n_neighbors=100)
evaluate_model(knn_model, "KNN (K=100)")

# Display plots
plt.show()
```

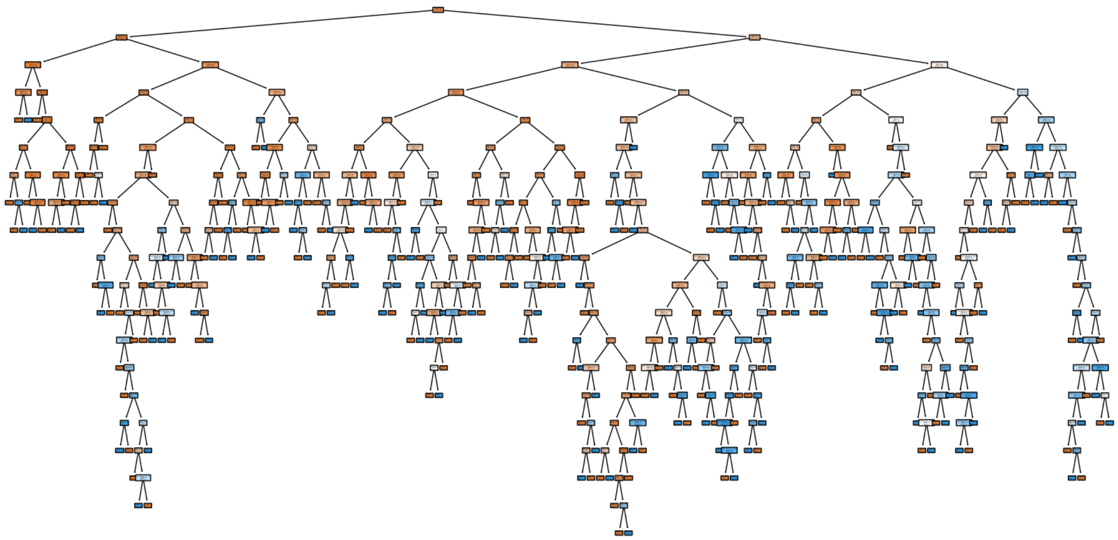
```
Confusion Matrix for LDA:
          Predicted 0  Predicted 1
Actual 0          902           32
Actual 1          118           33

Accuracy Score for LDA: 0.8617511520737328

Confusion Matrix for QDA:
          Predicted 0  Predicted 1
Actual 0          810          124
Actual 1           60           91

Accuracy Score for QDA: 0.8304147465437788

Confusion Matrix for KNN (K=1):
          Predicted 0  Predicted 1
Actual 0          908           26
Actual 1            0          151

Accuracy Score for KNN (K=1): 0.976036866359447

Confusion Matrix for KNN (K=10):
          Predicted 0  Predicted 1
Actual 0          888           46
Actual 1           92           59

Accuracy Score for KNN (K=10): 0.8728110599078341

Confusion Matrix for KNN (K=100):
          Predicted 0  Predicted 1
Actual 0          919           15
Actual 1          141           10

Accuracy Score for KNN (K=100): 0.8562211981566821
```

[12]:
```python
# Classification Tree Model

# Initialize tree model
tree_model = DecisionTreeClassifier(random_state=42)
```

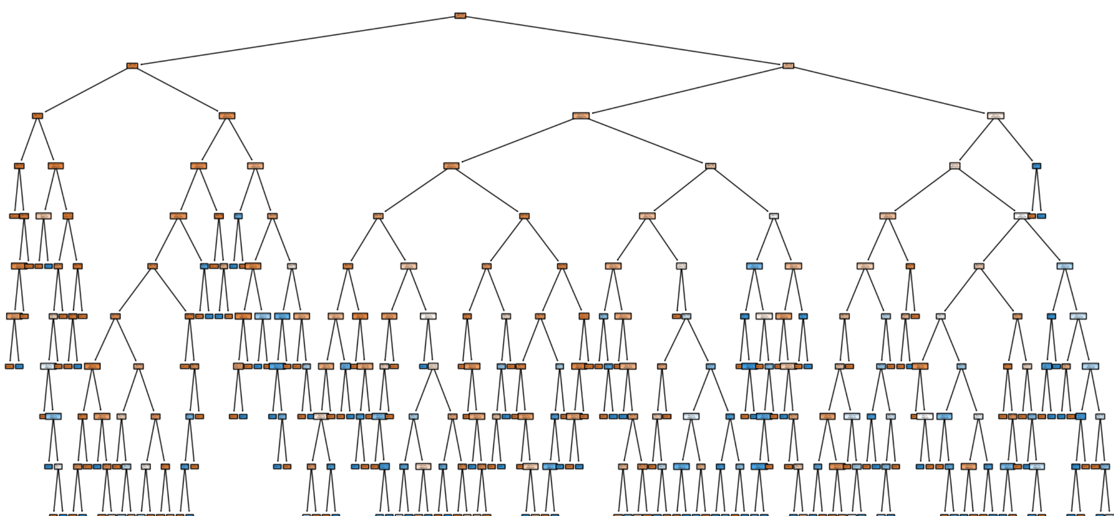
```
# Fit the model
tree_model.fit(X_train, y_train)

# Predictions on the test set
y_pred = tree_model.predict(X_test)

# Create confusion matrix
conf_matrix = confusion_matrix(y_test, y_pred)
conf_matrix_labels = pd.DataFrame(conf_matrix, index=['Actual 0', 'Actual 1'],␣
↪columns=['Predicted 0', 'Predicted 1'])
print("Confusion Matrix for Decision Tree (Before CV):")
print(conf_matrix_labels)

# Calculate accuracy score
accuracy = accuracy_score(y_test, y_pred)
print(f"\nAccuracy Score (Before CV): {accuracy}")

# Print the number of nodes in the tree before CV
print(f"\nNumber of nodes in the tree before CV: {tree_model.tree_.node_count}")

# Plot the decision tree
plt.figure(figsize=(20, 10))
plot_tree(tree_model, feature_names=features, class_names=['0', '1'],␣
↪filled=True, rounded=True)
plt.show()

# Define the parameter grid for grid search using optimal hyperparameters
param_grid = {
    'max_depth': [10],
    'min_samples_split': [2],
    'min_samples_leaf': [1]
}

# Create and perform grid search
grid_search = GridSearchCV(tree_model, param_grid, cv=5, scoring='accuracy')
grid_search.fit(X, y)

# Get the best decision tree from grid search
best_tree_model = grid_search.best_estimator_

# Print the number of nodes in the best tree after CV
print(f"\nNumber of nodes in the best tree after CV: {best_tree_model.tree_.
↪node_count}")

# Plot the best decision tree
plt.figure(figsize=(20, 10))
```

```python
plot_tree(best_tree_model, feature_names=features, class_names=['0', '1'],
    filled=True, rounded=True)
plt.show()

# Make predictions using the best tree model
y_pred = best_tree_model.predict(X_test)

# Create confusion matrix
conf_matrix = confusion_matrix(y_test, y_pred)
conf_matrix_labels = pd.DataFrame(conf_matrix, index=['Actual 0', 'Actual 1'],
    columns=['Predicted 0', 'Predicted 1'])
print("Confusion Matrix for Decision Tree (After CV):")
print(conf_matrix_labels)

# Accuracy Score
accuracy = accuracy_score(y_test, y_pred)
print(f"\nAccuracy Score (After CV): {accuracy}")

# Plot the decision tree with smaller max depth
plt.figure(figsize=(20, 10))
plot_tree(best_tree_model, feature_names=features, class_names=['0', '1'],
    filled=True, rounded=True, max_depth=2)
plt.show()

# Plot feature importances
feature_importance = best_tree_model.feature_importances_
feature_importance_df = pd.DataFrame({'Feature': features, 'Importance':
    feature_importance})
feature_importance_df = feature_importance_df.sort_values(by='Importance',
    ascending=False)

plt.figure(figsize=(6, 3))
sns.barplot(x='Importance', y='Feature', data=feature_importance_df,
    palette='viridis')
plt.title('Feature Importance Plot')
plt.show()
```

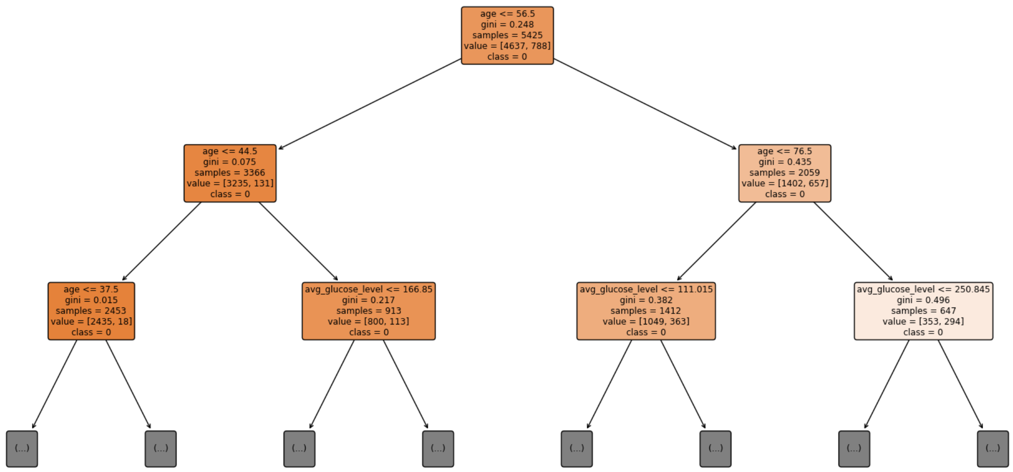
```
Confusion Matrix for Decision Tree (Before CV):
          Predicted 0  Predicted 1
Actual 0          908           26
Actual 1            0          151

Accuracy Score (Before CV): 0.976036866359447

Number of nodes in the tree before CV: 547
```

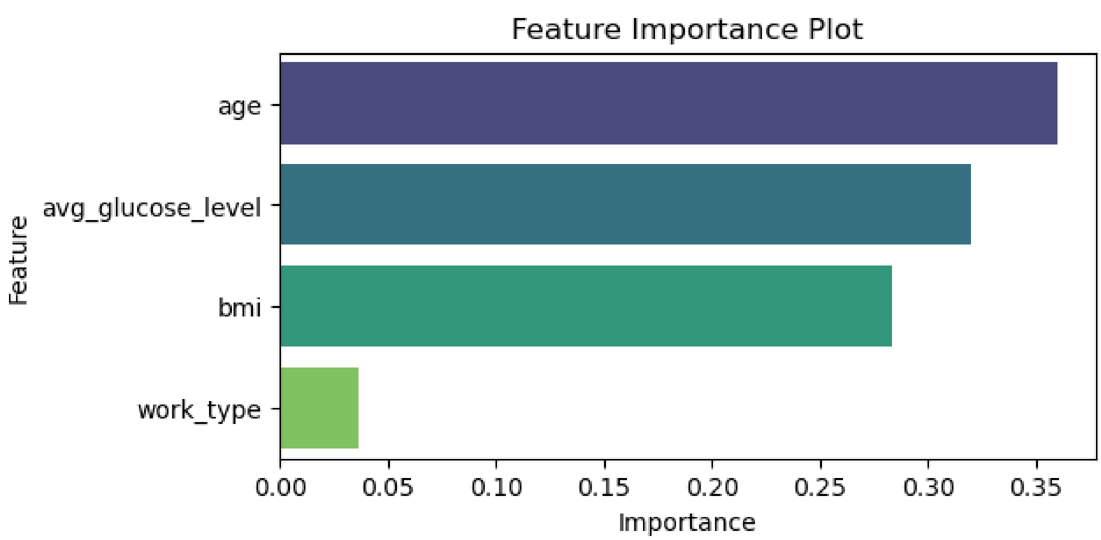


```
Number of nodes in the best tree after CV: 367
```



```
Confusion Matrix for Decision Tree (After CV):
          Predicted 0  Predicted 1
Actual 0          913           21
Actual 1           22          129

Accuracy Score (After CV): 0.96036866359447
```

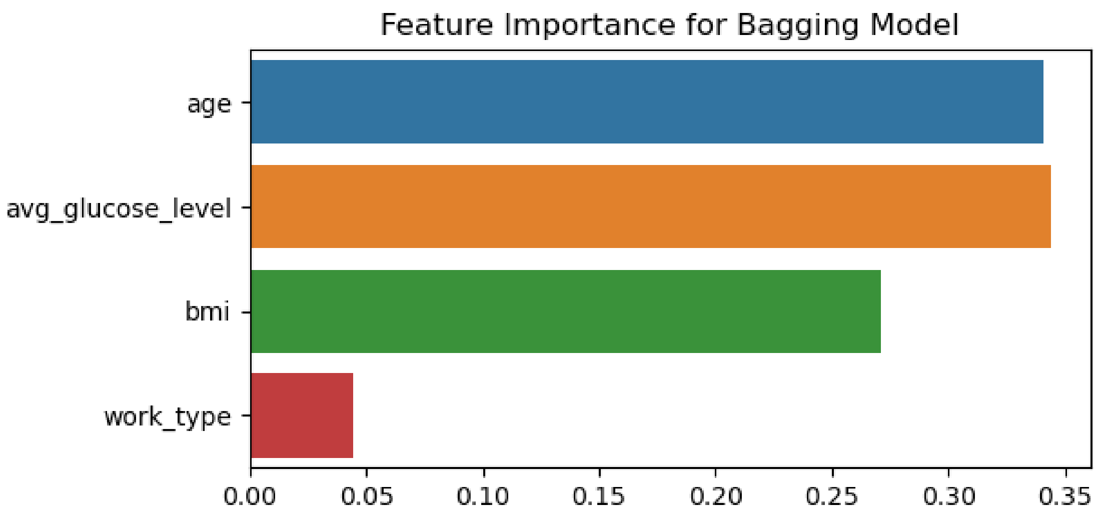



[13]:
```python
# Bagging Model

# Initialize base regressor
base_regressor = DecisionTreeRegressor()

# Create a bagging regressor with 100 base regressors
bagging_model = BaggingRegressor(base_regressor, n_estimators=100,
 ↪random_state=42)
bagging_model.fit(X_train, y_train)
```

```
# Make predictions using the bagging model
y_pred = bagging_model.predict(X_test)

# Convert predictions to binary (1 if prediction > 0.5, else 0)
y_pred_binary = (y_pred > 0.5).astype(int)

# Create confusion matrix
conf_matrix = confusion_matrix(y_test, y_pred_binary)
conf_matrix_labels = pd.DataFrame(conf_matrix, index=['Actual 0', 'Actual 1'],␣
↪columns=['Predicted 0', 'Predicted 1'])
print("Confusion Matrix for Bagging:")
print(conf_matrix_labels)

# Accuracy Score
accuracy = accuracy_score(y_test, y_pred_binary)
print(f"\nAccuracy Score for Bagging: {accuracy}")

# Extract feature importances
feature_importance = np.mean([tree.feature_importances_ for tree in␣
↪bagging_model.estimators_], axis=0)

# Plot feature importance
plt.figure(figsize=(6, 3))
sns.barplot(x=feature_importance, y=features)
plt.title('Feature Importance for Bagging Model')
plt.show()
```

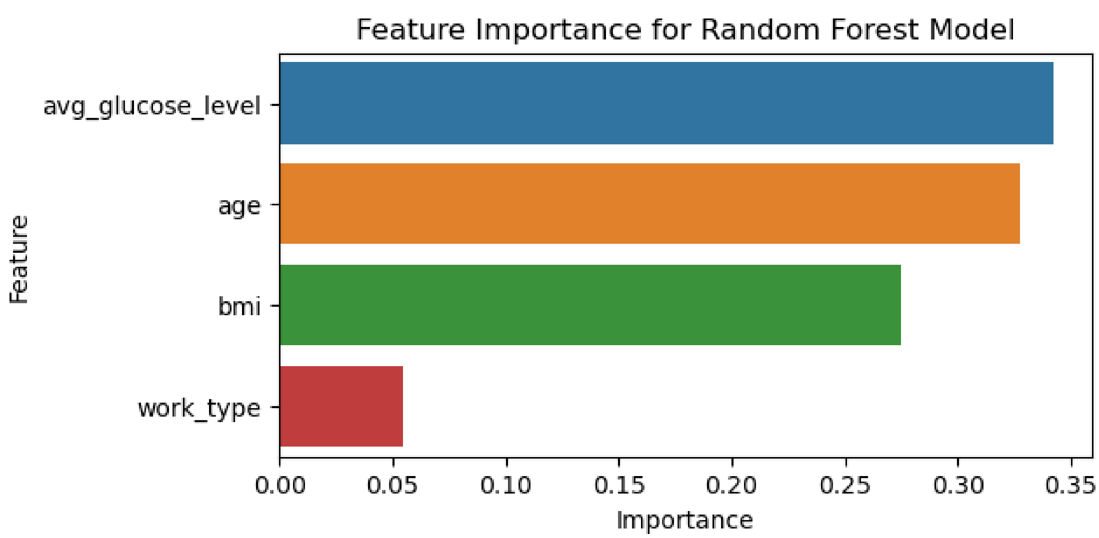
```
Confusion Matrix for Bagging:
          Predicted 0  Predicted 1
Actual 0          919           15
Actual 1            0          151

Accuracy Score for Bagging: 0.9861751152073732
```




[14]:
```
# Random Forest Model

# Initialize Random Forest Classifier
random_forest_classifier = RandomForestClassifier(n_estimators=100,␣
 ↪random_state=0)

# Fit Random Forest model
random_forest_classifier.fit(X_train, y_train)

# Predict on the test set
y_pred_rf = random_forest_classifier.predict(X_test)

# Create confusion matrix
conf_matrix_rf = confusion_matrix(y_test, y_pred_rf)
conf_matrix_labels_rf = pd.DataFrame(conf_matrix_rf, index=['Actual 0', 'Actual␣
 ↪1'], columns=['Predicted 0', 'Predicted 1'])
print("Confusion Matrix for RandomForest:")
print(conf_matrix_labels_rf)

# Accuracy Score
accuracy_rf = accuracy_score(y_test, y_pred_rf)
print(f"\nAccuracy Score for Random Forest: {accuracy_rf}")

# Determine variables' importances
feature_importances_rf = random_forest_classifier.feature_importances_
feature_importance_rf = pd.DataFrame({'Feature': X_train.columns, 'Importance':␣
 ↪feature_importances_rf})
feature_importance_rf = feature_importance_rf.sort_values(by='Importance',␣
 ↪ascending=False)
```

```
# Display the feature importances
print("\nFeature Importance:")
print(feature_importance_rf)

# Plot feature importances
plt.figure(figsize=(6, 3))
sns.barplot(x='Importance', y='Feature', data=feature_importance_rf)
plt.title('Feature Importance for Random Forest Model')
plt.show()
```

```
Confusion Matrix for RandomForest:
          Predicted 0  Predicted 1
Actual 0          922           12
Actual 1            0          151

Accuracy Score for Random Forest: 0.9889400921658986

Feature Importance:
             Feature  Importance
1  avg_glucose_level    0.342344
0                age    0.327715
2                bmi    0.275027
3          work_type    0.054914
```




[15]:
```
# Quantitative Analysis

# Life Expectancy Data Dictionary
```

```
# status: Developing or Developed nation (Developing = 0 and Developed = 1)
# adult_mortality: Adult Mortality Rates of both sexes (probability of dying␣
↪between 15 and 60 years per 1000 population)
# alcohol: Recorded per capita (ages 15+) consumption (in litres) of pure␣
↪alcohol per year
# percentage_expenditure: Expenditure on health as a percentage of Gross␣
↪Domestic Product per capita(%)
# hepatitis_b: Hepatitis B (HepB) immunization coverage among 1-year-olds (%)
# bmi: Average Body Mass Index of entire country population
# under_five_deaths: Number of under-five deaths per 1000 population
# polio: Pol3 immunization coverage among 1-year-olds (%)
# total_expenditure: General government expenditure on health as a percentage of␣
↪total government expenditure (%)
# diphtheria: DTP3 immunization coverage among 1-year-olds (%)
# hiv_aids: Deaths per 1000 live births HIV/AIDS (0-4 years)
# country_gdp: Gross Domestic Product per capita (in USD)
# country_population: Population of the country
# thinness_5_to_19_years: Prevalence of thinness among children and adolescents␣
↪for Age 5 to 19 (% )
# income_composition_resources: Human Development Index in terms of income␣
↪composition of resources (index ranging from 0 to 1)
# schooling: Number of years of Schooling
# life_expectancy: Life Expectancy in age
```

[16]:
```
# Clean Life Expectancy Data

# Rename columns
column_mapping = {
    'Status': 'status',
    'Life expectancy ': 'life_expectancy',
    'Adult Mortality': 'adult_mortality',
    'infant deaths': 'infant_deaths',
    'Alcohol': 'alcohol',
    'percentage expenditure': 'percentage_expenditure',
    'Hepatitis B': 'hepatitis_b',
    'Measles ': 'measles',
    ' BMI ': 'bmi',
    'under-five deaths ': 'under_five_deaths',
    'Polio': 'polio',
    'Total expenditure': 'total_expenditure',
    'Diphtheria ': 'diphtheria',
    ' HIV/AIDS': 'hiv_aids',
    'GDP': 'country_gdp',
    'Population': 'country_population',
    ' thinness  1-19 years': 'thinness_10_to_19_years',
    ' thinness 5-9 years': 'thinness_5_to_9_years',
    'Income composition of resources': 'income_composition_resources',
```

```
    'Schooling': 'schooling'
}

life_expectancy_renamed = life_expectancy.rename(columns=column_mapping)

# Drop 'Country', 'Year', and infant_deaths columns. Country and year aren't␣
↪necessary for this analysis. Infant deaths and under-five deaths closely␣
↪mirror eachother and are highly correlated (0.99 correlation coefficient). I␣
↪removed infant deaths to avoid possible issues with collinearity later on. I␣
↪also dropped the 'measles' column because the dictionary that came with the␣
↪data says it's per 1000 individuals, however, most of the values in this␣
↪column are >1000
life_expectancy_no_country_year = life_expectancy_renamed.drop(['Country',␣
↪'Year', 'infant_deaths', 'measles'], axis=1)

# Percent expenditure exceeds 100% in some cases, however, this is sensible in␣
↪some cases. As >100% PE doesn't necessarily imply exceeding available income,␣
↪but rather the proportion of income dedicated to health

# Country GDP was considered to be removed as this is highly correlated with␣
↪percentage expenditure (0.959), however, keeping country GDP in the models did␣
↪not have a significant impact on model performance, so, it did not get removed

# The other highly correlated pairs are Income Composition of Resources with␣
↪Schooling (0.785) and Under-Five Deaths with Country Population. These were␣
↪considered for transformation or removal, however, they did not affect the␣
↪models' performance significantly. All four of these variables were selected␣
↪in the Backward Stepwise Selection model and did not perform significantly␣
↪different than the Forward Selection Model (Forward MSE = 13.568 Backward MSE␣
↪= 13.465) which did not include any of these four variables

# Map values in the 'status' column
status_mapping = {'Developed': 1, 'Developing': 0}
life_expectancy_mapped = life_expectancy_no_country_year.copy()
life_expectancy_mapped['status'] = life_expectancy_no_country_year['status'].
↪map(status_mapping)

# Remove any null values and reset index
life_expectancy_no_null = life_expectancy_mapped.dropna()
life_expectancy_df = life_expectancy_no_null.reset_index(drop=True)

# Create new column by combining 'thinness_5_to_19_years' and␣
↪'thinness_10_to_19_years'. These two variables are highly correlated with␣
↪eachother and made sense to combine them
```

```
life_expectancy_df['thinness_5_to_19_years'] =␣
↪life_expectancy_df['thinness_10_to_19_years'] +␣
↪life_expectancy_df['thinness_5_to_9_years']

# Drop individual columns
life_expectancy_df.drop(['thinness_10_to_19_years', 'thinness_5_to_9_years'],␣
↪axis=1, inplace=True)

# Display the working dataframe for modeling
print(life_expectancy_df.head())
```

```
   status  life_expectancy  adult_mortality  alcohol  percentage_expenditure  \
0       0             65.0            263.0     0.01               71.279624
1       0             59.9            271.0     0.01               73.523582
2       0             59.9            268.0     0.01               73.219243
3       0             59.5            272.0     0.01               78.184215
4       0             59.2            275.0     0.01                7.097109

   hepatitis_b   bmi  under_five_deaths  polio  total_expenditure  diphtheria  \
0         65.0  19.1                 83    6.0               8.16        65.0
1         62.0  18.6                 86   58.0               8.18        62.0
2         64.0  18.1                 89   62.0               8.13        64.0
3         67.0  17.6                 93   67.0               8.52        67.0
4         68.0  17.2                 97   68.0               7.87        68.0

   hiv_aids  country_gdp  country_population  income_composition_resources  \
0       0.1   584.259210          33736494.0                         0.479
1       0.1   612.696514            327582.0                         0.476
2       0.1   631.744976          31731688.0                         0.470
3       0.1   669.959000           3696958.0                         0.463
4       0.1    63.537231           2978599.0                         0.454

   schooling  thinness_5_to_19_years
0       10.1                    34.5
1       10.0                    35.0
2        9.9                    35.4
3        9.8                    35.9
4        9.5                    36.4
```

[17]:
```
# Life Expectancy Data Summary and Exploration

# Generate numerical summary
summary_stats = life_expectancy_df.describe()
print(summary_stats)

# Developed (1) versus Developing (0)
status_counts = life_expectancy_df['status'].value_counts()
```

```python
# Display counts
print("Number of Developed (1) and Developing (0) Values:")
print(status_counts)

# Generate correlation matrix and heatmap
le_correlation_matrix = life_expectancy_df.corr()

print(le_correlation_matrix)

# Plot heatmap
plt.figure(figsize=(7, 3))
sns.heatmap(le_correlation_matrix, annot=True, cmap='coolwarm', fmt=".2f",␣
↪linewidths=.5)
plt.title('Correlation Heatmap of Life Expectancy Features')
plt.show()

# Look for highly correlated pairs for possible collinearity

# Correlation threshold
le_correlation_threshold = 0.65

# Find highly correlated pairs
le_highly_correlated_pairs = []

for i in range(len(le_correlation_matrix.columns)):
    for j in range(i+1, len(le_correlation_matrix.columns)):
        if abs(le_correlation_matrix.iloc[i, j]) > le_correlation_threshold:
            pair = (le_correlation_matrix.columns[i], le_correlation_matrix.
↪columns[j], le_correlation_matrix.iloc[i, j])
            le_highly_correlated_pairs.append(pair)

# Print pairs
for pair in le_highly_correlated_pairs:
    print(f"Highly Correlated Pair: {pair}")

# Create boxplot matrix of variables

# Select variables of interest
le_selected_variables = ['adult_mortality', 'alcohol', 'percentage_expenditure',
                         'hepatitis_b', 'bmi', 'under_five_deaths', 'polio',
                         'total_expenditure', 'diphtheria', 'hiv_aids',␣
↪'country_gdp',
                         'country_population', 'thinness_5_to_19_years',
                         'income_composition_resources', 'schooling',␣
↪'life_expectancy']
```

```python
# Subset selected variables
le_subset_df = life_expectancy_df[le_selected_variables]

# Set number of rows and columns in the matrix
num_columns = 4
num_rows = -(-len(le_selected_variables) // num_columns)

# Create matrix
fig, axes = plt.subplots(num_rows, num_columns, figsize=(15, 20))
fig.subplots_adjust(hspace=0.5)
axes = axes.flatten()

# Create boxplots for each variable
for i, variable in enumerate(le_selected_variables):
    sns.boxplot(x=life_expectancy_df[variable], ax=axes[i])
    axes[i].set_title(variable)

# Hide empty plots
for i in range(len(le_selected_variables), len(axes)):
    axes[i].axis('off')

# Display boxplot matrix
plt.show()

# Create histogram matrix of variables

# Set the number of rows and columns in the matrix
num_columns = 4
num_rows = -(-len(le_selected_variables) // num_columns)

# Create a matrix of subplots for histograms
fig, axes = plt.subplots(num_rows, num_columns, figsize=(15, 20))
fig.subplots_adjust(hspace=0.5)
axes = axes.flatten()

# Create histograms for each variable
for i, variable in enumerate(le_selected_variables):
    sns.histplot(life_expectancy_df[variable], kde=True, ax=axes[i], bins=20)
    axes[i].set_title(variable)

# Hide empty plots
for i in range(len(le_selected_variables), len(axes)):
    axes[i].axis('off')

# Display histogram matrix
plt.show()
```

```python
# Create function that creates scatterplot matrix with best-fit line for all␣
↪variables vs life expectancy
def scatterplot_matrix_with_fit(data, variables, target_variable, num_columns=3,␣
↪figsize=(15, 12), hspace=0.6, wspace=0.4):
    num_plots = len(variables) - 1
    num_rows = math.ceil(num_plots / num_columns)

    fig, axes = plt.subplots(num_rows, num_columns, figsize=figsize)
    fig.subplots_adjust(hspace=hspace, wspace=wspace)

    for i, variable in enumerate(variables):
        if variable != target_variable:
            row = i // num_columns
            col = i % num_columns
            ax = axes[row, col]

            # Scatterplot
            sns.scatterplot(data=data, x=variable, y=target_variable, ax=ax)

            # Fit linear regression line
            sns.regplot(x=variable, y=target_variable, data=data, ax=ax,␣
↪line_kws={"color": "red"})

            ax.set_title(f'{variable} vs {target_variable}')
            ax.set_xlabel(variable)
            ax.set_ylabel(target_variable)

    # Remove empty subplots
    for i in range(num_plots, num_rows * num_columns):
        fig.delaxes(axes.flatten()[i])

    plt.show()

# Use function to create the scatterplot matrix
scatterplot_matrix_with_fit(life_expectancy_df, le_selected_variables,␣
↪'life_expectancy', hspace=0.8, wspace=0.4)
```

```
            status  life_expectancy  adult_mortality      alcohol  \
count  1649.000000      1649.000000      1649.000000  1649.000000
mean      0.146756        69.302304       168.215282     4.533196
std       0.353969         8.796834       125.310417     4.029189
min       0.000000        44.000000         1.000000     0.010000
25%       0.000000        64.400000        77.000000     0.810000
50%       0.000000        71.700000       148.000000     3.790000
75%       0.000000        75.000000       227.000000     7.340000
max       1.000000        89.000000       723.000000    17.870000
```

| | percentage_expenditure | hepatitis_b | bmi | under_five_deaths | \ |
|---|---|---|---|---|---|
| count | 1649.000000 | 1649.000000 | 1649.000000 | 1649.000000 | |
| mean | 698.973558 | 79.217708 | 38.128623 | 44.220133 | |
| std | 1759.229336 | 25.604664 | 19.754249 | 162.897999 | |
| min | 0.000000 | 2.000000 | 2.000000 | 0.000000 | |
| 25% | 37.438577 | 74.000000 | 19.500000 | 1.000000 | |
| 50% | 145.102253 | 89.000000 | 43.700000 | 4.000000 | |
| 75% | 509.389994 | 96.000000 | 55.800000 | 29.000000 | |
| max | 18961.348600 | 99.000000 | 77.100000 | 2100.000000 | |

| | polio | total_expenditure | diphtheria | hiv_aids | \ |
|---|---|---|---|---|---|
| count | 1649.000000 | 1649.000000 | 1649.000000 | 1649.000000 | |
| mean | 83.564585 | 5.955925 | 84.155246 | 1.983869 | |
| std | 22.450557 | 2.299385 | 21.579193 | 6.032360 | |
| min | 3.000000 | 0.740000 | 2.000000 | 0.100000 | |
| 25% | 81.000000 | 4.410000 | 82.000000 | 0.100000 | |
| 50% | 93.000000 | 5.840000 | 92.000000 | 0.100000 | |
| 75% | 97.000000 | 7.470000 | 97.000000 | 0.700000 | |
| max | 99.000000 | 14.390000 | 99.000000 | 50.600000 | |

| | country_gdp | country_population | income_composition_resources | \ |
|---|---|---|---|---|
| count | 1649.000000 | 1.649000e+03 | 1649.000000 | |
| mean | 5566.031887 | 1.465363e+07 | 0.631551 | |
| std | 11475.900117 | 7.046039e+07 | 0.183089 | |
| min | 1.681350 | 3.400000e+01 | 0.000000 | |
| 25% | 462.149650 | 1.918970e+05 | 0.509000 | |
| 50% | 1592.572182 | 1.419631e+06 | 0.673000 | |
| 75% | 4718.512910 | 7.658972e+06 | 0.751000 | |
| max | 119172.741800 | 1.293859e+09 | 0.936000 | |

| | schooling | thinness_5_to_19_years |
|---|---|---|
| count | 1649.000000 | 1649.000000 |
| mean | 12.119891 | 9.758399 |
| std | 2.795388 | 9.084707 |
| min | 4.200000 | 0.200000 |
| 25% | 10.300000 | 3.300000 |
| 50% | 12.300000 | 6.500000 |
| 75% | 14.000000 | 14.000000 |
| max | 20.700000 | 55.400000 |

```
Number of Developed (1) and Developing (0) Values:
0    1407
1     242
Name: status, dtype: int64
```

| | status | life_expectancy | adult_mortality | \ |
|---|---|---|---|---|
| status | 1.000000 | 0.442798 | -0.278173 | |
| life_expectancy | 0.442798 | 1.000000 | -0.702523 | |
| adult_mortality | -0.278173 | -0.702523 | 1.000000 | |
| alcohol | 0.607782 | 0.402718 | -0.175535 | |

```
percentage_expenditure        0.461688         0.409631         -0.237610
hepatitis_b                   0.140351         0.199935         -0.105225
bmi                           0.298380         0.542042         -0.351542
under_five_deaths            -0.109847        -0.192265          0.060365
polio                         0.201917         0.327294         -0.199853
total_expenditure             0.192538         0.174718         -0.085227
diphtheria                    0.201654         0.341331         -0.191429
hiv_aids                     -0.129555        -0.592236          0.550691
country_gdp                   0.484801         0.441322         -0.255035
country_population           -0.034790        -0.022305         -0.015012
income_composition_resources  0.463615         0.721083         -0.442203
schooling                     0.512543         0.727630         -0.421171
thinness_5_to_19_years       -0.313338        -0.466150          0.284697

                               alcohol  percentage_expenditure  hepatitis_b  \
status                        0.607782                0.461688     0.140351
life_expectancy               0.402718                0.409631     0.199935
adult_mortality              -0.175535               -0.237610    -0.105225
alcohol                       1.000000                0.417047     0.109889
percentage_expenditure        0.417047                1.000000     0.016760
hepatitis_b                   0.109889                0.016760     1.000000
bmi                           0.353396                0.242738     0.143302
under_five_deaths            -0.101082               -0.092158    -0.240766
polio                         0.240315                0.128626     0.463331
total_expenditure             0.214885                0.183872     0.113327
diphtheria                    0.242951                0.134813     0.588990
hiv_aids                     -0.027113               -0.095085    -0.094802
country_gdp                   0.443433                0.959299     0.041850
country_population           -0.028880               -0.016792    -0.129723
income_composition_resources  0.561074                0.402170     0.184921
schooling                     0.616975                0.422088     0.215182
thinness_5_to_19_years       -0.402245               -0.260066    -0.133773

                                   bmi  under_five_deaths     polio  \
status                        0.298380          -0.109847  0.201917
life_expectancy               0.542042          -0.192265  0.327294
adult_mortality              -0.351542           0.060365 -0.199853
alcohol                       0.353396          -0.101082  0.240315
percentage_expenditure        0.242738          -0.092158  0.128626
hepatitis_b                   0.143302          -0.240766  0.463331
bmi                           1.000000          -0.242137  0.186268
under_five_deaths            -0.242137           1.000000 -0.171164
polio                         0.186268          -0.171164  1.000000
total_expenditure             0.189469          -0.145803  0.119768
diphtheria                    0.176295          -0.178448  0.609245
hiv_aids                     -0.210897           0.019476 -0.107885
country_gdp                   0.266114          -0.100331  0.156809
country_population           -0.081416           0.658680 -0.045387
```

| | | | |
|---|---|---|---|
| income_composition_resources | 0.510505 | -0.148097 | 0.314682 |
| schooling | 0.554844 | -0.226013 | 0.350147 |
| thinness_5_to_19_years | -0.560775 | 0.472116 | -0.172446 |

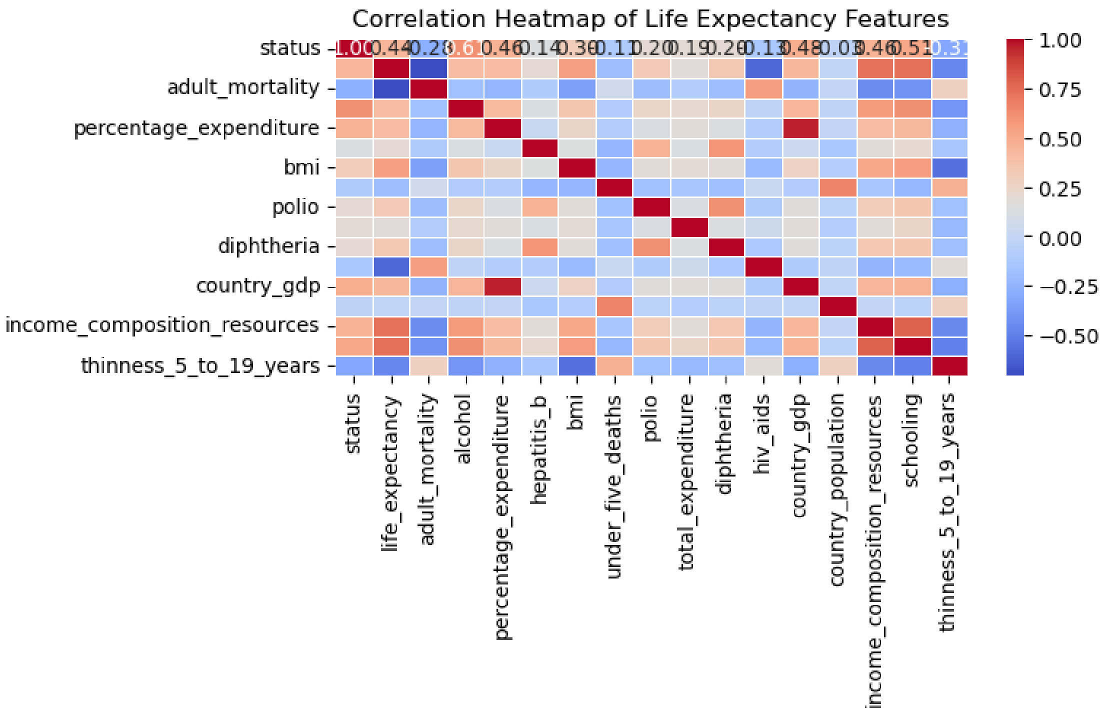
| | total_expenditure | diphtheria | hiv_aids | \ |
|---|---|---|---|---|
| status | 0.192538 | 0.201654 | -0.129555 | |
| life_expectancy | 0.174718 | 0.341331 | -0.592236 | |
| adult_mortality | -0.085227 | -0.191429 | 0.550691 | |
| alcohol | 0.214885 | 0.242951 | -0.027113 | |
| percentage_expenditure | 0.183872 | 0.134813 | -0.095085 | |
| hepatitis_b | 0.113327 | 0.588990 | -0.094802 | |
| bmi | 0.189469 | 0.176295 | -0.210897 | |
| under_five_deaths | -0.145803 | -0.178448 | 0.019476 | |
| polio | 0.119768 | 0.609245 | -0.107885 | |
| total_expenditure | 1.000000 | 0.129915 | 0.043101 | |
| diphtheria | 0.129915 | 1.000000 | -0.117601 | |
| hiv_aids | 0.043101 | -0.117601 | 1.000000 | |
| country_gdp | 0.180373 | 0.158438 | -0.108081 | |
| country_population | -0.079962 | -0.039898 | -0.027801 | |
| income_composition_resources | 0.183653 | 0.343262 | -0.248590 | |
| schooling | 0.243783 | 0.350398 | -0.211840 | |
| thinness_5_to_19_years | -0.217854 | -0.187488 | 0.181196 | |

| | country_gdp | country_population | \ |
|---|---|---|---|
| status | 0.484801 | -0.034790 | |
| life_expectancy | 0.441322 | -0.022305 | |
| adult_mortality | -0.255035 | -0.015012 | |
| alcohol | 0.443433 | -0.028880 | |
| percentage_expenditure | 0.959299 | -0.016792 | |
| hepatitis_b | 0.041850 | -0.129723 | |
| bmi | 0.266114 | -0.081416 | |
| under_five_deaths | -0.100331 | 0.658680 | |
| polio | 0.156809 | -0.045387 | |
| total_expenditure | 0.180373 | -0.079962 | |
| diphtheria | 0.158438 | -0.039898 | |
| hiv_aids | -0.108081 | -0.027801 | |
| country_gdp | 1.000000 | -0.020369 | |
| country_population | -0.020369 | 1.000000 | |
| income_composition_resources | 0.446856 | -0.008132 | |
| schooling | 0.467947 | -0.040312 | |
| thinness_5_to_19_years | -0.282874 | 0.285398 | |

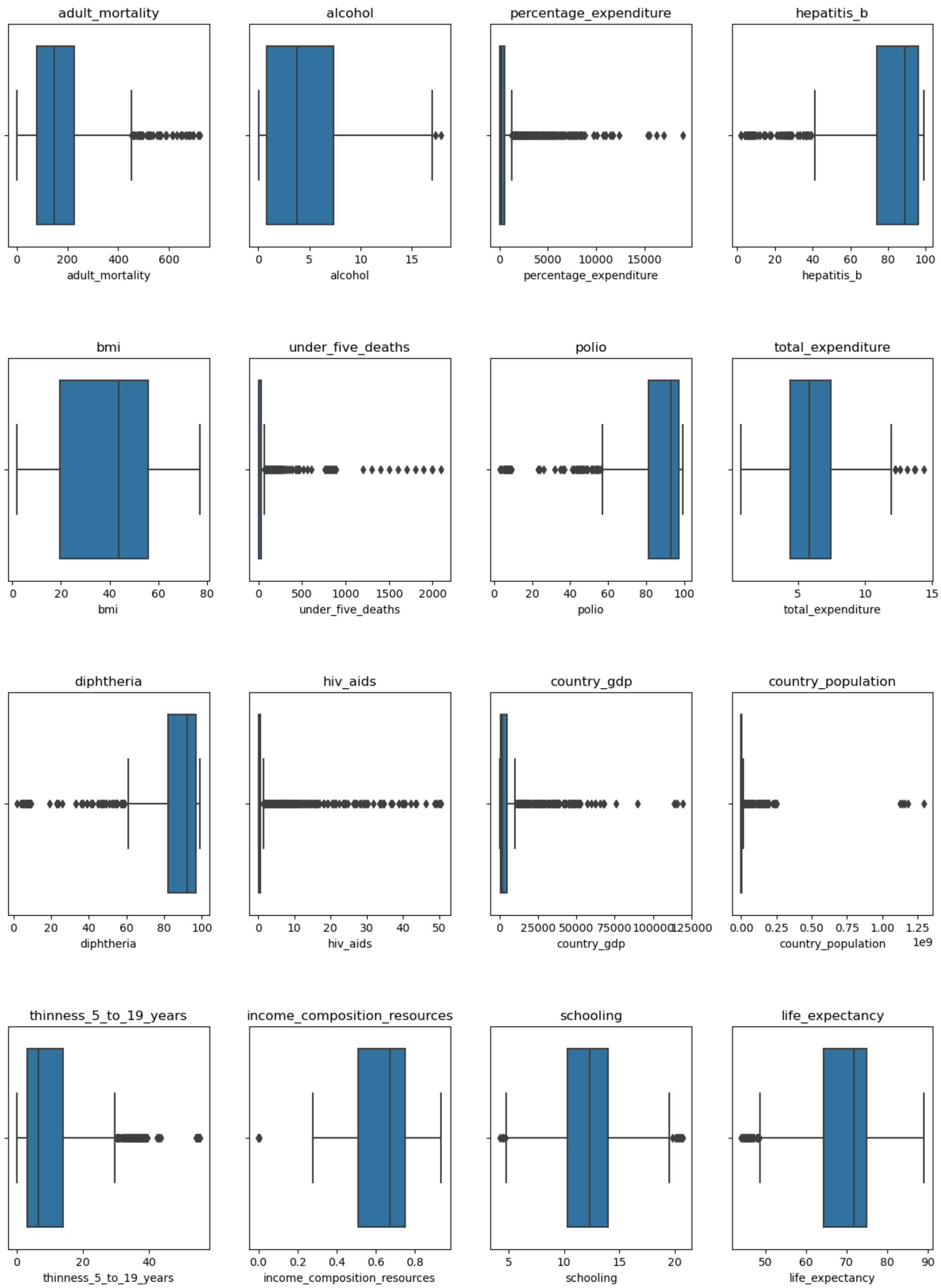
| | income_composition_resources | schooling | \ |
|---|---|---|---|
| status | 0.463615 | 0.512543 | |
| life_expectancy | 0.721083 | 0.727630 | |
| adult_mortality | -0.442203 | -0.421171 | |
| alcohol | 0.561074 | 0.616975 | |
| percentage_expenditure | 0.402170 | 0.422088 | |

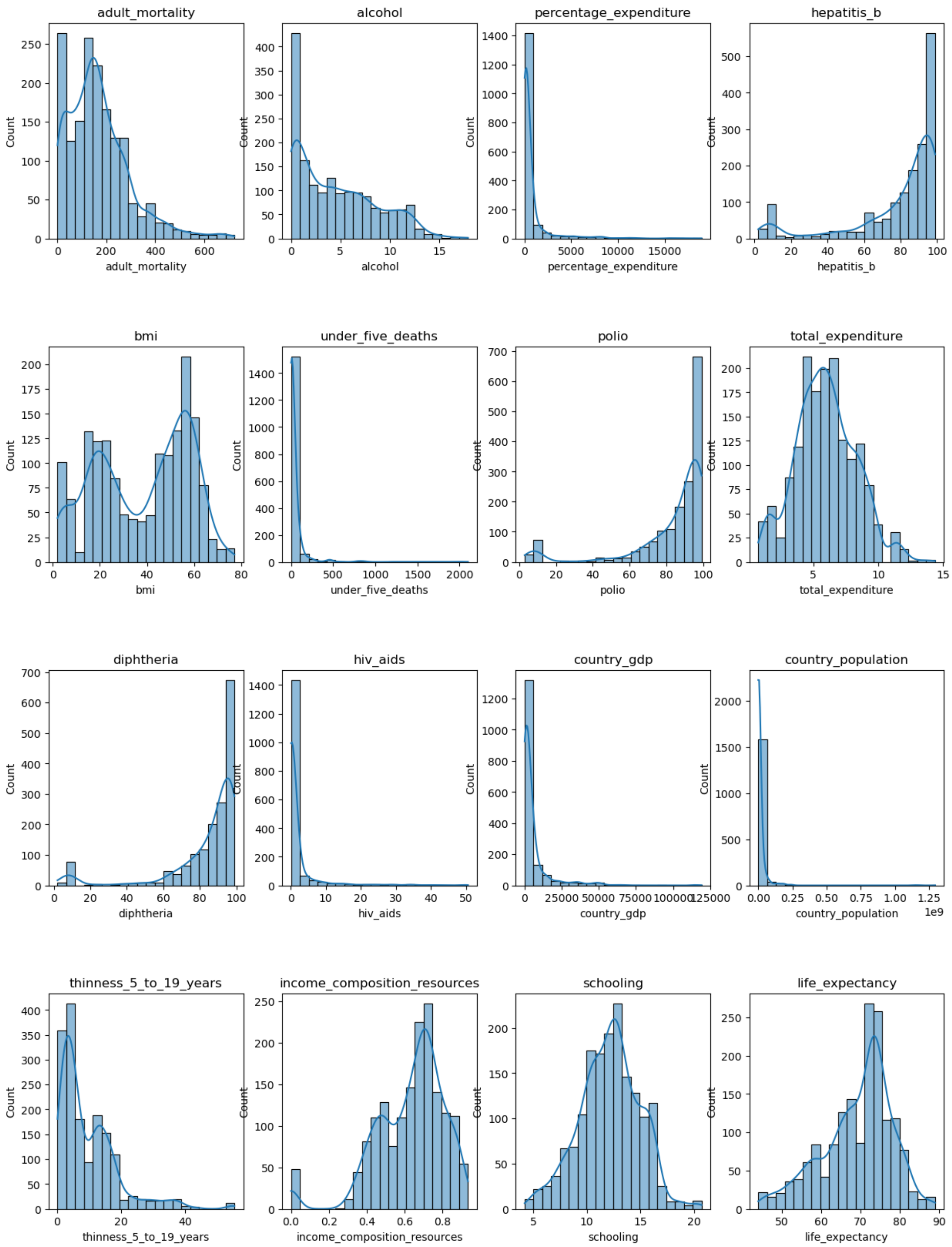
| | | |
|---|---|---|
| hepatitis_b | 0.184921 | 0.215182 |
| bmi | 0.510505 | 0.554844 |
| under_five_deaths | -0.148097 | -0.226013 |
| polio | 0.314682 | 0.350147 |
| total_expenditure | 0.183653 | 0.243783 |
| diphtheria | 0.343262 | 0.350398 |
| hiv_aids | -0.248590 | -0.211840 |
| country_gdp | 0.446856 | 0.467947 |
| country_population | -0.008132 | -0.040312 |
| income_composition_resources | 1.000000 | 0.784741 |
| schooling | 0.784741 | 1.000000 |
| thinness_5_to_19_years | -0.454299 | -0.490710 |

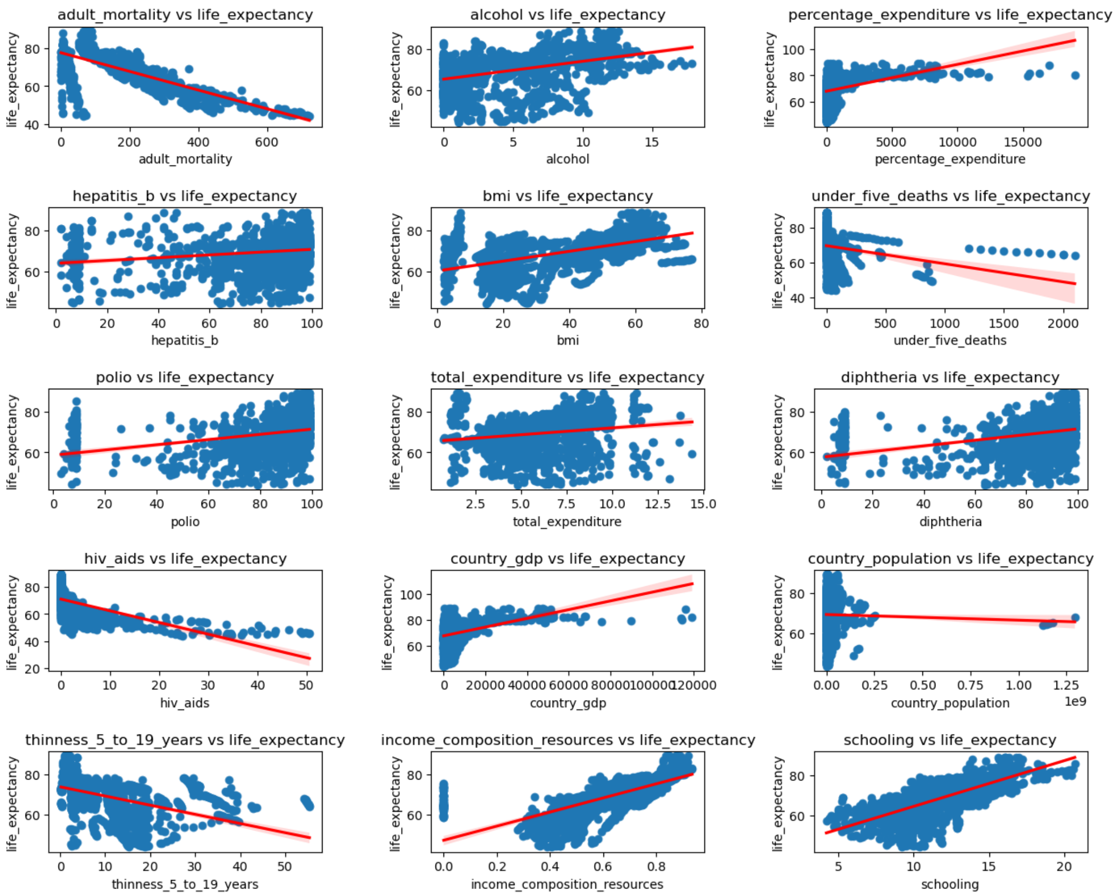
| | thinness_5_to_19_years |
|---|---|
| status | -0.313338 |
| life_expectancy | -0.466150 |
| adult_mortality | 0.284697 |
| alcohol | -0.402245 |
| percentage_expenditure | -0.260066 |
| hepatitis_b | -0.133773 |
| bmi | -0.560775 |
| under_five_deaths | 0.472116 |
| polio | -0.172446 |
| total_expenditure | -0.217854 |
| diphtheria | -0.187488 |
| hiv_aids | 0.181196 |
| country_gdp | -0.282874 |
| country_population | 0.285398 |
| income_composition_resources | -0.454299 |
| schooling | -0.490710 |
| thinness_5_to_19_years | 1.000000 |




```
Highly Correlated Pair: ('life_expectancy', 'adult_mortality',
-0.7025230623069735)
Highly Correlated Pair: ('life_expectancy', 'income_composition_resources',
0.7210825929172864)
Highly Correlated Pair: ('life_expectancy', 'schooling', 0.7276300323211043)
Highly Correlated Pair: ('percentage_expenditure', 'country_gdp',
0.9592988569672184)
Highly Correlated Pair: ('under_five_deaths', 'country_population',
0.6586796907106565)
Highly Correlated Pair: ('income_composition_resources', 'schooling',
0.7847405811682984)
```


adult_mortality
0 200 400 600
adult_mortality
alcohol
0 5 10 15
alcohol
percentage_expenditure
0 5000 10000 15000
percentage_expenditure
hepatitis_b
0 20 40 60 80 100
hepatitis_b
bmi
0 20 40 60 80
bmi
under_five_deaths
0 500 1000 1500 2000
under_five_deaths
polio
0 20 40 60 80 100
polio
total_expenditure
5 10 15
total_expenditure
diphtheria
0 20 40 60 80 100
diphtheria
hiv_aids
0 10 20 30 40 50
hiv_aids
country_gdp
0 25000 50000 75000 100000 125000
country_gdp
country_population
0.00 0.25 0.50 0.75 1.00 1.25
1e9
country_population
thinness_5_to_19_years
0 20 40
thinness_5_to_19_years
income_composition_resources
0.0 0.2 0.4 0.6 0.8
income_composition_resources
schooling
5 10 15 20
schooling
life_expectancy
50 60 70 80 90
life_expectancy


adult_mortality
alcohol
percentage_expenditure
hepatitis_b
bmi
under_five_deaths
polio
total_expenditure
diphtheria
hiv_aids
country_gdp
country_population
thinness_5_to_19_years
income_composition_resources
schooling
life_expectancy
Count
1e9




[18]:
```python
# Select Predictors, Define X and y, Split into test and train sets, Normalize␣
↪Data

# Select predictors
predictors = ['status', 'adult_mortality', 'alcohol', 'percentage_expenditure',
              'hepatitis_b', 'bmi', 'under_five_deaths', 'polio', 'country_gdp',
              'total_expenditure', 'diphtheria', 'hiv_aids',␣
↪'country_population',
              'thinness_5_to_19_years', 'schooling',␣
↪'income_composition_resources']

# Define X and y
X = sm.add_constant(life_expectancy_df[predictors])
y = life_expectancy_df['life_expectancy']

# Split data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state=42)
```

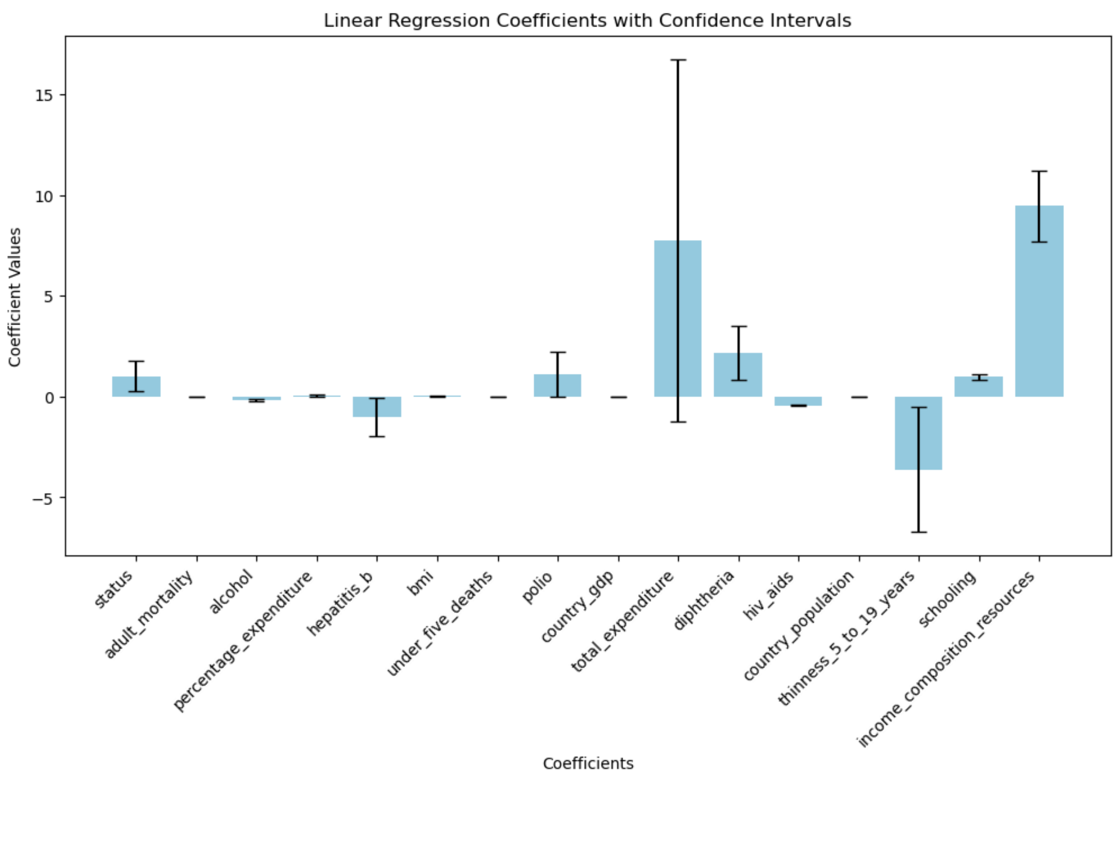
```
# Data Normalization (on both test and train sets)

# Convert percentage variables to decimals
percentage_columns = ['hepatitis_b', 'polio', 'total_expenditure', 'diphtheria',␣
↪'thinness_5_to_19_years', 'percentage_expenditure']
X_train[percentage_columns] /= 100
X_test[percentage_columns] /= 100

# Define X and y
X_train = sm.add_constant(X_train[predictors])
X_test = sm.add_constant(X_test[predictors])
y_train = life_expectancy_df.loc[X_train.index, 'life_expectancy']
y_test = life_expectancy_df.loc[X_test.index, 'life_expectancy']
```

[19]:
```
# Linear Regression Model

# Initialize linear regression model
linear_model = LinearRegression()

# Fit model
linear_model.fit(X_train, y_train)

# Make predictions on test set
linear_pred = linear_model.predict(X_test)

# Evaluate model with MSE
linear_mse = mean_squared_error(y_test, linear_pred)

print(f"Test Error (MSE) for Linear Regression: {linear_mse}")

# Summary of Linear Regression Model
X_with_intercept = sm.add_constant(X_train)
sm_model = sm.OLS(y_train, X_with_intercept).fit()

print(sm_model.summary())

# Plot coefficients with confidence intervals
plt.figure(figsize=(12, 6))
sns.barplot(x=sm_model.params.index[1:], y=sm_model.params.values[1:],␣
↪color='skyblue')
plt.errorbar(x=sm_model.params.index[1:], y=sm_model.params.values[1:],␣
↪yerr=sm_model.conf_int()[1:][1] - sm_model.params.values[1:], fmt='none',␣
↪color='black', capsize=5)
plt.title('Linear Regression Coefficients with Confidence Intervals')
plt.xlabel('Coefficients')
plt.ylabel('Coefficient Values')
```

```python
plt.xticks(rotation=45, ha='right')
plt.show()
```

```
Test Error (MSE) for Linear Regression: 13.912785384724556
                            OLS Regression Results
==============================================================================
Dep. Variable:        life_expectancy   R-squared:                       0.832
Model:                            OLS   Adj. R-squared:                  0.830
Method:                 Least Squares   F-statistic:                     402.2
Date:                Sat, 17 Aug 2024   Prob (F-statistic):               0.00
Time:                        21:37:03   Log-Likelihood:                -3576.2
No. Observations:                1319   AIC:                             7186.
Df Residuals:                    1302   BIC:                             7274.
Df Model:                          16
Covariance Type:            nonrobust
================================================================================
================
                                 coef    std err          t      P>|t|
[0.025      0.975]
--------------------------------------------------------------------------------
----------------
const                         52.4693      0.834     62.934      0.000
50.834      54.105
status                         1.0152      0.393      2.584      0.010
0.244       1.786
adult_mortality               -0.0175      0.001    -16.563      0.000
-0.020      -0.015
alcohol                       -0.1692      0.037     -4.608      0.000
-0.241      -0.097
percentage_expenditure         0.0398      0.021      1.858      0.063
-0.002       0.082
hepatitis_b                   -1.0117      0.495     -2.042      0.041
-1.983      -0.040
bmi                            0.0291      0.007      4.290      0.000
0.016       0.042
under_five_deaths             -0.0021      0.001     -2.204      0.028
-0.004      -0.000
polio                          1.0984      0.575      1.911      0.056
-0.029       2.226
country_gdp                -3.066e-06   3.38e-05     -0.091      0.928
-6.93e-05    6.32e-05
total_expenditure              7.7530      4.591      1.689      0.091
-1.253      16.759
diphtheria                     2.1556      0.678      3.177      0.002
0.825       3.487
hiv_aids                      -0.4332      0.020    -21.891      0.000
-0.472      -0.394
country_population          2.494e-09   2.17e-09      1.149      0.251
```

```
-1.77e-09    6.75e-09
thinness_5_to_19_years          -3.6151      1.567     -2.306      0.021
-6.690      -0.540
schooling                        0.9795      0.067     14.585      0.000
0.848       1.111
income_composition_resources     9.4645      0.892     10.605      0.000
7.714      11.215
==============================================================================
Omnibus:                       29.236   Durbin-Watson:                   2.053
Prob(Omnibus):                  0.000   Jarque-Bera (JB):               43.742
Skew:                          -0.215   Prob(JB):                     3.17e-10
Kurtosis:                       3.782   Cond. No.                     2.89e+09
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
[2] The condition number is large, 2.89e+09. This might indicate that there are
strong multicollinearity or other numerical problems.
```

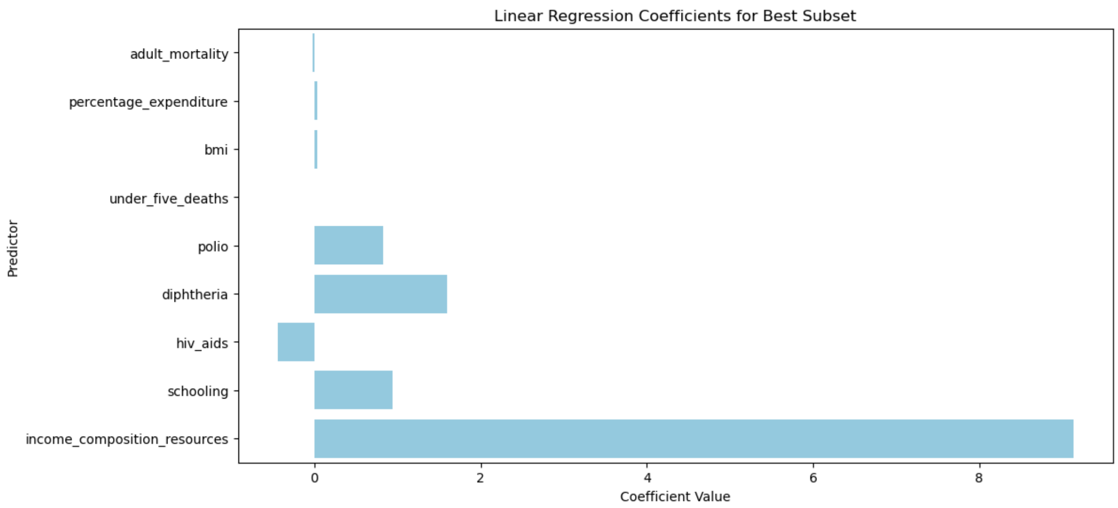



[20]:
```
# Best Subset Selection Model
```

```
# I adjusted the predictors by removing country_gdp and country_population, as␣
↪those features had really high p-values in the linear regression summary and␣
↪limited computing power capability
best_subset_predictors = ['adult_mortality', 'alcohol', 'percentage_expenditure',
              'hepatitis_b', 'bmi', 'under_five_deaths', 'polio',
              'total_expenditure', 'diphtheria', 'hiv_aids',␣
↪'thinness_5_to_19_years',
              'schooling', 'income_composition_resources']

best_model = None
best_mse = float('inf')

for L in range(1, len(best_subset_predictors) + 1):
    for subset in itertools.combinations(best_subset_predictors, L):
        subset_X_train = X_train[list(subset)]
        subset_X_test = X_test[list(subset)]

        model = LinearRegression()
        model.fit(subset_X_train, y_train)
        predictions = model.predict(subset_X_test)
        mse = mean_squared_error(y_test, predictions)

        if mse < best_mse:
            best_mse = mse
            best_model = model
            best_subset = list(subset)

print(f"Best Subset: {best_subset}")
print(f"Test Error (MSE) for Best Subset: {best_mse}")

# Slight improvement in MSE with Best Subset Model

# Get the coefficients and corresponding predictors
coefficients = best_model.coef_
predictors = best_subset

# Create a df
coefficients_df = pd.DataFrame({'Predictor': predictors, 'Coefficient':␣
↪coefficients})

# Plot coefficients
plt.figure(figsize=(12, 6))
sns.barplot(x='Coefficient', y='Predictor', data=coefficients_df,␣
↪color='skyblue')
plt.title('Linear Regression Coefficients for Best Subset')
plt.xlabel('Coefficient Value')
plt.ylabel('Predictor')
```

```
plt.show()
```

```
Best Subset: ['adult_mortality', 'percentage_expenditure', 'bmi',
'under_five_deaths', 'polio', 'diphtheria', 'hiv_aids', 'schooling',
'income_composition_resources']
Test Error (MSE) for Best Subset: 13.610841001767238
```




[21]:
```
# Forward Stepwise Selection

def forward_stepwise_selection(X_train, X_test, y_train, y_test, predictors):
    selected_predictors = []
    best_mse = float('inf')

    for _ in range(len(predictors)):
        remaining_predictors = list(set(predictors) - set(selected_predictors))
        best_subset = None

        for predictor in remaining_predictors:
            subset = selected_predictors + [predictor]
            subset_X_train = X_train[subset]
            subset_X_test = X_test[subset]

            model = LinearRegression()
            model.fit(subset_X_train, y_train)
            predictions = model.predict(subset_X_test)
            mse = mean_squared_error(y_test, predictions)

            if mse < best_mse:
                best_mse = mse
                best_subset = subset
```

```
        if best_subset:
            selected_predictors = best_subset

    return selected_predictors, best_mse

forward_selected_predictors, forward_best_mse =␣
↪forward_stepwise_selection(X_train, X_test, y_train, y_test, predictors)

print(f"Forward Stepwise Selection Predictors: {forward_selected_predictors}")
print(f"Test Error (MSE) for Forward Stepwise Selection: {forward_best_mse}")

# Backward Stepwise Selection

def backward_stepwise_selection(X_train, X_test, y_train, y_test, predictors):
    selected_predictors = predictors.copy()
    best_mse = float('inf')

    for _ in range(len(predictors) - 1):
        best_subset = None

        for predictor in selected_predictors:
            remaining_predictors = list(set(selected_predictors) -␣
↪set([predictor]))
            subset_X_train = X_train[remaining_predictors]
            subset_X_test = X_test[remaining_predictors]

            model = LinearRegression()
            model.fit(subset_X_train, y_train)
            predictions = model.predict(subset_X_test)
            mse = mean_squared_error(y_test, predictions)

            if mse < best_mse:
                best_mse = mse
                best_subset = remaining_predictors

        if best_subset:
            selected_predictors = best_subset

    return selected_predictors, best_mse

backward_selected_predictors, backward_best_mse =␣
↪backward_stepwise_selection(X_train, X_test, y_train, y_test, predictors)

print(f"Backward Stepwise Selection Predictors: {backward_selected_predictors}")
print(f"Test Error (MSE) for Backward Stepwise Selection: {backward_best_mse}")
```

```
Forward Stepwise Selection Predictors: ['income_composition_resources',
'hiv_aids', 'adult_mortality', 'bmi', 'diphtheria', 'percentage_expenditure',
'polio']
Test Error (MSE) for Forward Stepwise Selection: 13.624697136527905
Backward Stepwise Selection Predictors: ['hiv_aids', 'schooling',
'under_five_deaths', 'diphtheria', 'bmi', 'percentage_expenditure',
'income_composition_resources', 'adult_mortality']
Test Error (MSE) for Backward Stepwise Selection: 13.639252315189907
```

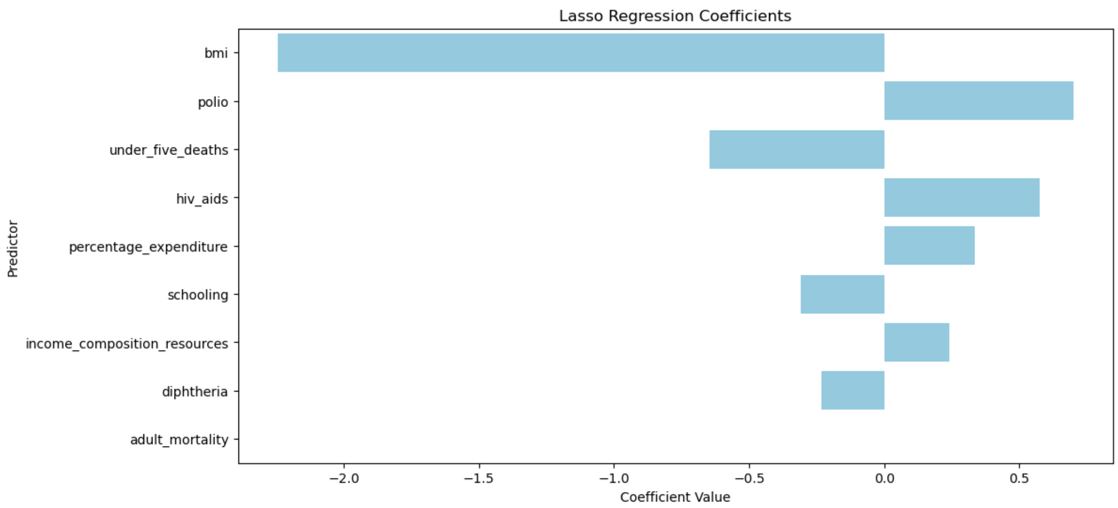
[22]:

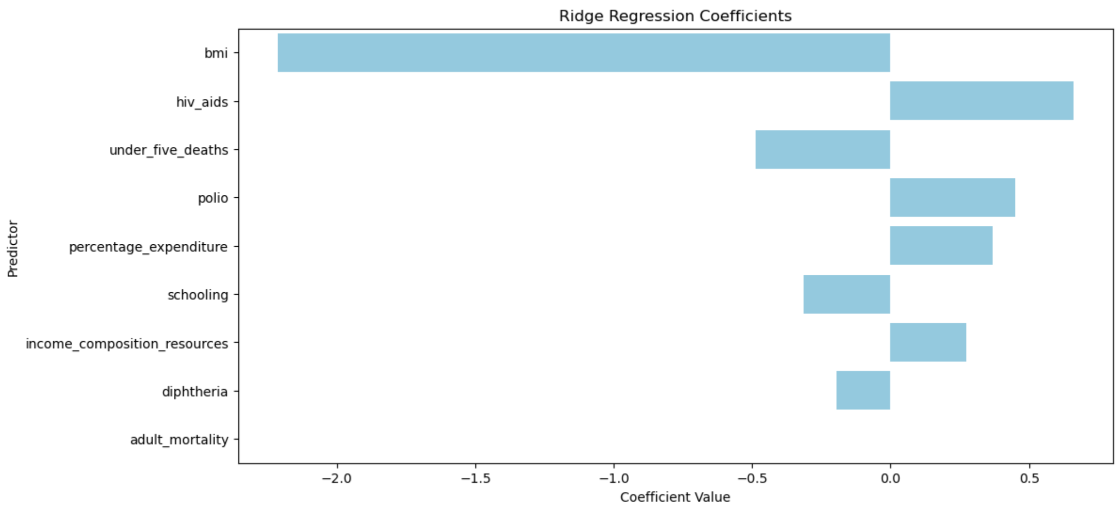
```
# Lasso and Ridge Regression Models

# Initialize scaler
scaler = StandardScaler()

# Fit scaler on train data and transform both train and test set
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

# Lasso with CV and Feature Scaling
lasso_params = {'alpha': np.logspace(-4, 4, 9)}
lasso_model = LassoCV(alphas=lasso_params['alpha'], cv=5)
lasso_model.fit(X_train_scaled, y_train)
lasso_pred = lasso_model.predict(X_test_scaled)
lasso_mse = mean_squared_error(y_test, lasso_pred)

print(f"Lasso Regression Best Alpha: {lasso_model.alpha_}")
print(f"Test Error (MSE) for Lasso Regression: {lasso_mse}")

# Get Lasso Coefficients
lasso_coefs = lasso_model.coef_

# Print Lasso Coefficients
sorted_lasso_coefs = sorted(zip(predictors, lasso_coefs), key=lambda x:␣
↪abs(x[1]), reverse=True)
print("Lasso Coefficients:")
for feature, coef in sorted_lasso_coefs:
    print(f"{feature}: {coef}")

# Ridge with CV and Feature Scaling
ridge_params = {'alpha': np.logspace(-4, 4, 9)}
ridge_model = RidgeCV(alphas=ridge_params['alpha'], cv=5)
ridge_model.fit(X_train_scaled, y_train)
ridge_pred = ridge_model.predict(X_test_scaled)
ridge_mse = mean_squared_error(y_test, ridge_pred)

print(f"Ridge Regression Best Alpha: {ridge_model.alpha_}")
print(f"Test Error (MSE) for Ridge Regression: {ridge_mse}")
```

```python
# Get Ridge Coefficients
ridge_coefs = ridge_model.coef_

# Print Ridge Coefficients
sorted_ridge_coefs = sorted(zip(predictors, ridge_coefs), key=lambda x:
↪abs(x[1]), reverse=True)
print("Ridge Coefficients:")
for feature, coef in sorted_ridge_coefs:
    print(f"{feature}: {coef}")

# Extract features and coefficients
features = [feature for feature, coef in sorted_lasso_coefs]
coefficients = [coef for feature, coef in sorted_lasso_coefs]

# Plot Lasso coefficients
plt.figure(figsize=(12, 6))
sns.barplot(x=coefficients, y=features, color='skyblue')
plt.title('Lasso Regression Coefficients')
plt.xlabel('Coefficient Value')
plt.ylabel('Predictor')
plt.show()

# Extract features and coefficients for Ridge Regression
ridge_features = [feature for feature, coef in sorted_ridge_coefs]
ridge_coefficients = [coef for feature, coef in sorted_ridge_coefs]

# Plot Ridge Regression coefficients
plt.figure(figsize=(12, 6))
sns.barplot(x=ridge_coefficients, y=ridge_features, color='skyblue')
plt.title('Ridge Regression Coefficients')
plt.xlabel('Coefficient Value')
plt.ylabel('Predictor')
plt.show()
```

```
Lasso Regression Best Alpha: 0.01
Test Error (MSE) for Lasso Regression: 13.895711091324577
Lasso Coefficients:
bmi: -2.2434612232196884
polio: 0.698721763941445
under_five_deaths: -0.6465963777816681
hiv_aids: 0.5743211805680589
percentage_expenditure: 0.3362297706715429
schooling: -0.3085431958482918
income_composition_resources: 0.2396820622240113
diphtheria: -0.2305580112219805
adult_mortality: 0.0
Ridge Regression Best Alpha: 100.0
```

```
Test Error (MSE) for Ridge Regression: 13.843180968055705
Ridge Coefficients:
bmi: -2.2128468574655855
hiv_aids: 0.659022262548571
under_five_deaths: -0.48675012358342384
polio: 0.450570589669475
percentage_expenditure: 0.3684517042753042
schooling: -0.31567817309625473
income_composition_resources: 0.27498420309674887
diphtheria: -0.19517525020260246
adult_mortality: 0.0
```



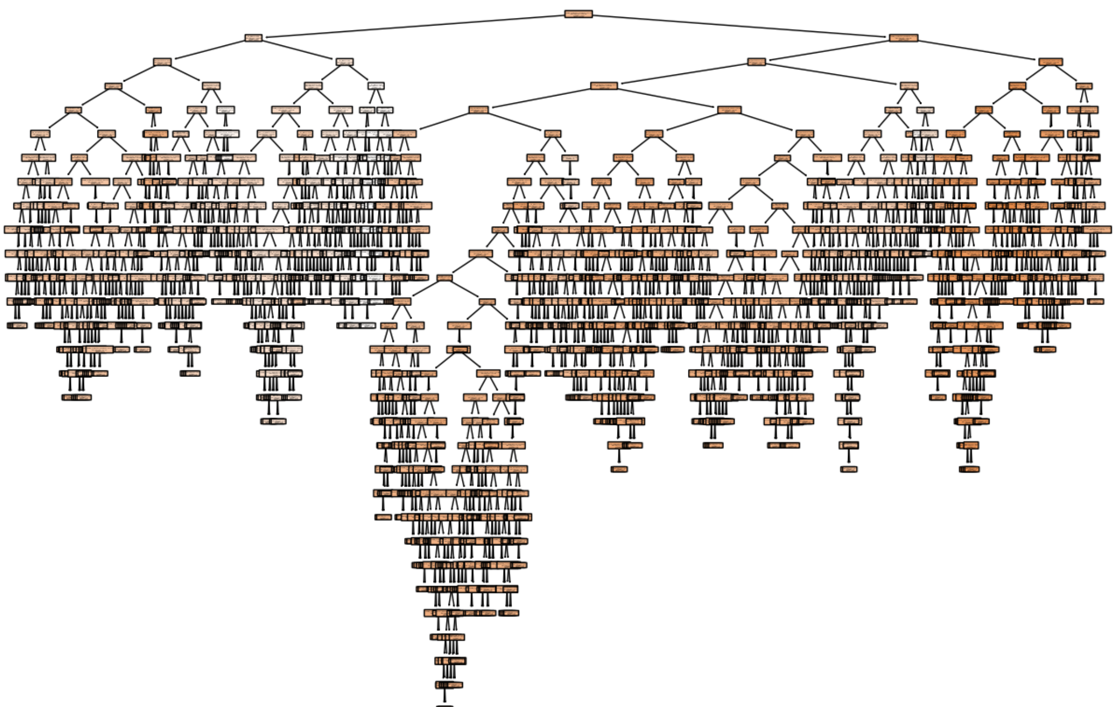



[23]:
```
# Decision Tree Model

# Initialize Decision Tree Regressor
tree_regressor = DecisionTreeRegressor(random_state=42)

# Fit model on training data
tree_regressor.fit(X_train, y_train)

# Make predictions on test set
y_pred = tree_regressor.predict(X_test)

# Evaluate the model using MSE
mse = mean_squared_error(y_test, y_pred)
print(f"Mean Squared Error for Decision Tree (Before Pruning): {mse}")

# Display tree
plt.figure(figsize=(15, 10))
plot_tree(tree_regressor, feature_names=X.columns, filled=True, rounded=True)
plt.show()

# Prune tree for optimal tree size

# Define parameters
param_grid = {'max_leaf_nodes': range(2, 200)}

# Create decision tree regressor
tree_regressor_cv = DecisionTreeRegressor(random_state=42)

# Cross Validation
grid_search = GridSearchCV(tree_regressor_cv, param_grid, cv=5,␣
 ↪scoring='neg_mean_squared_error')
grid_search.fit(X_train, y_train)

# Print optimal tree size
best_tree_size = grid_search.best_params_['max_leaf_nodes']
print("Optimal Tree Size:", best_tree_size)

# Create a pruned tree with the optimal tree size
pruned_tree = DecisionTreeRegressor(max_leaf_nodes=best_tree_size,␣
 ↪random_state=42)
pruned_tree.fit(X_train, y_train)

# Make predictions on the test set
y_pred_pruned = pruned_tree.predict(X_test)

# Evaluate the pruned tree using MSE
mse_pruned = mean_squared_error(y_test, y_pred_pruned)
```

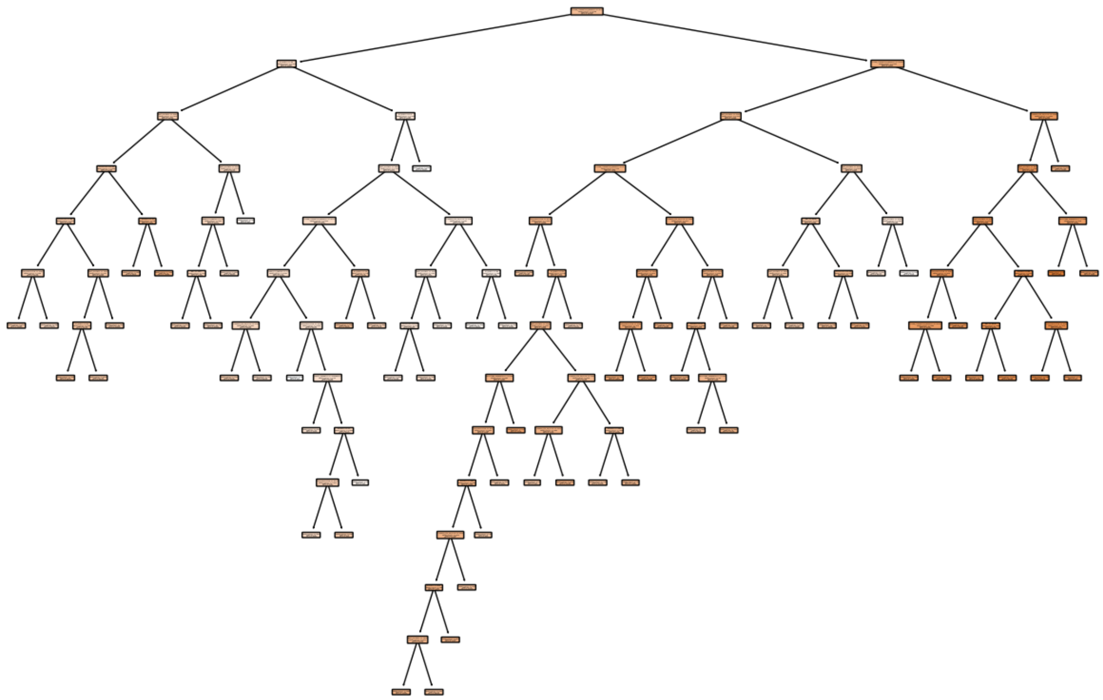
```
print(f"Mean Squared Error For Decision Tree (Pruned): {mse_pruned}")

# Display Pruned Tree
plt.figure(figsize=(15, 10))
plot_tree(pruned_tree, feature_names=X_train.columns, filled=True, rounded=True)
plt.show()

# Display Pruned Tree Structure
tree_structure_pruned = export_text(pruned_tree, feature_names=list(X_train.
↪columns))
print("\nDecision Tree Structure (Pruned):\n", tree_structure_pruned)

# Display Un-Pruned Tree Information
print("Original Decision Tree Information:")
print("Number of nodes in the original tree:", tree_regressor.tree_.node_count)
print("Depth of the original tree:", tree_regressor.get_depth())

# Display Pruned Tree Information
print("\nPruned Decision Tree Information:")
print("Number of nodes in the pruned tree:", pruned_tree.tree_.node_count)
print("Depth of the pruned tree:", pruned_tree.get_depth())

# Get feature importances from pruned tree
feature_importances_pruned = pruned_tree.feature_importances_

feature_importance_pruned_df = pd.DataFrame({'Feature': X.columns, 'Importance':␣
↪feature_importances_pruned})
feature_importance_pruned_df = feature_importance_pruned_df.
↪sort_values(by='Importance', ascending=False)

# Display feature importances
print("Feature Importances of Pruned Tree:")
print(feature_importance_pruned_df)

# Create a df
feature_importance_pruned_df = pd.DataFrame({'Feature': X.columns, 'Importance':␣
↪feature_importances_pruned})
feature_importance_pruned_df = feature_importance_pruned_df.
↪sort_values(by='Importance', ascending=False)

# Plot Importances
plt.figure(figsize=(5, 3))
sns.barplot(x='Importance', y='Feature', data=feature_importance_pruned_df,␣
↪color='skyblue')
plt.title('Feature Importances of Pruned Decision Tree')
plt.xlabel('Importance')
```

```python
plt.ylabel('Feature')
plt.show()
```

```
Mean Squared Error for Decision Tree (Before Pruning): 8.628424242424243
```



```
Optimal Tree Size: 62
Mean Squared Error For Decision Tree (Pruned): 8.447601596001256
```



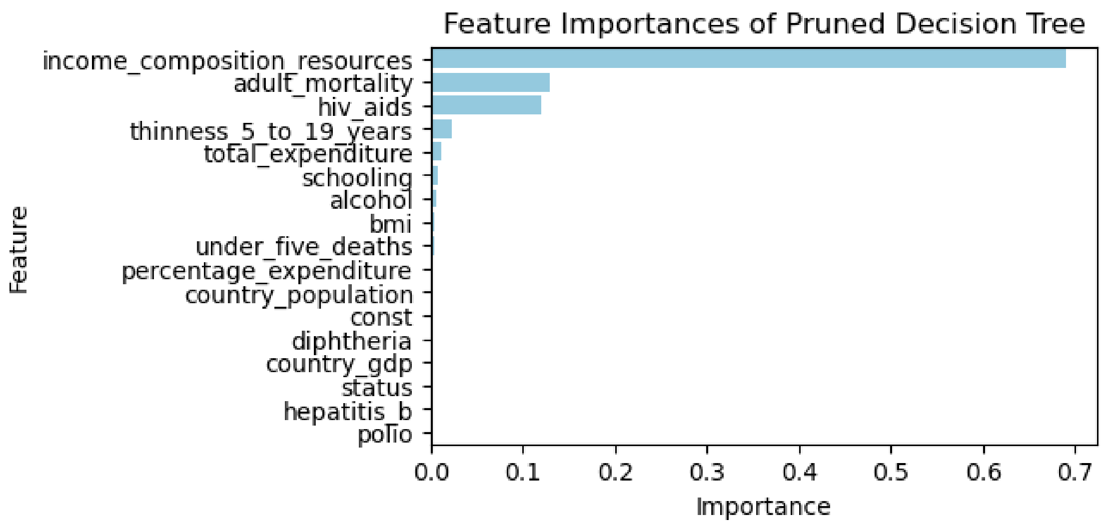
```
Decision Tree Structure (Pruned):
 |--- income_composition_resources <= 0.56
|   |--- hiv_aids <= 1.65
|   |   |--- adult_mortality <= 248.00
|   |   |   |--- schooling <= 12.25
|   |   |   |   |--- schooling <= 7.85
|   |   |   |   |   |--- total_expenditure <= 0.06
|   |   |   |   |   |   |--- value: [63.96]
|   |   |   |   |   |--- total_expenditure >  0.06
|   |   |   |   |   |   |--- value: [59.42]
|   |   |   |   |--- schooling >  7.85
|   |   |   |   |   |--- adult_mortality <= 197.50
|   |   |   |   |   |   |--- hiv_aids <= 0.25
|   |   |   |   |   |   |   |--- value: [68.18]
|   |   |   |   |   |   |--- hiv_aids >  0.25
|   |   |   |   |   |   |   |--- value: [65.11]
|   |   |   |   |   |--- adult_mortality >  197.50
|   |   |   |   |   |   |--- value: [64.51]
|   |   |   |--- schooling >  12.25
|   |   |   |   |--- alcohol <= 1.21
|   |   |   |   |   |--- value: [68.15]
|   |   |   |   |--- alcohol >  1.21
|   |   |   |   |   |--- value: [73.59]
```

```
|   |   |--- adult_mortality >  248.00
|   |   |   |--- adult_mortality <= 373.50
|   |   |   |   |--- under_five_deaths <= 59.00
|   |   |   |   |   |--- bmi <= 16.90
|   |   |   |   |   |   |--- value: [63.49]
|   |   |   |   |   |--- bmi >  16.90
|   |   |   |   |   |   |--- value: [60.83]
|   |   |   |   |--- under_five_deaths >  59.00
|   |   |   |   |   |--- value: [58.32]
|   |   |   |--- adult_mortality >  373.50
|   |   |   |   |--- value: [48.70]
|   |--- hiv_aids >  1.65
|   |   |--- hiv_aids <= 16.10
|   |   |   |--- adult_mortality <= 359.50
|   |   |   |   |--- income_composition_resources <= 0.52
|   |   |   |   |   |--- under_five_deaths <= 32.00
|   |   |   |   |   |   |--- thinness_5_to_19_years <= 0.13
|   |   |   |   |   |   |   |--- value: [62.43]
|   |   |   |   |   |   |--- thinness_5_to_19_years >  0.13
|   |   |   |   |   |   |   |--- value: [58.19]
|   |   |   |   |   |--- under_five_deaths >  32.00
|   |   |   |   |   |   |--- total_expenditure <= 0.01
|   |   |   |   |   |   |   |--- value: [45.30]
|   |   |   |   |   |   |--- total_expenditure >  0.01
|   |   |   |   |   |   |   |--- country_population <= 34608812.00
|   |   |   |   |   |   |   |   |--- value: [56.05]
|   |   |   |   |   |   |   |--- country_population >  34608812.00
|   |   |   |   |   |   |   |   |--- alcohol <= 5.71
|   |   |   |   |   |   |   |   |   |--- total_expenditure <= 0.04
|   |   |   |   |   |   |   |   |   |   |--- value: [58.85]
|   |   |   |   |   |   |   |   |   |--- total_expenditure >  0.04
|   |   |   |   |   |   |   |   |   |   |--- value: [65.50]
|   |   |   |   |   |   |   |   |--- alcohol >  5.71
|   |   |   |   |   |   |   |   |   |--- value: [49.20]
|   |   |   |   |--- income_composition_resources >  0.52
|   |   |   |   |   |--- hiv_aids <= 2.15
|   |   |   |   |   |   |--- value: [68.67]
|   |   |   |   |   |--- hiv_aids >  2.15
|   |   |   |   |   |   |--- value: [61.78]
|   |   |   |--- adult_mortality >  359.50
|   |   |   |   |--- thinness_5_to_19_years <= 0.17
|   |   |   |   |   |--- adult_mortality <= 442.00
|   |   |   |   |   |   |--- schooling <= 10.15
|   |   |   |   |   |   |   |--- value: [54.21]
|   |   |   |   |   |   |--- schooling >  10.15
|   |   |   |   |   |   |   |--- value: [57.37]
|   |   |   |   |   |--- adult_mortality >  442.00
|   |   |   |   |   |   |--- value: [52.35]
```

```
|   |   |   |   |--- thinness_5_to_19_years >  0.17
|   |   |   |   |   |--- hiv_aids <= 2.85
|   |   |   |   |   |   |--- value: [48.53]
|   |   |   |   |   |--- hiv_aids >  2.85
|   |   |   |   |   |   |--- value: [51.91]
|   |   |--- hiv_aids >  16.10
|   |   |   |--- value: [46.62]
|--- income_composition_resources >  0.56
|   |--- income_composition_resources <= 0.80
|   |   |--- adult_mortality <= 216.50
|   |   |   |--- income_composition_resources <= 0.70
|   |   |   |   |--- total_expenditure <= 0.03
|   |   |   |   |   |--- value: [67.29]
|   |   |   |   |--- total_expenditure >  0.03
|   |   |   |   |   |--- hiv_aids <= 3.45
|   |   |   |   |   |   |--- adult_mortality <= 175.50
|   |   |   |   |   |   |   |--- percentage_expenditure <= 10.29
|   |   |   |   |   |   |   |   |--- total_expenditure <= 0.11
|   |   |   |   |   |   |   |   |   |--- alcohol <= 7.00
|   |   |   |   |   |   |   |   |   |   |--- thinness_5_to_19_years <= 0.30
|   |   |   |   |   |   |   |   |   |   |   |--- truncated branch of depth 3
|   |   |   |   |   |   |   |   |   |   |--- thinness_5_to_19_years >  0.30
|   |   |   |   |   |   |   |   |   |   |   |--- value: [67.63]
|   |   |   |   |   |   |   |   |   |--- alcohol >  7.00
|   |   |   |   |   |   |   |   |   |   |--- value: [65.50]
|   |   |   |   |   |   |   |   |--- total_expenditure >  0.11
|   |   |   |   |   |   |   |   |   |--- value: [65.15]
|   |   |   |   |   |   |   |--- percentage_expenditure >  10.29
|   |   |   |   |   |   |   |   |--- value: [77.75]
|   |   |   |   |   |   |--- adult_mortality >  175.50
|   |   |   |   |   |   |   |--- thinness_5_to_19_years <= 0.05
|   |   |   |   |   |   |   |   |--- thinness_5_to_19_years <= 0.01
|   |   |   |   |   |   |   |   |   |--- value: [65.00]
|   |   |   |   |   |   |   |   |--- thinness_5_to_19_years >  0.01
|   |   |   |   |   |   |   |   |   |--- value: [72.71]
|   |   |   |   |   |   |   |--- thinness_5_to_19_years >  0.05
|   |   |   |   |   |   |   |   |--- alcohol <= 4.29
|   |   |   |   |   |   |   |   |   |--- value: [67.48]
|   |   |   |   |   |   |   |   |--- alcohol >  4.29
|   |   |   |   |   |   |   |   |   |--- value: [70.54]
|   |   |   |   |   |--- hiv_aids >  3.45
|   |   |   |   |   |   |--- value: [61.43]
|   |   |   |--- income_composition_resources >  0.70
|   |   |   |   |--- thinness_5_to_19_years <= 0.05
|   |   |   |   |   |--- adult_mortality <= 127.50
|   |   |   |   |   |   |--- total_expenditure <= 0.08
|   |   |   |   |   |   |   |--- value: [75.87]
|   |   |   |   |   |   |--- total_expenditure >  0.08
```

```
|   |   |   |   |   |   |   |--- value: [77.52]
|   |   |   |   |   |--- adult_mortality >  127.50
|   |   |   |   |   |   |--- value: [73.92]
|   |   |   |   |--- thinness_5_to_19_years >  0.05
|   |   |   |   |   |--- adult_mortality <= 177.50
|   |   |   |   |   |   |--- alcohol <= 9.77
|   |   |   |   |   |   |   |--- value: [73.71]
|   |   |   |   |   |   |--- alcohol >  9.77
|   |   |   |   |   |   |   |--- percentage_expenditure <= 0.19
|   |   |   |   |   |   |   |   |--- value: [65.75]
|   |   |   |   |   |   |   |--- percentage_expenditure >  0.19
|   |   |   |   |   |   |   |   |--- value: [71.73]
|   |   |   |   |   |--- adult_mortality >  177.50
|   |   |   |   |   |   |--- value: [71.07]
|   |   |--- adult_mortality >  216.50
|   |   |   |--- adult_mortality <= 371.00
|   |   |   |   |--- bmi <= 55.35
|   |   |   |   |   |--- adult_mortality <= 262.50
|   |   |   |   |   |   |--- value: [66.74]
|   |   |   |   |   |--- adult_mortality >  262.50
|   |   |   |   |   |   |--- value: [63.59]
|   |   |   |   |--- bmi >  55.35
|   |   |   |   |   |--- schooling <= 15.45
|   |   |   |   |   |   |--- value: [68.96]
|   |   |   |   |   |--- schooling >  15.45
|   |   |   |   |   |   |--- value: [74.33]
|   |   |   |--- adult_mortality >  371.00
|   |   |   |   |--- adult_mortality <= 575.00
|   |   |   |   |   |--- value: [55.71]
|   |   |   |   |--- adult_mortality >  575.00
|   |   |   |   |   |--- value: [47.25]
|   |--- income_composition_resources >  0.80
|   |   |--- thinness_5_to_19_years <= 0.04
|   |   |   |--- adult_mortality <= 80.00
|   |   |   |   |--- adult_mortality <= 67.50
|   |   |   |   |   |--- total_expenditure <= 0.08
|   |   |   |   |   |   |--- income_composition_resources <= 0.88
|   |   |   |   |   |   |   |--- value: [78.44]
|   |   |   |   |   |   |--- income_composition_resources >  0.88
|   |   |   |   |   |   |   |--- value: [81.61]
|   |   |   |   |   |--- total_expenditure >  0.08
|   |   |   |   |   |   |--- value: [82.05]
|   |   |   |   |--- adult_mortality >  67.50
|   |   |   |   |   |--- alcohol <= 9.86
|   |   |   |   |   |   |--- bmi <= 60.35
|   |   |   |   |   |   |   |--- value: [80.33]
|   |   |   |   |   |   |--- bmi >  60.35
|   |   |   |   |   |   |   |--- value: [83.78]
```

```
|   |   |   |   |   |--- alcohol >  9.86
|   |   |   |   |   |   |--- total_expenditure <= 0.11
|   |   |   |   |   |   |   |--- value: [85.28]
|   |   |   |   |   |   |--- total_expenditure >  0.11
|   |   |   |   |   |   |   |--- value: [81.30]
|   |   |   |--- adult_mortality >  80.00
|   |   |   |   |--- percentage_expenditure <= 0.69
|   |   |   |   |   |--- value: [89.00]
|   |   |   |   |--- percentage_expenditure >  0.69
|   |   |   |   |   |--- value: [79.54]
|   |   |--- thinness_5_to_19_years >  0.04
|   |   |   |--- value: [74.09]

Original Decision Tree Information:
Number of nodes in the original tree: 2351
Depth of the original tree: 29

Pruned Decision Tree Information:
Number of nodes in the pruned tree: 123
Depth of the pruned tree: 13
Feature Importances of Pruned Tree:
                         Feature  Importance
16  income_composition_resources    0.689602
2                adult_mortality    0.129980
12                      hiv_aids    0.119355
14        thinness_5_to_19_years    0.022546
10             total_expenditure    0.011108
15                     schooling    0.008734
3                        alcohol    0.006877
6                            bmi    0.004306
7               under_five_deaths    0.003819
4         percentage_expenditure    0.002594
13            country_population    0.001078
0                          const    0.000000
11                    diphtheria    0.000000
9                    country_gdp    0.000000
1                         status    0.000000
5                    hepatitis_b    0.000000
8                          polio    0.000000
```




[24]:
```python
# Random Forest Model

# Initialize Random Forest Regressor
random_forest_model = RandomForestRegressor(n_estimators=100, random_state=42)

# Fit model on training data
random_forest_model.fit(X_train, y_train)

# Predict on test set
y_pred_rf = random_forest_model.predict(X_test)

# Calculate test MSE for Random Forest
test_mse_rf = mean_squared_error(y_test, y_pred_rf)
print("Test MSE for Random Forest:", test_mse_rf)

# Determine feature importances
feature_importances_rf = random_forest_model.feature_importances_
feature_importance_rf = pd.DataFrame({'Feature': X_train.columns, 'Importance':␣
↪feature_importances_rf})
feature_importance_rf = feature_importance_rf.sort_values(by='Importance',␣
↪ascending=False)

# Display feature importances
print("Feature Importance:")
print(feature_importance_rf)
```

```
Test MSE for Random Forest: 3.5643493545454628
Feature Importance:
                        Feature  Importance
```

```
16  income_composition_resources    0.607003
12                      hiv_aids    0.182911
2                adult_mortality    0.125515
14          thinness_5_to_19_years  0.023084
10             total_expenditure    0.010435
15                     schooling    0.010107
3                        alcohol    0.008716
7              under_five_deaths    0.006283
6                            bmi    0.005759
4         percentage_expenditure    0.003997
9                    country_gdp    0.003745
13            country_population    0.003543
8                          polio    0.003443
11                    diphtheria    0.002787
5                    hepatitis_b    0.002544
1                         status    0.000127
0                          const    0.000000
```

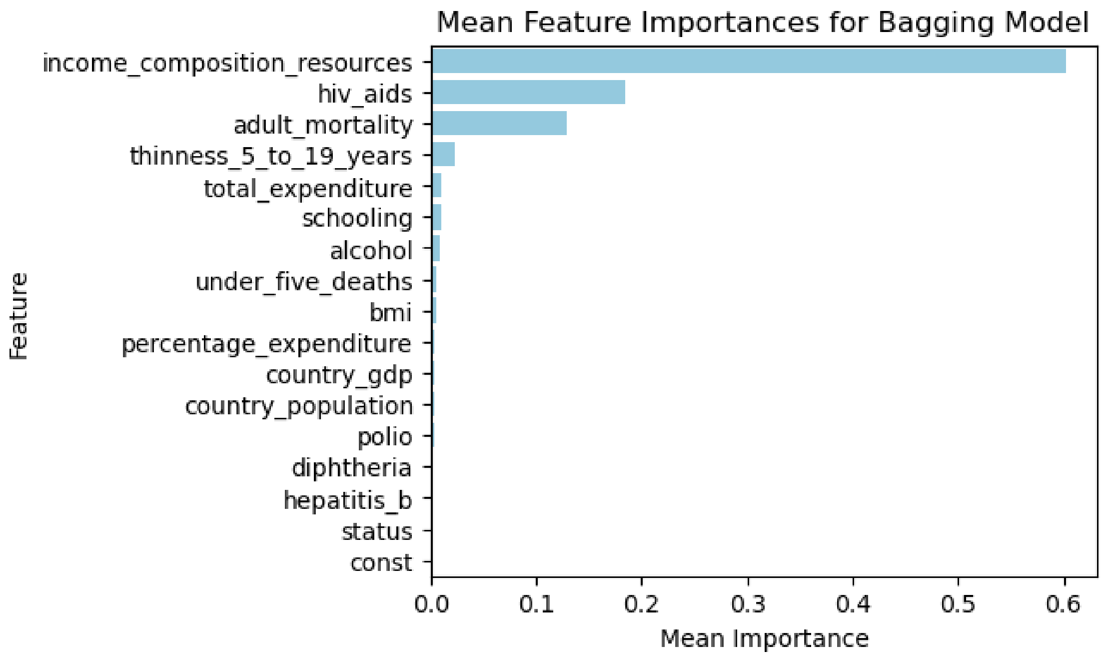
[25]:

```
# Bagging Model

# Initialize base regressor. Decision tree regressor used here instead of␣
↪gradient, as the decision tree regressor performs better. This is perhaps due␣
↪to possible overfitting of gradient boosting regressor
base_regressor = DecisionTreeRegressor(random_state=42)

# Initialize bagging regressor
bagging_regressor = BaggingRegressor(base_regressor, n_estimators=50,␣
↪random_state=42)

# Fit bagging regression to the training set
bagging_regressor.fit(X_train, y_train)

# Predict on the test set
bagging_preds = bagging_regressor.predict(X_test)

# Calculate test set MSE
bagging_mse = mean_squared_error(y_test, bagging_preds)

# Print test set MSE for bagging
print(f"Test Set MSE for Bagging: {bagging_mse}")


# Find feature importances, average all base estimators together and display list

# Get the list of base estimators fitted by bagging regressor
base_estimators = bagging_regressor.estimators_
```

```python
# Initialize an array for base estimator storage
all_feature_importances = np.zeros((len(base_estimators), X_train.shape[1]))

# Iterate through each base estimator and get feature importances
for i, base_estimator in enumerate(base_estimators):
    all_feature_importances[i, :] = base_estimator.feature_importances_

# Calculate mean importance across all iterations
mean_feature_importances = np.mean(all_feature_importances, axis=0)

feature_importance_df = pd.DataFrame({'Feature': X.columns, 'Mean_Importance':␣
↪mean_feature_importances})
feature_importance_df = feature_importance_df.sort_values(by='Mean_Importance',␣
↪ascending=False)

# Display mean feature importances
print("Mean Feature Importances for Bagging:")
print(feature_importance_df)

# Plot Feature Importances
plt.figure(figsize=(5, 4))
sns.barplot(x='Mean_Importance', y='Feature', data=feature_importance_df,␣
↪color='skyblue')
plt.title('Mean Feature Importances for Bagging Model')
plt.xlabel('Mean Importance')
plt.ylabel('Feature')
plt.show()
```

```
Test Set MSE for Bagging: 3.676756909090907
Mean Feature Importances for Bagging:
                         Feature  Mean_Importance
16  income_composition_resources         0.601978
12                      hiv_aids         0.184755
2                adult_mortality         0.129262
14          thinness_5_to_19_years       0.022835
10             total_expenditure         0.010366
15                     schooling         0.010257
3                        alcohol         0.008608
7               under_five_deaths        0.005798
6                            bmi         0.005739
4          percentage_expenditure        0.004233
9                    country_gdp         0.003830
13            country_population         0.003514
8                          polio         0.003494
11                    diphtheria         0.002770
5                    hepatitis_b         0.002471
1                         status         0.000091
```

```
0                             const         0.000000
```

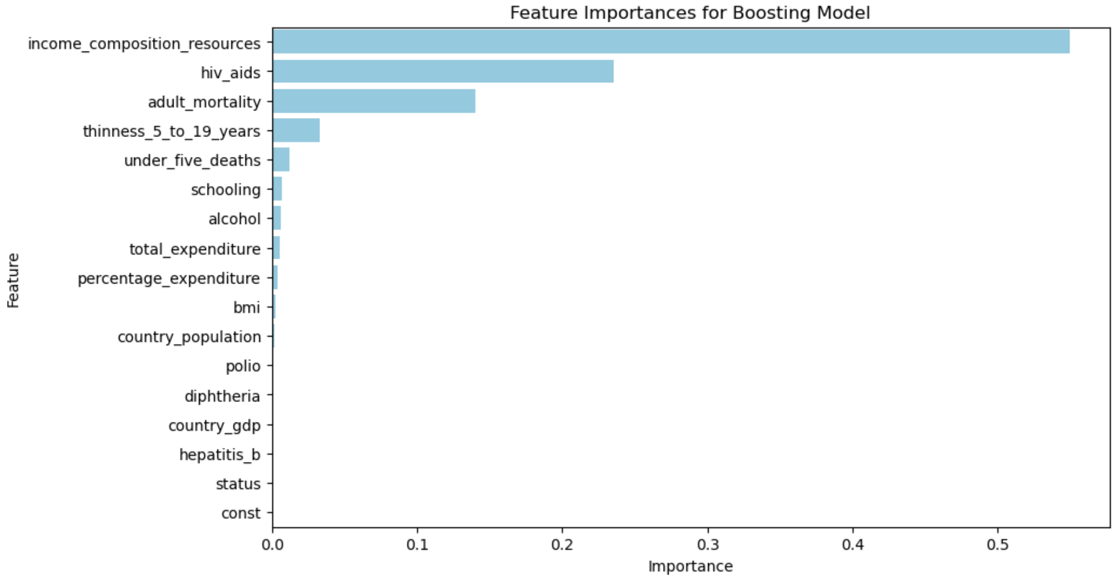



[26]:

```python
# Boosting Model

# Initialize the boosting regressor
boost_regressor = GradientBoostingRegressor(n_estimators=100, learning_rate=0.1,␣
↪random_state=42)

# Fit the boosting model on the training data
boost_regressor.fit(X_train, y_train)

# Predict on the test set
y_pred_boost = boost_regressor.predict(X_test)

# Calculate the test MSE
test_mse_boost = mean_squared_error(y_test, y_pred_boost)
print("Test Error (MSE) for Boosting :", test_mse_boost)

# Get feature importances
feature_importance = boost_regressor.feature_importances_

feature_importance_df = pd.DataFrame({'Feature': X_train.columns, 'Importance':␣
↪feature_importance})
feature_importance_df = feature_importance_df.sort_values(by='Importance',␣
↪ascending=False)
```

```
# Print feature importance
print("Feature Importances for Boosting:")
print(feature_importance_df)

# Plot Feature Importances
plt.figure(figsize=(10, 6))
sns.barplot(x='Importance', y='Feature', data=feature_importance_df,␣
 ↪color='skyblue')
plt.title('Feature Importances for Boosting Model')
plt.xlabel('Importance')
plt.ylabel('Feature')
plt.show()
```

```
Test Error (MSE) for Boosting : 5.017524037267107
Feature Importances for Boosting:
                         Feature  Importance
16  income_composition_resources    0.549505
12                      hiv_aids    0.235133
2                adult_mortality    0.140226
14          thinness_5_to_19_years    0.033077
7               under_five_deaths    0.011768
15                     schooling    0.007011
3                        alcohol    0.005941
10             total_expenditure    0.005557
4         percentage_expenditure    0.003669
6                            bmi    0.002548
13            country_population    0.001523
8                          polio    0.001245
11                    diphtheria    0.001240
9                    country_gdp    0.000955
5                    hepatitis_b    0.000444
1                         status    0.000160
0                          const    0.000000
```



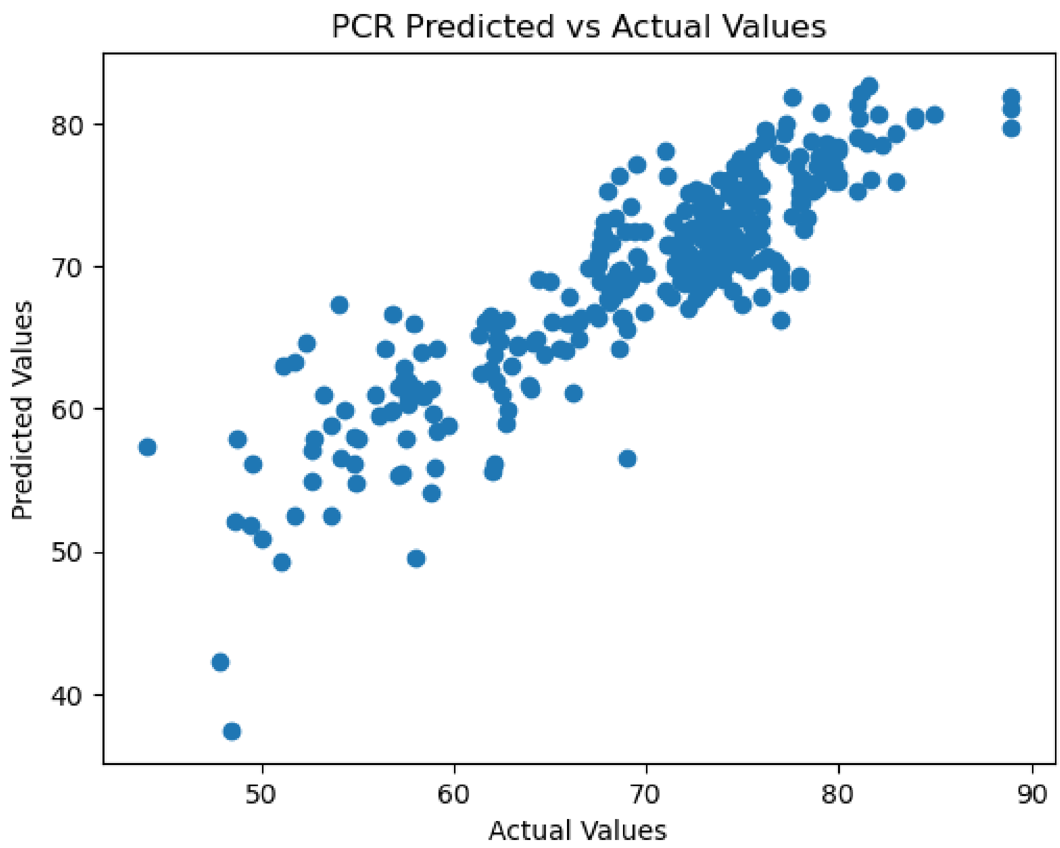

[27]:
```
# Partial Least Squares Model

# Initialize PLS regression model
pls_regressor = PLSRegression(n_components=3)

# Fit the PLS model on the training data
pls_regressor.fit(X_train, y_train)

# Predict on the test set
y_pred_pls = pls_regressor.predict(X_test)

# Calculate the test MSE
test_mse_pls = mean_squared_error(y_test, y_pred_pls)
print("PLS Test MSE:", test_mse_pls)

# Find Absolute Mean of each feature in the model and list in descending order

# Get Loadings
loadings = pls_regressor.x_loadings_

# Define feature names and put in df
feature_names = list(X.columns)
n_components = 3
loadings_df = pd.DataFrame(loadings, columns=[f'Component_{i+1}' for i in␣
 ↪range(n_components)])
loadings_df.index = feature_names
```

```python
# Calculate absolute mean for each feature
loadings_df['Absolute_Mean'] = loadings_df.abs().mean(axis=1)

# Sort df by absolute mean in descending order
loadings_df = loadings_df.sort_values(by='Absolute_Mean', ascending=False)

# Display Loadings
print(loadings_df)
```

```
PLS Test MSE: 13.847597559123793
                              Component_1  Component_2  Component_3  \
under_five_deaths               -0.139352    -0.232765    -0.687548
country_population              -0.044013    -0.228999    -0.730638
alcohol                          0.292114     0.301698    -0.330864
hiv_aids                        -0.194359     0.580887    -0.070790
adult_mortality                 -0.284462     0.463528    -0.011021
total_expenditure                0.138540     0.235638     0.338624
status                           0.293845     0.209124    -0.200710
schooling                        0.385298     0.048440     0.152277
country_gdp                      0.288171     0.241973     0.028085
percentage_expenditure           0.273866     0.246192     0.030274
bmi                              0.292712    -0.038532    -0.201162
polio                            0.203526     0.121874    -0.166183
income_composition_resources     0.366462    -0.023188     0.099598
diphtheria                       0.214479     0.121224    -0.143546
hepatitis_b                      0.145007     0.148748    -0.141164
thinness_5_to_19_years          -0.285279    -0.101390     0.013115
const                            0.000000     0.000000     0.000000

                              Absolute_Mean
under_five_deaths                  0.353222
country_population                 0.334550
alcohol                            0.308225
hiv_aids                           0.282012
adult_mortality                    0.253004
total_expenditure                  0.237601
status                             0.234559
schooling                          0.195338
country_gdp                        0.186077
percentage_expenditure             0.183444
bmi                                0.177468
polio                              0.163861
income_composition_resources       0.163083
diphtheria                         0.159750
hepatitis_b                        0.144973
thinness_5_to_19_years             0.133261
const                              0.000000
```

[28]:
```
# Principal Components Regression

# PCR with Cross-Validation
pca_params = {'pca__n_components': range(1, len(predictors) + 1)}
pca_model = Pipeline([
    ('pca', PCA()),
    ('regression', LinearRegression())
])

pca_grid = GridSearchCV(pca_model, param_grid=pca_params, cv=5,␣
↪scoring='neg_mean_squared_error')
pca_grid.fit(X_train, y_train)

# Predict using the best estimator
pcr_pred = pca_grid.predict(X_test)

# Calculate MSE
pcr_mse = mean_squared_error(y_test, pcr_pred)
print(f"PCR M: {pca_grid.best_params_['pca__n_components']}")
print(f"Test Error (MSE) for PCR: {pcr_mse}")

# Plot Predicted vs Actual Values
plt.scatter(y_test, pcr_pred)
plt.xlabel("Actual Values")
plt.ylabel("Predicted Values")
plt.title("PCR Predicted vs Actual Values")
plt.show()
```

```
PCR M: 9
Test Error (MSE) for PCR: 15.485975939003584
```




[29]:
```
# Linear Model Input

input_data = {
    'const': 52.47,
    'status': 1,
    'adult_mortality': 18.35,
    'alcohol': 9.5,
    'percentage_expenditure': 0.17,
    'hepatitis_b': 0.92,
    'bmi': 26.5,
    'under_five_deaths': 7.2,
    'polio': 0.93,
    'country_gdp': 70248.63,
    'total_expenditure': 0.29,
    'diphtheria': 0.80,
    'hiv_aids': 0.1,
    'country_population': 331900000,
    'thinness_5_to_19_years': 0.04,
    'schooling': 14,
    'income_composition_resources': 0.921
```

```
}

# Convert input data to df
input_df = pd.DataFrame([input_data])

# Make prediction linear
life_expectancy_prediction = linear_model.predict(input_df)


# Best Subset Selection Input

best_subset_input_data = {
    'adult_mortality': 18.35,
    'percentage_expenditure': 0.17,
    'bmi': 26.5,
    'under_five_deaths': 7.2,
    'polio': 0.93,
    'diphtheria': 0.80,
    'hiv_aids': 0.1,
    'schooling': 14,
    'income_composition_resources': 0.921
}

# Convert input data to df
best_subset_input_df = pd.DataFrame([best_subset_input_data])

# Make prediction best subset
best_subset_prediction = best_model.predict(best_subset_input_df)


# Standardize the input data
input_scaled = scaler.transform(input_df)

# Make prediction lasso
lasso_prediction = lasso_model.predict(input_scaled)

# Make prediction ridge
ridge_prediction = ridge_model.predict(input_scaled)

# Decision Tree Model
tree_pred = tree_regressor.predict(input_df)

# Random Forest Model
rf_pred = random_forest_model.predict(input_df)

# Bagging Model
bagging_pred = bagging_regressor.predict(input_df)
```

```
# Boosting Model
boost_pred = boost_regressor.predict(input_df)

# PLS Model
pls_pred = pls_regressor.predict(input_df)

# PCR Input data in the correct order
PCR_input_data_ordered = {
    'const': 52.47,
    'status': 1,
    'adult_mortality': 18.35,
    'alcohol': 9.5,
    'percentage_expenditure': 0.17,
    'hepatitis_b': 0.92,
    'bmi': 26.5,
    'under_five_deaths': 7.2,
    'polio': 0.93,
    'country_gdp': 70248.63,
    'total_expenditure': 0.29,
    'diphtheria': 0.80,
    'hiv_aids': 0.1,
    'country_population': 331900000,
    'thinness_5_to_19_years': 0.04,
    'schooling': 14,
    'income_composition_resources': 0.921
}

# Convert input data to df
PCR_input_df_ordered = pd.DataFrame([PCR_input_data_ordered])

# PCR Prediction
pca_input_ordered = pca_grid.best_estimator_.named_steps['pca'].
 ↪transform(PCR_input_df_ordered)
pcr_pred_ordered = pca_grid.predict(PCR_input_df_ordered)

# Actual Life Expectancy in the USA 2023 is 79.11, according to macrotrends.net
actual_us_life_expectancy = 79.11

# Display Predictions
print(f"Linear Regression Predicted Life Expectancy (USA 2023):␣
 ↪{life_expectancy_prediction[0]}")
print(f"Best Subset Selection Predicted Life Expectancy (USA 2023):␣
 ↪{best_subset_prediction[0]}")
print(f"Lasso Regression Predicted Life Expectancy (USA 2023):␣
 ↪{lasso_prediction[0]}")
```

```
print(f"Ridge Regression Predicted Life Expectancy (USA 2023):␣
↪{ridge_prediction[0]}")
print(f"Decision Tree Predicted Life Expectancy: {tree_pred[0]}")
print(f"Random Forest Predicted Life Expectancy: {rf_pred[0]}")
print(f"Bagging Predicted Life Expectancy: {bagging_pred[0]}")
print(f"Boosting Predicted Life Expectancy: {boost_pred[0]}")
print(f"PLS Predicted Life Expectancy: {pls_pred[0]}")
print(f"PCR Predicted Life Expectancy: {pcr_pred[0]}")

# Calculate residual errors for each model
linear_regression_error = actual_us_life_expectancy -␣
↪life_expectancy_prediction[0]
best_subset_error = actual_us_life_expectancy - best_subset_prediction[0]
lasso_regression_error = actual_us_life_expectancy - lasso_prediction[0]
ridge_regression_error = actual_us_life_expectancy - ridge_prediction[0]
decision_tree_error = actual_us_life_expectancy - tree_pred[0]
random_forest_error = actual_us_life_expectancy - rf_pred[0]
bagging_error = actual_us_life_expectancy - bagging_pred[0]
boosting_error = actual_us_life_expectancy - boost_pred[0]
pls_error = actual_us_life_expectancy - pls_pred[0]
pcr_error = actual_us_life_expectancy - pcr_pred[0]

# Create dictionary with errors
errors = {
    'Linear Regression': linear_regression_error,
    'Best Subset Selection': best_subset_error,
    'Lasso Regression': lasso_regression_error,
    'Ridge Regression': ridge_regression_error,
    'Decision Tree': decision_tree_error,
    'Random Forest': random_forest_error,
    'Bagging': bagging_error,
    'Boosting': boosting_error,
    'PLS': pls_error,
    'PCR': pcr_error,
}

# Sort order of errors
sorted_errors = sorted(errors.items(), key=lambda x: abs(x[1]), reverse=True)

# Display Residual Errors
print("\nResidual Errors:")
for model, error in sorted_errors:
    print(f"{model}: {error}")
```

```
# This data set includes WHO data from 2000 - 2015. I Would like to follow the␣
↪trend in each variable up to a future date, such as 2027. Then take that input␣
↪data and test it in these models to predict future life expectancy
# I would also like to run predictions on feature value inputs from other␣
↪countries to see how each model performs with different inputs.
```

```
Linear Regression Predicted Life Expectancy (USA 2023): 79.23609149104493
Best Subset Selection Predicted Life Expectancy (USA 2023): 76.64001894885261
Lasso Regression Predicted Life Expectancy (USA 2023): 79.22946797977693
Ridge Regression Predicted Life Expectancy (USA 2023): 81.0125065636481
Decision Tree Predicted Life Expectancy: 76.3
Random Forest Predicted Life Expectancy: 75.49000000000001
Bagging Predicted Life Expectancy: 75.386
Boosting Predicted Life Expectancy: 78.29134134238686
PLS Predicted Life Expectancy: 81.37115545052427
PCR Predicted Life Expectancy: 70.10706799687415

Residual Errors:
PCR: 9.00293200312585
Bagging: 3.7240000000000038
Random Forest: 3.6199999999999903
Decision Tree: 2.8100000000000023
Best Subset Selection: 2.4699810511473856
PLS: -2.261155450524271
Ridge Regression: -1.902506563648103
Boosting: 0.8186586576131418
Linear Regression: -0.12609149104493156
Lasso Regression: -0.11946797977692825
```

[30]:
```
# Principal Components Regression w/ Income Composition Resources as the Target

# Define predictors and target variable
predictors = ['status', 'alcohol', 'percentage_expenditure', 'hepatitis_b',␣
↪'bmi',
              'under_five_deaths', 'polio', 'total_expenditure', 'diphtheria',
              'hiv_aids', 'country_gdp', 'country_population',
              'thinness_5_to_19_years', 'adult_mortality',
              'schooling', 'life_expectancy']

target_variable = 'income_composition_resources'

X = life_expectancy_df[predictors]
y = life_expectancy_df[target_variable]

# Split data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state=42)
```

```python
# PCR with Cross Validation
pca_params = {'pca__n_components': range(1, len(predictors) + 1)}
pca_model = Pipeline([
    ('pca', PCA()),
    ('regression', LinearRegression())
])

pca_grid = GridSearchCV(pca_model, param_grid=pca_params, cv=5,␣
 ↪scoring='neg_mean_squared_error')
pca_grid.fit(X_train, y_train)

# Predict using the best estimator
pcr_pred = pca_grid.predict(X_test)

# Calculate MSE
pcr_mse = mean_squared_error(y_test, pcr_pred)
print(f"M: {pca_grid.best_params_['pca__n_components']}")
print(f"Test Error (MSE) for PCR (Income Composition Resources): {pcr_mse}")

# Use PCR model to predict income_composition_resources given current US␣
 ↪stastistics
icr_input_data = {
    'status': 1,
    'alcohol': 9.5,
    'percentage_expenditure': 0.17,
    'hepatitis_b': 0.92,
    'bmi': 26.5,
    'under_five_deaths': 7.2,
    'polio': 0.93,
    'total_expenditure': 0.29,
    'diphtheria': 0.80,
    'hiv_aids': 0.1,
    'country_gdp': 70248.63,
    'country_population': 331900000,
    'thinness_5_to_19_years': 0.04,
    'adult_mortality': 18.35,
    'schooling': 14,
    'life_expectancy': 79.11
}

# Create df with the input data
icr_input_data_df = pd.DataFrame([icr_input_data])

# Apply PCA transformation
icr_pca_transformed_data = pca_grid.best_estimator_['pca'].
 ↪transform(icr_input_data_df)
```

```python
# Make prediction on target
prediction = pca_grid.best_estimator_['regression'].
 ↪predict(icr_pca_transformed_data)

print(f"Predicted income_composition_resources: {prediction[0]}")

actual_us_icr = 0.921

# Calculate Residual Error
residual_error = actual_us_icr - prediction[0]

# Print Error
print(f"Residual Error: {residual_error}")
```

```
M: 15
Test Error (MSE) for PCR (Income Composition Resources): 0.005087865112819682
Predicted income_composition_resources: 0.8789390951466994
Residual Error: 0.04206090485330061
```

[ ]:

```python

```