Data Preporcessing:

The data has been uploaded and pre-processed to ensure that it is cleaned,formatted and outliers are addressed before exploring relationships between variables and analyzing correlations.

1. **Column Names:** Rename columns to have clear, short and lowercase names.
2. **Data Types:** assign / Convert the data type of ech column to appropriate ones.
3. **Duplicate Rows:** Identify and drop duplicate rows.1635 duplicates found
4. **Missing Values:** Check for missing values and handle them appropriately. No missing value found
5. **Aggregation of feature categories** to fewer levels: Age, Education and Income
6. **Frequency distribution** of the target/outcome variable, diabetes
7. **Outliers:** Detect, vizualize and remove outliers.
8. **Histograms:** Plot histograms to visualize the distribution of numeric features.
9. **Scatter Plot/Bar Plot:** Plot scatter plots or bar plots to explore relationships between variables.
10. **Summary Statistics:** Calculate summary statistics for numeric features.
11. **Correlation Matrix/Heat Map:** Calculate and visualize the correlation between numeric features
12. **Chi-square test** for independence of categorical variables against 'diabetes'
13. **The Frequency distribution** of some categorical variables:'age', 'education', 'income'
14. **The distribution of 'diabetes' outcome** by risk factors
15. **The distribution of diabetes outcome** by good habit features
16. **Prevalence of Diabetes** by age, gender, education and income level

Import necessary libraries

In [ ]:
```
## IMPORT NECESSARY PYTHON LIBRARIES

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import sklearn
import scipy.stats as stats
```

Read the diabetes dataset

In [ ]:
```
df_diabetes = pd.read_csv("C:/Users\yitay/Documents/CIND820_BigDataAnalyticsProject
```

In [ ]:
```
# see the first 5 observations
df_diabetes.head()
```

Out[ ]:

	Diabetes_binary	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDiseaseorAt
0	0.0	1.0	0.0	1.0	26.0	0.0	0.0	
1	0.0	1.0	1.0	1.0	26.0	1.0	1.0	
2	0.0	0.0	0.0	1.0	26.0	0.0	0.0	
3	0.0	1.0	1.0	1.0	28.0	1.0	0.0	
4	0.0	0.0	0.0	1.0	29.0	1.0	0.0	

5 rows × 22 columns

1.Column Names: renamed columns to have clear, short and lowercase names.

In [ ]:
```python
# lowercase, shorter, clear names
new_column_names = ['diabetes', 'bp', 'chol', 'cholcheck', 'bmi', 'smoker', 'stroke
'education', 'income']
df_diabetes.columns = new_column_names
```

In [ ]:
```python
# Check the new column names
df_diabetes.columns
```

Out[ ]:
```
Index(['diabetes', 'bp', 'chol', 'cholcheck', 'bmi', 'smoker', 'stroke',
       'heart_disease', 'activity', 'fruits', 'veggies', 'alcohol',
       'healthcare', 'nodocbccost', 'genhlth', 'menthlth', 'phyhlth', 'walk',
       'sex', 'age', 'education', 'income'],
      dtype='object')
```

In [ ]:
```python
# the first 5 obsrvations/rows after renaming the col
df_diabetes.head()
```

Out[ ]:

	diabetes	bp	chol	cholcheck	bmi	smoker	stroke	heart_disease	activity	fruits	...
0	0.0	1.0	0.0	1.0	26.0	0.0	0.0	0.0	1.0	0.0	...
1	0.0	1.0	1.0	1.0	26.0	1.0	1.0	0.0	0.0	1.0	...
2	0.0	0.0	0.0	1.0	26.0	0.0	0.0	0.0	1.0	1.0	...
3	0.0	1.0	1.0	1.0	28.0	1.0	0.0	0.0	1.0	1.0	...
4	0.0	0.0	0.0	1.0	29.0	1.0	0.0	0.0	1.0	1.0	...

5 rows × 22 columns

2. Data Types and structure: check and assign appropriate data types to each attribute

Check data types of attributes

In [ ]:
```
# check the data type of attributes
print("Data Types of Attributes:")
df_diabetes.dtypes
```

```
Data Types of Attributes:
```

Out[ ]:
```
diabetes         float64
bp               float64
chol             float64
cholcheck        float64
bmi              float64
smoker           float64
stroke           float64
heart_disease    float64
activity         float64
fruits           float64
veggies          float64
alcohol          float64
healthcare       float64
nodocbccost      float64
genhlth          float64
menthlth         float64
phyhlth          float64
walk             float64
sex              float64
age              float64
education        float64
income           float64
dtype: object
```

Check the data structure (rows and columns)

In [ ]:
```
# (row, columns)
print(df_diabetes.shape)
print("Number of rows:", df_diabetes.shape[0])      # 0 for rows
print("Number of columns:", df_diabetes.shape[1])   # 1 for columns
```

```
(70692, 22)
Number of rows: 70692
Number of columns: 22
```

Count the number of unique values for each column

In [ ]:
```
# Dictionary to store the count of unique values for each column
unique_counts = {}

# Loop through each column and get the count of unique values
for column in df_diabetes.columns:
    unique_counts[column] = df_diabetes[column].nunique()

# Print the number of unique values for each column
for column, count in unique_counts.items():
    print(f"Number of unique values - '{column}': {count}")
```

```
Number of unique values - 'diabetes': 2
Number of unique values - 'bp': 2
Number of unique values - 'chol': 2
Number of unique values - 'cholcheck': 2
Number of unique values - 'bmi': 80
Number of unique values - 'smoker': 2
Number of unique values - 'stroke': 2
Number of unique values - 'heart_disease': 2
Number of unique values - 'activity': 2
Number of unique values - 'fruits': 2
Number of unique values - 'veggies': 2
Number of unique values - 'alcohol': 2
Number of unique values - 'healthcare': 2
Number of unique values - 'nodocbccost': 2
Number of unique values - 'genhlth': 5
Number of unique values - 'menthlth': 31
Number of unique values - 'phyhlth': 31
Number of unique values - 'walk': 2
Number of unique values - 'sex': 2
Number of unique values - 'age': 13
Number of unique values - 'education': 6
Number of unique values - 'income': 8
```

Convert the data type of categorical features

In [ ]:
```
# List of columns to convert to integer dtype
columns_to_integer = ['diabetes', 'bp', 'chol', 'cholcheck', 'smoker', 'stroke', 'h

# Convert the specified columns to integer dtype
for column in columns_to_integer:
    # Fill NaN values with 0 and convert to integer
    df_diabetes[column] = df_diabetes[column].astype(int)

# Check the data types
print(df_diabetes.dtypes)

# Print the DataFrame
print(df_diabetes)
```

```
diabetes          int32
bp                int32
chol              int32
cholcheck         int32
bmi             float64
smoker            int32
stroke            int32
heart_disease     int32
activity          int32
fruits            int32
veggies           int32
alcohol           int32
healthcare        int32
nodocbccost       int32
genhlth           int32
menthlth        float64
phyhlth         float64
walk              int32
sex               int32
age               int32
education         int32
income            int32
dtype: object
       diabetes  bp  chol  cholcheck   bmi  smoker  stroke  heart_disease  \
0             0   1     0          1  26.0       0       0              0
1             0   1     1          1  26.0       1       1              0
2             0   0     0          1  26.0       0       0              0
3             0   1     1          1  28.0       1       0              0
4             0   0     0          1  29.0       1       0              0
...         ...  ..   ...        ...   ...     ...     ...            ...
70687         1   0     1          1  37.0       0       0              0
70688         1   0     1          1  29.0       1       0              1
70689         1   1     1          1  25.0       0       0              1
70690         1   1     1          1  18.0       0       0              0
70691         1   1     1          1  25.0       0       0              1

       activity  fruits  ...  healthcare  nodocbccost  genhlth  menthlth  \
0             1       0  ...           1            0        3       5.0
1             0       1  ...           1            0        3       0.0
2             1       1  ...           1            0        1       0.0
3             1       1  ...           1            0        3       0.0
4             1       1  ...           1            0        2       0.0
...         ...     ...  ...         ...          ...      ...       ...
70687         0       0  ...           1            0        4       0.0
70688         0       1  ...           1            0        2       0.0
70689         0       1  ...           1            0        5      15.0
70690         0       0  ...           1            0        4       0.0
70691         1       1  ...           1            0        2       0.0

       phyhlth  walk  sex  age  education  income
0         30.0     0    1    4          6       8
1          0.0     0    1   12          6       8
2         10.0     0    1   13          6       8
3          3.0     0    1   11          6       8
4          0.0     0    0    8          5       8
...        ...   ...  ...  ...        ...     ...
```

```
70687      0.0     0    0    6          4        1
70688      0.0     1    1   10          3        6
70689      0.0     1    0   13          6        4
70690      0.0     1    0   11          2        4
70691      0.0     0    0    9          6        2

[70692 rows x 22 columns]
```

3. Duplicate Rows: Identify and drop duplicate rows

- 1635 duplicate rows found

In [ ]:
```
# Check for duplicate rows
duplicate_rows = df_diabetes[df_diabetes.duplicated()]

# Print the duplicate rows
if not duplicate_rows.empty:
    print("Duplicate rows found:")
    print(duplicate_rows)
else:
    print("No duplicate rows found.")

# Drop duplicates, keeping the first occurrence
df_diabetes = df_diabetes.drop_duplicates(keep='first')

# Print the cleaned DataFrame
print("\nDataFrame after removing duplicates:")
print(df_diabetes)
```

```
Duplicate rows found:
       diabetes  bp  chol  cholcheck   bmi  smoker  stroke  heart_disease  \
602           0   0     0          1  22.0       0       0              0   
689           0   0     0          1  26.0       0       0              0   
891           0   0     0          1  24.0       0       0              0   
1092          0   0     0          1  21.0       0       0              0   
1326          0   1     0          1  29.0       0       0              0   
...         ...  ..   ...        ...   ...     ...     ...            ...   
69865         1   1     1          1  27.0       1       0              0   
69939         1   1     1          1  27.0       1       0              0   
70305         1   1     0          1  30.0       0       0              0   
70591         1   1     1          1  30.0       0       0              1   
70663         1   1     1          1  33.0       0       0              0   

       activity  fruits  ...  healthcare  nodocbccost  genhlth  menthlth  \
602           1       1  ...           1            0        1       0.0   
689           1       1  ...           1            0        1       0.0   
891           1       1  ...           1            0        1       0.0   
1092          1       1  ...           1            0        1       0.0   
1326          1       0  ...           1            0        2       0.0   
...         ...     ...  ...         ...          ...      ...       ...   
69865         1       1  ...           1            0        4       0.0   
69939         1       1  ...           1            0        3       0.0   
70305         0       0  ...           1            0        3       0.0   
70591         1       1  ...           1            0        2       0.0   
70663         1       1  ...           1            0        3       0.0   

       phyhlth  walk  sex  age  education  income  
602        0.0     0    0    6          6       8  
689        0.0     0    0    6          6       8  
891        0.0     0    0    6          6       8  
1092       0.0     0    0    5          6       8  
1326       0.0     0    1   10          5       6  
...        ...   ...  ...  ...        ...     ...  
69865      0.0     0    1   12          6       8  
69939      0.0     0    1   12          6       8  
70305      0.0     0    1    9          4       7  
70591      0.0     0    1   10          6       8  
70663      0.0     0    1    9          6       6  

[1635 rows x 22 columns]

DataFrame after removing duplicates:
       diabetes  bp  chol  cholcheck   bmi  smoker  stroke  heart_disease  \
0             0   1     0          1  26.0       0       0              0   
1             0   1     1          1  26.0       1       1              0   
2             0   0     0          1  26.0       0       0              0   
3             0   1     1          1  28.0       1       0              0   
4             0   0     0          1  29.0       1       0              0   
...         ...  ..   ...        ...   ...     ...     ...            ...   
70687         1   0     1          1  37.0       0       0              0   
70688         1   0     1          1  29.0       1       0              1   
70689         1   1     1          1  25.0       0       0              1   
70690         1   1     1          1  18.0       0       0              0   
70691         1   1     1          1  25.0       0       0              1   
```

```
       activity  fruits  ...  healthcare  nodocbccost  genhlth  menthlth  \
0             1       0  ...           1            0        3       5.0
1             0       1  ...           1            0        3       0.0
2             1       1  ...           1            0        1       0.0
3             1       1  ...           1            0        3       0.0
4             1       1  ...           1            0        2       0.0
...         ...     ...  ...         ...          ...      ...       ...
70687         0       0  ...           1            0        4       0.0
70688         0       1  ...           1            0        2       0.0
70689         0       1  ...           1            0        5      15.0
70690         0       0  ...           1            0        4       0.0
70691         1       1  ...           1            0        2       0.0

       phyhlth  walk  sex  age  education  income
0         30.0     0    1    4          6       8
1          0.0     0    1   12          6       8
2         10.0     0    1   13          6       8
3          3.0     0    1   11          6       8
4          0.0     0    0    8          5       8
...        ...   ...  ...  ...        ...     ...
70687      0.0     0    0    6          4       1
70688      0.0     1    1   10          3       6
70689      0.0     1    0   13          6       4
70690      0.0     1    0   11          2       4
70691      0.0     0    0    9          6       2

[69057 rows x 22 columns]
```

4. Missing Values: Identify and handle missing values.

- No missing value found

In [ ]:

```
# Count the number of missing values in each column
missing_count_per_column = df_diabetes.isnull().sum()
missing_count_per_column
```

Out[ ]:
```
diabetes         0
bp               0
chol             0
cholcheck        0
bmi              0
smoker           0
stroke           0
heart_disease    0
activity         0
fruits           0
veggies          0
alcohol          0
healthcare       0
nodocbccost      0
genhlth          0
menthlth         0
phyhlth          0
walk             0
sex              0
age              0
education        0
income           0
dtype: int64
```

In [ ]:
```
## Count the total number of missing values in the entire DataFrame
total_missing_count = df_diabetes.isnull().sum().sum()
print("Total number of missing values:",total_missing_count)
```

```
Total number of missing values: 0
```

5. Aggregation of feature categories to fewer levels: Age, Education and Income

Age

The age category levels have been reduced from 13 to 4. Levels 1 and 2 assigned to level 0 (young adults); 3 to 6 to level 1 (middle aged),7 to 9 to level 2 (older adults) and 10 to 13 to level 3 (elderly)

In [ ]:
```
# Define age mapping: maps original age levels to new categorical levels
age_mapping = {
    1: 0,   # Levels 1 & 2 map to 0 (Young Adults)
    2: 0,
    3: 1,   # Levels 3 - 6 map to 1 (Middle Aged)
    4: 1,
    5: 1,
    6: 1,
    7: 2,   # Levels 7 - 9 map to 2 (Older Adults)
    8: 2,
    9: 2,
    10: 3,   # Levels 10 – 13 map to 3 (Elderly)
    11: 3,
    12: 3,
    13: 3
}
```

```
## Replace the age levels in the DataFrame
df_diabetes['age'] = df_diabetes['age'].map(age_mapping)

## Rename the age levels to Young Adults, Middle Aged, Older Adults, and Elderly
#df_diabetes['age'] = df_diabetes['age'].replace({0: 'Young Adults', 1: 'Middle Age

##  We can skip the renaming step if we prefer using numerical values instead of st
## Now, 'age' column will have levels 'Young Adults', 'Middle Aged', 'Older Adults'
```

In [ ]:
```
# Get unique levels of the 'age' column
#new_age_levels = df_diabetes['age'].unique()

# Print each unique level in a new line
##print("Unique levels in 'age' column:")
#for level in new_age_levels:
#    print('-',level)
```

Education

The education levels have been reduced from 6 to 3. Levels 1 and 2 assigned to level 0 (Elementary); 3 and 4 to level 1 (High school), 5 and 6 to level 2 (collage)

In [ ]:
```
education_mapping = {
        1: 0, # Levels 1 and 2 map to 0 (up to grade 8)
    2: 0,
    3: 1, # Levels 3 and 4 map to 1 (grade 9 to 12th)
    4: 1,
    5: 2, # Levels 5 and 6 map to 1 (collage or university)
    6: 2
}
## Replace the aeducation levels in the DataFrame
df_diabetes['education'] = df_diabetes['education'].map(education_mapping)

## Rename the education levels to Elementary, High School and Collage
#df_diabetes['education'] = df_diabetes['education'].replace({0: 'Elementary', 1: '

##  We can skip the renaming step if we prefer using numerical values instead of st
## Now, 'Education' column will have levels 'Elementary', 'High Schhol', & 'Collage
```

In [ ]:
```
# Get unique levels of the 'education' column
#new_education_levels = df_diabetes['education'].unique()

# Print each unique level in a new line
#print("Unique levels in 'education' column:")
#for level in new_education_levels:
 #    print('-',level)
```

Income

The income levels have been reduced from 8 to 3. Levels 1 to 5 assigned to level 0 (Low income); 6 and 7 to level 1 (Middle income), 8 to level 2 (High income)

In [ ]:
```
income_mapping = {
        1: 0,  # Levels 1 and 5 map to 0 (low income)
```

```
    2: 0,
    3: 0,
    4: 0,
    5: 0,
    6: 1,  # Levels 6 and 7  map to 1 (middle income)
    7: 1,
    8: 2   # Levels 8 map to 2 (high income)
}

## Then replace the income levels in the DataFrame
df_diabetes['income'] = df_diabetes['income']. map(income_mapping)

## Finally, rename the income levels to low income, middle income, and high income

# df_diabetes['income'] = df_diabetes['income'].replace({0: 'Low income', 1: 'Middl
##  we can skip the renaming step if we prefer using numerical values instead of st
## Now 'income' column will have levels 'low income', 'middle income', 'high income
```

In [ ]:
```
# Get unique levels of the 'education' column
# new_income_levels = df_diabetes['income'].unique()

# Print each unique level in a new line
#print("Unique levels in 'income' column:")
#for level in new_income_levels:
#    print('-',level)
```

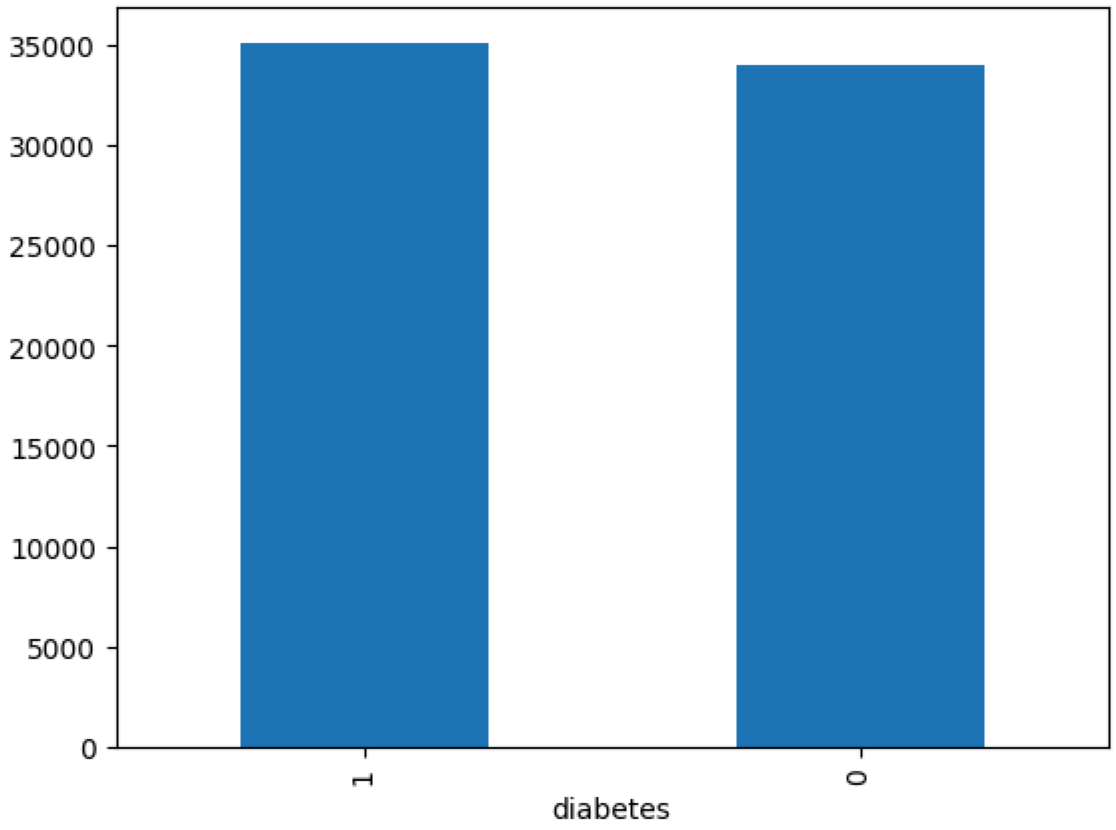
6. Frequency distribution of the target/outcome variable, diabetes

In [ ]:
```
import pandas as pd
class_diabetes = df_diabetes['diabetes'].value_counts()

# Display the class frequencies
print("class diabetes:")
print(class_diabetes)
```

```
class diabetes:
diabetes
1    35097
0    33960
Name: count, dtype: int64
```

In [ ]:
```
df_diabetes['diabetes'].value_counts().plot(kind ='bar')
```

Out[ ]:
```
<Axes: xlabel='diabetes'>
```



7. Outliers: Detect, vizualize and remove outliers.

7.1. Detect outliers

The lower and upper boundaries beyond which data points are considered outliers are given as follows

- The lower bound is the value at the first quartile (Q1) minus 1.5 times the interquartile range (IQR).
  - Lower Bound = Q1 − 1.5*IQR
- The upper bound is the value at the third quartile (Q3) plus 1.5 times the interquartile range (IQR).
  - Upper Bound = Q3 + 1.5*IQR

Detect outliers using IQR and count them by features

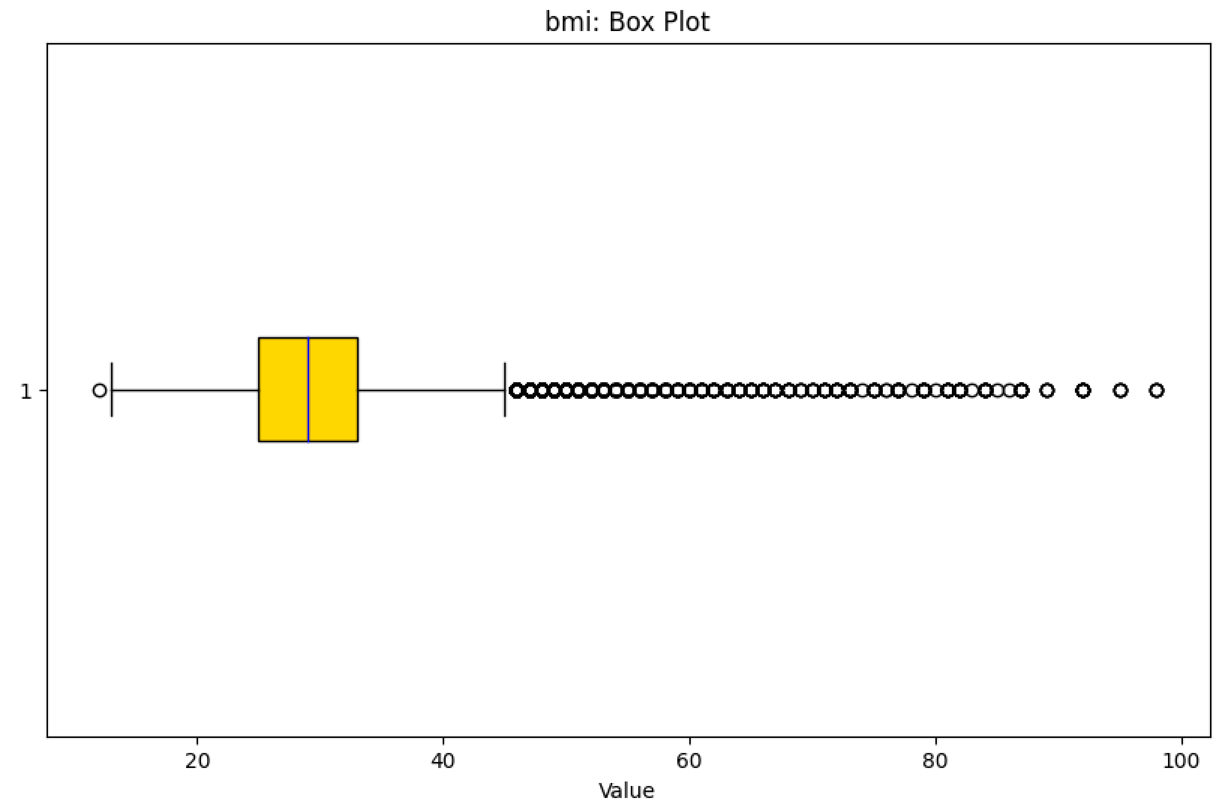
In [ ]:
```
import pandas as pd

# Function to detect outliers using IQR and count them by feature
def detect_outliers_iqr(df_diabetes, columns_with_outliers):
    outliers_count = {col: 0 for col in columns_with_outliers}

    for col in columns_with_outliers:
        q1 = df_diabetes[col].quantile(0.25)
        q3 = df_diabetes[col].quantile(0.75)
        iqr = q3 - q1
        lower_bound = q1 - 1.5 * iqr
        upper_bound = q3 + 1.5 * iqr
        for val in df_diabetes[col]:
            if val < lower_bound or val > upper_bound:
                outliers_count[col] += 1

    return outliers_count

columns_with_outliers = ['bmi', 'menthlth', 'phyhlth']
outliers_count = detect_outliers_iqr(df_diabetes, columns_with_outliers)

# Create a DataFrame to tabulate the number of outliers by feature
outliers_count_df = pd.DataFrame(list(outliers_count.items()), columns=['Feature',

print("\nNumber of outliers by feature:")
print(outliers_count_df)
```

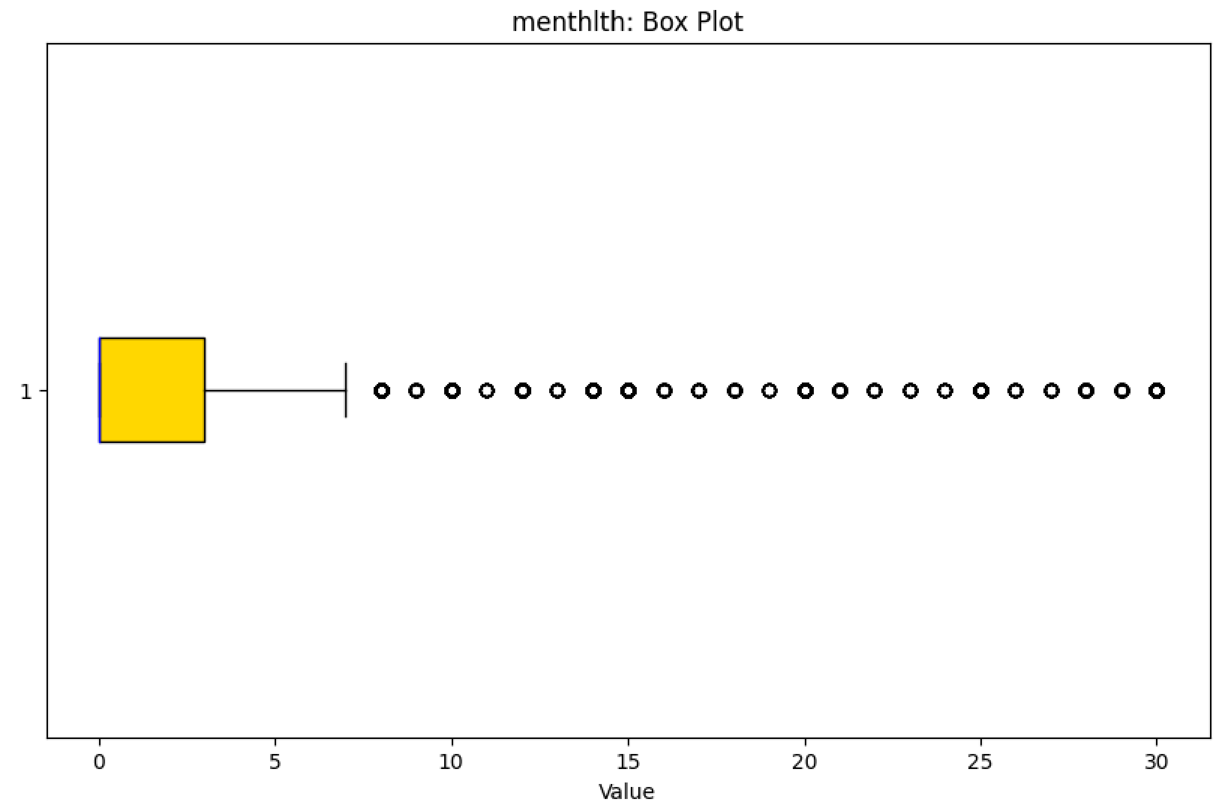
```
Number of outliers by feature:
    Feature  Number of Outliers
0       bmi                2181
1  menthlth               10703
2   phyhlth               10620
```

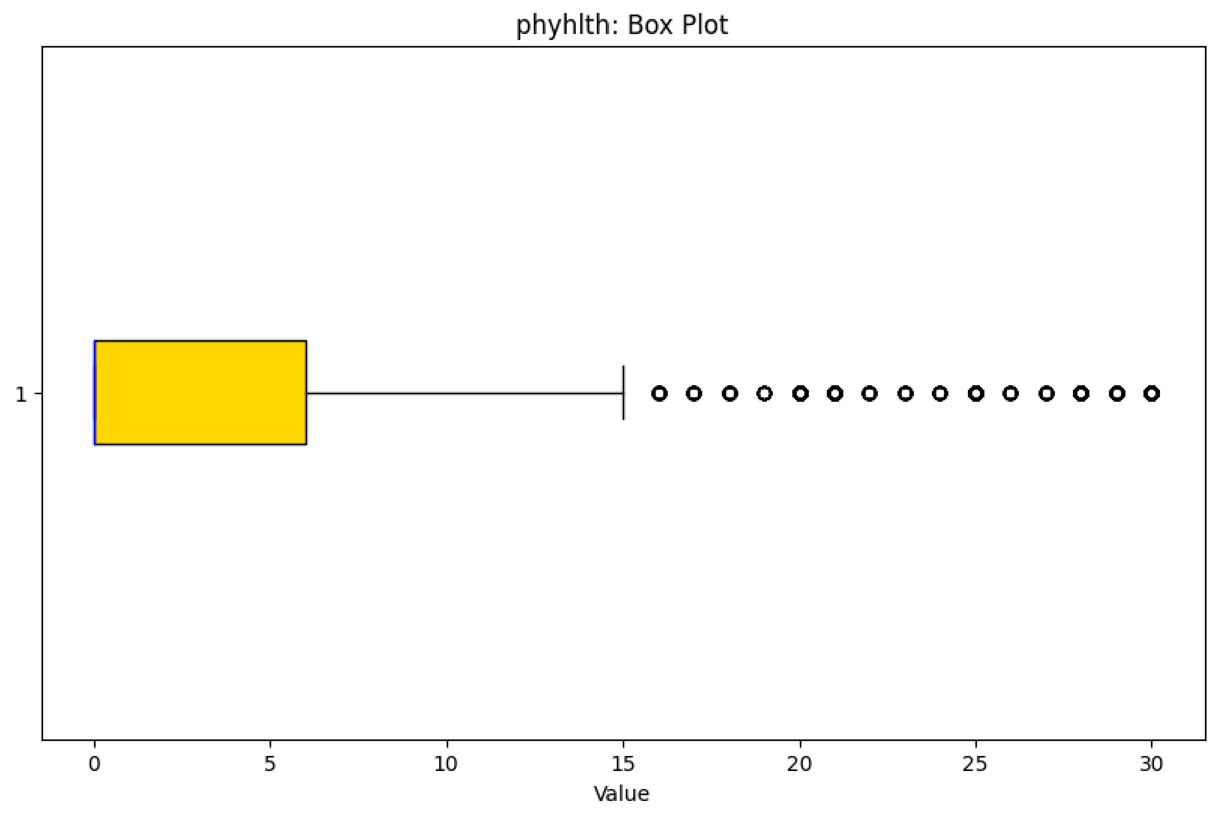
7.2.Vizualize Outliers using Box Plots

In [ ]:

```
# List of features to plot
columns_with_outliers = ['bmi', 'menthlth', 'phyhlth']

# Loop through each feature and create a box plot
for feature in columns_with_outliers:
    plt.figure(figsize=(10, 6))

    # Create box plot
    plt.boxplot(df_diabetes[feature], vert=False, patch_artist=True, boxprops=dict(

    # Add labels and title
    plt.xlabel('Value')
    plt.title(f'{feature}: Box Plot')

    # Show the plot
    plt.show()
```


bmi: Box Plot
1
20
40
60
80
100
Value


menthlth: Box Plot
1
0
5
10
15
20
25
30
Value



7.3. Detect and drop outliers from the dataframe

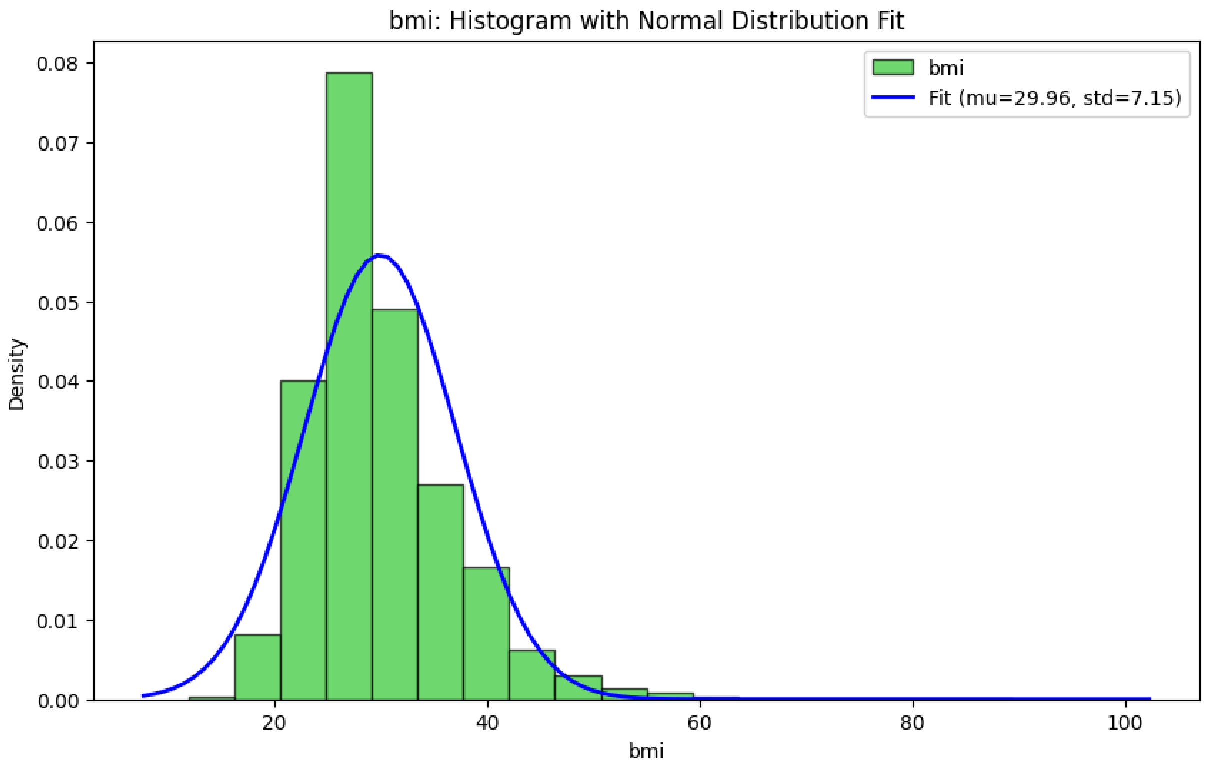
- Drop the outliers using the indices of the outliers obtained from the detect_outliers_iqr function

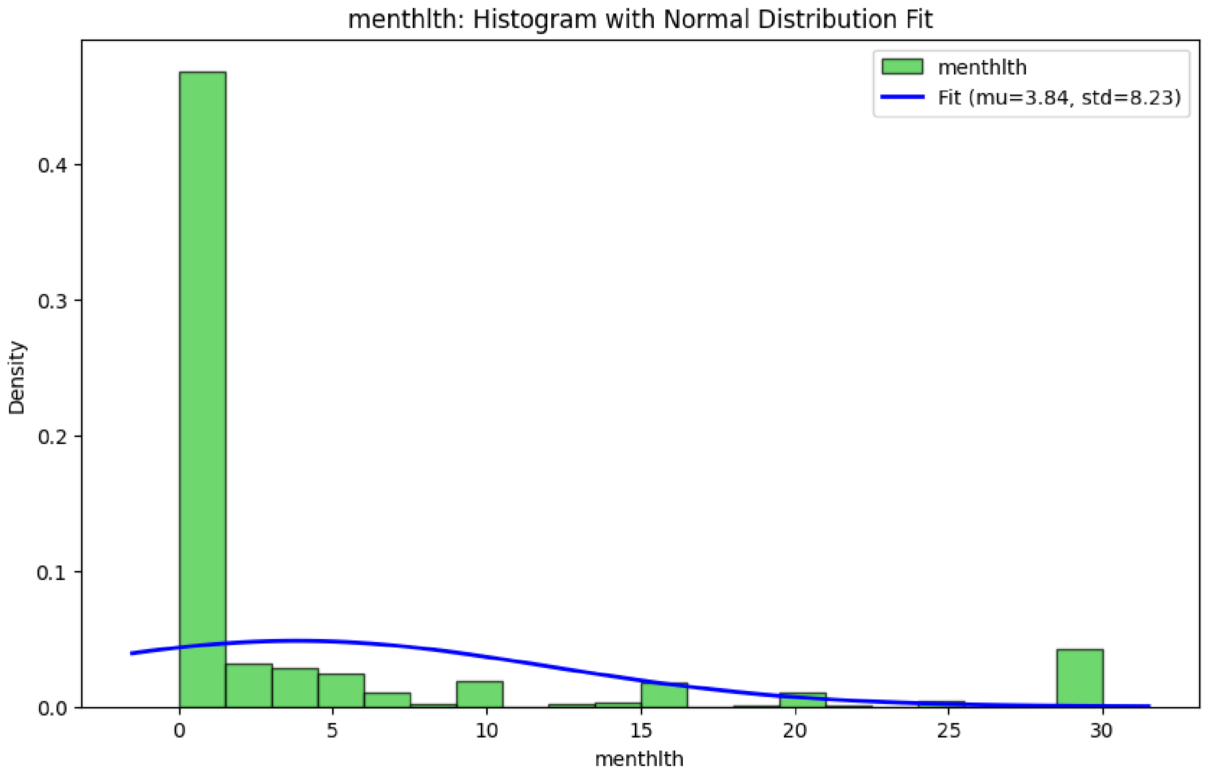
```
In [ ]: import pandas as pd

# Function to detect outliers using IQR for specified columns
def detect_outliers_iqr(df_diabetes, columns_with_outliers):
    outliers = set()
    for col in columns_with_outliers:
        q1 = df_diabetes[col].quantile(0.25)
        q3 = df_diabetes[col].quantile(0.75)
        iqr = q3 - q1
        lower_bound = q1 - 1.5 * iqr
        upper_bound = q3 + 1.5 * iqr
        for i, val in enumerate(df_diabetes[col]):
            if val < lower_bound or val > upper_bound:
                outliers.add(i)  # Add index to the set of outliers
    return list(outliers)

columns_with_outliers = ['bmi', 'menthlth', 'phyhlth']
outliers_indices = detect_outliers_iqr(df_diabetes, columns_with_outliers)

# Drop outliers from the DataFrame
#diabetes_clean = diabetes_clean.drop(outliers_indices)
#
# Print the cleaned DataFrame
```

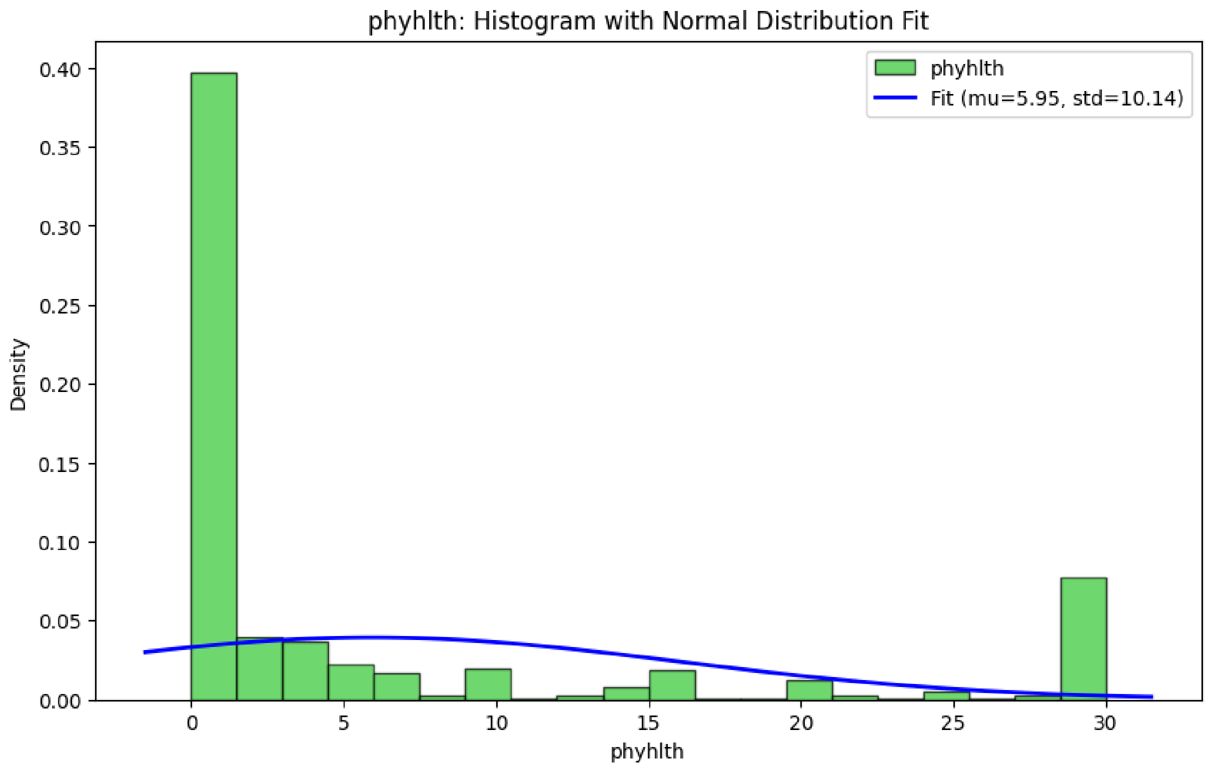
```
#print("DataFrame after removing outliers:")
# print(diabetes_clean)
```

8.Histogram- numerical features

In [ ]:
```
#import pandas as pd
#import numpy as np
#import matplotlib.pyplot as plt
#from scipy.stats import norm


# List of features to plot
features = ['bmi',  'menthlth', 'phyhlth']

# Loop through each feature and create histogram with normal distribution fit
for feature in features:
    plt.figure(figsize=(10, 6))

    # Create histogram
    plt.hist(df_diabetes[feature], bins=20, color='limegreen', edgecolor='black', a

    # Fit a normal distribution to the data
    mu, std = norm.fit(df_diabetes[feature])

    # Overlay normal distribution curve
    xmin, xmax = plt.xlim()
    x_range = np.linspace(xmin, xmax, 100)
    p = norm.pdf(x_range, mu, std)

    plt.plot(x_range, p, 'blue', linewidth=2, label=f'Fit (mu={mu:.2f}, std={std:.2

    # Add labels and title
    plt.xlabel(feature)
    plt.ylabel('Density')
    plt.title(f'{feature}: Histogram with Normal Distribution Fit')
    plt.legend()

    # Show the plot
    plt.show()
```

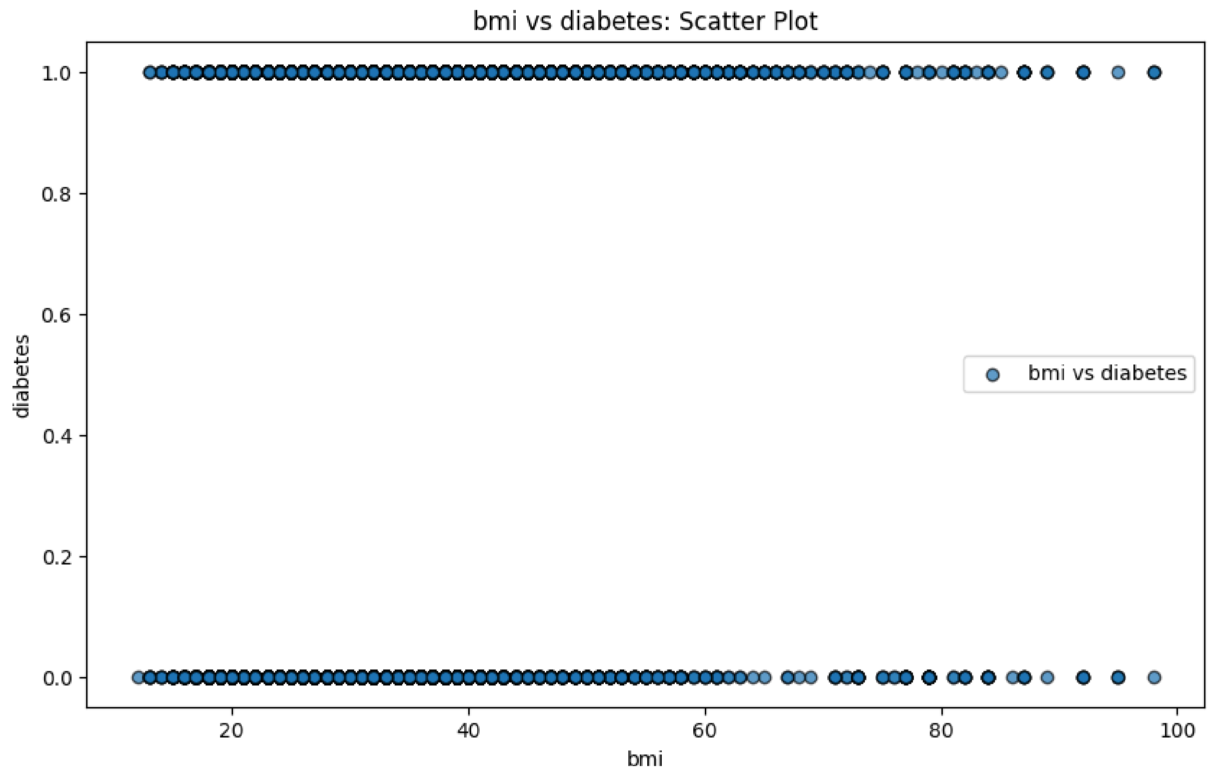

bmi: Histogram with Normal Distribution Fit
bmi
Fit (mu=29.96, std=7.15)
Density
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0.07
0.08
20
40
60
80
100
bmi

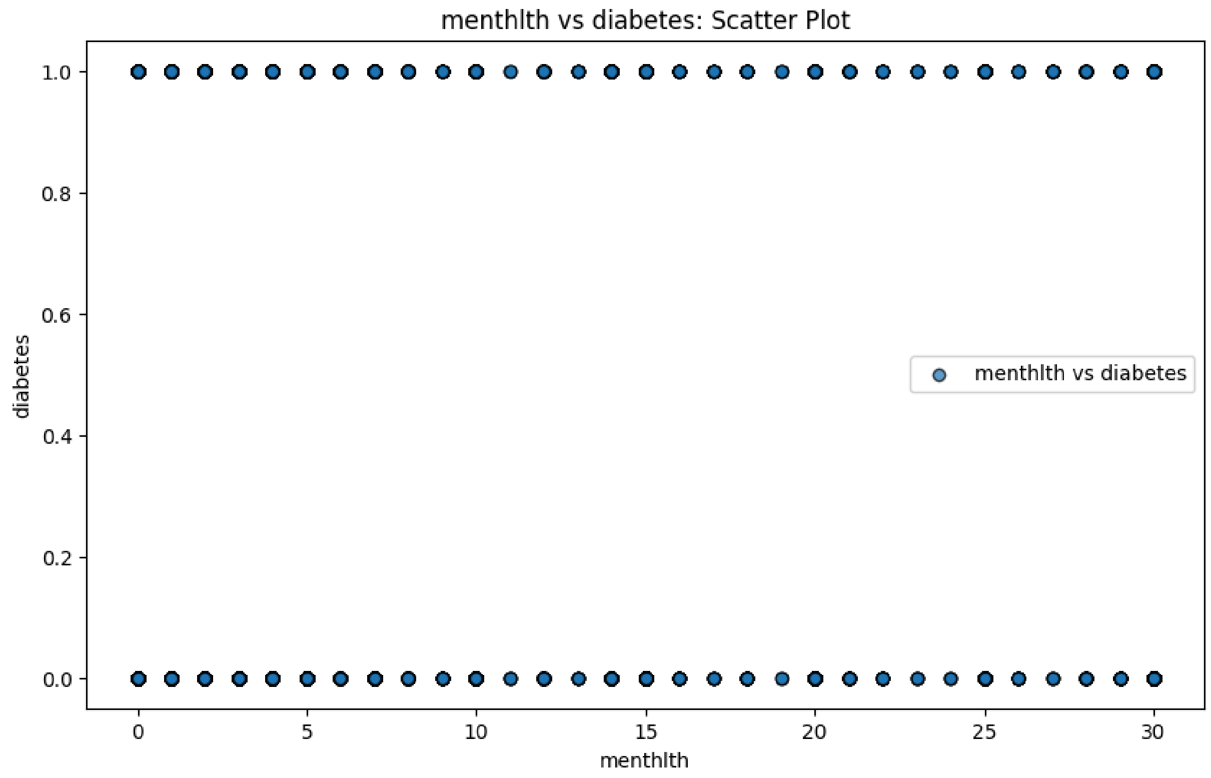

menthlth: Histogram with Normal Distribution Fit
menthlth
Fit (mu=3.84, std=8.23)
Density
0.0
0.1
0.2
0.3
0.4
0
5
10
15
20
25
30
menthlth

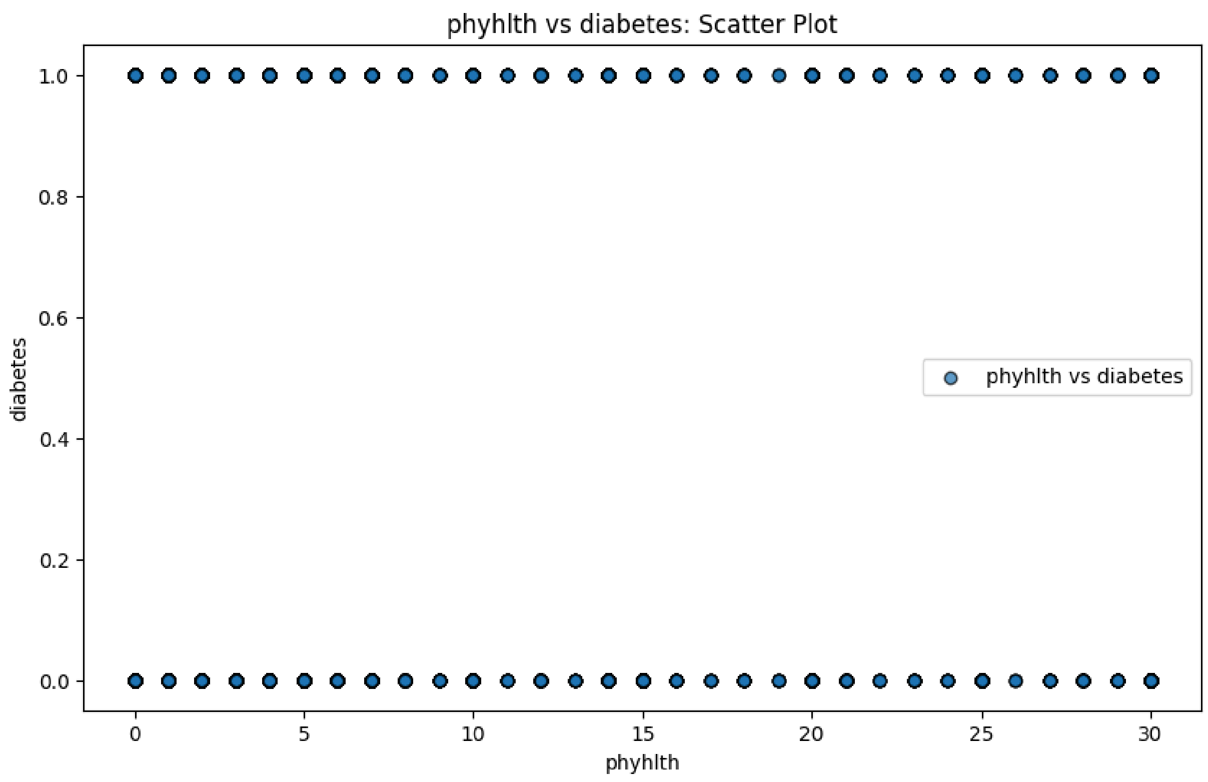


9. Scatter Plot/Bar Plot: used to explore relationships between variables.

```
In [ ]: # List of features to plot
        features = ['bmi',      'menthlth',     'phyhlth']

        # Target variable
        target = 'diabetes'

        # Loop through each feature and create a scatter plot
        for feature in features:
            plt.figure(figsize=(10, 6))

            # Create scatter plot
            plt.scatter(df_diabetes[feature], df_diabetes[target], alpha=0.7, edgecolor='bl

            # Add labels and title
            plt.xlabel(feature)
            plt.ylabel(target)
            plt.title(f'{feature} vs {target}: Scatter Plot')
            plt.legend()

            # Show the plot
            plt.show()
```


bmi vs diabetes: Scatter Plot
1.0
0.8
0.6
0.4
0.2
0.0
diabetes
bmi vs diabetes
20
40
60
80
100
bmi


menthlth vs diabetes: Scatter Plot
1.0
0.8
0.6
0.4
0.2
0.0
diabetes
menthlth vs diabetes
0
5
10
15
20
25
30
menthlth



10. Summary Statistics: numeric features.

In [ ]:
```
# df_diabetes.describe()

# For readability, transpose the summary statistics
df_diabetes.describe().T
```

Out[ ]:

	count	mean	std	min	25%	50%	75%	max
diabetes	69057.0	0.508232	0.499936	0.0	0.0	1.0	1.0	1.0
bp	69057.0	0.571224	0.494905	0.0	0.0	1.0	1.0	1.0
chol	69057.0	0.531329	0.499021	0.0	0.0	1.0	1.0	1.0
cholcheck	69057.0	0.974803	0.156723	0.0	1.0	1.0	1.0	1.0
bmi	69057.0	29.955834	7.147972	12.0	25.0	29.0	33.0	98.0
smoker	69057.0	0.481935	0.499677	0.0	0.0	0.0	1.0	1.0
stroke	69057.0	0.063643	0.244118	0.0	0.0	0.0	0.0	1.0
heart_disease	69057.0	0.150875	0.357930	0.0	0.0	0.0	0.0	1.0
activity	69057.0	0.696483	0.459780	0.0	0.0	1.0	1.0	1.0
fruits	69057.0	0.605659	0.488712	0.0	0.0	1.0	1.0	1.0
veggies	69057.0	0.784120	0.411434	0.0	1.0	1.0	1.0	1.0
alcohol	69057.0	0.043515	0.204014	0.0	0.0	0.0	0.0	1.0
healthcare	69057.0	0.953908	0.209687	0.0	1.0	1.0	1.0	1.0
nodocbccost	69057.0	0.096138	0.294782	0.0	0.0	0.0	0.0	1.0
genhlth	69057.0	2.863692	1.107950	1.0	2.0	3.0	4.0	5.0
menthlth	69057.0	3.840103	8.231164	0.0	0.0	0.0	3.0	30.0
phyhlth	69057.0	5.945306	10.139113	0.0	0.0	0.0	6.0	30.0
walk	69057.0	0.258612	0.437875	0.0	0.0	0.0	1.0	1.0
sex	69057.0	0.456464	0.498105	0.0	0.0	0.0	1.0	1.0
age	69057.0	2.174160	0.843393	0.0	2.0	2.0	3.0	3.0
education	69057.0	1.619329	0.534450	0.0	1.0	2.0	2.0	2.0
income	69057.0	0.870049	0.819899	0.0	0.0	1.0	2.0	2.0

11.Correlation Matrix:

Visualize the correlation between features & between features and the outcome variable(diabetes)

In [ ]:

```
## Compute the correlation matrix including the outcome variable, 'diabetes'
correlation_matrix = df_diabetes.corr()

## Compute the correlation matrix by dropping the outcome variable, 'diabetes'
# df_diabetes_drop_target = df_diabetes.drop(columns=['diabetes'])
# correlation_matrix = df_diabetes_drop_target.corr()
# Display the correlation matrix
print(correlation_matrix)
```

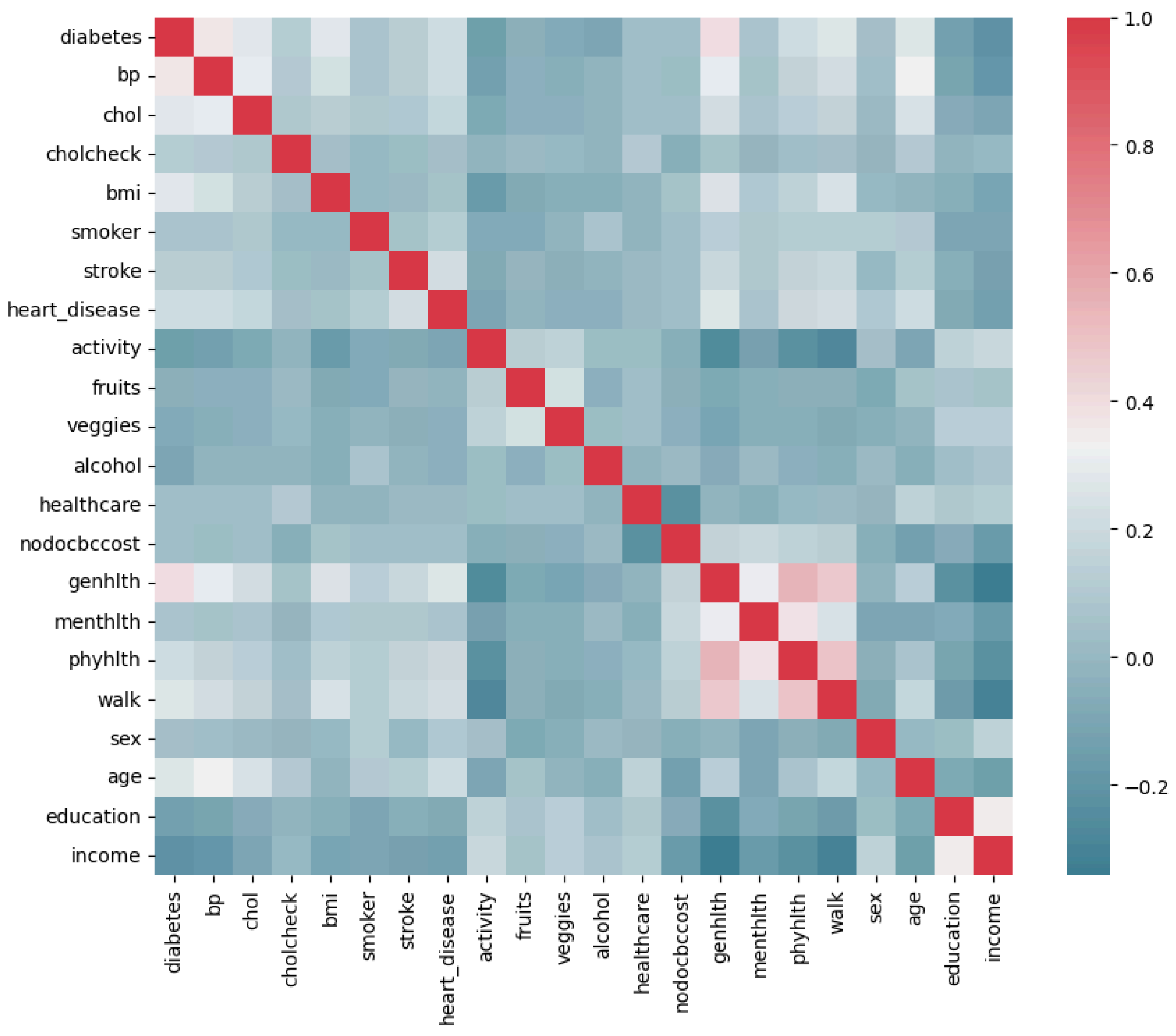
```
               diabetes        bp      chol  cholcheck       bmi    smoker  \
diabetes       1.000000  0.372048  0.281399   0.118900  0.285643  0.075853   
bp             0.372048  1.000000  0.308987   0.106593  0.232372  0.078123   
chol           0.281399  0.308987  1.000000   0.088231  0.123917  0.086522   
cholcheck      0.118900  0.106593  0.088231   1.000000  0.047779 -0.002854   
bmi            0.285643  0.232372  0.123917   0.047779  1.000000  0.002761   
smoker         0.075853  0.078123  0.086522  -0.002854  0.002761  1.000000   
stroke         0.122727  0.126869  0.098166   0.023368  0.019503  0.061957   
heart_disease  0.207229  0.206776  0.178207   0.044795  0.055345  0.120457   
activity      -0.150281 -0.128307 -0.084469  -0.010072 -0.164179 -0.072401   
fruits        -0.044560 -0.031818 -0.040783   0.015853 -0.076933 -0.068192   
veggies       -0.072181 -0.059824 -0.037801  -0.001040 -0.050163 -0.023760   
alcohol       -0.098709 -0.029764 -0.027259  -0.026850 -0.060795  0.076394   
healthcare     0.027034  0.039659  0.034352   0.106549 -0.010527 -0.010228   
nodocbccost    0.036145  0.021802  0.029976  -0.061975  0.061861  0.031896   
genhlth        0.396571  0.308459  0.227588   0.063116  0.256642  0.140658   
menthlth       0.080688  0.058133  0.079929  -0.009365  0.099286  0.086354   
phyhlth        0.206868  0.167821  0.138266   0.036442  0.155661  0.114730   
walk           0.267082  0.229638  0.157859   0.046421  0.240667  0.113713   
sex            0.042538  0.037824  0.013250  -0.008116 -0.002822  0.113422   
age            0.270581  0.325906  0.236471   0.100686 -0.026132  0.108439   
education     -0.131569 -0.109807 -0.067133  -0.012338 -0.061120 -0.094346   
income        -0.210774 -0.177433 -0.095025   0.003931 -0.105602 -0.098975   

                 stroke  heart_disease  activity    fruits  ...  healthcare  \
diabetes       0.122727       0.207229 -0.150281 -0.044560  ...    0.027034   
bp             0.126869       0.206776 -0.128307 -0.031818  ...    0.039659   
chol           0.098166       0.178207 -0.084469 -0.040783  ...    0.034352   
cholcheck      0.023368       0.044795 -0.010072  0.015853  ...    0.106549   
bmi            0.019503       0.055345 -0.164179 -0.076933  ...   -0.010527   
smoker         0.061957       0.120457 -0.072401 -0.068192  ...   -0.010228   
stroke         1.000000       0.222062 -0.076771 -0.005811  ...    0.007801   
heart_disease  0.222062       1.000000 -0.093858 -0.014931  ...    0.017603   
activity      -0.076771      -0.093858  1.000000  0.127578  ...    0.024168   
fruits        -0.005811      -0.014931  0.127578  1.000000  ...    0.026964   
veggies       -0.044869      -0.032327  0.143392  0.234505  ...    0.026832   
alcohol       -0.024496      -0.038745  0.021624 -0.031518  ...   -0.012691   
healthcare     0.007801       0.017603  0.024168  0.026964  ...    1.000000   
nodocbccost    0.034305       0.033397 -0.059079 -0.042215  ...   -0.220451   
genhlth        0.186537       0.271502 -0.264142 -0.086836  ...   -0.028477   
menthlth       0.084800       0.071530 -0.124535 -0.057019  ...   -0.047689   
phyhlth        0.161824       0.194963 -0.228329 -0.041836  ...   -0.000416   
walk           0.189714       0.229188 -0.270988 -0.044017  ...    0.011066   
sex            0.004149       0.099020  0.052069 -0.088017  ...   -0.006804   
age            0.113841       0.205764 -0.088975  0.055290  ...    0.144226   
education     -0.056268      -0.075456  0.154878  0.075876  ...    0.090365   
income        -0.120743      -0.134466  0.182744  0.056529  ...    0.117616   

               nodocbccost   genhlth  menthlth   phyhlth      walk       sex  \
diabetes          0.036145  0.396571  0.080688  0.206868  0.267082  0.042538   
bp                0.021802  0.308459  0.058133  0.167821  0.229638  0.037824   
chol              0.029976  0.227588  0.079929  0.138266  0.157859  0.013250   
cholcheck        -0.061975  0.063116 -0.009365  0.036442  0.046421 -0.008116   
bmi               0.061861  0.256642  0.099286  0.155661  0.240667 -0.002822   
smoker            0.031896  0.140658  0.086354  0.114730  0.113713  0.113422   
stroke            0.034305  0.186537  0.084800  0.161824  0.189714  0.004149   
```

```
heart_disease     0.033397  0.271502  0.071530  0.194963  0.229188  0.099020
activity         -0.059079 -0.264142 -0.124535 -0.228329 -0.270988  0.052069
fruits           -0.042215 -0.086836 -0.057019 -0.041836 -0.044017 -0.088017
veggies          -0.033643 -0.106136 -0.047458 -0.060875 -0.078098 -0.053422
alcohol           0.008453 -0.063705  0.013914 -0.038739 -0.051894  0.015437
healthcare       -0.220451 -0.028477 -0.047689 -0.000416  0.011066 -0.006804
nodocbccost       1.000000  0.164758  0.191108  0.153952  0.123415 -0.048469
genhlth           0.164758  1.000000  0.310093  0.550138  0.472338 -0.016880
menthlth          0.191108  0.310093  1.000000  0.376625  0.246948 -0.089926
phyhlth           0.153952  0.550138  0.376625  1.000000  0.484092 -0.045929
walk              0.123415  0.472338  0.246948  0.484092  1.000000 -0.082858
sex              -0.048469 -0.016880 -0.089926 -0.045929 -0.082858  1.000000
age              -0.131942  0.137805 -0.102646  0.075041  0.176205  0.000452
education        -0.066338 -0.228809 -0.072687 -0.119683 -0.155786  0.021732
income           -0.176346 -0.339565 -0.168691 -0.232727 -0.298935  0.149290

                    age  education    income
diabetes       0.270581  -0.131569 -0.210774
bp             0.325906  -0.109807 -0.177433
chol           0.236471  -0.067133 -0.095025
cholcheck      0.100686  -0.012338  0.003931
bmi           -0.026132  -0.061120 -0.105602
smoker         0.108439  -0.094346 -0.098975
stroke         0.113841  -0.056268 -0.120743
heart_disease  0.205764  -0.075456 -0.134466
activity      -0.088975   0.154878  0.182744
fruits         0.055290   0.075876  0.056529
veggies       -0.015007   0.133288  0.138043
alcohol       -0.052377   0.035449  0.070686
healthcare     0.144226   0.090365  0.117616
nodocbccost   -0.131942  -0.066338 -0.176346
genhlth        0.137805  -0.228809 -0.339565
menthlth      -0.102646  -0.072687 -0.168691
phyhlth        0.075041  -0.119683 -0.232727
walk           0.176205  -0.155786 -0.298935
sex            0.000452   0.021732  0.149290
age            1.000000  -0.087148 -0.149126
education     -0.087148   1.000000  0.355316
income        -0.149126   0.355316  1.000000

[22 rows x 22 columns]
```

Correlation Heatmap

In [ ]:
```
#import pandas as pd
#import matplotlib.pyplot as plt
#import seaborn as sns

# Run correlation matrix and plot
f, ax = plt.subplots(figsize=(10, 8))
corr = df_diabetes.corr()

sns.heatmap(corr, mask=np.zeros_like(corr, dtype=bool),
            cmap=sns.diverging_palette(220, 10, as_cmap=True),
            square=True, ax=ax)
```

```
plt.show()
```



Correlation of features with the outcome variable, diabetes

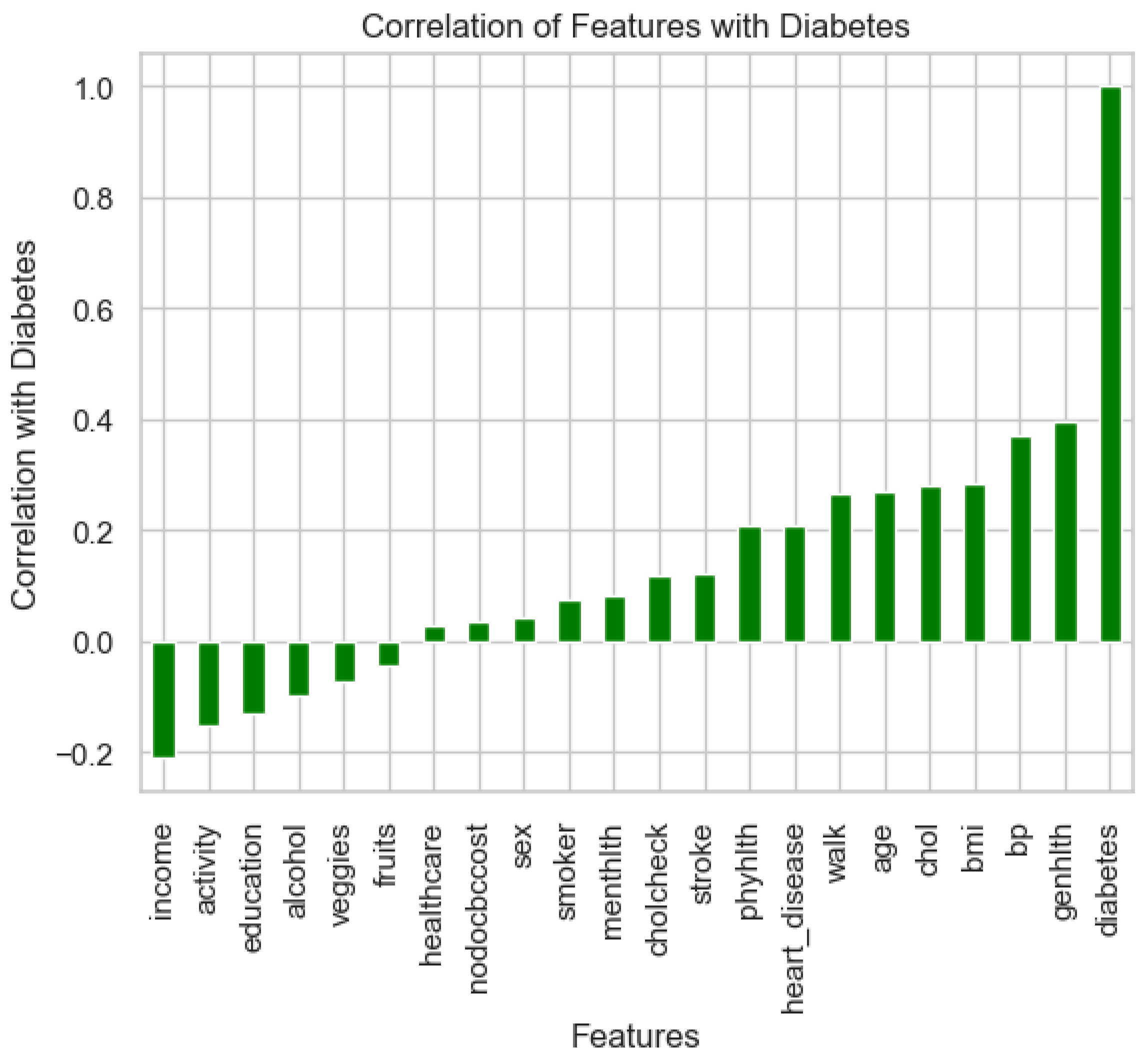
- sort the results, ascending order

In [ ]:
```
df_diabetes.corr()['diabetes'].sort_values()
```

```
Out[ ]: income          -0.210774
        activity        -0.150281
        education       -0.131569
        alcohol         -0.098709
        veggies         -0.072181
        fruits          -0.044560
        healthcare       0.027034
        nodocbccost      0.036145
        sex              0.042538
        smoker           0.075853
        menthlth         0.080688
        cholcheck        0.118900
        stroke           0.122727
        phyhlth          0.206868
        heart_disease    0.207229
        walk             0.267082
        age              0.270581
        chol             0.281399
        bmi              0.285643
        bp               0.372048
        genhlth          0.396571
        diabetes         1.000000
        Name: diabetes, dtype: float64
```

Bar graph: Correlation of features with the outcome variable, Diabetes

```
In [ ]: df_diabetes.corr()['diabetes'].sort_values().plot(kind='bar', color='green')
        plt.xlabel('Features')
        plt.ylabel('Correlation with Diabetes')
        plt.title('Correlation of Features with Diabetes')
        plt.show()
```



12. Chi-square test for independence of categorical variables against 'diabetes'

- The null hypothesis (Ho) in Chi-square test of independence states that there is no relationship between the categorical variables being tested.
- Given a significance level of 0.05, if we reject the null hypothesis(False), it indicates that there is evidence to suggest a relationship between the variables.

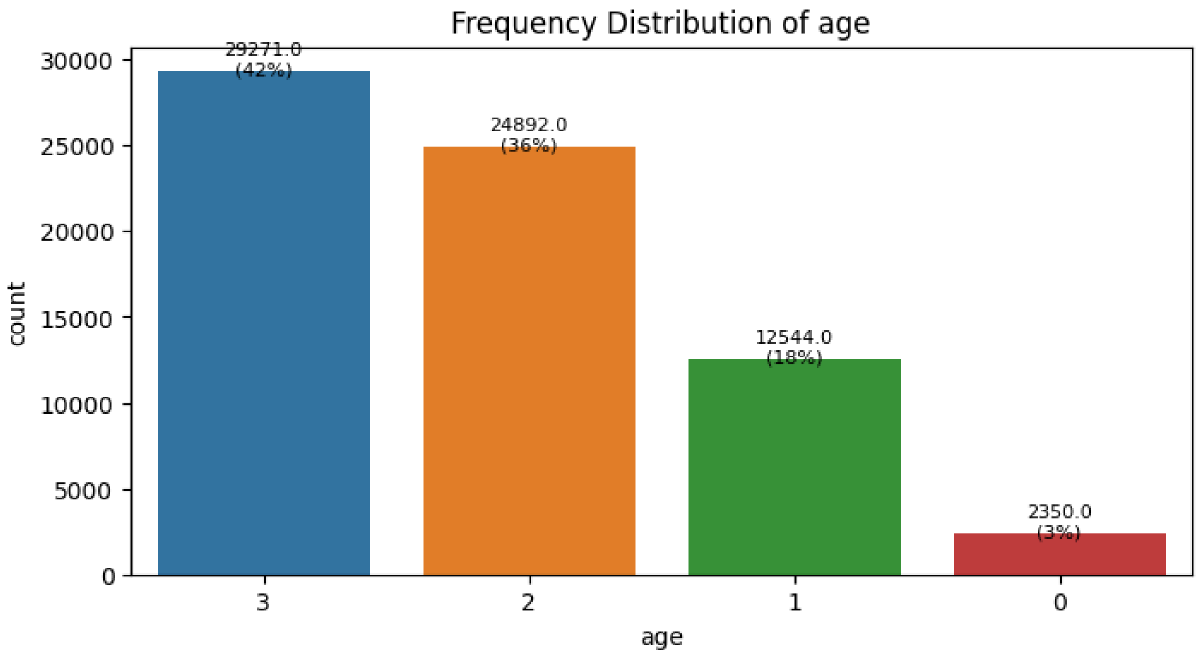
In [ ]:
```
import pandas as pd
from scipy.stats import chi2_contingency

# List to store the results
chi2_results = []

# Define the significance level
alpha = 0.05

df_diabetes_drop_target = df_diabetes.drop(columns=['diabetes'])

# Iterate over each column in the DataFrame
for column in df_diabetes.columns:
    # Create a contingency table between the current column and the target column
    contingency_table = pd.crosstab(df_diabetes[column], df_diabetes['diabetes'])

    # Perform the Chi-square test
    chi2_stat, p_val, _, _ = chi2_contingency(contingency_table)

    # Store the results
    chi2_results.append((column, chi2_stat, p_val, p_val > alpha))

# Convert the results to a DataFrame for easier analysis
chi2_results_df = pd.DataFrame(chi2_results, columns=['Column', 'Chi-square statist

# Print the DataFrame
print(" Chi-square Test of Independence")

print(chi2_results_df)
```

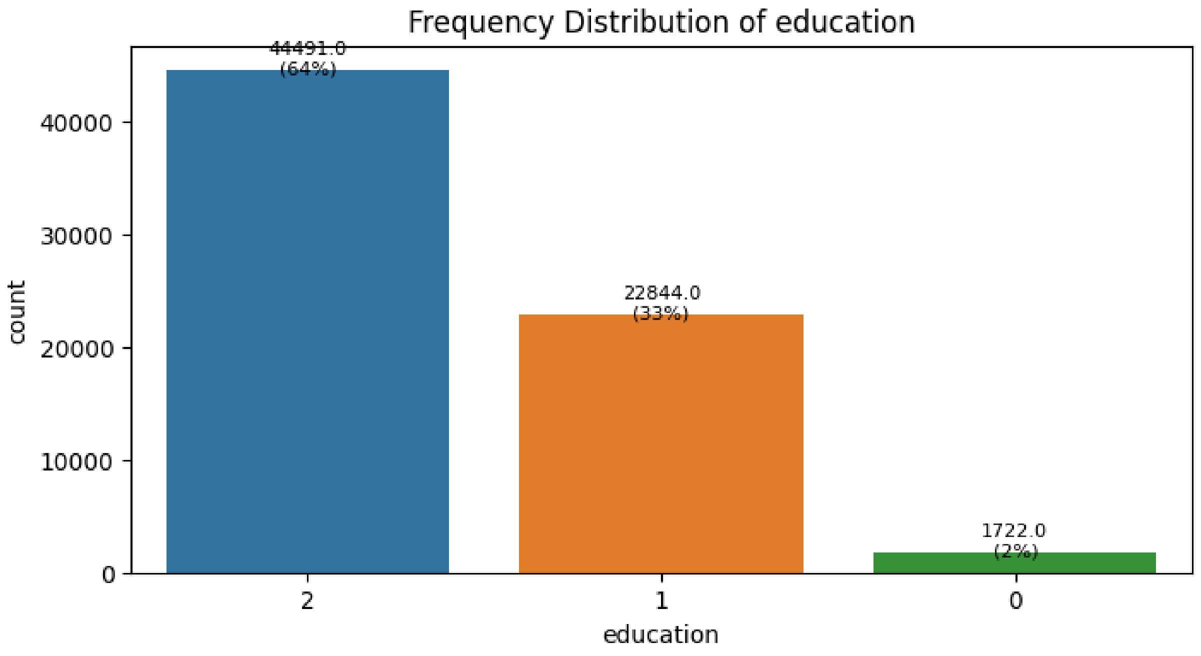
```
 Chi-square Test of Independence
           Column  Chi-square statistic        p-value  Null Hypothesis (Ho)
0        diabetes          69052.998973   0.000000e+00                 False
1              bp           9557.323086   0.000000e+00                 False
2            chol           5467.178055   0.000000e+00                 False
3       cholcheck            974.756080  5.513841e-214                 False
4             bmi           7206.276100   0.000000e+00                 False
5          smoker            397.032404   2.437524e-88                 False
6          stroke           1039.121611  5.633771e-228                 False
7   heart_disease           2964.403557   0.000000e+00                 False
8        activity           1558.959632   0.000000e+00                 False
9          fruits            136.935677   1.245551e-31                 False
10        veggies            359.443376   3.722096e-80                 False
11        alcohol            671.888634  3.880471e-148                 False
12     healthcare             50.212286   1.379812e-12                 False
13     nodocbccost            89.975138   2.411716e-21                 False
14        genhlth          11355.569296   0.000000e+00                 False
15       menthlth            596.821393  1.347932e-106                 False
16        phyhlth           3362.803539   0.000000e+00                 False
17           walk           4924.796104   0.000000e+00                 False
18            sex            124.787363   5.665131e-29                 False
19            age           5345.689918   0.000000e+00                 False
20      education           1195.820177  2.142633e-260                 False
21         income           3069.107535   0.000000e+00                 False
```

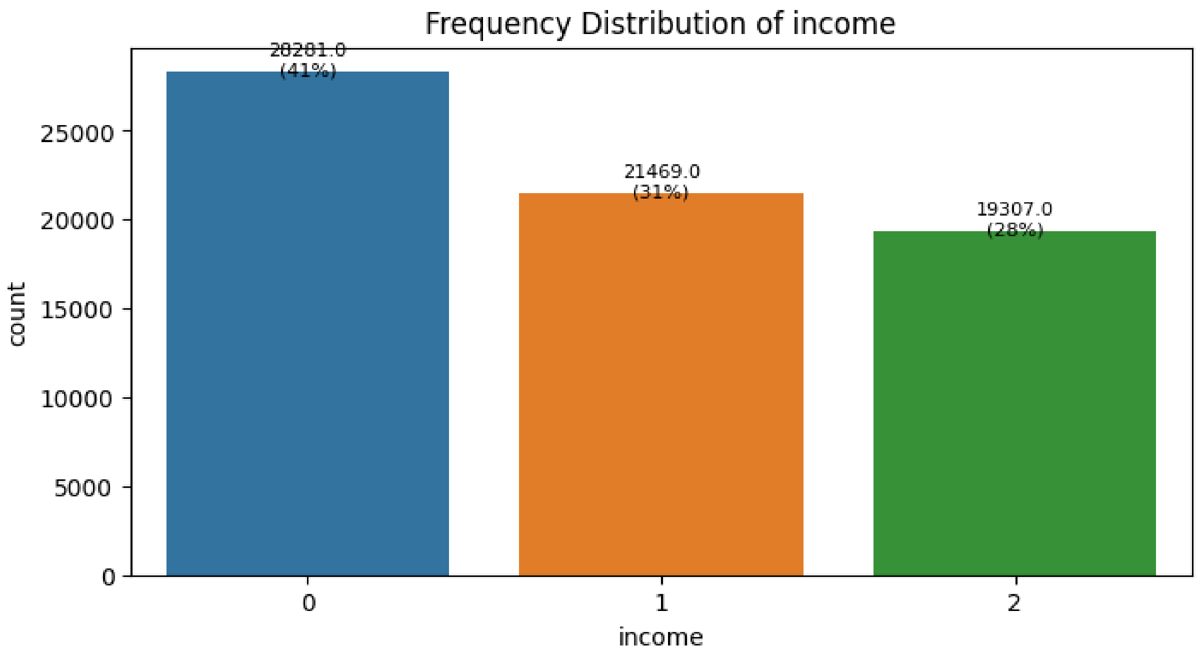
13. Frequency distribution of some categorical variables:'age', 'education', 'income'

In [ ]:

```
import matplotlib.pyplot as plt
import seaborn as sns

# Plot the frequency distribution of each categorical variable
# categorical_columns = df_diabetes.select_dtypes(include=['category', 'object']).c
age_education_income_features = ['age', 'education', 'income']

for column in age_education_income_features:
    plt.figure(figsize=(8, 4))
    ax = sns.countplot(data=df_diabetes, x=column, order=df_diabetes[column].value_
    plt.title(f'Frequency Distribution of {column}')
    plt.xticks(rotation=0)

    # Add count and percentage above each bar
    total_count = len(df_diabetes[column])
    for p in ax.patches:
        count = p.get_height()
        percentage = (count / total_count) * 100
        ax.annotate(f'{count}\n({percentage:.0f}%)', (p.get_x() + p.get_width() / 2
                    ha='center', va='center', fontsize=8, xytext=(0, 5), textcoords

    plt.show()
```



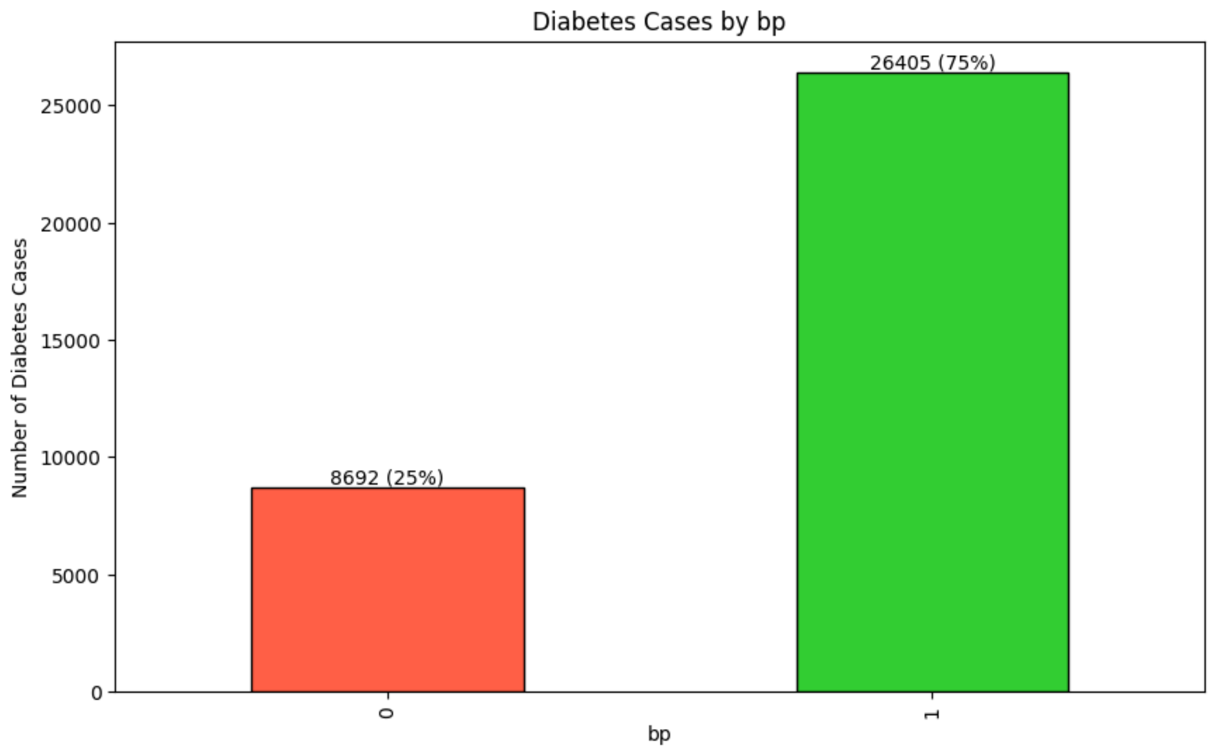


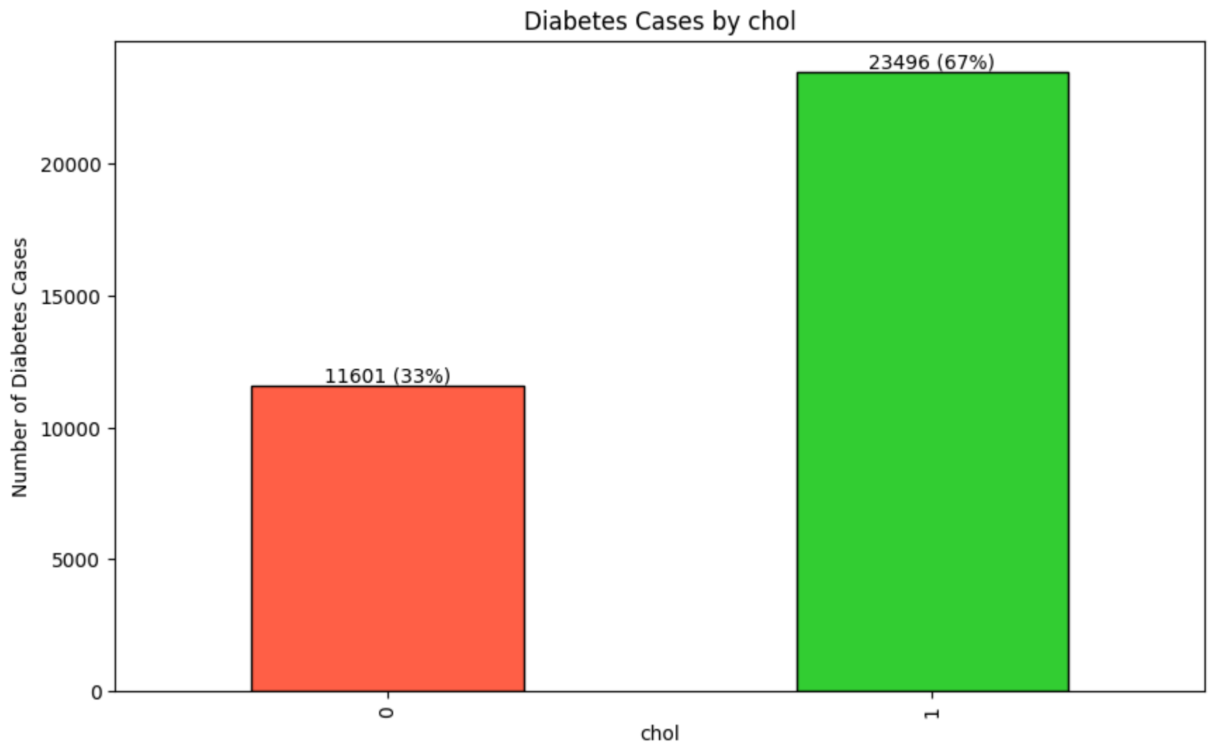


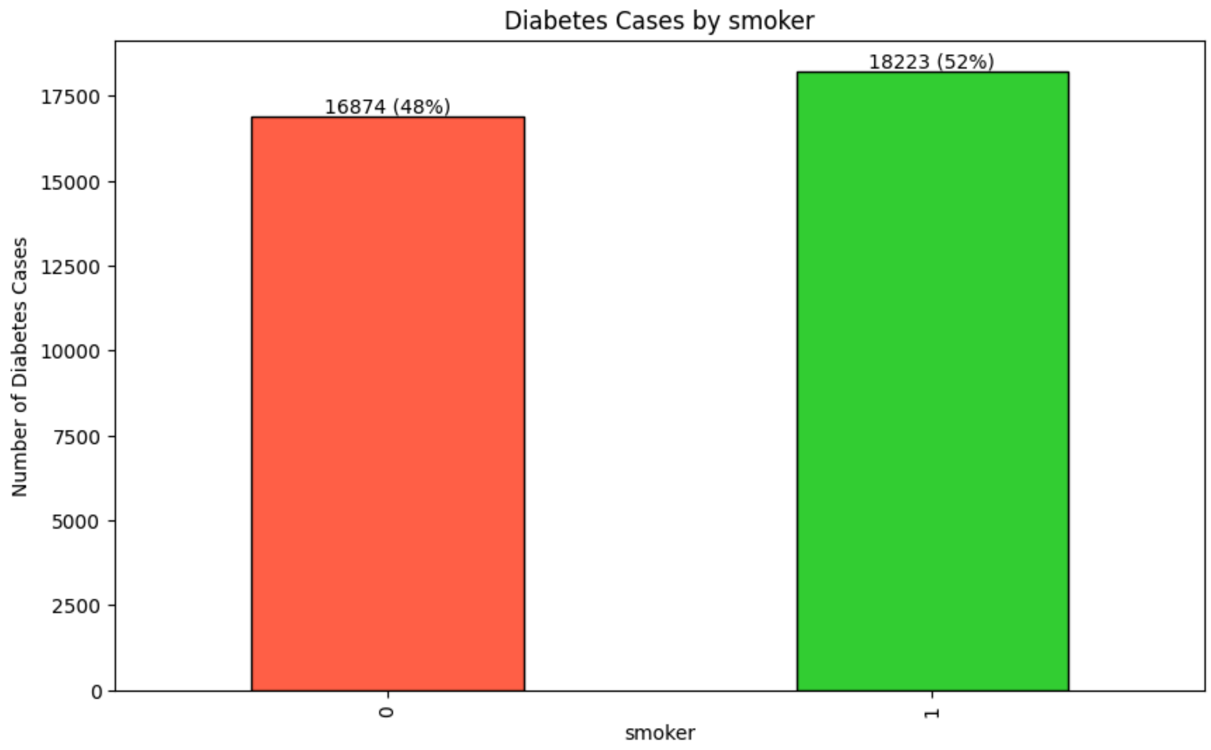
14.The distribution of 'diabetes' outcome by risk factors

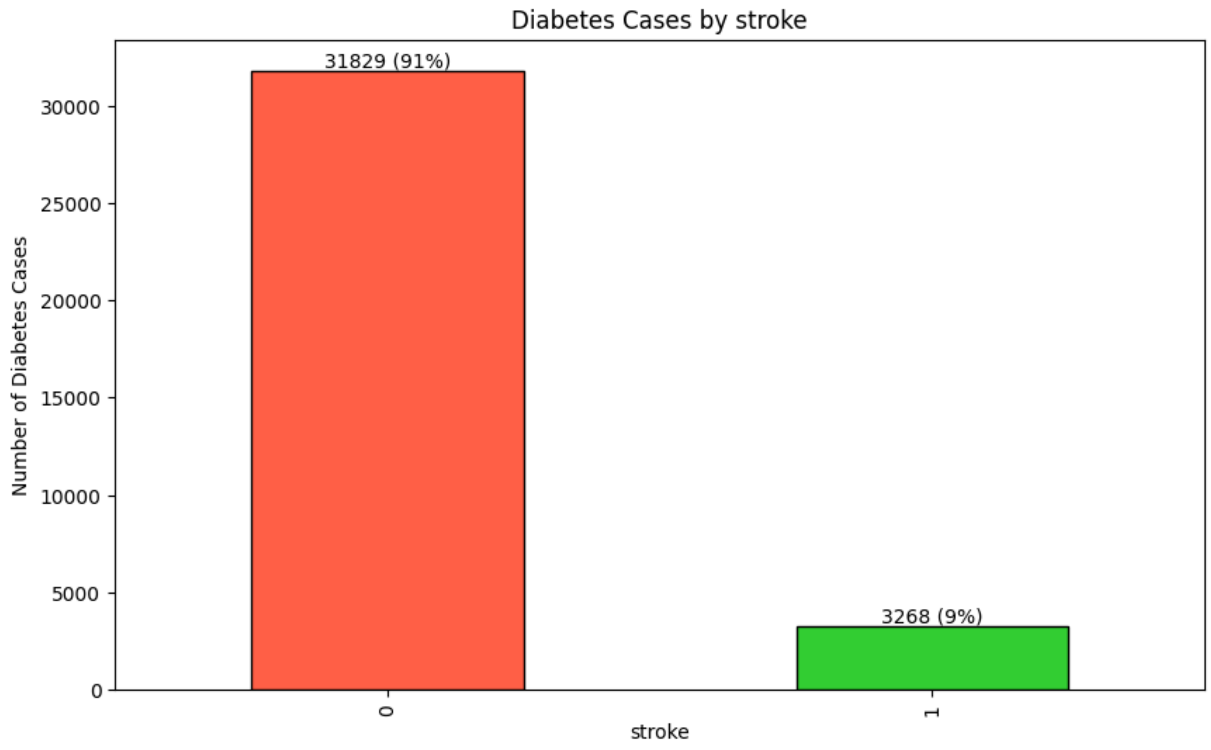
Cross Tabulation: diabetes with bp,chol,smoker,stroke, heart_disease and alchol

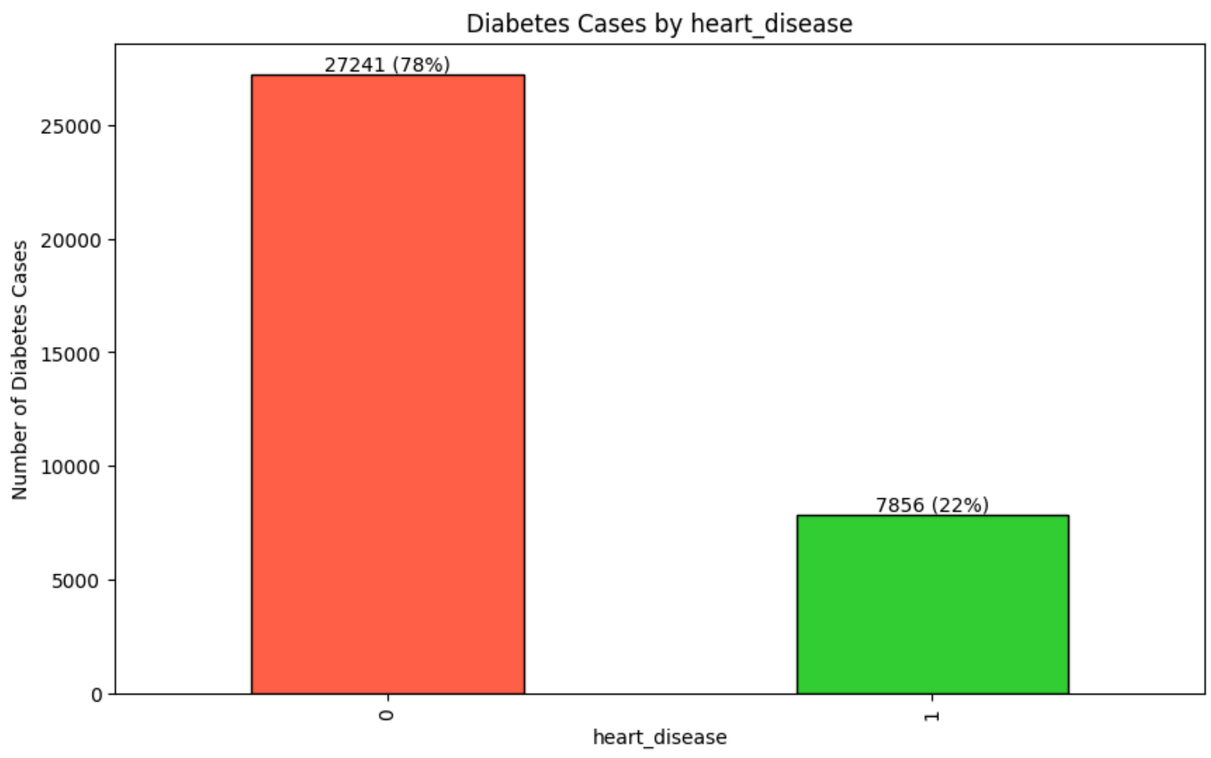
In [ ]:
```
# List of features to plot
risk_facors_features = ['bp', 'chol', 'smoker', 'stroke', 'heart_disease', 'alcohol

# Iterate through each feature and create a bar plot
for feature in risk_facors_features:
    # Create cross-tabulation
    cross_tab = pd.crosstab(df_diabetes[feature], df_diabetes['diabetes'])

    # Sum of diabetes cases for each category
    grouped = cross_tab[1]

    plt.figure(figsize=(10, 6))

    # Create alternating colors
    colors = ['tomato' if i % 2 == 0 else 'limegreen' for i in range(len(grouped))]

    # Plot with alternating colors
    ax = grouped.plot(kind='bar', color=colors, edgecolor='black')

    # Calculate the total sum for percentage calculation
    total = grouped.sum()

    # Annotate the bars with the sum and percentage
    for i, value in enumerate(grouped):
        percentage = (value / total) * 100
        ax.text(i, value, f'{int(round(value))} ({round(percentage)}%)', ha='center

    # Add labels and title
    plt.xlabel(feature)
    plt.ylabel('Number of Diabetes Cases')
    plt.title(f'Diabetes Cases by {feature}')
    # Show the plot
    plt.show()
```

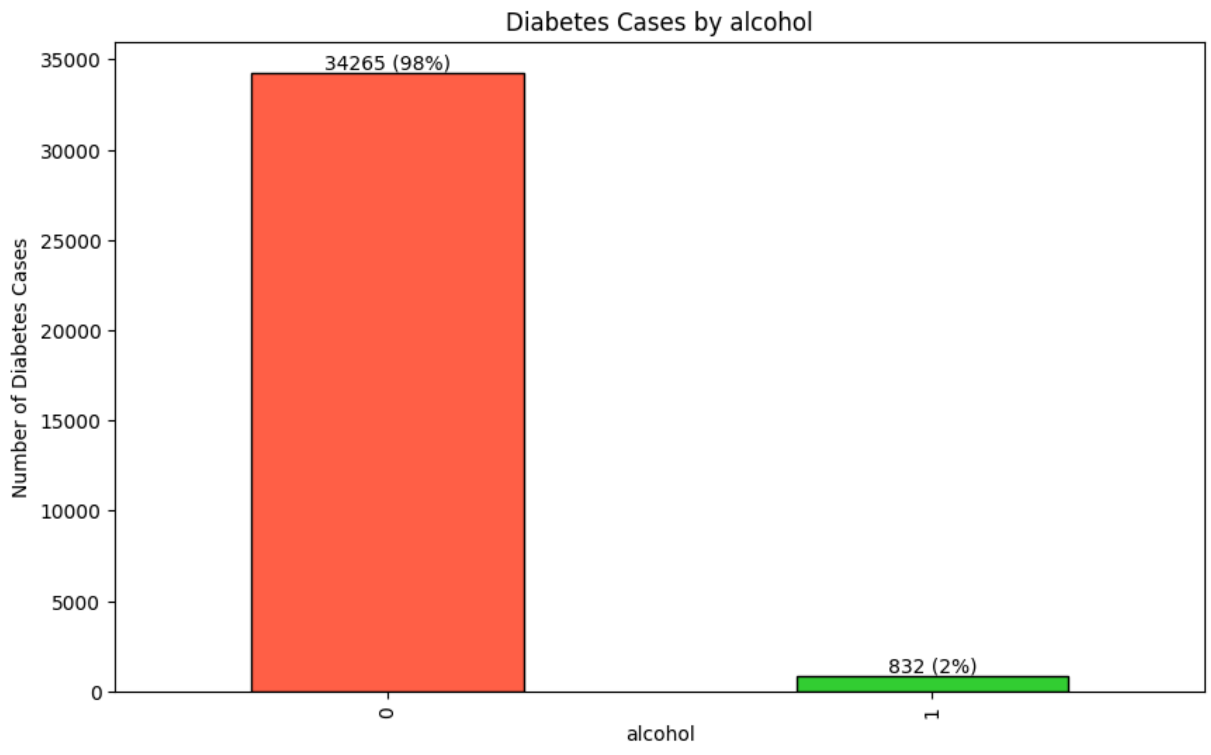





Diabetes Cases by smoker
Number of Diabetes Cases
16874 (48%)
18223 (52%)
0
1
smoker
0
2500
5000
7500
10000
12500
15000
17500


Diabetes Cases by stroke
Number of Diabetes Cases
31829 (91%)
3268 (9%)
0
1
stroke
0
5000
10000
15000
20000
25000
30000





15. The distribution of diabetes outcome by good habit features

Croos Tabulation: diabetes with activity, fruits and veggies

In [ ]:
```
# croos tabulation of good_habit_features with diabetes outcome

# List of features to generate crosstabs for
good_habit_features = ['activity', 'fruits', 'veggies']

# Iterate through each feature and create a crosstab
```

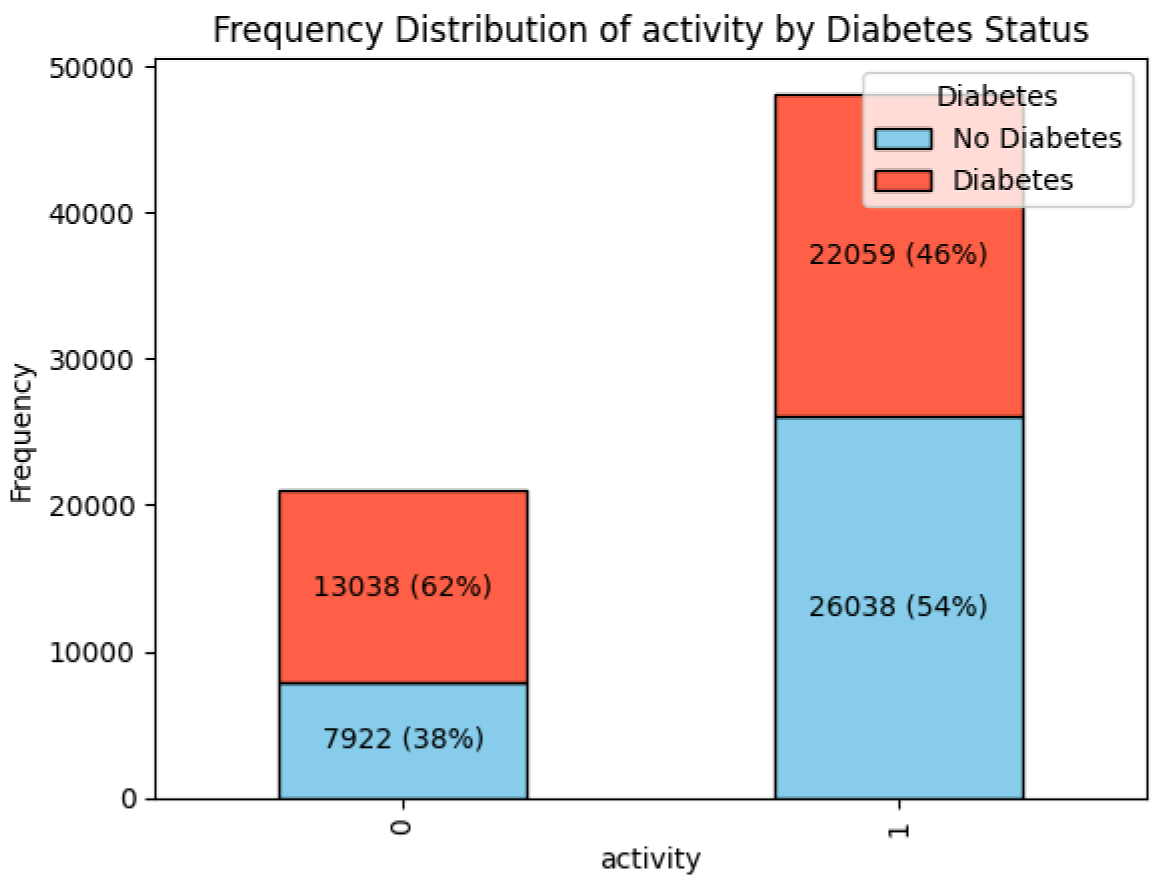
```
for feature in good_habit_features:
    crosstab = pd.crosstab(df_diabetes[feature], df_diabetes['diabetes'])
    crosstab.columns = ['No Diabetes', 'Diabetes']  # Rename columns for clarity
    print(f'Crosstab for {feature}:\n', crosstab, '\n')
```

```
Crosstab for activity:
            No Diabetes  Diabetes
activity
0                  7922     13038
1                 26038     22059

Crosstab for fruits:
          No Diabetes  Diabetes
fruits
0               12640     14592
1               21320     20505

Crosstab for veggies:
           No Diabetes  Diabetes
veggies
0                 6306      8602
1                27654     26495
```

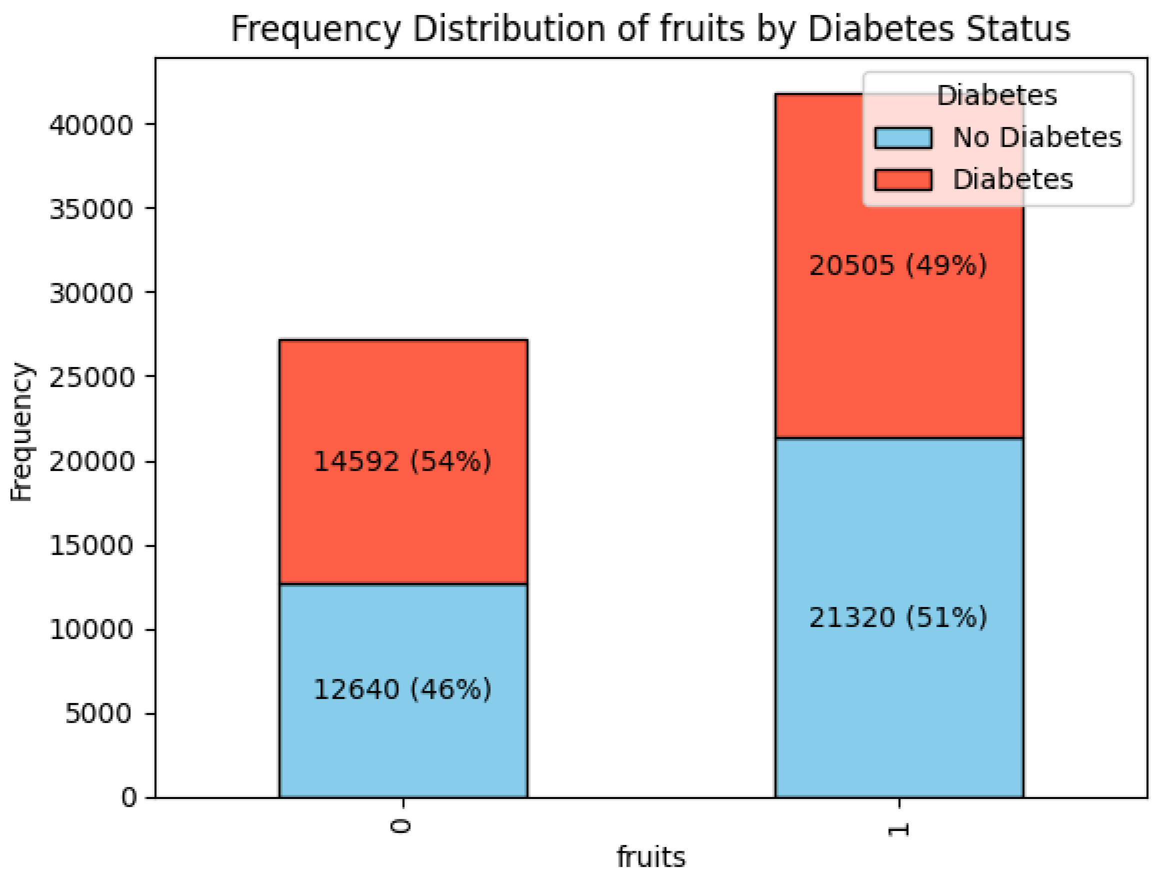
Bar graph: Good habit features with diabetes outcome

In [ ]:
```
# List of features to plot
good_habit_features = ['activity', 'fruits', 'veggies']

# Iterate through each feature and create a frequency table
for feature in good_habit_features:
    # Create a frequency table using crosstab
    frequency_table = pd.crosstab(df_diabetes[feature], df_diabetes['diabetes'])

    plt.figure(figsize=(8, 4))

    # Plot the frequency table as a bar plot
    ax = frequency_table.plot(kind='bar', stacked=True, color=['skyblue', 'tomato']

    # Annotate the bars with the counts and percentages
    for i, row in enumerate(frequency_table.values):
        for j, value in enumerate(row):
            percentage = (value / row.sum()) * 100
            ax.text(i, row[:j].sum() + value/2, f'{value} ({int(round(percentage))}

    # Add labels and title
    plt.xlabel(feature)
    plt.ylabel('Frequency')
    plt.title(f'Frequency Distribution of {feature} by Diabetes Status')

    # Add legend
    plt.legend(title='Diabetes', labels=['No Diabetes', 'Diabetes'], loc='upper rig

    # Show the plot
    plt.show()
```

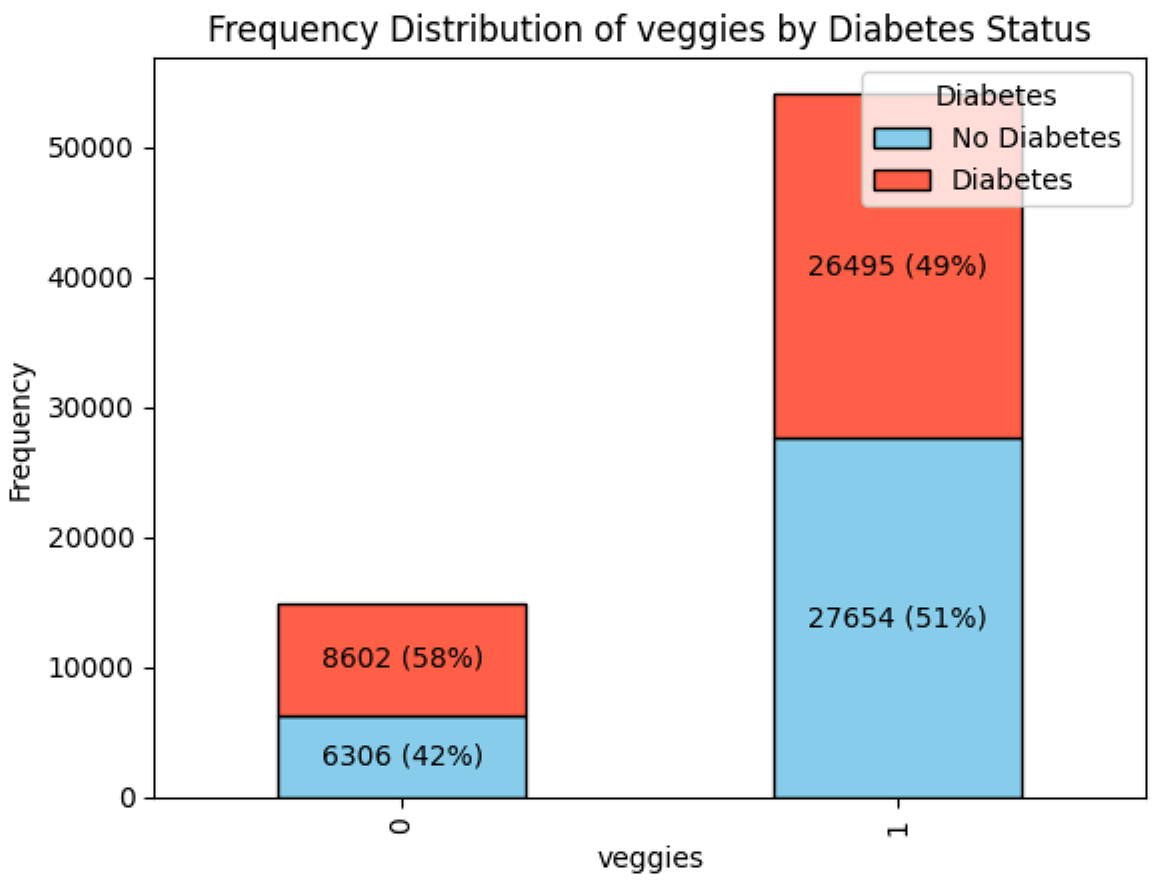
```
<Figure size 800x400 with 0 Axes>
```


Frequency Distribution of activity by Diabetes Status
Frequency
activity
0
1
Diabetes
No Diabetes
Diabetes
7922 (38%)
13038 (62%)
26038 (54%)
22059 (46%)
0
10000
20000
30000
40000
50000

```
<Figure size 800x400 with 0 Axes>
```


Frequency Distribution of fruits by Diabetes Status
Frequency
fruits
0
1
Diabetes
No Diabetes
Diabetes
12640 (46%)
14592 (54%)
21320 (51%)
20505 (49%)
0
5000
10000
15000
20000
25000
30000
35000
40000

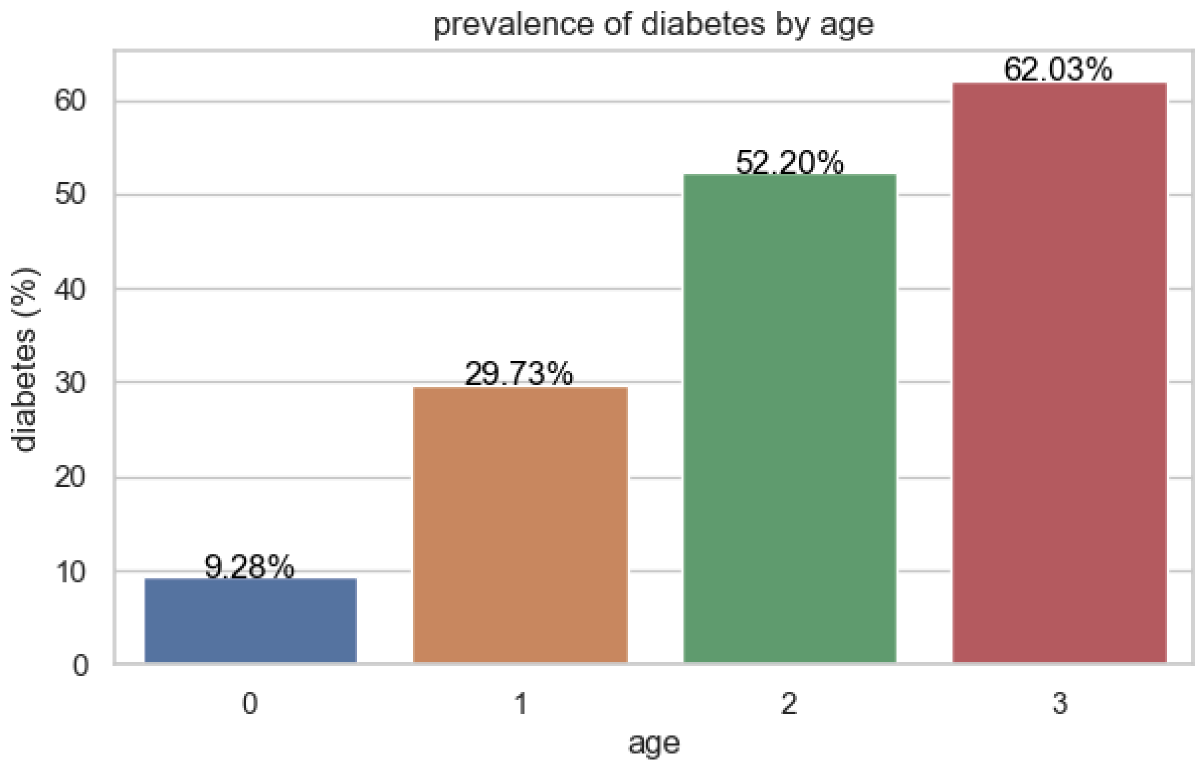
```
<Figure size 800x400 with 0 Axes>
```



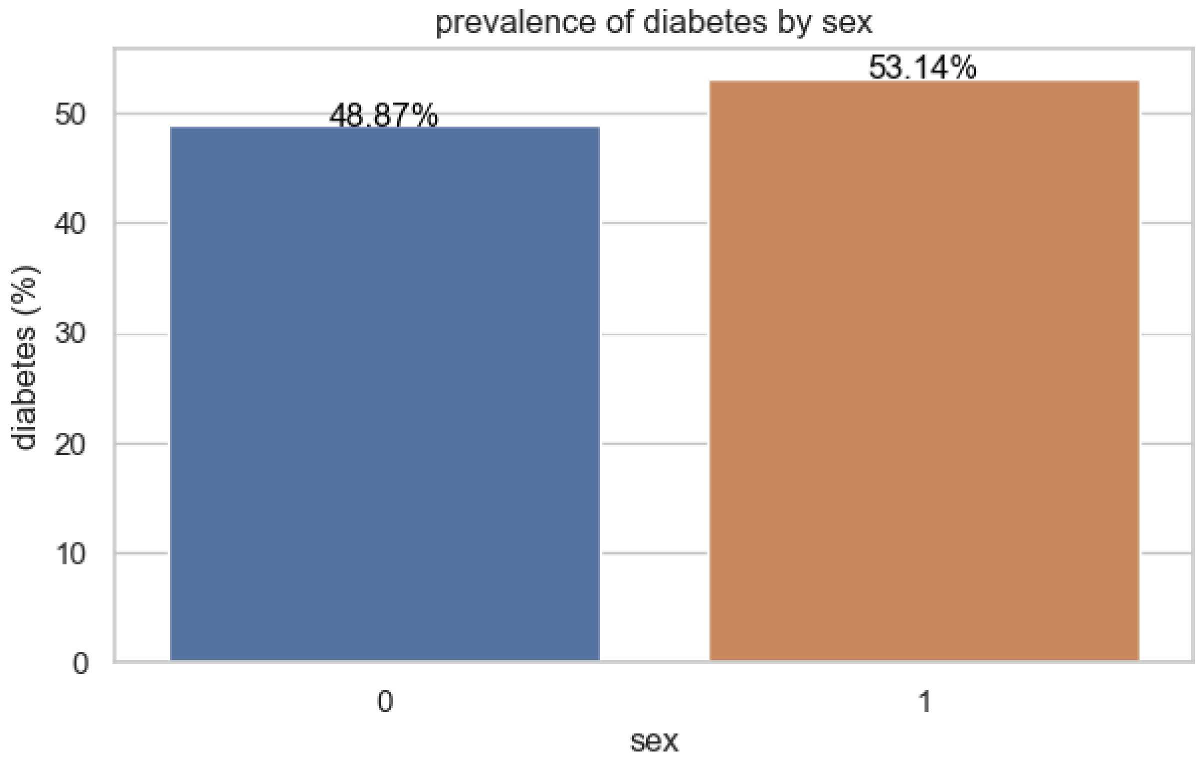
16. Prevalence of Diabetes by age, gender, education and income level

```
In [ ]: import pandas as pd
        import matplotlib.pyplot as plt
        import seaborn as sns

        # Plot settings
        sns.set(style="whitegrid")

        # List of categorical features to plot
        features = ['age', 'sex', 'education', 'income']

        # Creating plots using a for loop
        for feature in features:
            plt.figure(figsize=(7, 4))
            prevalence = df_diabetes.groupby(feature)['diabetes'].mean().reset_index()
            prevalence['diabetes'] = prevalence['diabetes'] * 100  # Convert to percentage
            prevalence = prevalence.sort_values(by='diabetes', ascending=False)  # Sort by
            sns.barplot(data=prevalence, x=feature, y='diabetes', ci=None)
            plt.title(f'prevalence of diabetes by {feature}')
            plt.ylabel('diabetes (%)')
            plt.xlabel(feature)
            plt.xticks(rotation=0)

            # Adding percentages on top of the bars
            for index, row in prevalence.iterrows():
                plt.text(index, row['diabetes'], f"{row['diabetes']:.2f}%", color='black',
    plt.show()
```

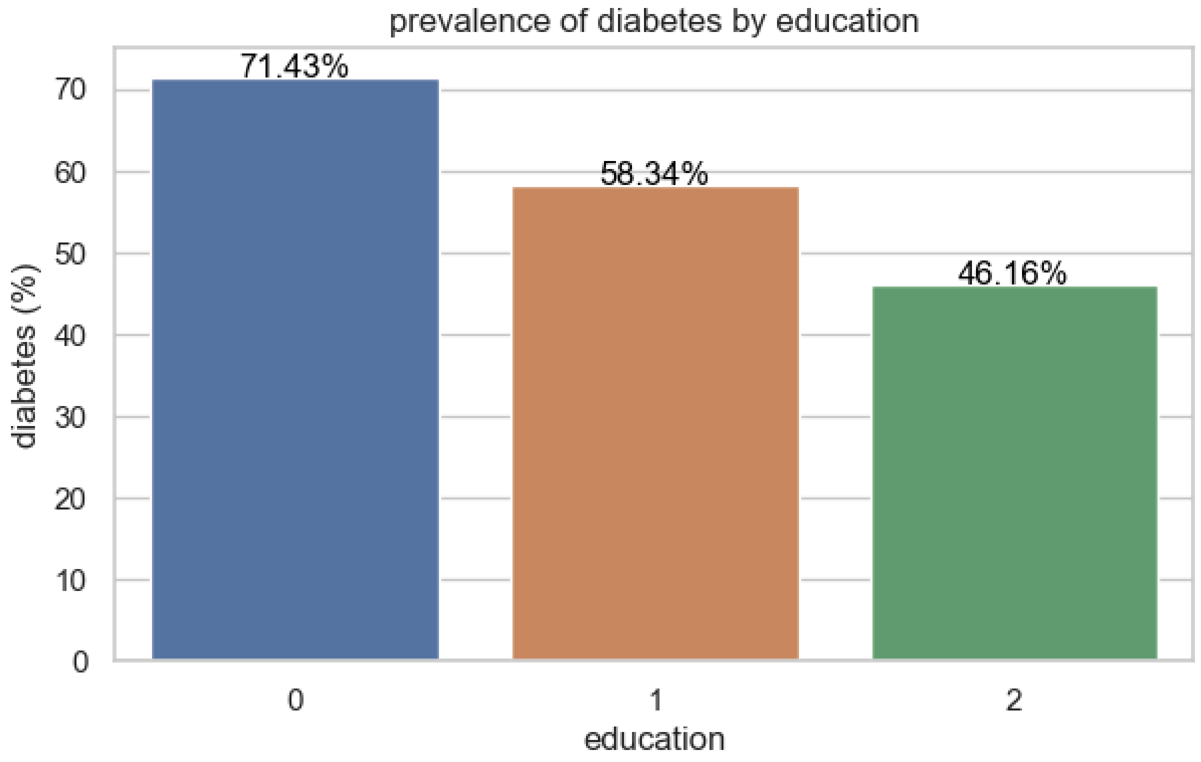
```
C:\Users\yitay\AppData\Local\Temp\ipykernel_8224\3554196671.py:17: FutureWarning:

The `ci` parameter is deprecated. Use `errorbar=None` for the same effect.

  sns.barplot(data=prevalence, x=feature, y='diabetes', ci=None)
```



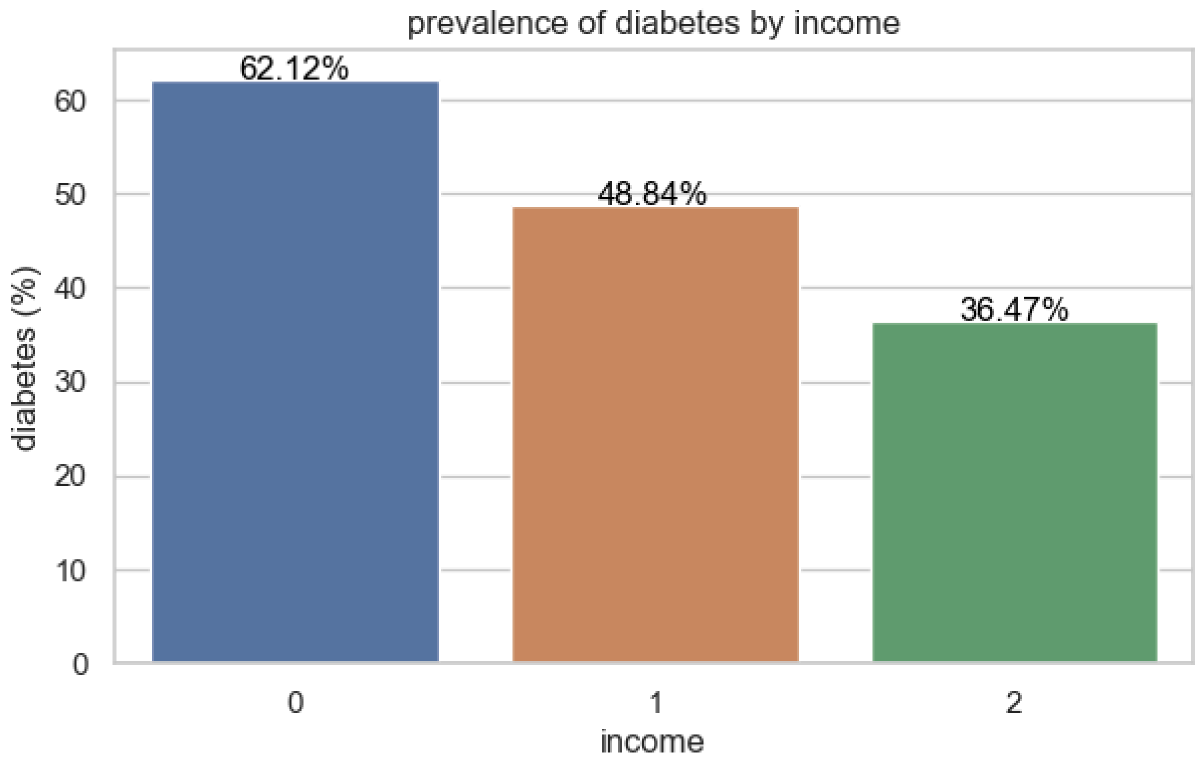
```
C:\Users\yitay\AppData\Local\Temp\ipykernel_8224\3554196671.py:17: FutureWarning:

The `ci` parameter is deprecated. Use `errorbar=None` for the same effect.

  sns.barplot(data=prevalence, x=feature, y='diabetes', ci=None)
```



```
C:\Users\yitay\AppData\Local\Temp\ipykernel_8224\3554196671.py:17: FutureWarning: 

The `ci` parameter is deprecated. Use `errorbar=None` for the same effect.

  sns.barplot(data=prevalence, x=feature, y='diabetes', ci=None)
```



```
C:\Users\yitay\AppData\Local\Temp\ipykernel_8224\3554196671.py:17: FutureWarning:

The `ci` parameter is deprecated. Use `errorbar=None` for the same effect.

  sns.barplot(data=prevalence, x=feature, y='diabetes', ci=None)
```

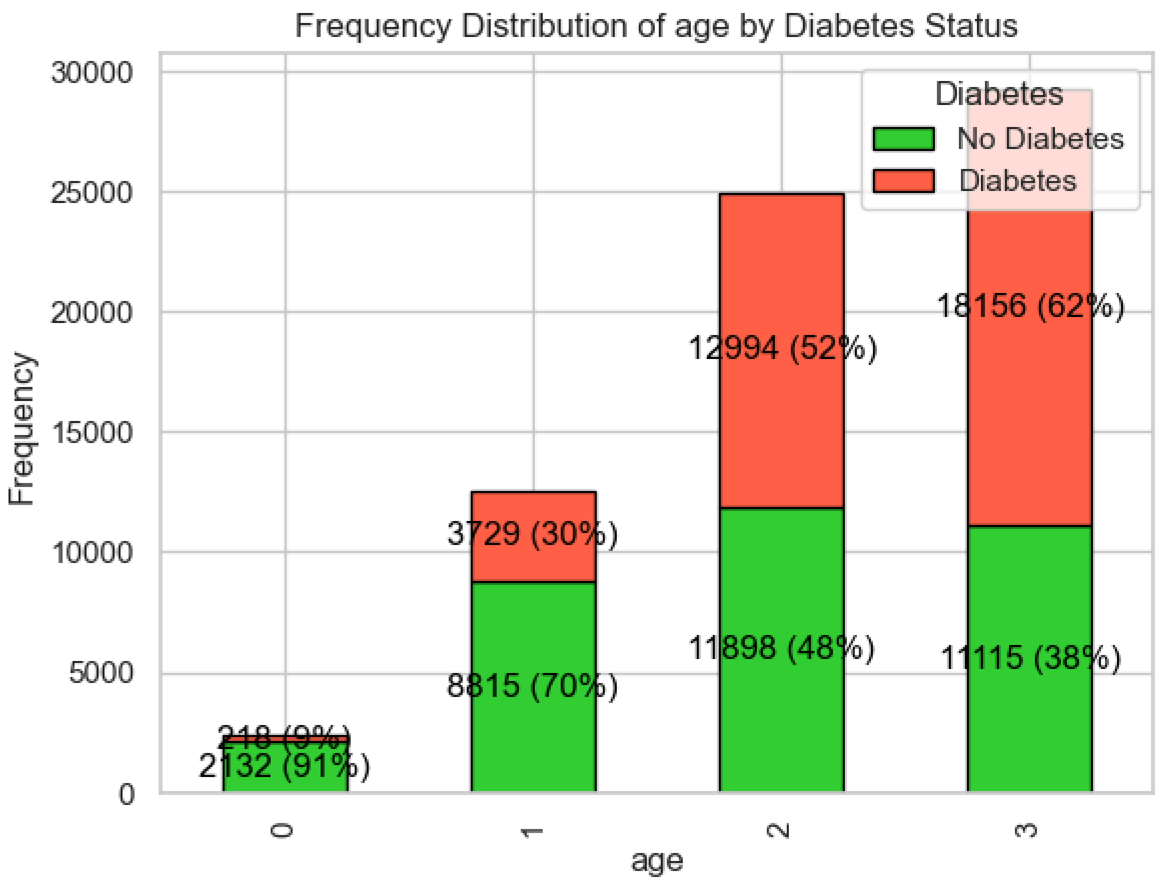


option 2

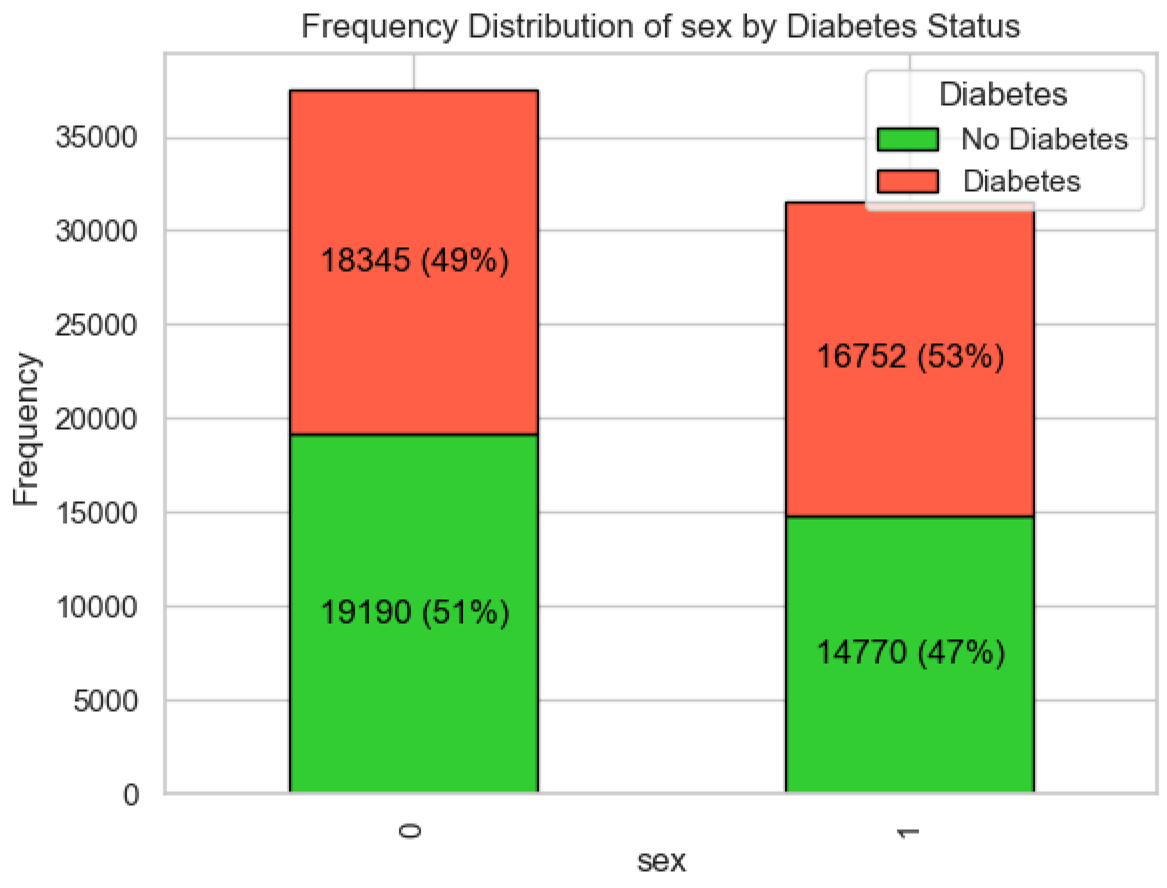
Prevalence of Diabetes by age, gender, education and income level

```
In [ ]: # List of features to plot
prevalence_features = ['age', 'sex', 'education', 'income']

# Iterate through each feature and create a frequency table
for feature in prevalence_features:
    # Create a frequency table using crosstab
    frequency_table = pd.crosstab(df_diabetes[feature], df_diabetes['diabetes'])

    plt.figure(figsize=(8, 4))

    # Plot the frequency table as a bar plot
    ax = frequency_table.plot(kind='bar', stacked=True, color=['limegreen', 'tomato

    # Annotate the bars with the counts and percentages
    for i, row in enumerate(frequency_table.values):
        for j, value in enumerate(row):
            percentage = (value / row.sum()) * 100
            ax.text(i, row[:j].sum() + value/2, f'{value} ({int(round(percentage))}

    # Add labels and title
    plt.xlabel(feature)
    plt.ylabel('Frequency')
    plt.title(f'Frequency Distribution of {feature} by Diabetes Status')

    # Add legend
    plt.legend(title='Diabetes', labels=['No Diabetes', 'Diabetes'], loc='upper rig

    # Show the plot
    plt.show()
```

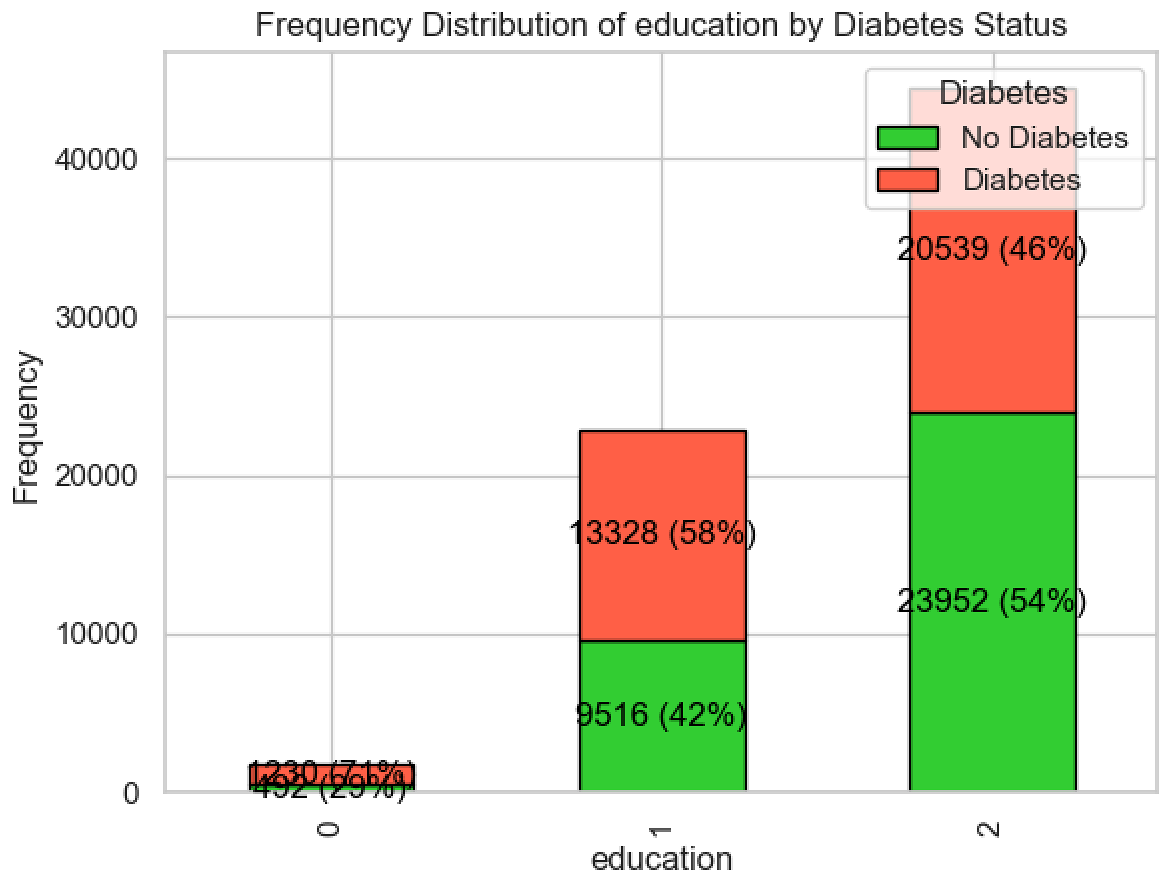
```
<Figure size 800x400 with 0 Axes>
```



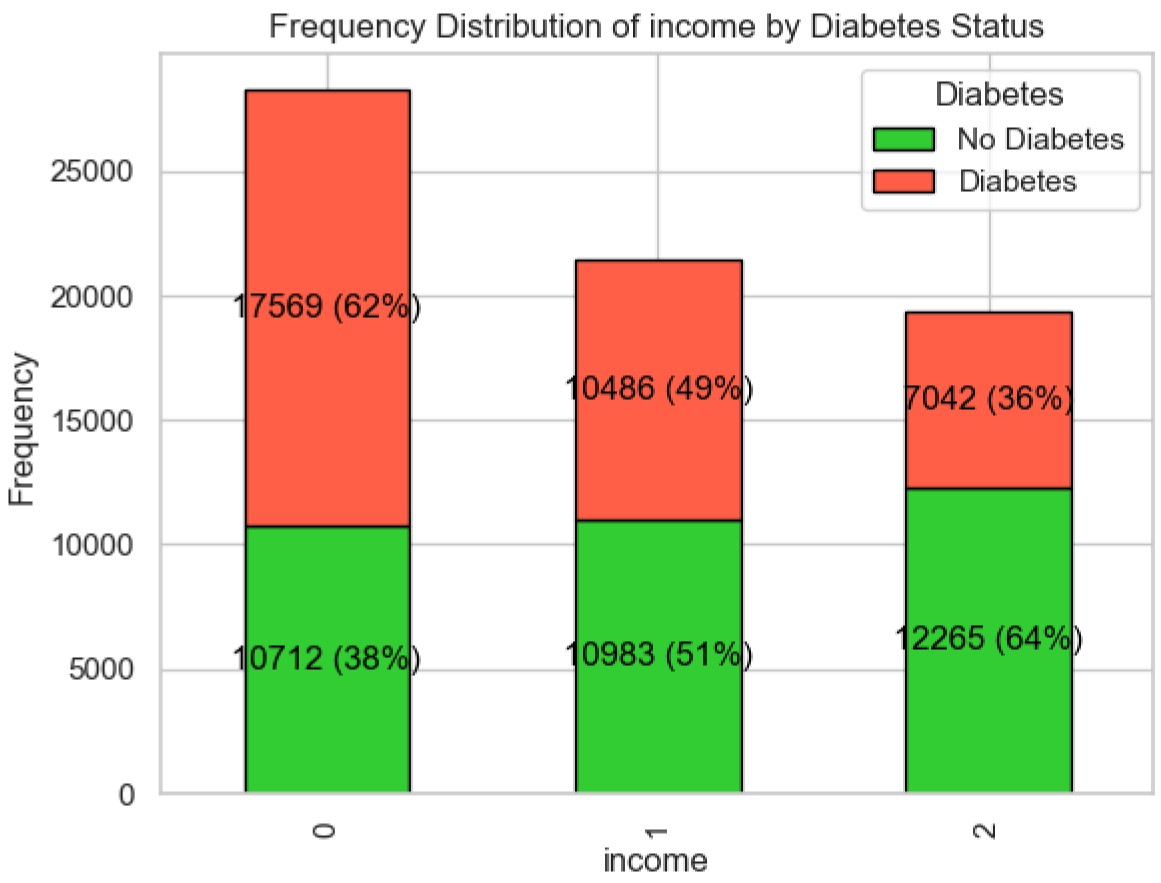
```
<Figure size 800x400 with 0 Axes>
```


Frequency Distribution of sex by Diabetes Status
Diabetes
🟩 No Diabetes
🟥 Diabetes
18345 (49%)
19190 (51%)
16752 (53%)
14770 (47%)
Frequency
35000
30000
25000
20000
15000
10000
5000
0
0
1
sex

```
<Figure size 800x400 with 0 Axes>
```


Frequency Distribution of education by Diabetes Status
Diabetes
🟩 No Diabetes
🟥 Diabetes
1230 (71%)
492 (29%)
13328 (58%)
9516 (42%)
20539 (46%)
23952 (54%)
Frequency
40000
30000
20000
10000
0
0
1
2
education

```
<Figure size 800x400 with 0 Axes>
```



```
============================
```

Save the 'df.diabetes' dataset as a separate clean CSV file

- The location of the saved 'diabetes_clean.csv' file will be in the current working directory of my Python environment at the time i run this script

In [ ]:
```
import pandas as pd
from sklearn.datasets import load_diabetes

# Load diabetes dataset
diabetes = load_diabetes(as_frame=True)
df_diabetes = diabetes.frame

# Save the DataFrame to a CSV file without the index
df_diabetes.to_csv('diabetes_clean.csv', index=False)
```