In [1]:
```python
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.impute import SimpleImputer
from sklearn.pipeline import Pipeline
from sklearn.compose import ColumnTransformer
from sklearn.feature_selection import SelectKBest, f_classif
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score, precision_score, recall_score,
```

In [2]:
```python
data = pd.read_csv("C:/Users/PAVILION/Downloads/diabetes_012_health_indica
```

In [3]:
```python
data
```

Out[3]:

	Diabetes_012	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDiseaseoı
0	0.0	1.0	1.0	1.0	40.0	1.0	0.0	
1	0.0	0.0	0.0	0.0	25.0	1.0	0.0	
2	0.0	1.0	1.0	1.0	28.0	0.0	0.0	
3	0.0	1.0	0.0	1.0	27.0	0.0	0.0	
4	0.0	1.0	1.0	1.0	24.0	0.0	0.0	
...	...	...	...	...	...	...	...	
253675	0.0	1.0	1.0	1.0	45.0	0.0	0.0	
253676	2.0	1.0	1.0	1.0	18.0	0.0	0.0	
253677	0.0	0.0	0.0	1.0	28.0	0.0	0.0	
253678	0.0	1.0	0.0	1.0	23.0	0.0	0.0	
253679	2.0	1.0	1.0	1.0	25.0	0.0	0.0	

253680 rows × 22 columns

In [4]:

```
# Check for missing values
print(data.isnull().sum())

# Handle missing values (e.g., impute with mean or mode)
data.fillna(data.mean(), inplace=True)

# Explore data using descriptive statistics
print(data.describe())
```

```
Diabetes_012            0
HighBP                  0
HighChol                0
CholCheck               0
BMI                     0
Smoker                  0
Stroke                  0
HeartDiseaseorAttack    0
PhysActivity            0
Fruits                  0
Veggies                 0
HvyAlcoholConsump       0
AnyHealthcare           0
NoDocbcCost             0
GenHlth                 0
MentHlth                0
PhysHlth                0
DiffWalk                0
Sex                     0
Age                     0
Education               0
Income                  0
dtype: int64
        Diabetes_012         HighBP       HighChol      CholCheck  \
count  253680.000000  253680.000000  253680.000000  253680.000000   
mean        0.296921       0.429001       0.424121       0.962670   
std         0.698160       0.494934       0.494210       0.189571   
min         0.000000       0.000000       0.000000       0.000000   
25%         0.000000       0.000000       0.000000       1.000000   
50%         0.000000       0.000000       0.000000       1.000000   
75%         0.000000       1.000000       1.000000       1.000000   
max         2.000000       1.000000       1.000000       1.000000   

                 BMI         Smoker         Stroke  HeartDiseaseorAttack  
\
count  253680.000000  253680.000000  253680.000000         253680.000000   
mean       28.382364       0.443169       0.040571              0.094186   
std         6.608694       0.496761       0.197294              0.292087   
min        12.000000       0.000000       0.000000              0.000000   
25%        24.000000       0.000000       0.000000              0.000000   
50%        27.000000       0.000000       0.000000              0.000000   
75%        31.000000       1.000000       0.000000              0.000000   
max        98.000000       1.000000       1.000000              1.000000   

        PhysActivity         Fruits  ...  AnyHealthcare    NoDocbcCost  \
count  253680.000000  253680.000000  ...  253680.000000  253680.000000   
mean        0.756544       0.634256  ...       0.951053       0.084177   
std         0.429169       0.481639  ...       0.215759       0.277654   
min         0.000000       0.000000  ...       0.000000       0.000000   
25%         1.000000       0.000000  ...       1.000000       0.000000   
50%         1.000000       1.000000  ...       1.000000       0.000000   
75%         1.000000       1.000000  ...       1.000000       0.000000   
max         1.000000       1.000000  ...       1.000000       1.000000   

             GenHlth       MentHlth       PhysHlth       DiffWalk  \
count  253680.000000  253680.000000  253680.000000  253680.000000   
mean        2.511392       3.184772       4.242081       0.168224   
```

```
std          1.068477       7.412847       8.717951       0.374066
min          1.000000       0.000000       0.000000       0.000000
25%          2.000000       0.000000       0.000000       0.000000
50%          2.000000       0.000000       0.000000       0.000000
75%          3.000000       2.000000       3.000000       0.000000
max          5.000000      30.000000      30.000000       1.000000

                  Sex            Age      Education         Income
count   253680.000000  253680.000000  253680.000000  253680.000000
mean         0.440342       8.032119       5.050434       6.053875
std          0.496429       3.054220       0.985774       2.071148
min          0.000000       1.000000       1.000000       1.000000
25%          0.000000       6.000000       4.000000       5.000000
50%          0.000000       8.000000       5.000000       7.000000
75%          1.000000      10.000000       6.000000       8.000000
max          1.000000      13.000000       6.000000       8.000000

[8 rows x 22 columns]
```

In [5]:

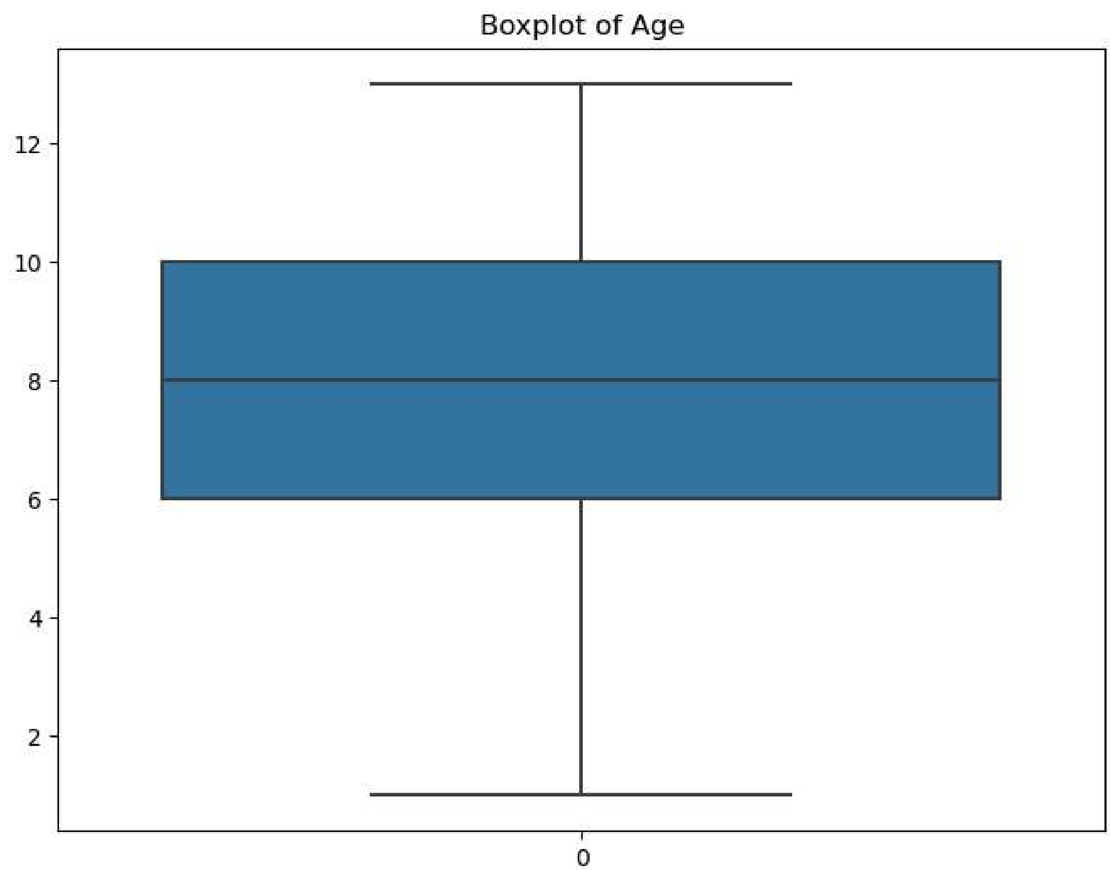
```python
# Check for duplicate rows
duplicates = data.duplicated()
print(duplicates.sum())

# Remove duplicate rows (if any)
data = data.drop_duplicates()
```

```
23899
```

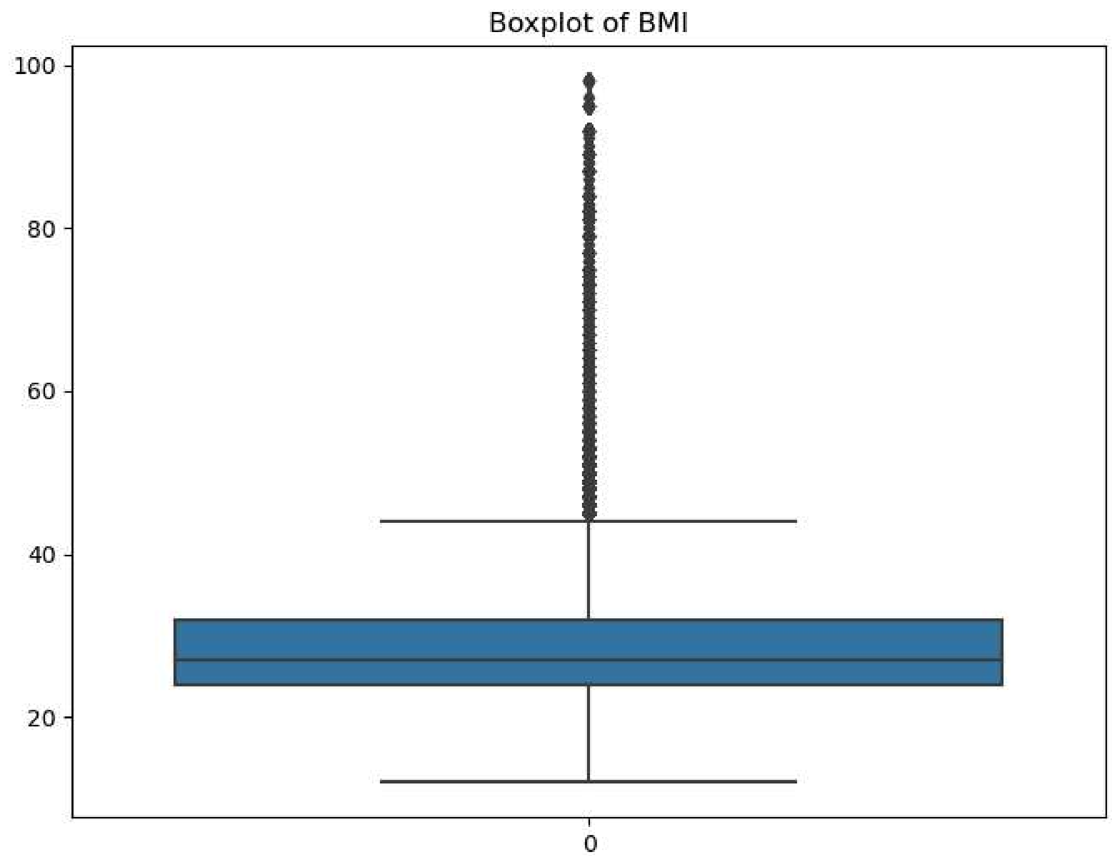
In [10]:

```
# Numerical columns for outlier detection
numerical_cols = ['Age', 'BMI']

# Function to detect outliers using IQR method
def detect_outliers_iqr(data):
    q1, q3 = np.percentile(data, [25, 75])
    iqr = q3 - q1
    lower_bound = q1 - 1.5 * iqr
    upper_bound = q3 + 1.5 * iqr
    outliers = data[(data < lower_bound) | (data > upper_bound)]
    return outliers

# Detect outliers in each numerical column
for col in numerical_cols:
    outliers = detect_outliers_iqr(data[col])
    print(f"Outliers in {col}: {outliers}")

    # Visualize outliers using boxplot
    plt.figure(figsize=(8, 6))
    sns.boxplot(data[col])
    plt.title(f"Boxplot of {col}")
    plt.show()
```

```
Outliers in Age: Series([], Name: Age, dtype: float64)
```



```
Outliers in BMI: 85        45.0
97        45.0
156       47.0
201       55.0
203       49.0
          ...
253370    46.0
253382    46.0
253402    49.0
253482    46.0
253675    45.0
Name: BMI, Length: 5638, dtype: float64
```



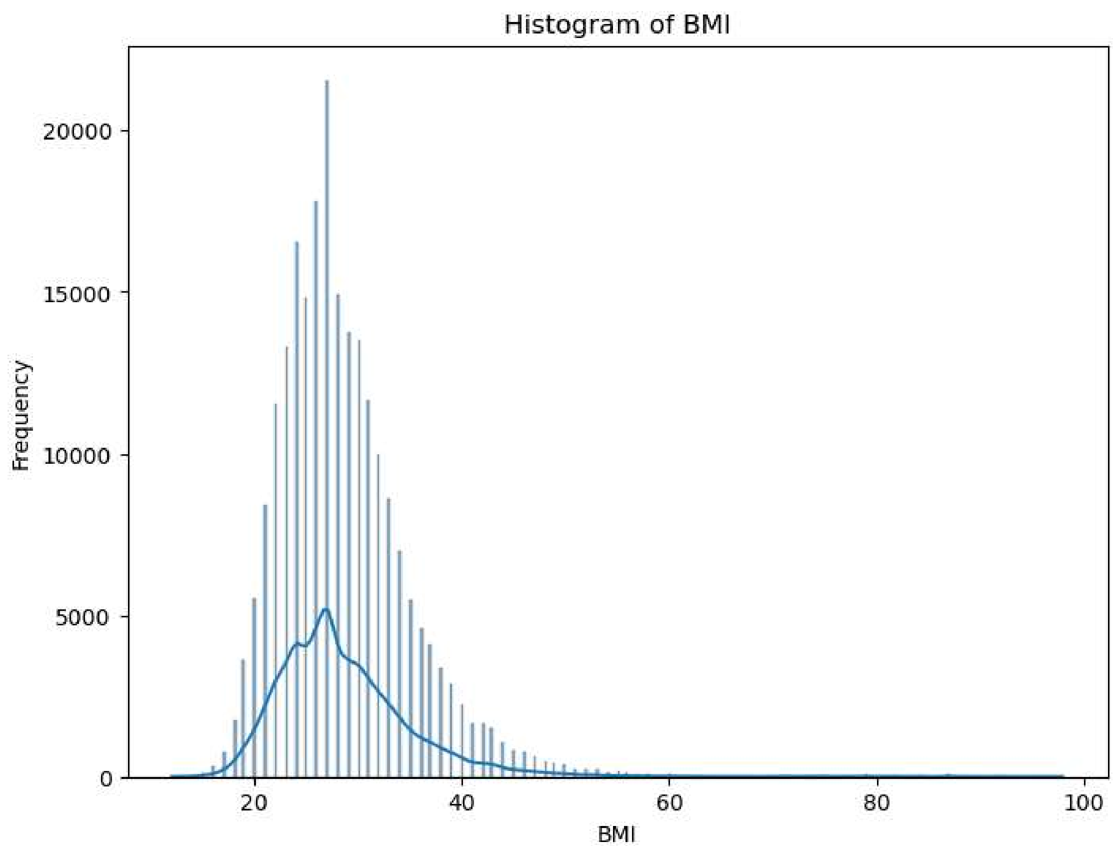
In [8]:

```
print(data.columns)
```

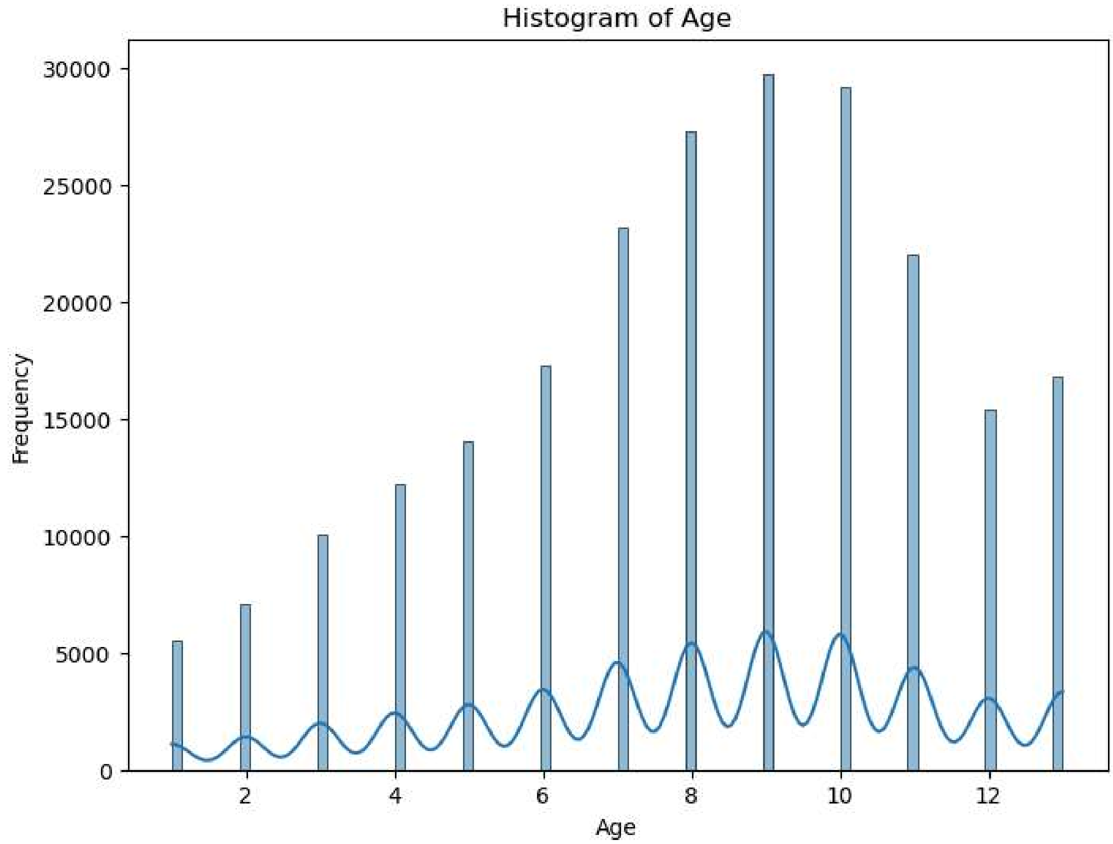
```
Index(['Diabetes_012', 'HighBP', 'HighChol', 'CholCheck', 'BMI', 'Smoke
r',
       'Stroke', 'HeartDiseaseorAttack', 'PhysActivity', 'Fruits', 'Veggi
es',
       'HvyAlcoholConsump', 'AnyHealthcare', 'NoDocbcCost', 'GenHlth',
       'MentHlth', 'PhysHlth', 'DiffWalk', 'Sex', 'Age', 'Education',
       'Income'],
      dtype='object')
```

In [11]:
```
# Numerical columns for skewness check
numerical_cols = ['BMI', 'Age']

# Calculate and print skewness for each numerical column
for col in numerical_cols:
    skewness = data[col].skew()
    print(f"Skewness of {col}: {skewness}")

    # Visualize the distribution using a histogram
    plt.figure(figsize=(8, 6))
    sns.histplot(data[col], kde=True)
    plt.title(f"Histogram of {col}")
    plt.xlabel(col)
    plt.ylabel("Frequency")
    plt.show()
```

```
Skewness of BMI: 2.063938014894699
```




```
Skewness of Age: -0.38514720011877446
```



In [12]:
```
import numpy as np

# Assuming 'data' is a Pandas Series or NumPy array
data_log = np.log(data + 1)  # Adding 1 to handle zero values
```

In [13]:
```
data_sqrt = np.sqrt(data)
```

In [18]:

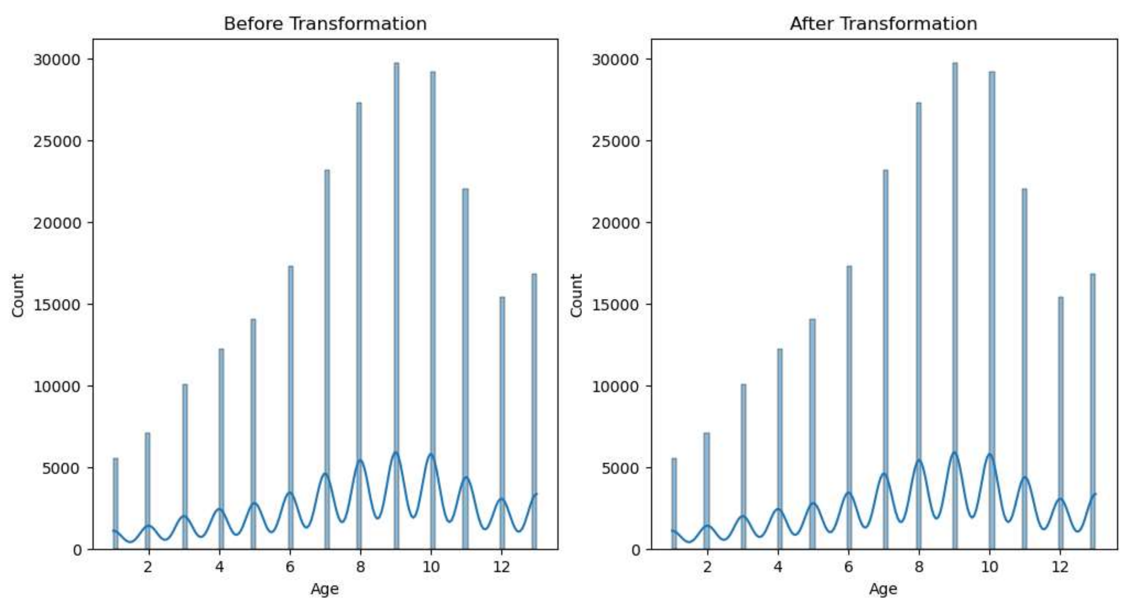
```
import pandas as pd
import numpy as np
from scipy.stats import boxcox



# Identify a skewed feature (e.g., 'Age')
skewness = data['Age'].skew()
print(f"Skewness of Age: {skewness}")

# Apply Box-Cox transformation
data['Age_transformed'], _ = boxcox(data['Age'])

# Check the skewness after transformation
skewness_transformed = data['Age_transformed'].skew()
print(f"Skewness of Age (transformed): {skewness_transformed}")
```

```
Skewness of Age: -0.38514720011877446
Skewness of Age (transformed): -0.21455876070301383

C:\Users\PAVILION\AppData\Local\Temp\ipykernel_21472\543037943.py:12: Set
tingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-do
cs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (http
s://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returni
ng-a-view-versus-a-copy)
  data['Age_transformed'], _ = boxcox(data['Age'])
```

In [19]:

```
# Numerical column to check for skewness (e.g., 'Age')
column_name = 'Age'

# Check skewness
skewness = data[column_name].skew()
print(f"Skewness of {column_name}: {skewness}")

# Apply logarithmic transformation if skewness is significant
if skewness > 1:  # Adjust the threshold as needed
    data[column_name] = np.log1p(data[column_name])

# Re-check skewness after transformation
skewness_after_transform = data[column_name].skew()
print(f"Skewness of {column_name} after transformation: {skewness_after_tr

# Visualize the distribution before and after transformation
plt.figure(figsize=(12, 6))
plt.subplot(1, 2, 1)
sns.histplot(data[column_name], kde=True)
plt.title('Before Transformation')

plt.subplot(1, 2, 2)
sns.histplot(data[column_name], kde=True)
plt.title('After Transformation')

plt.show()
```

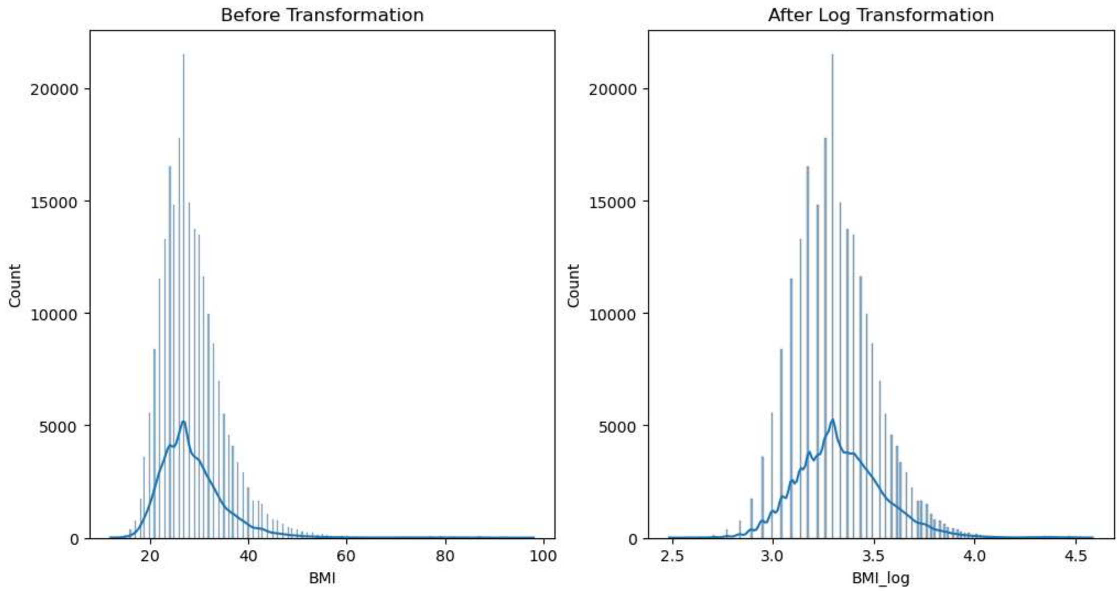
```
Skewness of Age: -0.38514720011877446
Skewness of Age after transformation: -0.38514720011877446
```



In [20]:

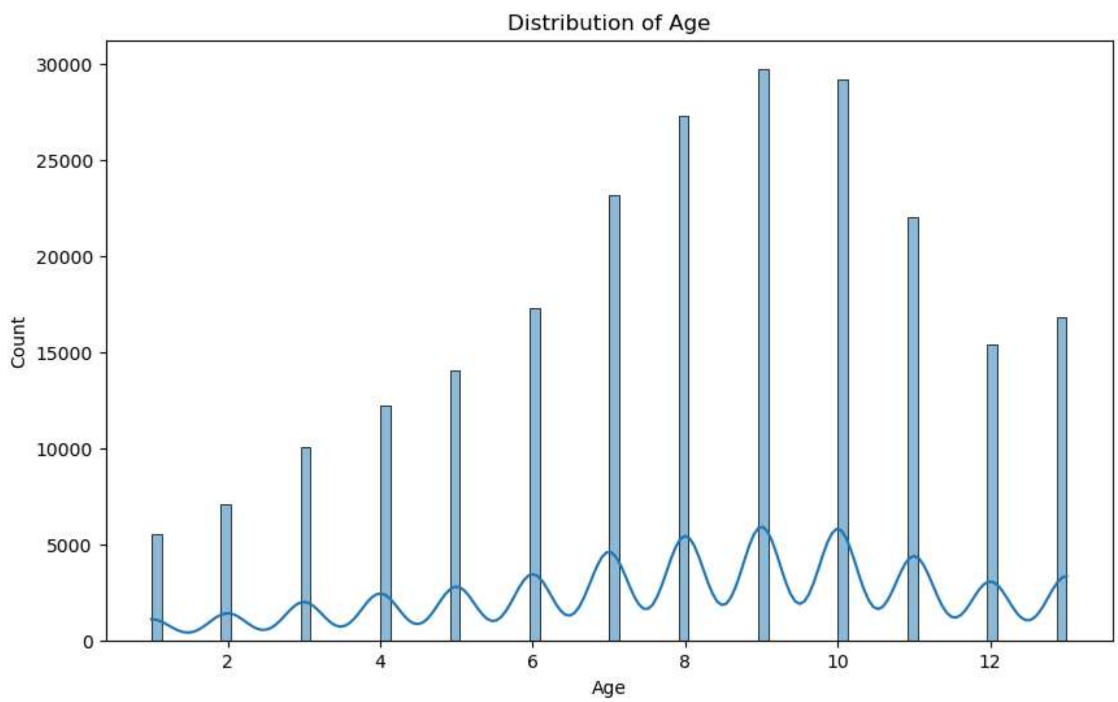
```
# Check the initial skewness
initial_skewness = data['BMI'].skew()
print(f"Initial skewness of BMI: {initial_skewness}")

# Apply logarithmic transformation
data['BMI_log'] = np.log(data['BMI'])

# Check the skewness after transformation
transformed_skewness = data['BMI_log'].skew()
print(f"Skewness of BMI after log transformation: {transformed_skewness}")

# Visualize the distributions
plt.figure(figsize=(12, 6))
plt.subplot(1, 2, 1)
sns.histplot(data['BMI'], kde=True)
plt.title('Before Transformation')

plt.subplot(1, 2, 2)
sns.histplot(data['BMI_log'], kde=True)
plt.title('After Log Transformation')

plt.show()
```

```
Initial skewness of BMI: 2.063938014894699
Skewness of BMI after log transformation: 0.6375339497416975

C:\Users\PAVILION\AppData\Local\Temp\ipykernel_21472\2597344881.py:6: Set
tingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-do
cs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (http
s://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returni
ng-a-view-versus-a-copy)
  data['BMI_log'] = np.log(data['BMI'])
```

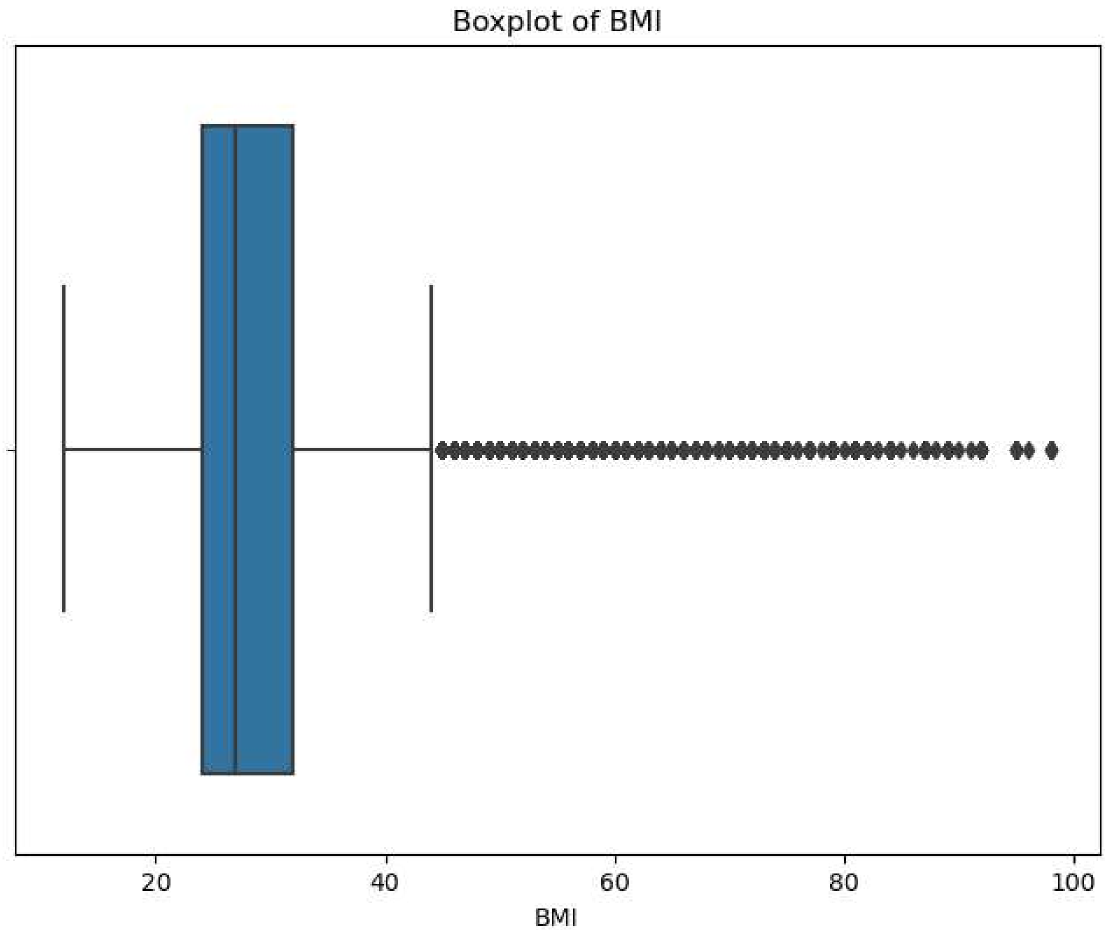


In [21]:

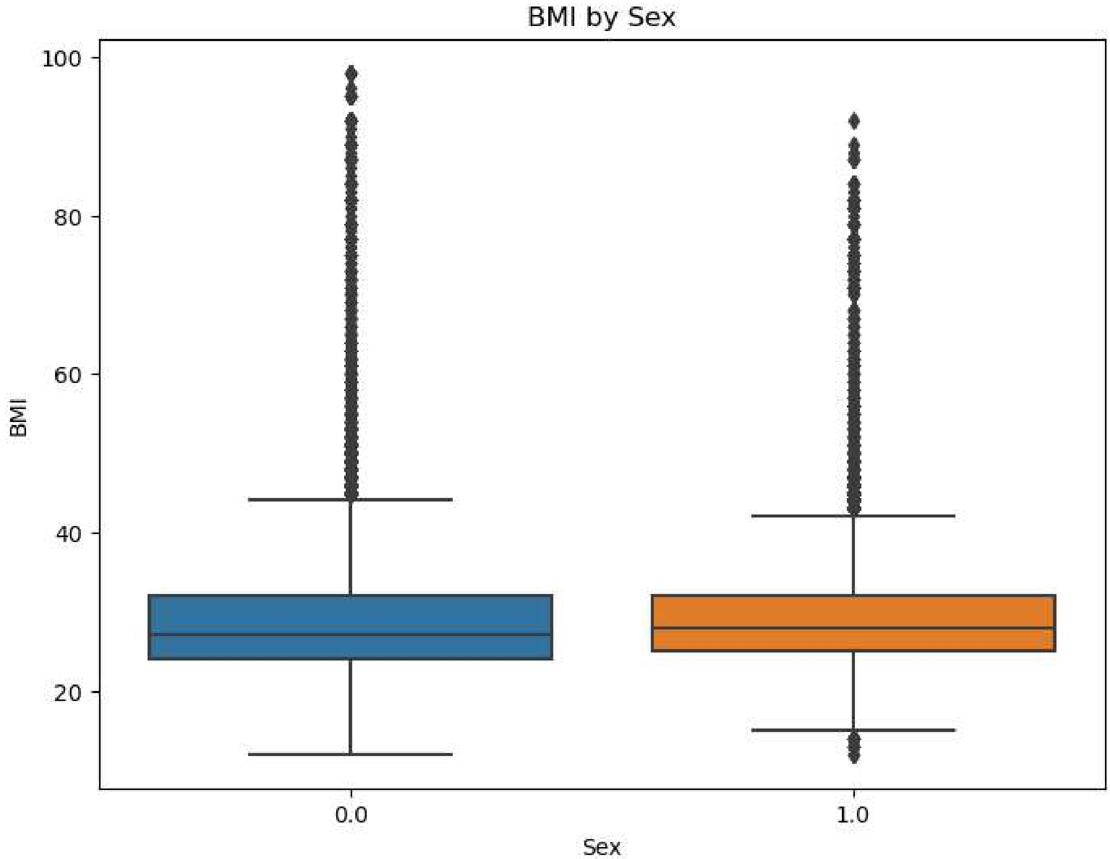
```
plt.figure(figsize=(10, 6))
sns.histplot(data['Age'], kde=True)
plt.title('Distribution of Age')
plt.xlabel('Age')
plt.ylabel('Count')
plt.show()
```



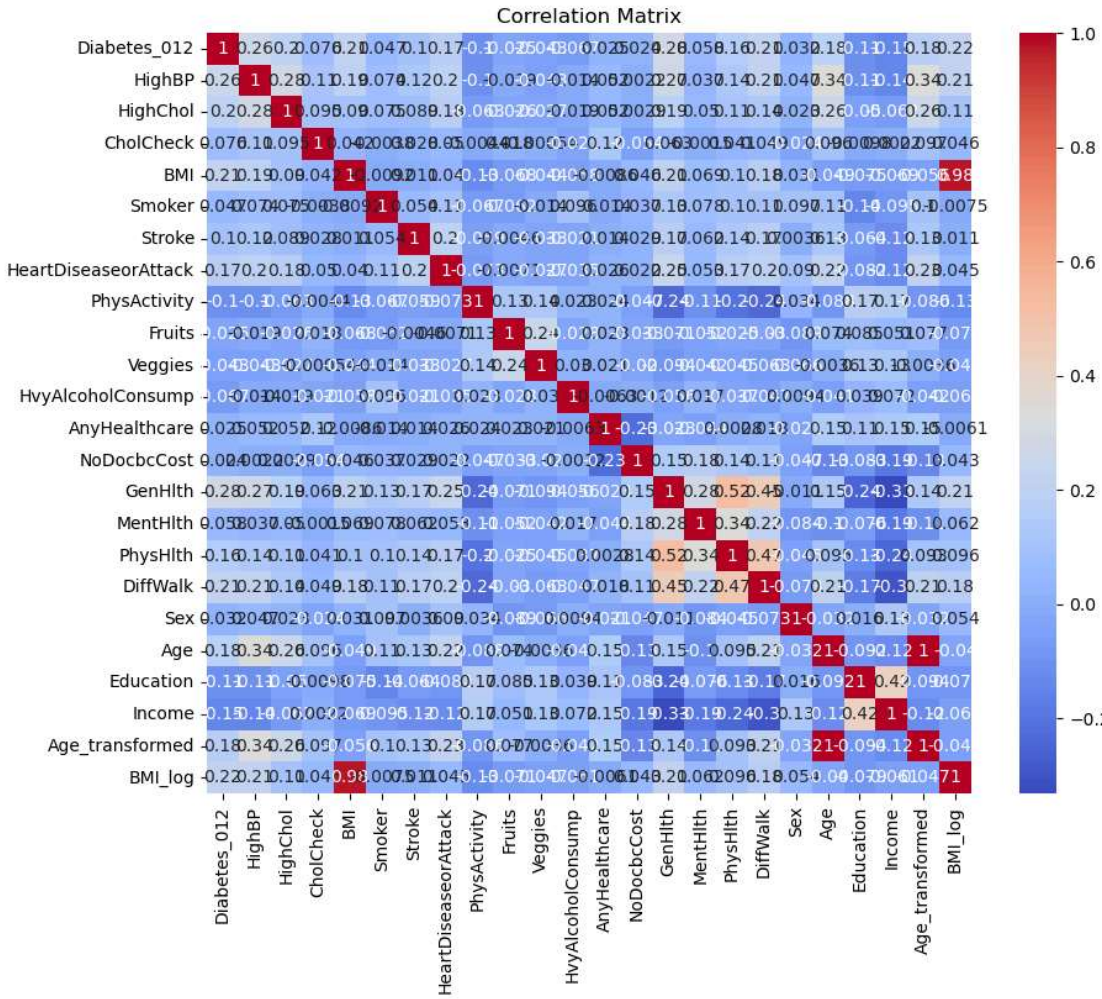
In [22]:
```
plt.figure(figsize=(8, 6))
sns.boxplot(x=data['BMI'])
plt.title('Boxplot of BMI')
plt.show()
```



In [23]:
```
plt.figure(figsize=(8, 6))
sns.boxplot(x='Sex', y='BMI', data=data)
plt.title('BMI by Sex')
plt.show()
```

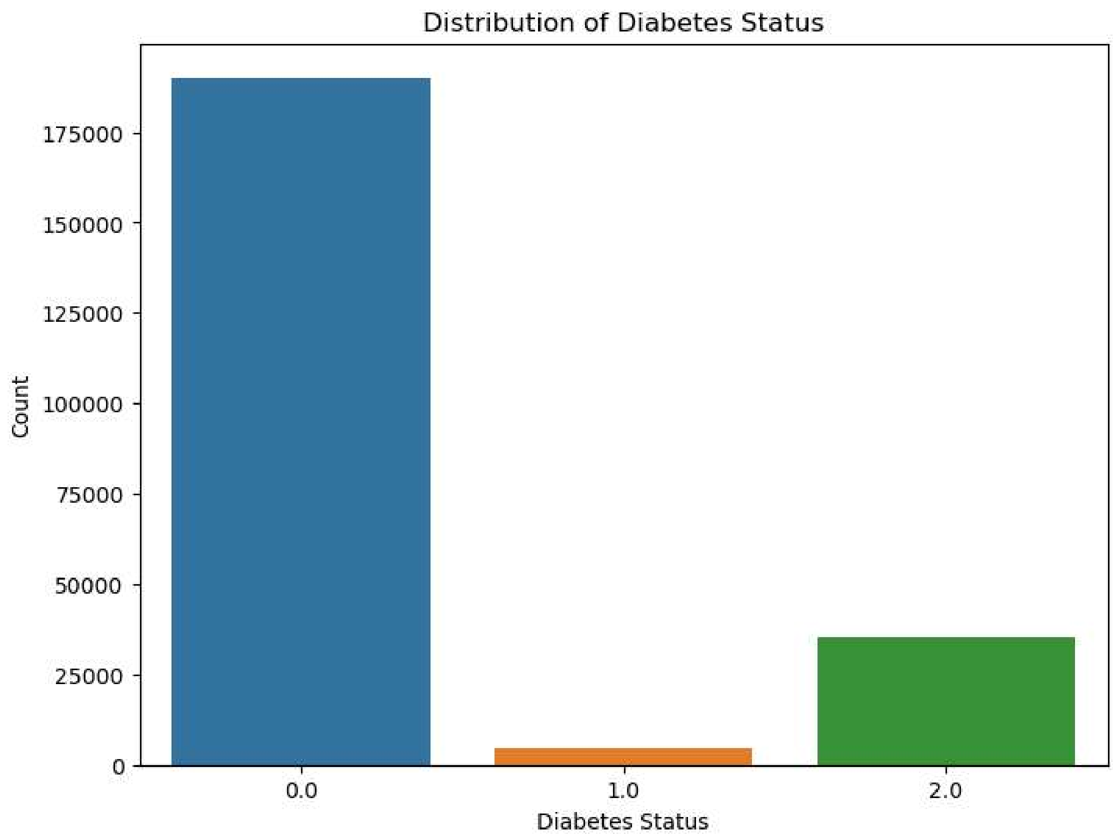


In [24]:
```
corr_matrix = data.corr()
plt.figure(figsize=(10, 8))
sns.heatmap(corr_matrix, annot=True, cmap='coolwarm')
plt.title('Correlation Matrix')
plt.show()
```

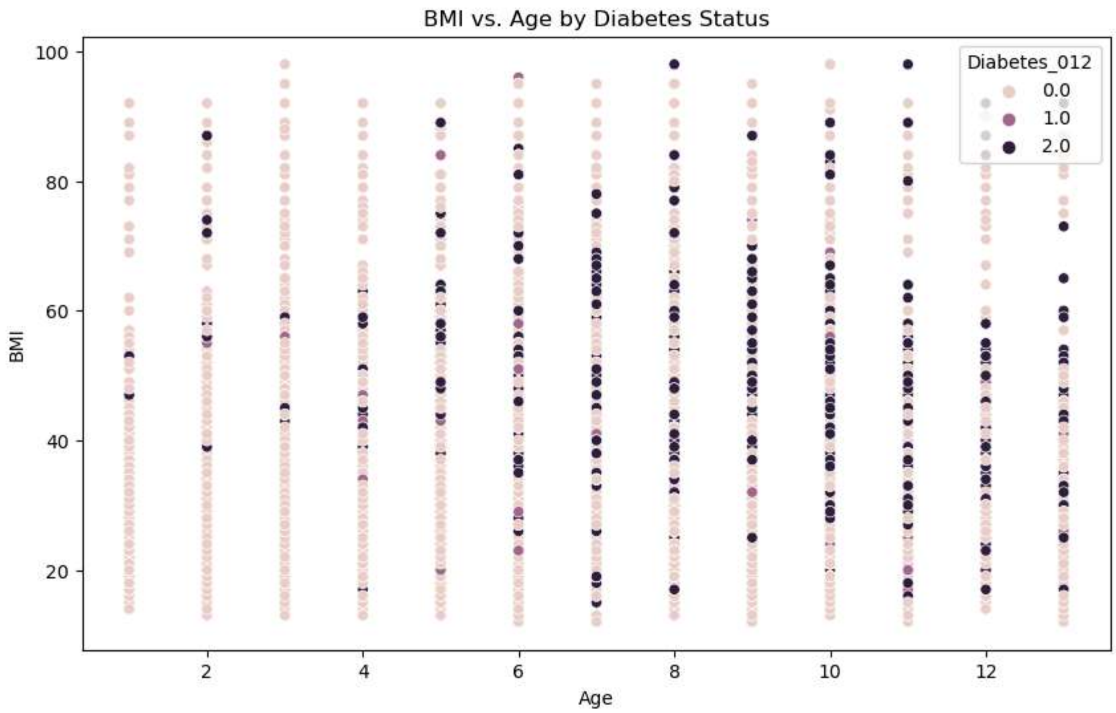


In [25]:

```
plt.figure(figsize=(8, 6))
sns.countplot(x='Diabetes_012', data=data)
plt.title('Distribution of Diabetes Status')
plt.xlabel('Diabetes Status')
plt.ylabel('Count')
plt.show()
```



In [26]:
```
plt.figure(figsize=(10, 6))
sns.scatterplot(x='Age', y='BMI', data=data, hue='Diabetes_012')
plt.title('BMI vs. Age by Diabetes Status')
plt.xlabel('Age')
plt.ylabel('BMI')
plt.show()
```



In [30]:
```
# Split the data into features (X) and target variable (y)
X = data.drop('Diabetes_012', axis=1)
y = data['Diabetes_012']

# 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, r

# Select the top 10 features using f_classif
selector = SelectKBest(score_func=f_classif, k=10)
selector.fit(X_train, y_train)

# Get the selected features
selected_features = X_train.columns[selector.get_support()]

# Create new DataFrames with selected features
X_train_selected = X_train[selected_features]
X_test_selected = X_test[selected_features]
```

In [31]:
```
mean = np.mean(X, axis=0)
std = np.std(X, axis=0)
```

In [32]:
```
X_standardized = (X - mean) / std
```

In [33]:
```
# Create a StandardScaler object
scaler = StandardScaler()

# Fit the scaler to the training data
scaler.fit(X_train)

# Transform the training and testing data
X_train_scaled = scaler.transform(X_train)
X_test_scaled = scaler.transform(X_test)
```

In [ ]: