In [ ]:

```
import sys
import pandas as pd
import numpy as np
import seaborn as sns
from matplotlib import pyplot as plt

from sklearn.model_selection import train_test_split
from sklearn.metrics import  accuracy_score
from sklearn.tree import  DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.feature_selection import mutual_info_classif
from scipy.stats import chi2_contingency, ttest_ind


# Packages created for this project
# Dependencies need to be installed using
# pip/pipenv install -e .
#If there is a problem importing the packages, try  use
#sys.path.insert(0, '../')
from src.visualization.visualize import plot_feature_importance, plot_confusion_matrix
from src.features.build_features import convert_dtypes, preprocess_and_encode_features, fea
from src.models.train_model import grid_search_and_predict, train_and_evaluate
from src.models.metrics import classification_metrics

# Palette of colors used for the plots
red  = '#BE3232'
blue = '#2D4471'
```

1. Data Preprocessing

In [ ]:

```
# Dataset from
# https://www.kaggle.com/datasets/alexteboul/diabetes-health-indicators-dataset?select=dial

df = pd.read_csv('../data/raw/diabetes-indicators-balanced-5050split.csv')
df.head(2)
```

Out[ ]:

	Diabetes_binary	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDiseaseorAttack	PhysActiv
0	0.0	1.0	0.0	1.0	26.0	0.0	0.0	0.0	
1	0.0	1.0	1.0	1.0	26.0	1.0	1.0	0.0	

2 rows × 22 columns

In [ ]:

```
print("before:",df.shape)
# Search for duplicated instances and drop
print("Duplications:",df.duplicated().sum())
#display(df.loc[df.duplicated(),:].head())
df.drop_duplicates(inplace=True)
print('After:',df.shape)
```

```
before: (70692, 22)
Duplications: 1635
After: (69057, 22)
```

Let's check if there are zeros in the categorical features where the range is above zero. This can be interpreted as missing values, so we need to change then to NaN.

In [ ]:

```
categorical_columns = ["GenHlth", "MentHlth", "PhysHlth",
                "Age", "Education", "Income"]
for column in categorical_columns:
    print('Missing Values:', f'{round(100*df[column].eq(0).sum()/df.shape[0], 2)} %', f'in
print(f"Missing Values: {df['BMI'].eq(0).sum()} % in BMI")
df.drop(columns=['MentHlth', 'PhysHlth'], inplace=True)
```

```
Missing Values: 0.0 % in GenHlth
Missing Values: 67.31 % in MentHlth
Missing Values: 55.48 % in PhysHlth
Missing Values: 0.0 % in Age
Missing Values: 0.0 % in Education
Missing Values: 0.0 % in Income
Missing Values: 0 % in BMI
```

There are indeed missing values for **MentHlth** and **PhysHlth**, both must have a range between 1-30. But because the missing values account for 67% of my dataset, it's concerning. Even if this feature correlate highly with the target, removing 67% of data might be worse. A straightforward solution was just to drop these features.

1.1 Split Dataset

In [ ]:

```
# Before split, change the target name to Diabetes
df.rename(columns={'Diabetes_binary': 'Diabetes'}, inplace=True)

# Split in 60% Train /20% Validation/ 20% Test
df_train_large, df_test = train_test_split(df, test_size = 0.2, random_state = 1)
df_train, df_val = train_test_split(df_train_large, train_size = 0.75, random_state = 1)


# Save target feature
Y_train_large = df_train_large['Diabetes'].values
Y_test = df_test['Diabetes'].values
Y_train = df_train['Diabetes'].values
Y_val = df_val['Diabetes'].values

# Drop target feature
df_train.drop('Diabetes', axis=1, inplace=True)
df_val.drop('Diabetes', axis=1, inplace=True)
df_test.drop('Diabetes', axis=1, inplace=True)
```

We will adjust the data types of `df_train_large` to optimize memory usage during the EDA process.

In [ ]:

```
# for better memory usage and interpretability for EDA
boolean_columns = ['Diabetes',"HighBP", "HighChol",
               "CholCheck", "Smoker", "Stroke", "HeartDiseaseorAttack",
               "PhysActivity", "Fruits", "Veggies", "HvyAlcoholConsump",
               "AnyHealthcare", "NoDocbcCost", "DiffWalk", "Sex"]

categorical_columns = ["GenHlth", "Age", "Education", "Income"]

dtype_dict = {
    'int32': categorical_columns + boolean_columns,
    'float32': ["BMI"]
}

df_train_large = convert_dtypes(df_train_large, dtype_dict)
display(df_train_large.info())
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 55245 entries, 15055 to 5239
Data columns (total 20 columns):
 #   Column                Non-Null Count  Dtype  
---  ------                --------------  -----  
 0   Diabetes              55245 non-null  int32  
 1   HighBP                55245 non-null  int32  
 2   HighChol              55245 non-null  int32  
 3   CholCheck             55245 non-null  int32  
 4   BMI                   55245 non-null  float32
 5   Smoker                55245 non-null  int32  
 6   Stroke                55245 non-null  int32  
 7   HeartDiseaseorAttack  55245 non-null  int32  
 8   PhysActivity          55245 non-null  int32  
 9   Fruits                55245 non-null  int32  
 10  Veggies               55245 non-null  int32  
 11  HvyAlcoholConsump     55245 non-null  int32  
 12  AnyHealthcare         55245 non-null  int32  
 13  NoDocbcCost           55245 non-null  int32  
 14  GenHlth               55245 non-null  int32  
 15  DiffWalk              55245 non-null  int32  
 16  Sex                   55245 non-null  int32  
 17  Age                   55245 non-null  int32  
 18  Education             55245 non-null  int32  
 19  Income                55245 non-null  int32  
dtypes: float32(1), int32(19)
memory usage: 4.6 MB
None
```

2. Exploratory Data Analysis (EDA)

Let's proceed with the EDA in the `df_train_large` dataset, which is the combination of both training and validation sets. To prevent data leakage, we don't include the test set for the EDA. This will ensure the trained model evaluation on the test set is unbiased, without information from the train set mistakenly leakage to the test.

2.1 Feature Distribution

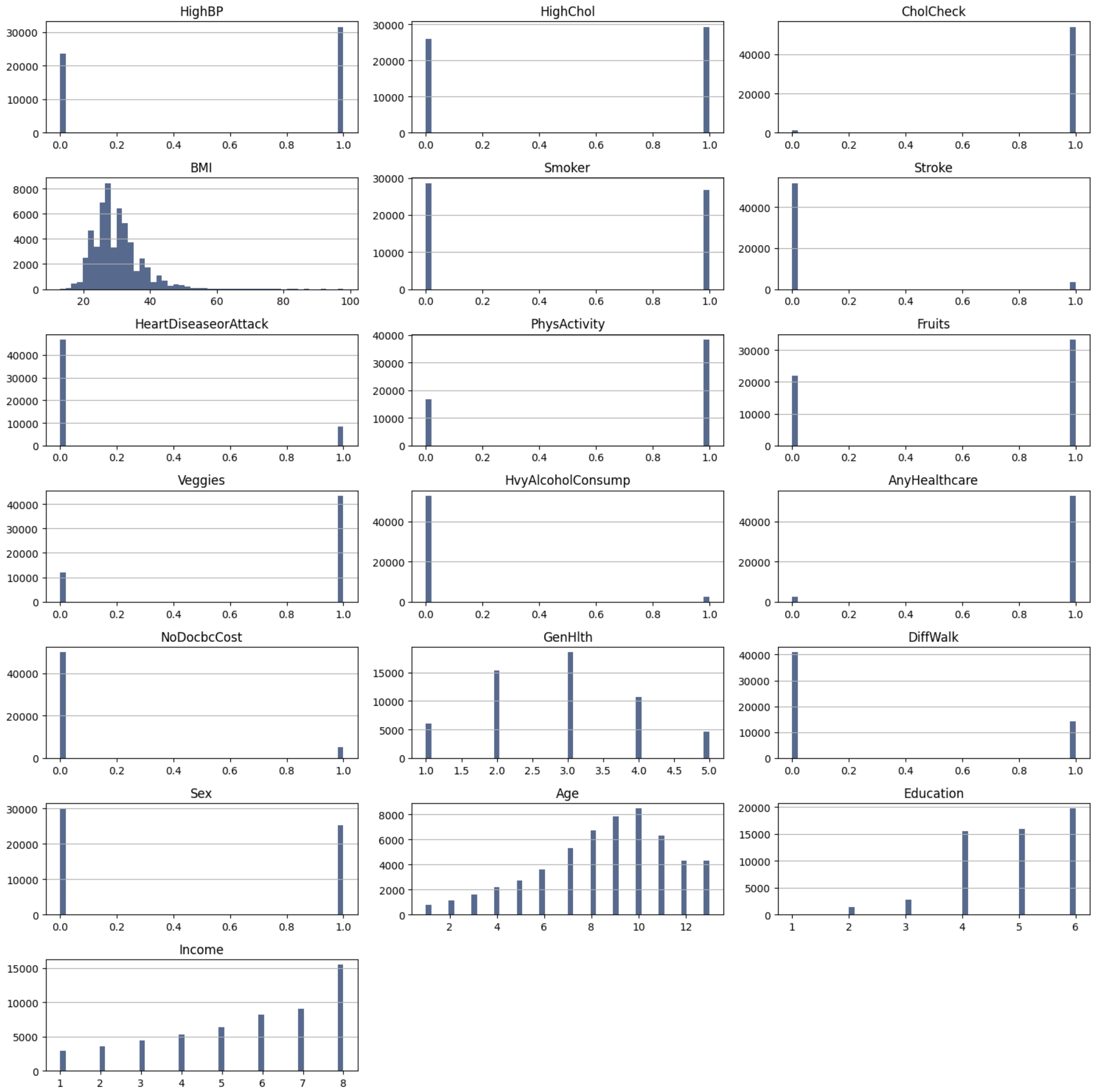
In [ ]:

```python
# Create a dataset without the target feature
df_train_dropped = df_train_large.drop('Diabetes', axis=1)
```

In [ ]:

```python
features = df_train_dropped.columns
n_features = len(features)

fig, axes = plt.subplots(nrows = 7, ncols=3, figsize=(15, 15))

for idx, feature in enumerate(features):
    # Identify row and column in the grid
    row, col = divmod(idx, 3)

    # Check if the feature is boolean type
    if np.issubdtype(df_train_dropped[feature].dtype, np.bool_):
        Yes_count = np.sum(df_train_large[feature])
        No_count = len(df_train_large[feature]) - Yes_count
        axes[row, col].bar(['Yes', 'No'], [Yes_count, No_count], color=blue, alpha = 0.4)
    else:
        # Plot histogram for the current feature
        axes[row, col].hist(df_train_dropped[feature], bins=50, color=blue, alpha = 0.8,)

    axes[row, col].set_title(feature)
    axes[row, col].grid(axis='y')

# remove empty plots
for ax in axes.ravel()[len(features):]:
    ax.axis('off')
```

```
# Adjust layout
plt.tight_layout()
plt.show()
```



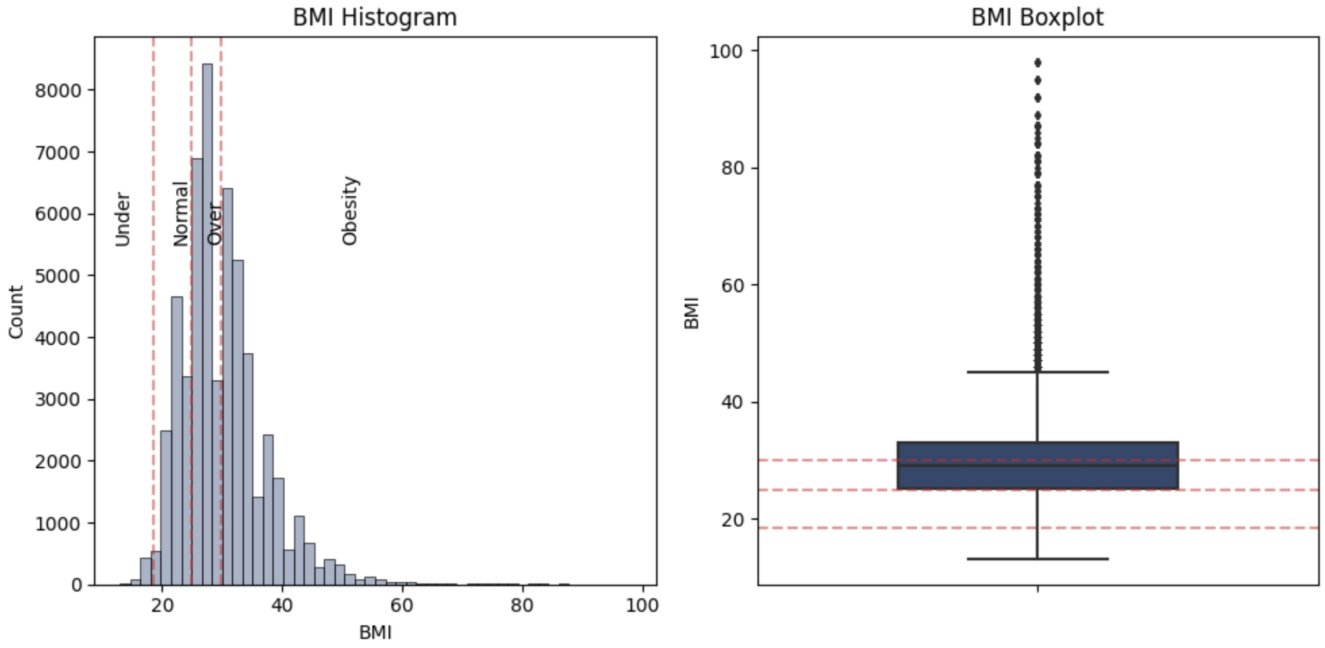
Most of our features are categorical. Features like **CholCHeck**, **Stroke**, **HeartDiseaseorAttack**, **Vaggies**, **HvyAlcoholConsump**, **AnyHealthcare**, **NoDocbcCost** are highly imbaleced. Such imbalances could influence the performance of machine learning models, often biasing them towards the majority class. Here I will not focus on balance those features, but we could try methods like class weights for a better performance in predictions.

Also, it's appear that the feature **BMI** has outliers that wee need to take a closer look.

In [ ]:

```
# From World Health Organization (WHO):
#--------------------------
# Under: BMI less than 18.5
# Normal: BMI between 18.5 and 24.9
# Over: BMI between 25 and 29.9
# Obesity: BMI of 30 or greater



fig, axes = plt.subplots(1, 2, figsize=(10, 5))
```

```
# Plot the histplot on the first axes
sns.histplot(df_train_dropped['BMI'], bins=50, alpha=0.4, color=blue, ax=axes[0])

# Add vertical lines
for line in [18.5, 24.9, 29.9]:
    axes[0].axvline(line, color= red, linestyle='--', alpha=0.5)

# Add text labels within the second subplot (histplot)
categories = ['Under', 'Normal', 'Over', 'Obesity']
positions = [12, 21.7, 27.45, 50]  # Midpoints between the lines and the ends

for x_pos, cat in zip(positions, categories):
    axes[0].text(x_pos, 5500, cat, rotation=90, size=10, va='bottom')

axes[0].set_title('BMI Histogram')

#-------
# Plot the boxplot on the second axes
sns.boxplot(data=df_train_dropped, y='BMI', color=blue, width=0.5, fliersize=3, ax=axes[1])
axes[1].set_title('BMI Boxplot')

# Add horizontal lines
for line in [18.5, 24.9, 29.9]:
    axes[1].axhline(line, color= red, linestyle='--', alpha=0.5)


# Display the plots
plt.tight_layout()
plt.show()
```



There are numerous outliers, indicating individuals with significantly higher BMI values. Given the skewed distribution and box plot, these outliers do not necessarily represent errors or anomalies in the data but rather a realistic representation of the upper bound of BMI within the population

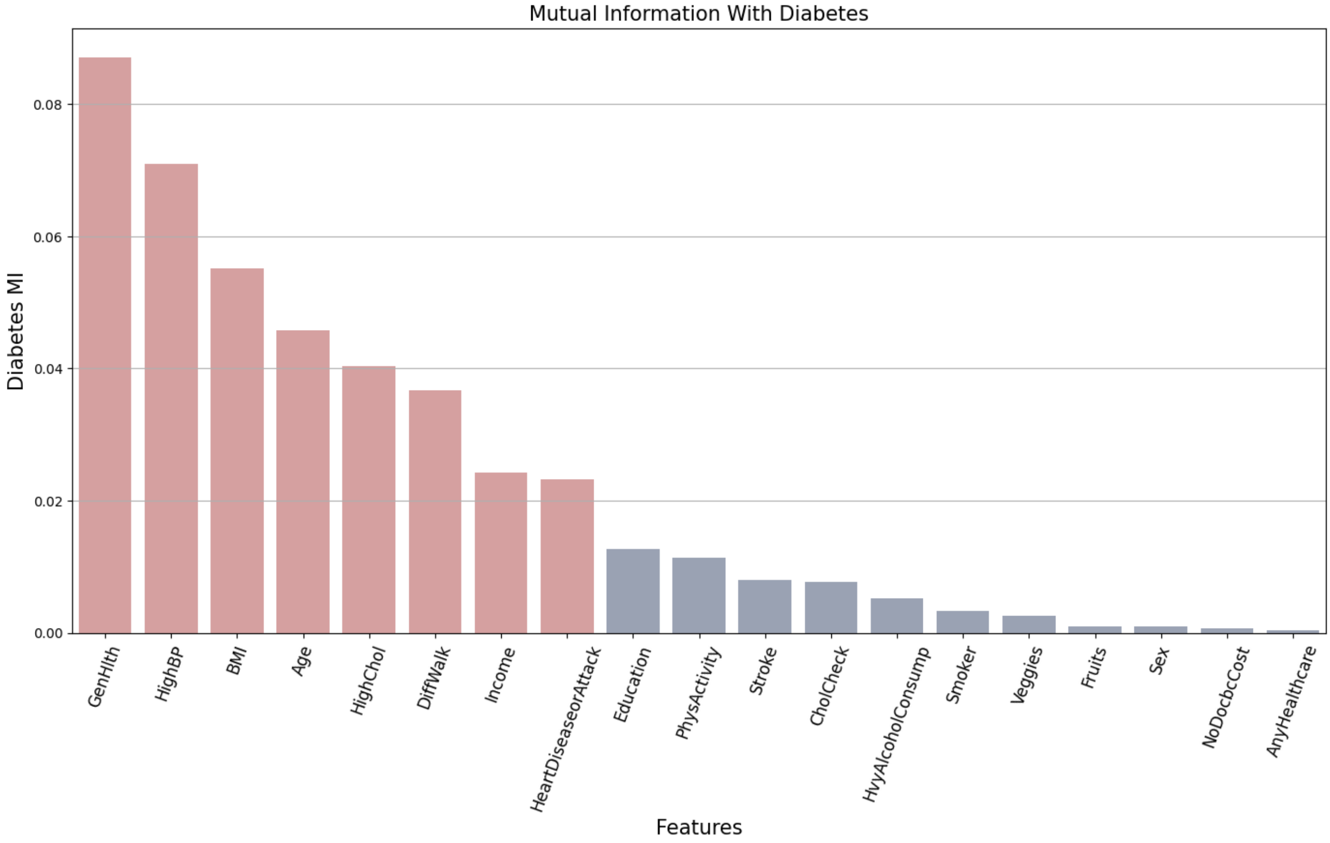
2.2 Feature Importance

Mutual Information

Given that most of our features are binary, having only one numerical feature for **BMI**, a first natural choice of metric to account correlation would be the Mutual information (MI). MI accounts for linear and non-linear relation, is robust against outliers and can be reliable for any numerical or categorical features.

Let's compare the MI of the features with the target variable **Diabetes**.

```
In [ ]: mi_values = mutual_info_classif(df_train_dropped, Y_train_large, discrete_features=True)

        mi_column = pd.DataFrame(mi_values, index=pd.Index(df_train_dropped.columns, name='features
                                 columns=['diabetes_MI']).sort_values(by='diabetes_MI', ascending=F

        # Convert the index 'Features' into a column for plotting
        mi_column_reset = mi_column.reset_index()

        # Plotting
        feature_threshold= 0.020
        fig, ax = plt.subplots(figsize=(15, 10))
        plot_feature_importance(mi_column_reset, x='features', y='diabetes_MI', ax=ax, threshold=fe
                                title="Mutual Information With Diabetes", xlabel="Features",
                                ylabel="Diabetes MI", palette=[blue, red])

        plt.show()

        # Select features with MI > feature_threshold
        best_mi_features = list(mi_column[mi_column['diabetes_MI'] > feature_threshold].index)
        print("Best correlated features:\n",best_mi_features)
```



```
Best correlated features:
 ['GenHlth', 'HighBP', 'BMI', 'Age', 'HighChol', 'DiffWalk', 'Income', 'HeartDiseaseorAttac
k']
```

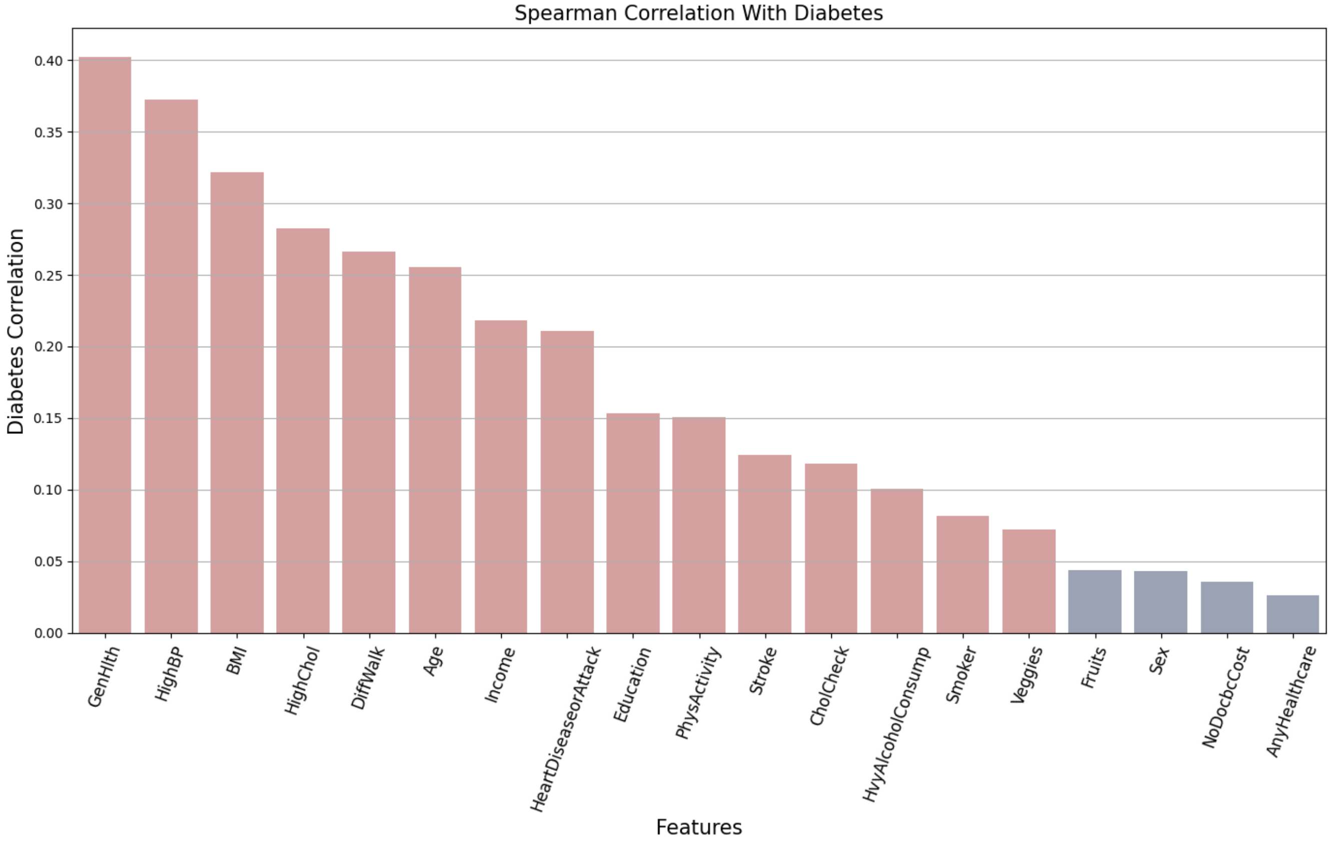
The bars in red represent the features related to the target variable **Diabetes** that preset the most significant entropy reduction. This means that these features provide significant information about the presence of diabetes.

Spearman Correlation

Some of our features, like **GenHlth**, **MentHlth**, **PhysHlth**, `**Age**, **Education**, **Income** are ordinal. A useful metric for this case is Spearman Correlation. Spearman Correlation is a non-parametric metric (does not assume any specific distribution for the data) and are more reliable to ordinal data. It captures monotonic relationships, whether linear or not.

Let's compare the Spearman Correlation of the features with the target variable **Diabetes**.

```
In [ ]: # Calculate Spearman correlation
        spearman_corr = df_train_large.corr(method='spearman')['Diabetes'].agg(np.abs)\
                                                                .sort_values(ascending=False)\
                                                                .drop('Diabetes')\
                                                                .to_frame()

        # Convert Spearman correlation to DataFrame and reset index
        spearman_column = spearman_corr.reset_index()
        spearman_column.columns = ['Features', 'spearman_correlation']

        # Plotting
        feature_threshold= 0.07
        fig, ax = plt.subplots(figsize=(15, 10))
        plot_feature_importance(spearman_column, x='Features', y='spearman_correlation', ax=ax, thr
                                title="Spearman Correlation With Diabetes", xlabel="Features",
                                ylabel="Diabetes Correlation", palette=[blue, red])

        plt.show()

        # Select features with Spearman correlation value > feature_threshold
        best_spearman_features = spearman_corr[spearman_corr['Diabetes'] >= feature_threshold].inde
        print("Best correlated features:\n", best_spearman_features)
```



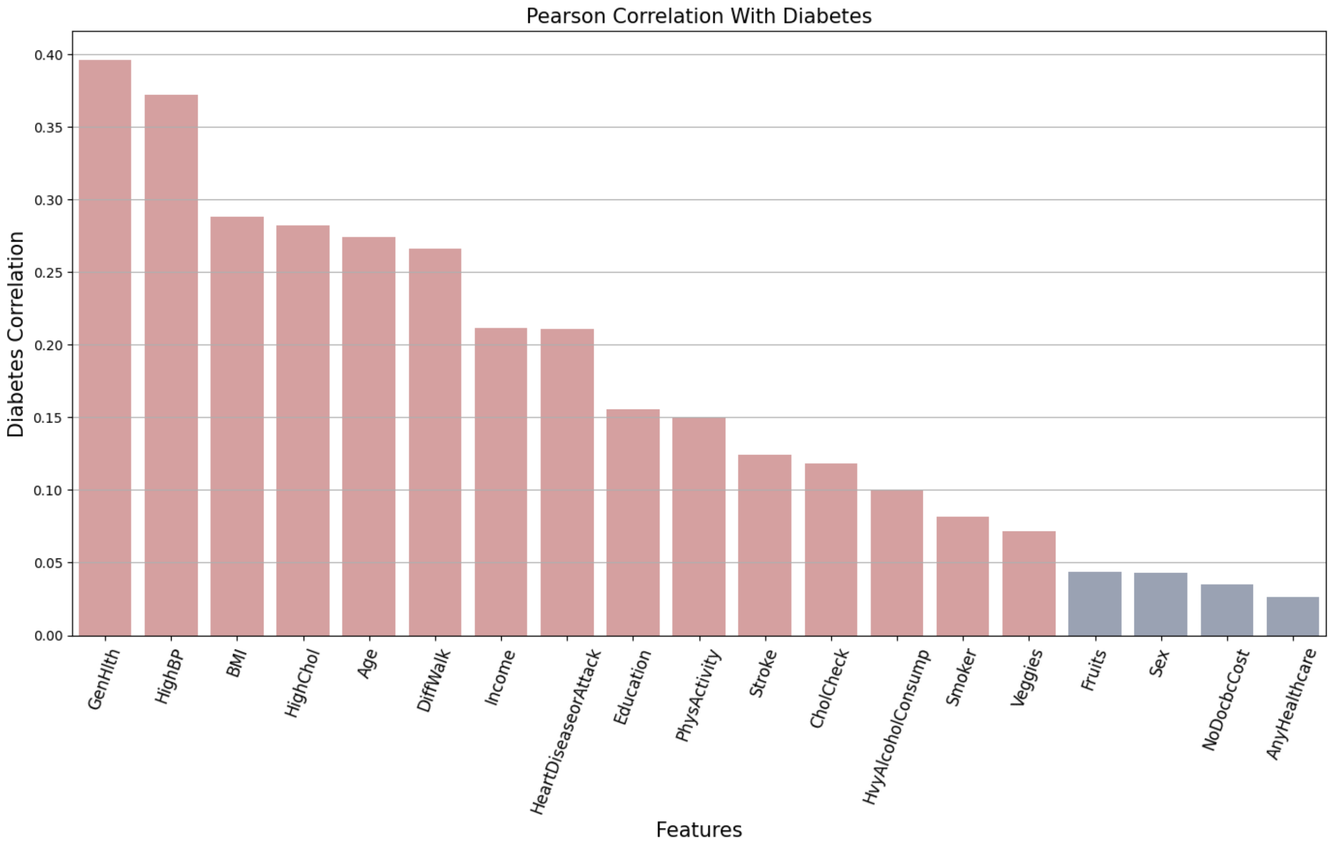
```
Best correlated features:
 ['GenHlth', 'HighBP', 'BMI', 'HighChol', 'DiffWalk', 'Age', 'Income', 'HeartDiseaseorAttac
k', 'Education', 'PhysActivity', 'Stroke', 'CholCheck', 'HvyAlcoholConsump', 'Smoker', 'Veg
gies']
```

Let's check one more metric, Pearson correlation. While Spearman detects monotonic relationships, Pearson captures linear relationships.

Pearson Correlation

The Pearson correlation accounts only for linear relationships and is very sensitive to outliers. It's not particularly reliable for categorical data, especially binary ones.

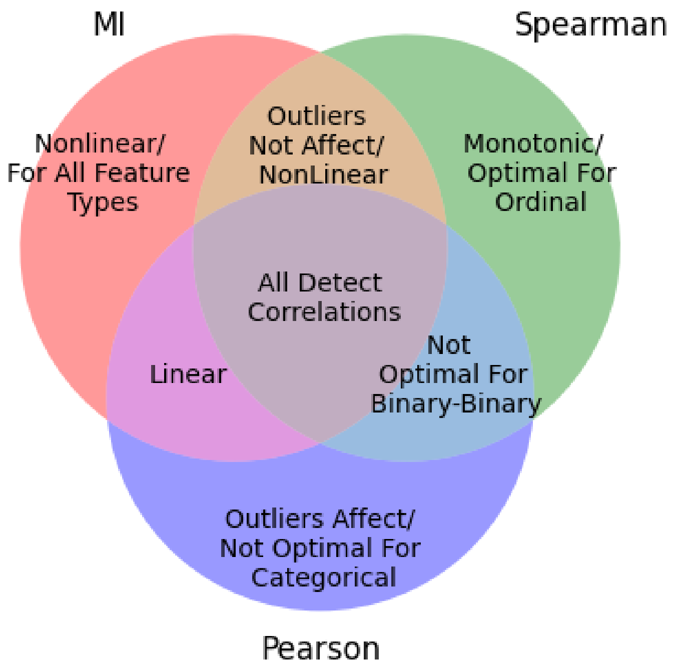
```
In [ ]: # Calculate Spearman correlation
        pearson_corr = df_train_large.corr(method='pearson')['Diabetes'].agg(np.abs)\
                                                                .sort_values(ascending=False)\
                                                                .drop('Diabetes')\
                                                .to_frame()

# Convert Spearman correlation to DataFrame and reset index
pearson_column = pearson_corr.reset_index()
pearson_column.columns = ['Features', 'pearson_correlation']

#
feature_threshold = 0.07
fig, ax = plt.subplots(figsize=(15, 10))
plot_feature_importance(pearson_column, x='Features', y='pearson_correlation', ax=ax, thres
                        title="Pearson Correlation With Diabetes", xlabel="Features",
                        ylabel="Diabetes Correlation", palette=[blue, red])

plt.show()


# Select features with correlation value > feature_threshold
best_pearson_features = pearson_corr[pearson_corr['Diabetes'] >= feature_threshold].index.t
print("Best correlated features:\n", best_pearson_features)
```



```
Best correlated features:
 ['GenHlth', 'HighBP', 'BMI', 'HighChol', 'Age', 'DiffWalk', 'Income', 'HeartDiseaseorAttac
k', 'Education', 'PhysActivity', 'Stroke', 'CholCheck', 'HvyAlcoholConsump', 'Smoker', 'Veg
gies']
```

Utilizing three distinct metrics — Mutual Information (MI), Pearson, and Spearman — I constructed a schematic representation of a diagram that illustrates the shared and unique characteristics of each metric.

The diagram can provide a better view of how these metrics intersect and which features emerge as a relevant correlation with the target variable.



Using this idea, let take the overlapping sets of features selected by each metric.

```
In [ ]: mi_set = set(best_mi_features)
        pearson_set = set(best_pearson_features)
        spearman_set = set(best_spearman_features)

        # Common features across pearson and mutual information
        pearson_mi_set = (pearson_set.intersection(mi_set))
        print("\n Pearson and MI intersection:\n",pearson_mi_set)

        # Common features across spearman and mutual information
        spearman_mi_set = (spearman_set.intersection(mi_set))
        print("\n Spearman and MI intersection:\n",spearman_mi_set)

        # Common features across spearman and pearson
        spearman_pearson_set = (spearman_set.intersection(pearson_set))
        print("\n Spearman and Pearson intersection:\n",spearman_pearson_set)

        # Common features across all three metrics
        small_feature_set = mi_set.intersection(pearson_set).intersection(spearman_set)
        print("\nAgreement between the three metrics:\n",small_feature_set)
```

```
 Pearson and MI intersection:
 {'BMI', 'GenHlth', 'HighBP', 'HighChol', 'Age', 'HeartDiseaseorAttack', 'Income', 'DiffWal
k'}

 Spearman and MI intersection:
 {'BMI', 'GenHlth', 'HighBP', 'HighChol', 'Age', 'HeartDiseaseorAttack', 'Income', 'DiffWal
k'}

 Spearman and Pearson intersection:
 {'BMI', 'PhysActivity', 'Education', 'HvyAlcoholConsump', 'GenHlth', 'HighBP', 'Veggies',
'HighChol', 'Stroke', 'Age', 'HeartDiseaseorAttack', 'Income', 'Smoker', 'CholCheck', 'Diff
Walk'}

Agreement between the three metrics:
 {'BMI', 'GenHlth', 'HighBP', 'HighChol', 'Age', 'HeartDiseaseorAttack', 'Income', 'DiffWal
k'}
```

From this analyze for the correlations we can conclude that the features **BMI**, **GenHlth**, **Age**, **Income**, **HeartDiseaseorAttack**, **DiffWalk**, **HighBP**, **HighChol** appear to have a higher degree of relevance compare to the target **Diabetes**. All three metrics show a agreement for the relevance of these features.

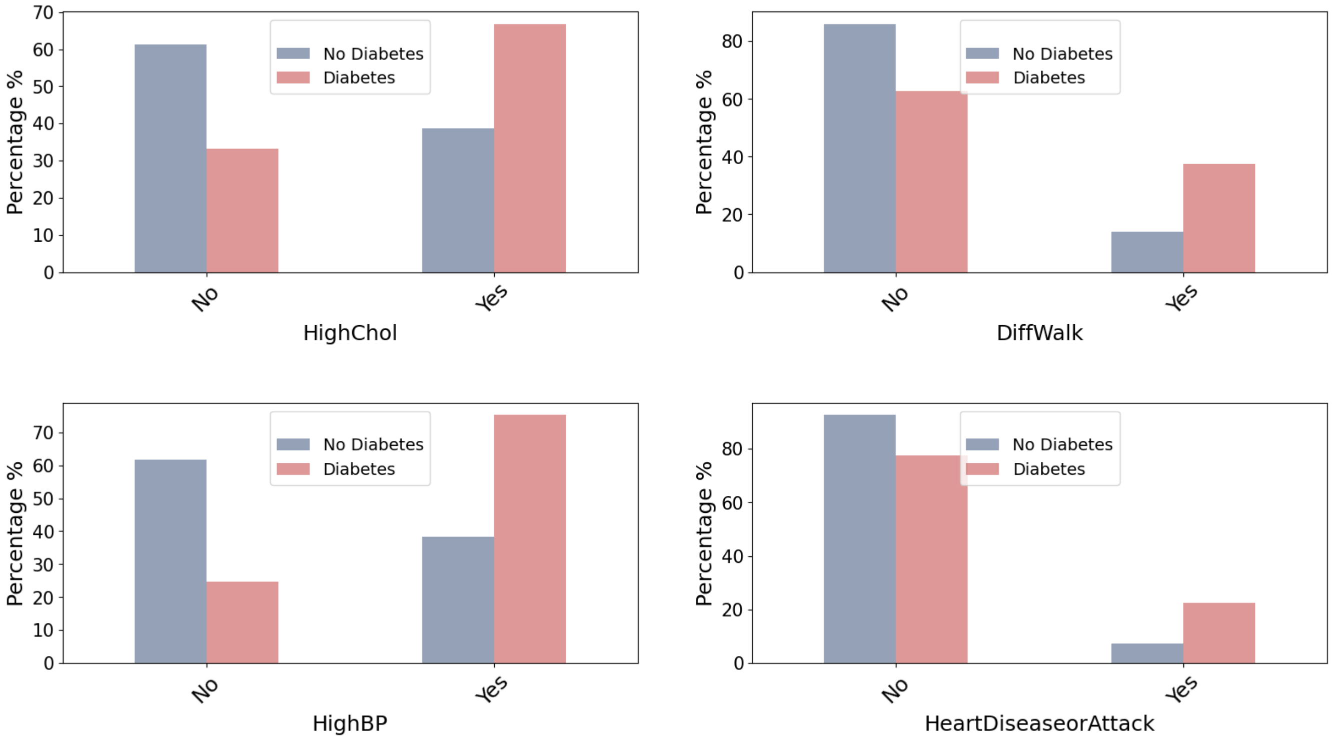
Now, with a more restricted set of features, it's essential to closely examine the relationship between the each feature and the target variable based on their frequency. To do this, we can create a frequency table and illustrate the results using a bar plot.

Let's take the set with the common feature across all three metrics to proceed with the analyze.

```
In [ ]: # Separate in binary and non binary
        numerical = ['BMI']
        categorical = ['GenHlth', 'Age', 'Income']
        binary = ['HighChol','DiffWalk', 'HighBP', 'HeartDiseaseorAttack']
```

Binary

```
In [ ]: fig, axes = plt.subplots(2, 2, figsize=(17, 10))

        for ax, feature in zip(axes.ravel(), binary):

            ct = pd.crosstab(df_train_dropped[feature], Y_train_large )
            ct_normalized = ct.divide(ct.sum(axis=0), axis=1)*100

            ct_normalized.plot(kind='bar', stacked=False, ax=ax, color = [blue, red],
                     alpha = 0.5, fontsize= 15, legend=False  )
            #sns.barplot(x=ct_normalized.index, y= ct_normalized[1], ax=ax, palette = ['#2D4471',

            ax.set_title('', fontsize=21)
            ax.set_ylabel('Percentage %', fontsize= 18)
            ax.set_xlabel(feature, fontsize= 18)

            ax.set_xticks([0, 1])
            ax.set_xticklabels(['No', 'Yes'], fontsize=18, rotation=45)
            ax.legend( ['No Diabetes', 'Diabetes'], title=' ',
                       loc='upper center', fontsize = 14)

        #for ax in axes.ravel()[len(binary):]:
        #    ax.axis('off')

        plt.tight_layout(pad=5.0)
        plt.show()
```



For Binary (categorical) data we can use the chi squared test to quantify how independent two categorical variables are, i.e. if there is an association between the two variables. This is achieved by this statistical test by comparing the observed frequencies to expected frequencies in a contingency table for the classes.

```
In [ ]: cts = {}
        for feature in binary:
```

```
    # Compute the contingency table
    ct = pd.crosstab(df_train_dropped[feature], Y_train_large)
    cts[feature] = ct
    # chi-squared test
    _, p_value, _, _ = chi2_contingency(cts[feature])

    # Null hypothesis: There is no association between the two variables
    if (p_value < 0.05):
        print(f"Significant association between diabetes status and {feature}.")

    else:
        print('Failed to reject Null Hypothesis')
```

```
Significant association between diabetes status and HighChol.
Significant association between diabetes status and DiffWalk.
Significant association between diabetes status and HighBP.
Significant association between diabetes status and HeartDiseaseorAttack.
```

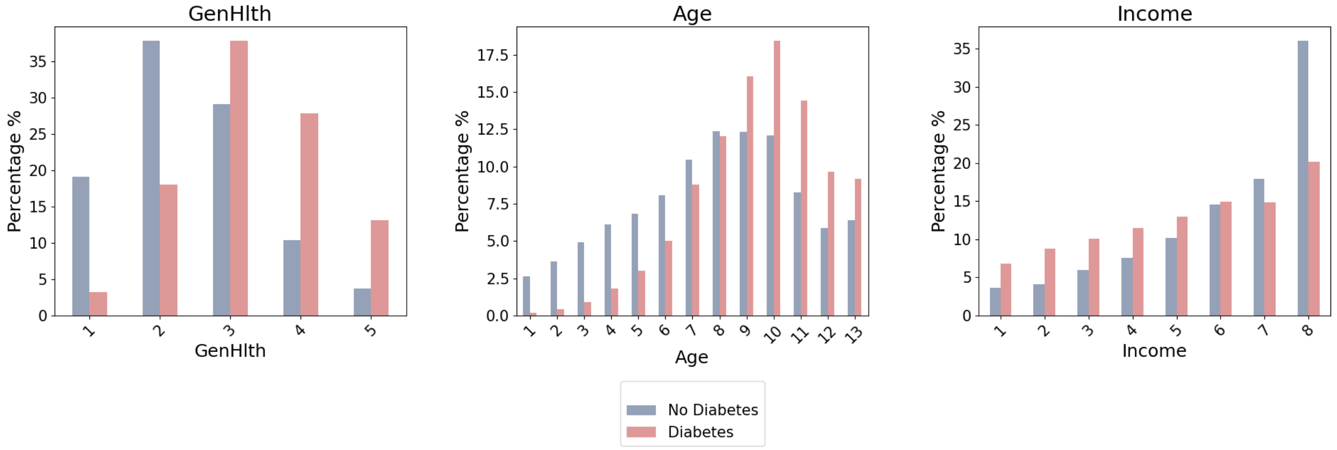
The visualization in a bar plot for **HighChol**, **DiffWalk**, **HighBP** demonstrates a tendency to **Diabetes** when the answer is **Yes**. The visual observation is further supported by the chi-squared test. Thus, it can be inferred that Diabetic patients tend to have higher cholesterol, difficulty walking, and higher blood pressure.

On the other hand, while **HeartDiseaseorAttack** seems to have an association with **Diabetes**, this link is less evident in the visual observation.

Categorical Ordinal

In [ ]:

```
fig, axes = plt.subplots(1, len(categorical), figsize=(20, 8))

for ax, feature in zip(axes.ravel(), categorical):

    ct = pd.crosstab(df_train_dropped[feature], Y_train_large)
    ct_normalized = ct.divide(ct.sum(axis=0), axis=1)*100

    ct_normalized.plot(kind='bar', stacked=False, ax=ax, color=[blue, red],
            alpha=0.5, fontsize=15, legend=False)

    ax.set_title(feature, fontsize=21)
    ax.set_ylabel('Percentage %', fontsize=18)
    ax.set_xlabel(feature, fontsize=18)

    # Allow x-axis tick labels to take on unique values for non-binary variables
    ax.tick_params(axis='x', rotation=45, labelsize=15)

axes[1].legend(['No Diabetes', 'Diabetes'], title=' ', loc='upper center',
               bbox_to_anchor=(0.5, -0.2), fontsize=15)

#for ax in axes.ravel()[len(non_binary):]:
#    ax.axis('off')

plt.tight_layout(pad=5.0)
plt.show()
```



In [ ]:

```python
cts = {}
for feature in categorical:
    # Compute the contingency table
    ct = pd.crosstab(df_train_dropped[feature], Y_train_large)
    cts[feature] = ct
    # chi-squared test
    _, p_value, _, _ = chi2_contingency(cts[feature])

    # Null hypothesis: There is no association between the two variables
    if (p_value < 0.05):
        print(f"Significant association between diabetes status and {feature}.")

    else:
        print('Failed to reject Null Hypothesis')
```

```
Significant association between diabetes status and GenHlth.
Significant association between diabetes status and Age.
Significant association between diabetes status and Income.
```

For **GenHlth** it shows a correlation with diabetes. Based on the categories of general health:

1. excellent : less than 5% has diabetes
2. very good : between $15-20\%$ has diabetes
3. good: more than 35% has diabetes
4. fair: between $25-30\%$ has diabetes
5. poor: between $10-15\%$ has diabetes

As general health gets worse, the percentage of individuals diagnosed with diabetes increases.

For the **Age** we have the following categories:

1. 18-24
2. 25-29
3. 30-34
4. 35-39
5. 40-44
6. 45-49
7. 50-54
8. 55-59
9. 60-64
10. 65-69
11. 70-74
12. 75-79
13. more then 80

There's an observed increment in the percentage of individuals with diabetes as age progresses, though there are some exceptions. This is a good sign, because it is in line with known medical data indicating that the risk of diabetes increases with age.

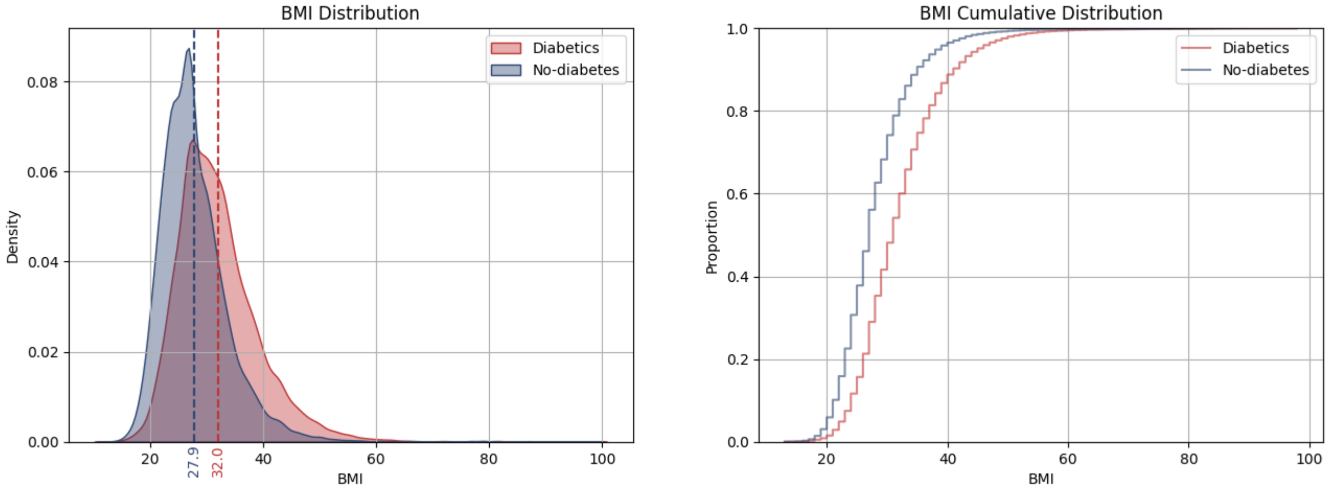
For **Income** , those individuals with the highest income tend to have an increase in the incidence of diabetes compared to lowest income. But is complex to say more than this, because it does not follow a simple linear trend as for **GenHlth** and **Age**.

Numerical

In [ ]:

```python
# Divide the dataset into two groups based on Diabetes status
df_train_no = df_train_large[df_train_large['Diabetes'] == 0]
df__train_yes = df_train_large[df_train_large['Diabetes'] == 1]

# Select the BMI feature from each group
df_no_bmi = df_train_no['BMI']
df_yes_bmi = df__train_yes['BMI']
```

```

fig, axes = plt.subplots(nrows=1, ncols=2, figsize=(14, 6))

# Plotting the distributions
sns.kdeplot(df_yes_bmi, ax=axes[0],color=red , alpha=0.4, fill=True)
sns.kdeplot(df_no_bmi, ax=axes[0],color=blue , alpha=0.4, fill=True)

axes[0].axvline(df_yes_bmi.mean(), color=red, linestyle='--', alpha = 1)
axes[0].axvline(df_no_bmi.mean(), color=blue, linestyle='--', alpha = 1)

axes[0].text(df_yes_bmi.mean(), -0.007, f'{df_yes_bmi.mean():.1f}',
              color=red, rotation=90, ha='center')

axes[0].text(df_no_bmi.mean(), -0.007, f'{df_no_bmi.mean():.1f}',
              color=blue, rotation=90, ha='center')



axes[0].grid()
axes[0].set_title('BMI Distribution')
axes[0].legend(['Diabetics', 'No-diabetes'])

# Plotting the CDFs
sns.ecdfplot(df_yes_bmi, ax=axes[1], label="Diabetics",
             color=red, alpha=0.6)

sns.ecdfplot(df_no_bmi, ax=axes[1], label="No-diabetes",
             color=blue, alpha=0.6)

axes[1].grid()
axes[1].set_title('BMI Cumulative Distribution')
axes[1].legend()

plt.tight_layout(pad=5.0)
plt.show()
```



For numerical data, we employ the t-test to compare the means of two groups: BMI for diabetic patients and BMI for non-diabetic patients. Because the variances of the groups differ, then Welch's t-test is employed, not assuming equal variances.

In [ ]:

```
print('Diff of Variances:', np.abs(df_yes_bmi.var() - df_no_bmi.var()))
# the variance of the two groups are different, so we use Welch's t-test
_, p_value  = ttest_ind(df_yes_bmi, df_no_bmi, equal_var=False)

# Null hypothesis: The two groups have the same mean
if p_value < 0.05:
    print('Diabetic and non-diabetic have different BMI')
else:
    print('Failed to reject Null Hypothesis')
```

```
Diff of Variances: 16.09348
Diabetic and non-diabetic have different BMI
```

The distributions and cumulative distribution for BMI in diabetic and non-diabetic patients has a significant difference. The BMI distribution for diabetics appears right-skewed, suggesting a tendency towards higher BMI values compared to the more symmetric distribution of non-diabetics. This difference is more evident in their cumulative distributions, which show a significant gap between the curves. This visual observation is further supported by a Welch's t-test, indicating a significant difference in the mean BMI values of the two groups. Thus, it can be inferred that diabetic patients tend to have higher BMIs than non-diabetics

2.3 Conclusion from EDA

After analyzing the data, we found that the best features for training our machine learning model are:

- HighBP
- GenHlth
- HighChol
- DiffWalk
- Age
- BMI
- HeartDiseaseorAttack
- Income

We saw a clear link between these features and the target variable **Diabetes**. But for the **HeartDiseaseorAttack** and **Income** features, it's harder to say exactly how they relate or if the relationship is significant for predicting whether an individual has diabetes. All we can infer is that the relationship is not linear. Also, **HeartDiseaseorAttack** is highly imbalanced, and this could have some influence in this relation withe the target variable.

3. Model Training and Validation

Now, with a better understanding of the features and their significance in relation to the target variable **Diabetes**, we can proceed to train a model to evaluate its performance on this set of features identified from the EDA. We consider both a consensus set of features, where all metrics agree, which results in a smaller feature set, and a large set of features selected based on the highest Pearson and mutual information. This approach will allow us to compare the models using different subsets of features, providing a more nuanced understanding of the relevance (or irrelevance) of each feature to the target variable.

In [ ]:

```
# Remove Diabetes, is not necessary anymore
boolean_features = boolean_columns.copy()
boolean_features.remove('Diabetes')
categorical_features  = categorical_columns.copy()

# Best set of features selected from EDA
small_feature_list = list(small_feature_set)

large_feature_set = spearman_pearson_set.union(mi_set)
large_feature_list= list(large_feature_set)
```

3.1 Logistic Regression

In [ ]:

```
# Best set of features selected from EDA
small_feature_list = list(small_feature_set)
large_feature_list= list(spearman_pearson_set.union(mi_set))
```

```
print('\n Small set of features:\n', small_feature_list)
print('\n Large set of features:\n', large_feature_list)

# Change dtypes for logistic regression
dtype_dict_lr = {
    'bool': boolean_features,
    'str': categorical_features,
    'float32': ["BMI"]
}

# Create a copy of dataframe to modify the dtypes
df_train_lr = df_train.copy()
df_val_lr = df_val.copy()
df_test_lr = df_test.copy()

X_train_small, X_val_small, _, _ = preprocess_and_encode_features(df_train_lr, df_val_lr, c
                                                                   dtype_dict_lr, featu

X_train_large, X_val_large, _, _ = preprocess_and_encode_features(df_train_lr, df_val_lr, c
                                                                     dtype_dict_lr, feat

#df_train.info()
```

```
 Small set of features:
 ['BMI', 'GenHlth', 'HighBP', 'HighChol', 'Age', 'HeartDiseaseorAttack', 'Income', 'DiffWal
k']

 Large set of features:
 ['PhysActivity', 'Education', 'HvyAlcoholConsump', 'HighChol', 'Income', 'CholCheck', 'BM
I', 'GenHlth', 'HighBP', 'Veggies', 'Stroke', 'Age', 'HeartDiseaseorAttack', 'Smoker', 'Dif
fWalk']
```

3.1.1 Hyperparameter tunning and validate

In [ ]:

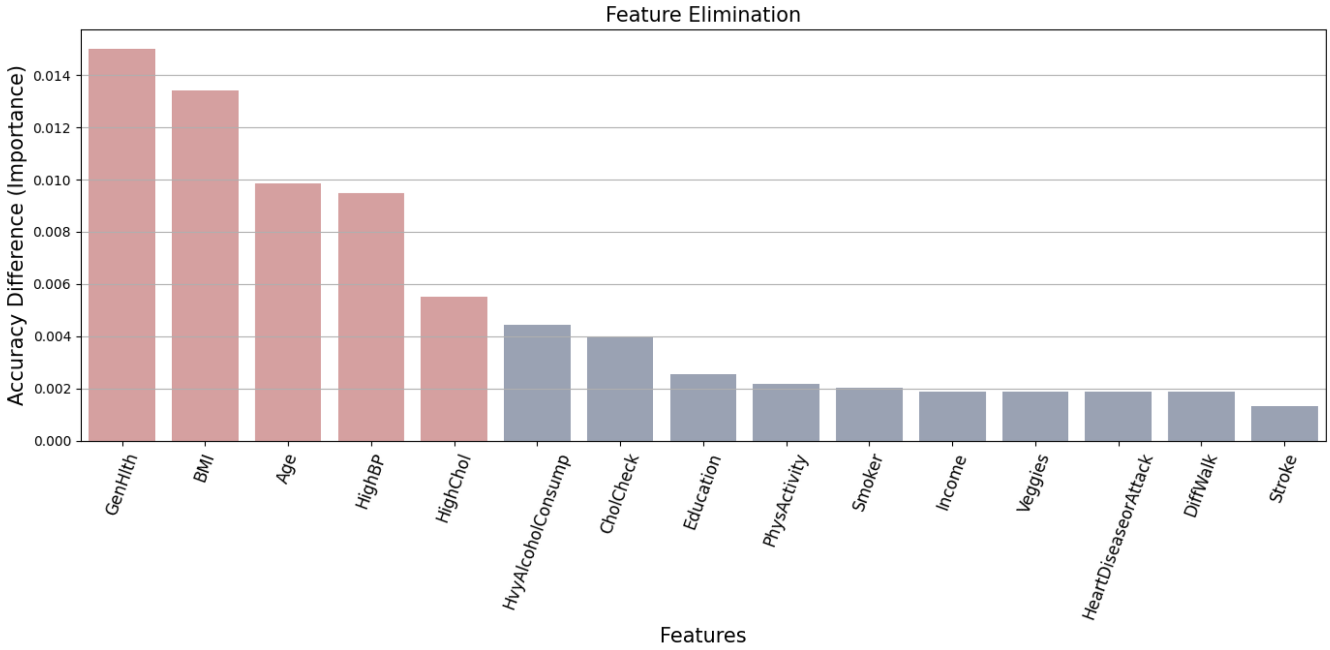
```
param_grid_lr = { "C":[0.001, 0.01, 1, 10, 100],
                  "penalty":["l1","l2"],
                  "solver": [ 'liblinear'],
                  'random_state': [42]}

# Grid search and predict on Large Feature Set
best_lr_params, best_score, \
best_estimator, Y_pred_lr_large, \
      val_accuracy = grid_search_and_predict(   LogisticRegression(),
                                                param_grid_lr, X_train_large, Y_train,
                                                X_val_large, Y_val)

print("\n Tuned hyperparameters :",best_lr_params)
print("\n Accuracy of the best hyperparameters :",round(best_score,3))
print('\n Accuracy for Large Feature Set:', round(val_accuracy, 3))

# Predict on Small Feature Set
accuracy, Y_pred_lr_small = train_and_evaluate( LogisticRegression,
                                                best_lr_params,
                                                X_train_small, Y_train,
                                                X_val_small, Y_val)



print('\n Accuracy for Small Feature Set:', round(accuracy, 3))
```

```
 Tuned hyperparameters : {'C': 1, 'penalty': 'l2', 'random_state': 42, 'solver': 'liblinea
r'}

 Accuracy of the best hyperparameters : 0.744

 Accuracy for Large Feature Set: 0.748

 Accuracy for Small Feature Set: 0.744
```

3.1.2 Feature importance

In [ ]:

```
lr_model = LogisticRegression(**best_lr_params)
feature_importance = feature_elimination(df_train, df_val, Y_train, Y_val,
                                           lr_model, accuracy_score, large_feature_list, accuracy_s

# Set up the figure and axis
fig, ax = plt.subplots(figsize=(15, 8))

importance_threshold = 0.005
plot_feature_importance(df = feature_importance,
                        x="eliminated_feature",
                        y="accuracy_score_diff",
                        ax=ax,
                        threshold=importance_threshold,
                        pad=5.0,
                        title='Feature Elimination',
                        xlabel='Features',
                        ylabel='Accuracy Difference (Importance)',
                        palette=[blue, red])

# Display the plot
plt.show()

feature_importance_lr = set(feature_importance[feature_importance['accuracy_score_diff'] >=
print('\nFeatures importance Logistic Regression:\n', feature_importance_lr)
```



```
Features importance Logistic Regression:
 {'BMI', 'GenHlth', 'HighBP', 'HighChol', 'Age'}
```

The bar plot indicates that the features **GenHlth**, **BMI**, **Age**, **HighBP**, **HighChol** are relevant for the model's accuracy. Removing any of these specific features leads to a large decline in accuracy compared to the others features.

3.1.3 Metrics

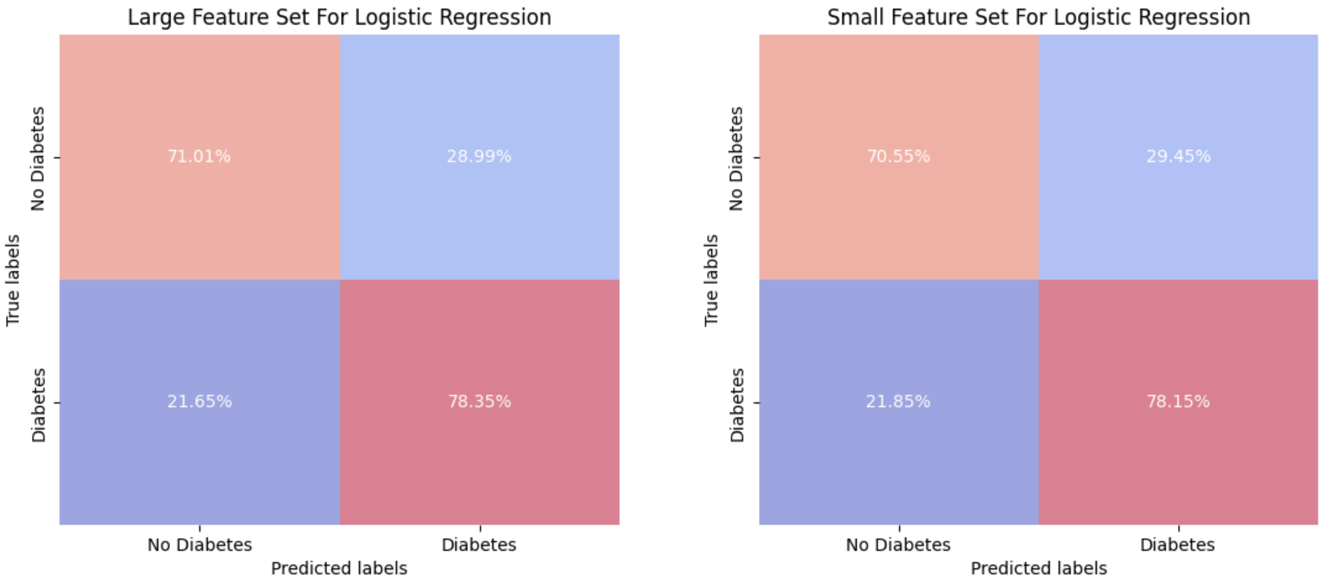
In [ ]:

```
lr_metrics_large = classification_metrics(Y_val, Y_pred_lr_large, 'lr_large_set')
lr_metrics_small = classification_metrics(Y_val, Y_pred_lr_small, 'lr_small_set')

lr_metrics = lr_metrics_large.merge(lr_metrics_small, on = 'metrics', how = 'outer')


display(lr_metrics)
```

	lr_large_set	lr_small_set
metrics		
Precision	0.738683	0.735145
Recall	0.783458	0.781476
AUC	0.746788	0.743500
F1 Score	0.760412	0.757603

Given that the smaller feature set provides almost equivalent performance to the larger set, specially for the F1 score and the recall metrics, we can conclude that the large set of features has some irrelevant features for the predictive power of the model.

```
In [ ]: predictions = {
            "Large Feature Set For Logistic Regression": Y_pred_lr_large,  # Predictions using larg
            "Small Feature Set For Logistic Regression": Y_pred_lr_small   # Predictions using sma
        }

        # Create plots
        fig, axes = plt.subplots(1, 2, figsize=(12, 6))

        for ax, (title, Y_pred) in zip(axes.ravel(), predictions.items()):
            plot_confusion_matrix(Y_val, Y_pred, title, ax, xy_legends=['No Diabetes', 'Diabetes'])

        plt.tight_layout(pad=5.0)
        plt.show()
```



The models exhibit a demonstrates a reasonably ability in correctly identifying individuals with and without diabetes, with True Positive (sensitivity) rates of 78.35% for the larger feature set and 78.15% for the smaller feature set, and True Negative (specificity) rates of 71.01% and 70.55% respectively. However, in a potential clinical setting, the observed False Negative rates of 21.65% for the larger set and 21.85% for the smaller set could be of problematic, as they represent the proportion of actual diabetic patients who were not identified by the model. Same for the False Positive rates.

While the balance between precision and recall suggests that the models perform reasonably well for a general application, the consequences of false predictions in a medical context could be bad.

3.2 Decision Tree and Random Forest

```
In [ ]: df_train_trees = df_train.copy()
        df_val_trees = df_val.copy()

        dtype_dict_trees = {
```

```
    'int32': categorical_features + boolean_features
}

df_train_trees = convert_dtypes(df_train_trees, dtype_dict_trees)
df_val_trees = convert_dtypes(df_val_trees, dtype_dict_trees)


# For decision three is need only to select the feature matrix from dataframe
X_train_small, X_val_small = df_train_trees[small_feature_list].values, df_val_trees[small_
X_train_large, X_val_large = df_train_trees[large_feature_list].values, df_val_trees[large_
```

3.2.1 Hyperparameter Tunning And Validate

Decision tree

In [ ]:

```
# Decision Tree
param_grid_dt = {
    'max_depth': [3 ,10, 15 ],
    'min_samples_split': [2, 5],
    'min_samples_leaf': [1, 8, 10],
    'criterion': ['gini'],
    'random_state': [42]
}

best_dt_params, best_score, best_estimator,\
      Y_pred_dt_large, val_accuracy  = grid_search_and_predict(  DecisionTreeClassifier(),
                                                        X_train_large, Y_train, \
                                                        X_val_large, Y_val, cv = 8)

print("\n Tuned hyperparameters :",best_dt_params)
print("\n Accuracy of the best hyperparameters :",round(best_score,3))
print('\n Accuracy for Large Feature Set:', round(val_accuracy, 3))

# Predict on Small Feature Set
accuracy, Y_pred_dt_small = train_and_evaluate( DecisionTreeClassifier,
                                                best_dt_params,
                                                X_train_small, Y_train,
                                                X_val_small, Y_val)

print('\nAccuracy for Small Feature Set::',round(accuracy, 3))
```

```
 Tuned hyperparameters : {'criterion': 'gini', 'max_depth': 10, 'min_samples_leaf': 10, 'mi
n_samples_split': 2, 'random_state': 42}

 Accuracy of the best hyperparameters : 0.73

 Accuracy for Large Feature Set: 0.731

Accuracy for Small Feature Set:: 0.735
```

Random Forest

In [ ]:

```
# Define the hyperparameter grid for RandomForestClassifier
param_grid_rf = {
    'max_depth': [10, 15, 20],
    'min_samples_split': [5, 10],
    'min_samples_leaf': [8, 10, 15, 20],
    'criterion': ['gini'],
    'n_estimators': [40, 50, 60],
    'random_state': [42]
}


# Use the grid_search_and_predict function to perform GridSearchCV and prediction on large
best_rf_params, best_score, best_estimator,\
      Y_pred_rf_large, val_accuracy= grid_search_and_predict(   RandomForestClassifier(),
                                                              param_grid_rf, X_train_larg
                                                              Y_train, X_val_large, Y_val
```

```
print("\n Tuned hyperparameters :",best_rf_params)
print("\n Accuracy of the best hyperparameters :",round(best_score,3))
print('\n Accuracy for Large Feature Set:', round(val_accuracy, 3))


accuracy_small, Y_pred_rf_small = train_and_evaluate(
    RandomForestClassifier, best_rf_params, X_train_small, Y_train, X_val_small, Y_val
)

print("\nAccuracy for Small Feature Set:", round(accuracy_small, 3))
```

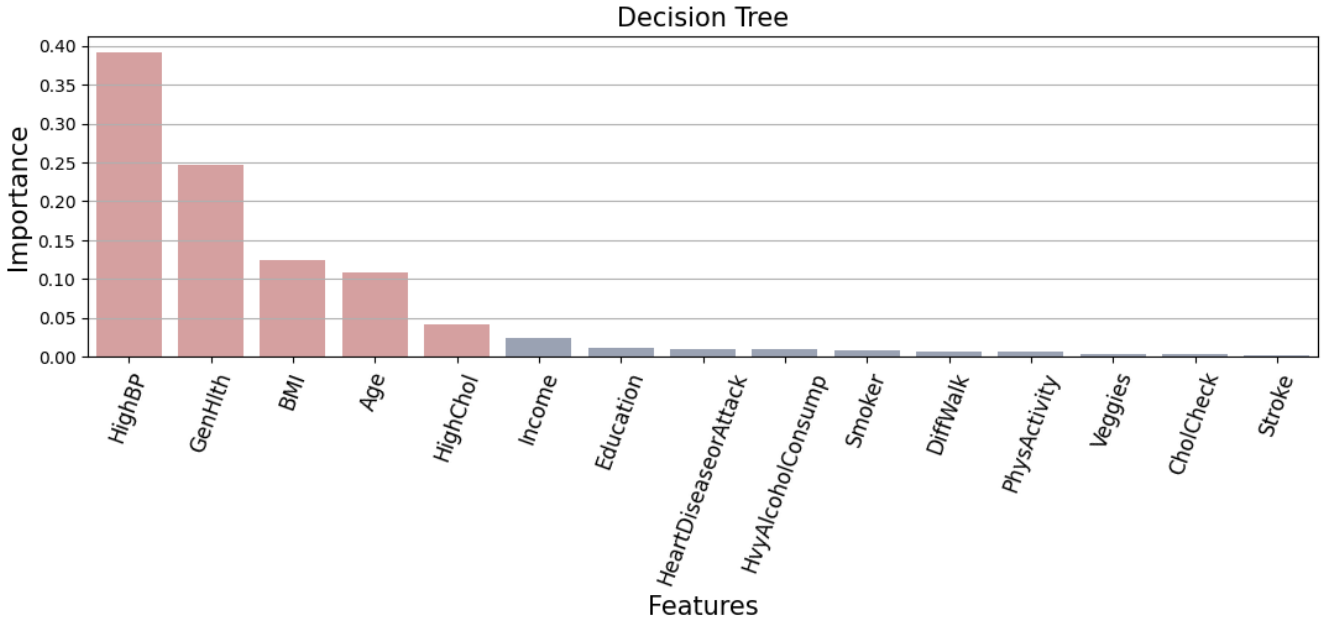
```
 Tuned hyperparameters : {'criterion': 'gini', 'max_depth': 10, 'min_samples_leaf': 15, 'mi
n_samples_split': 5, 'n_estimators': 60, 'random_state': 42}

 Accuracy of the best hyperparameters : 0.745

 Accuracy for Large Feature Set: 0.747

Accuracy for Small Feature Set: 0.747
```

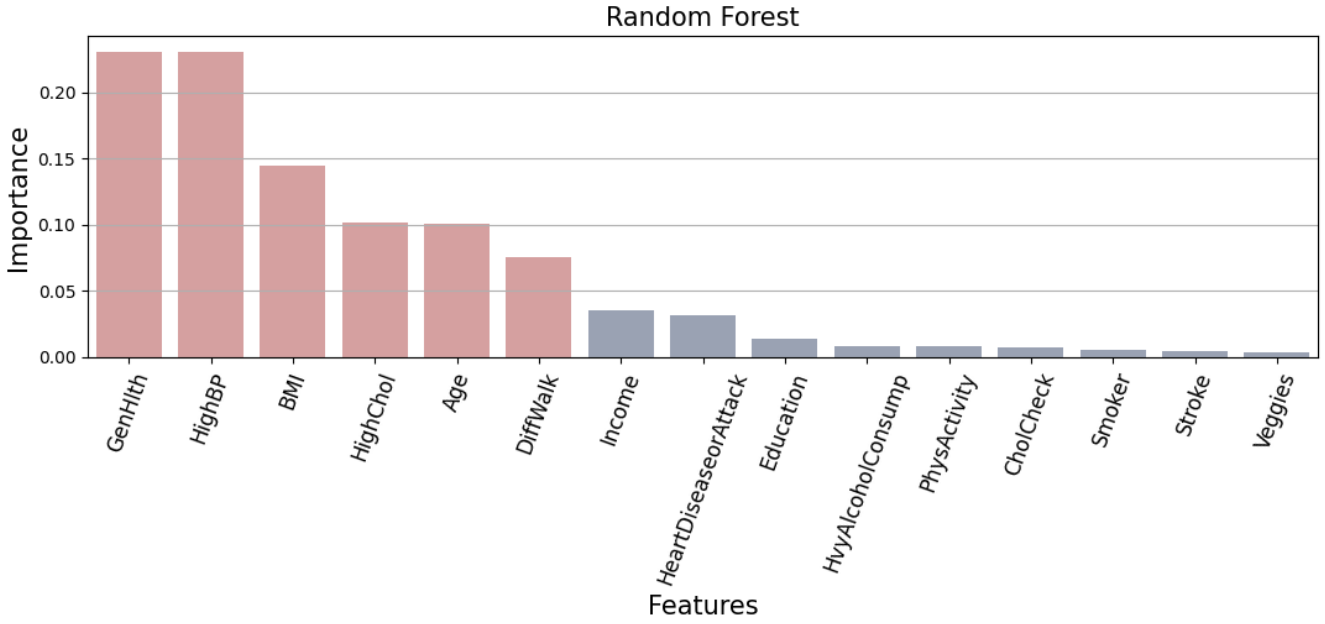
3.2.2 Feature Importance

Feature importance in most tree-ensembles is calculated based an importance score. The importance score is a measure of how often the feature was selected for splitting and how much gain in purity was achieved as a result of the selection.

In [ ]:

```
dt_model= DecisionTreeClassifier( **best_dt_params)
dt_model.fit(X_train_large, Y_train)

rf_model = RandomForestClassifier(**best_rf_params)
rf_model.fit(X_train_large, Y_train)

# Extract feature importance
importances_dt = pd.DataFrame( dt_model.feature_importances_ ,
                              index = pd.Index(large_feature_list, name='features'),
                              columns = ['feature_importance'])\
                              .sort_values(by='feature_importance', ascending=False)\
                              .reset_index()

importances_rf =  pd.DataFrame( rf_model.feature_importances_,
                                index = pd.Index(large_feature_list, name='features'),
                                columns = ['feature_importance'])\
                                .sort_values(by='feature_importance', ascending=False)\
                                .reset_index()


fig, axes = plt.subplots(nrows=2, ncols=1, figsize=(12, 12))

# Plot Decision Tree Feature Importance
feature_threshold = 0.04
plot_feature_importance( df=importances_dt, x='features', y='feature_importance', ax=axes[0
                         threshold=feature_threshold, title='Decision Tree', palette=[blue,

# Plot Random Forest Feature Importance
plot_feature_importance( df=importances_rf, x='features', y='feature_importance', ax=axes[1
                         threshold=feature_threshold, title='Random Forest', palette = [blu

plt.tight_layout(pad = 5)
plt.show()
```





In [ ]:

```
feature_importance_dt = set(importances_dt[importances_dt['feature_importance'] > feature_i
feature_importance_rf = set(importances_rf[importances_rf['feature_importance'] > feature_i

best_feature_set = feature_importance_dt.intersection(feature_importance_rf).intersection(f

print('Features importance Decision Tree:\n', feature_importance_dt)
print('\nFeatures importance Random Forest:\n', feature_importance_rf)
print('\nFeatures importance Logistic Regression:\n', feature_importance_lr)
print('\n Agreement between the three models:\n', best_feature_set)
```

```
Features importance Decision Tree:
 {'BMI', 'GenHlth', 'HighBP', 'HighChol', 'Age'}

Features importance Random Forest:
 {'BMI', 'GenHlth', 'HighBP', 'HighChol', 'Age', 'DiffWalk'}

Features importance Logistic Regression:
 {'BMI', 'GenHlth', 'HighBP', 'HighChol', 'Age'}

 Agreement between the three models:
 {'BMI', 'GenHlth', 'HighBP', 'HighChol', 'Age'}
```

3.2.3 Metrics

In [ ]:

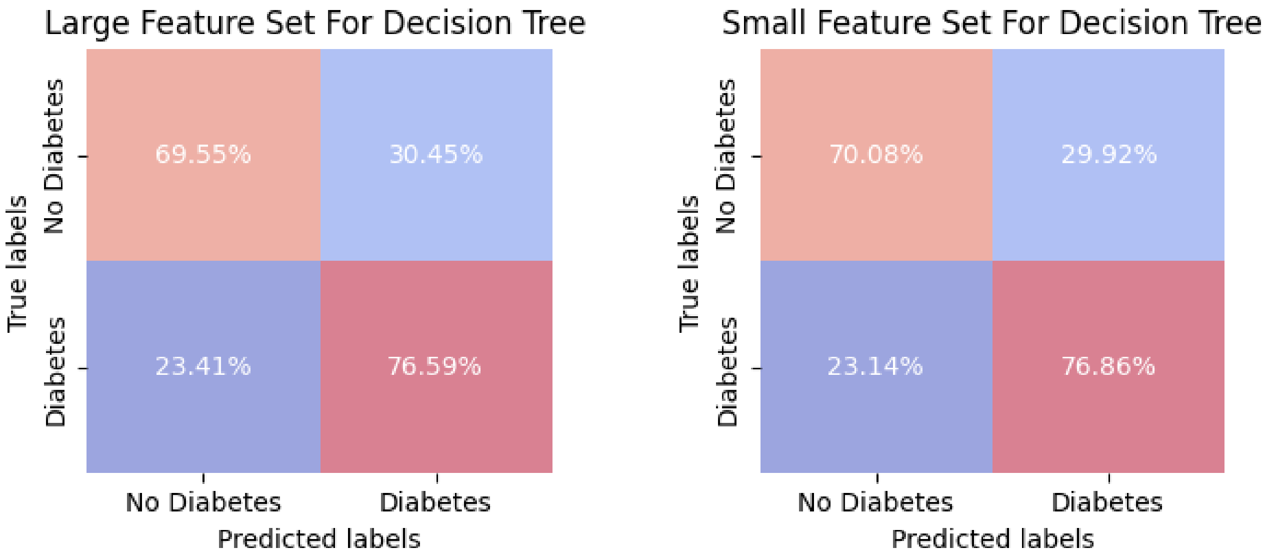
```python
dt_metrics_large = classification_metrics(Y_val, Y_pred_dt_large, 'dt_large_set')
dt_metrics_small = classification_metrics(Y_val, Y_pred_dt_small, 'dt_small_set')
dt_metrics = dt_metrics_large.merge(dt_metrics_small, on = 'metrics', how = 'outer')

rf_metrics_large = classification_metrics(Y_val, Y_pred_rf_large, 'rf_large_set')
rf_metrics_small = classification_metrics(Y_val, Y_pred_rf_small, 'rf_small_set')
rf_metrics = rf_metrics_large.merge(rf_metrics_small, on = 'metrics', how = 'outer')

trees_metrics = dt_metrics.merge(rf_metrics, on = 'metrics', how = 'outer')
display(trees_metrics)
```

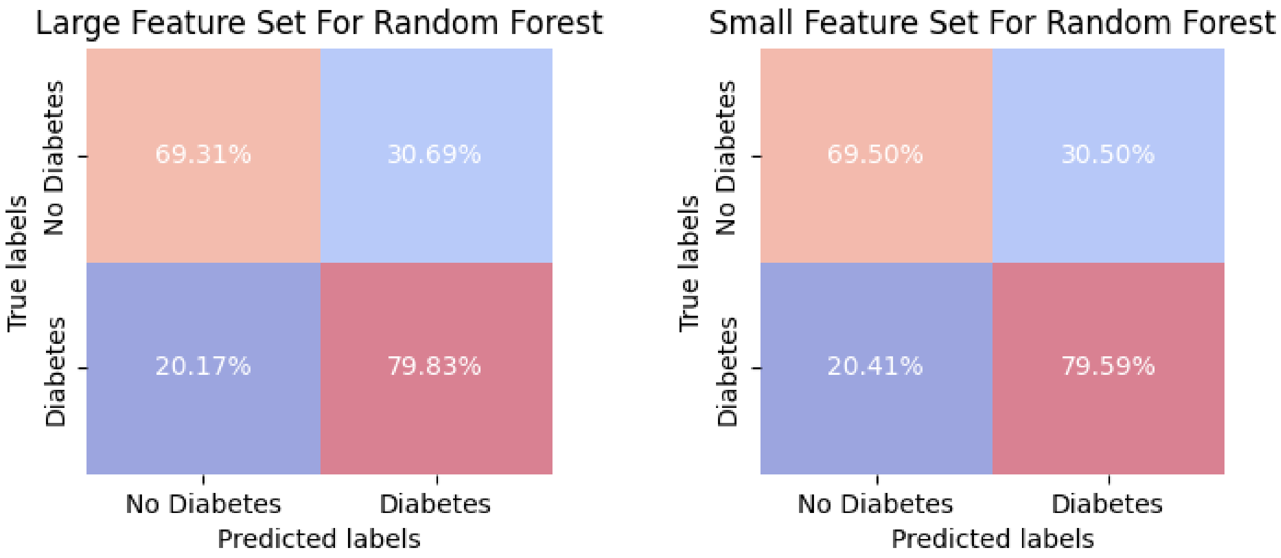
	dt_large_set	dt_small_set	rf_large_set	rf_small_set
metrics				
Precision	0.724544	0.728750	0.731223	0.731866
Recall	0.765897	0.768588	0.798329	0.795921
AUC	0.730675	0.734687	0.745706	0.745465
F1 Score	0.744647	0.748139	0.763304	0.762551

As we concluded for the logistic regression model, the smaller feature set provides almost equivalent performance to the larger set, specially for the F1 score and the recall metrics. which again suggests that the smaller feature set may contain the most relevant features.

In [ ]:

```python
predictions = {
    "Large Feature Set For Decision Tree ": Y_pred_dt_large,
    "Small Feature Set For Decision Tree": Y_pred_dt_small,
    "Large Feature Set For Random Forest": Y_pred_rf_large,
    "Small Feature Set For Random Forest": Y_pred_rf_small

}

# Create plots
fig, axes = plt.subplots(2, 2, figsize=((8, 8)))

for ax, (title, Y_pred) in zip(axes.ravel(), predictions.items()):
    plot_confusion_matrix(Y_val, Y_pred, title, ax, xy_legends=['No Diabetes', 'Diabetes'])

plt.tight_layout(pad=5.0)
plt.show()
```





The Decision Tree and Random Forest models perform similarly for the different sets, with Random Forest showing a better predictive power in identifying true positives (correctly classify a diabetic individual) with 79.66%. The false negative rates are relatively low for all models, which is critical for a clinical test. This also confirm a suspected about redundancy in the larger feature set.

3.3 Selecting Model And Best Set Of Features

In [ ]:

```
# Best set of features from the models
best_features_list = list(best_feature_set)

# Compare the difference between the sets of features
diff_feature_set = small_feature_set.difference(best_feature_set)

print('Features in small set but not in best set:\n', diff_feature_set)
```

```
Features in small set but not in best set:
 {'DiffWalk', 'HeartDiseaseorAttack', 'Income'}
```

In [ ]:

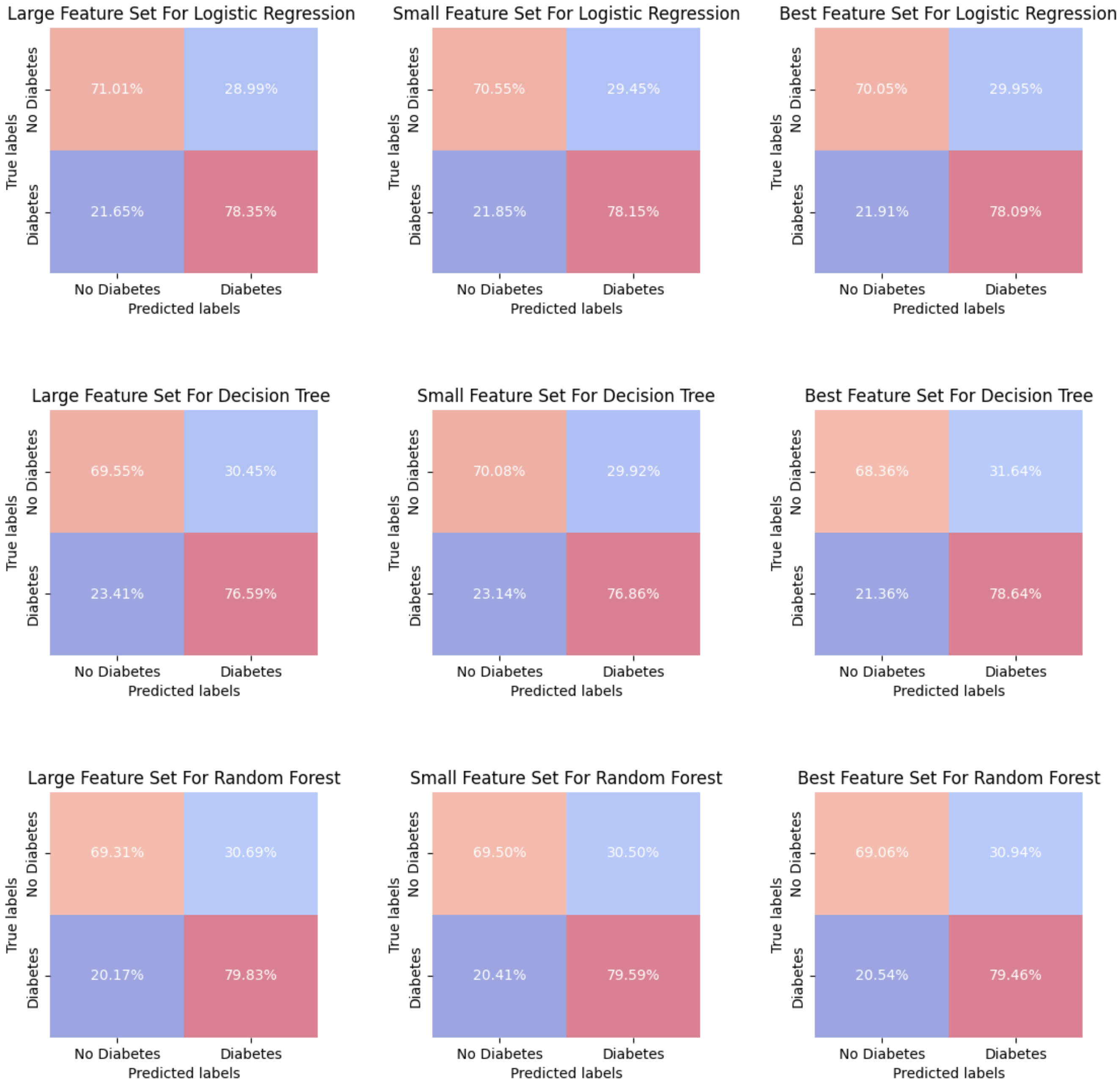
```
# Best set of features from the models
best_features_list = list(best_feature_set)

X_train_lr, X_val_lr, _, _ = preprocess_and_encode_features(df_train_lr, df_val_lr, df_test
                                                             dtype_dict_lr, featu

X_train_trees, X_val_trees = df_train_trees[best_features_list].values, df_val_trees[best_f
```

```python
# Logistic Regression
lr_accuracy, Y_pred_lr_best = train_and_evaluate(LogisticRegression,
                                                 best_lr_params,
                                                 X_train_lr, Y_train,
                                                 X_val_lr, Y_val)

# Decision Tree
dt_accuracy, Y_pred_dt_best = train_and_evaluate(DecisionTreeClassifier,
                                                 best_dt_params,
                                                 X_train_trees, Y_train,
                                                 X_val_trees, Y_val)

# Random Forest
rf_accuracy, Y_pred_rf_best = train_and_evaluate(RandomForestClassifier,
                                                 best_rf_params, X_train_trees,
                                                 Y_train, X_val_trees, Y_val)

# Print accuracy for each model
print("Logistic Regression Accuracy for best features set:", round(lr_accuracy, 3))
print("Decision Tree Accuracy for best features set:", round(dt_accuracy, 3))
print("Random Forest Accuracy for best features set:", round(rf_accuracy, 3))
```

```
Logistic Regression Accuracy for best features set: 0.742
Decision Tree Accuracy for best features set: 0.736
Random Forest Accuracy for best features set: 0.744
```

In [ ]:

```python
predictions = {
    "Large Feature Set For Logistic Regression ": Y_pred_lr_large,
    "Small Feature Set For Logistic Regression": Y_pred_lr_small,
    "Best Feature Set For Logistic Regression": Y_pred_lr_best,
    "Large Feature Set For Decision Tree ": Y_pred_dt_large,
    "Small Feature Set For Decision Tree": Y_pred_dt_small,
    "Best Feature Set For Decision Tree": Y_pred_dt_best,
    "Large Feature Set For Random Forest": Y_pred_rf_large,
    "Small Feature Set For Random Forest": Y_pred_rf_small,
    "Best Feature Set For Random Forest": Y_pred_rf_best
}

# Create plots
fig, axes = plt.subplots(3, 3, figsize=(12, 12))

for ax, (title, Y_pred) in zip(axes.ravel(), predictions.items()):
    plot_confusion_matrix(Y_val, Y_pred, title, ax, xy_legends=['No Diabetes', 'Diabetes'])

plt.tight_layout(pad=5.0)
plt.show()
```



The best feature set consistently outperforms or matches the performance of the large and small feature sets in predicting both classes across all models! This is very good news, because implies that feature selection has been effective in improving model performance, reducing the complexity of the model.

One conclusion that we could drawn from this analyze is that the minor differences between the feature set performances may suggest that the models are somewhat robust to the features selected, or it may indicate that all sets contain the most critical features needed for making predictions.

In [ ]:

```
lr_metrics_best = classification_metrics(Y_val, Y_pred_lr_best, 'lr_best_set')
dt_metrics_best = classification_metrics(Y_val, Y_pred_dt_best, 'dt_best_set')
rf_metrics_best = classification_metrics(Y_val, Y_pred_rf_best, 'rf_best_set')

metrics_best = lr_metrics_best.merge(dt_metrics_best, on = 'metrics', how = 'outer')\
                              .merge(rf_metrics_best, on = 'metrics', how = 'outer')

lr_metrics_large = classification_metrics(Y_val, Y_pred_lr_large, 'lr_large_set')
dt_metrics_large = classification_metrics(Y_val, Y_pred_dt_large, 'dt_large_set')
rf_metrics_large = classification_metrics(Y_val, Y_pred_rf_large, 'rf_large_set')

metrics_large = lr_metrics_large.merge(dt_metrics_large, on = 'metrics', how = 'outer')\
                                .merge(rf_metrics_large, on = 'metrics', how = 'outer')

metrics_small = lr_metrics_small.merge(dt_metrics_small, on = 'metrics', how = 'outer')\
                                .merge(rf_metrics_small, on = 'metrics', how = 'outer')
```

```
all_metrics = metrics_best.merge(metrics_large, on = 'metrics', how = 'outer')\
                          .merge(metrics_small, on = 'metrics', how = 'outer')

display(all_metrics)
```

metrics	lr_best_set	dt_best_set	rf_best_set	lr_large_set	dt_large_set	rf_large_set	lr_small_set	dt_sma
Precision	0.731688	0.722201	0.728701	0.738683	0.724544	0.731223	0.735145	0.7
Recall	0.780909	0.786433	0.794647	0.783458	0.765897	0.798329	0.781476	0.7
AUC	0.740699	0.735017	0.742606	0.746788	0.730675	0.745706	0.743500	0.7
F1 Score	0.755498	0.752949	0.760247	0.760412	0.744647	0.763304	0.757603	0.7

The minor differences between the metrics become clearer upon closer inspection. For example, the AUC values are quite close across all models, suggesting a consistent ability to distinguish between positive and negative classes. Furthermore, the F1 Score and Recall metrics indicate that the models excel at accurately identifying relevant cases with a low count of false negatives.

The most balanced model in terms of complexity and predictive power is the Random Forest with the best feature set, which contains only five features for this model.

4. Model Evaluation on Test Set

Next, we'll evaluate the models on the test set. This step is important to confirm that the models' performance is consistent with the validation results and to demonstrate their predictive stability on unseen data. For this section we only use the best set of features: **BMI**, **GenHlth**, **Age**, **HighBP**, and **HighChol**.

Logistic Regression

In [ ]:

```
best_features_list = list(best_feature_set)
X_train_lr, _, X_test_lr, _ = preprocess_and_encode_features(df_train_lr, df_val_lr, df_tes
                                                                     dtype_dict_lr, featu


# Logistic Regression
lr_accuracy, Y_pred_lr_test = train_and_evaluate(LogisticRegression,
                                                 best_lr_params,
                                                 X_train_lr, Y_train,
                                                 X_test_lr, Y_test)

print('Accuracy for Logistic Regression on test set:\n', round(lr_accuracy, 3))
```

```
Accuracy for Logistic Regression on test set:
 0.738
```

Decision Tree and Random Forest

In [ ]:

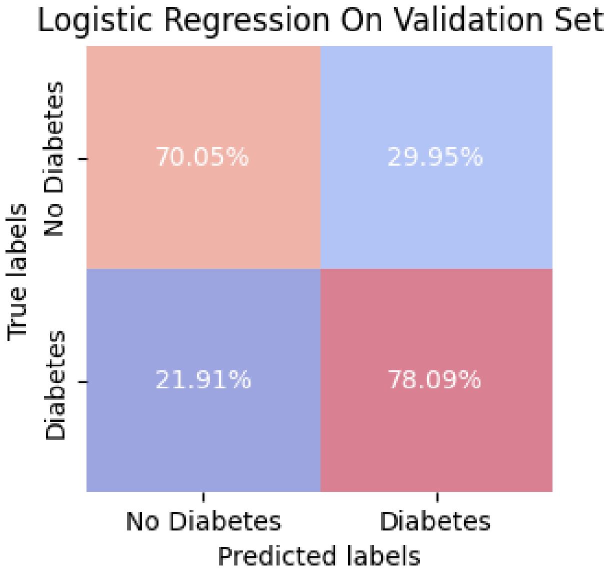
```
df_train_trees = df_train.copy()
df_test_trees = df_test.copy()

dtype_dict_trees = {
    'int32': categorical_features + boolean_features
}

df_train_trees = convert_dtypes(df_train_trees, dtype_dict_trees)
df_test_trees = convert_dtypes(df_test_trees, dtype_dict_trees)

# For decision three is need only to select the feature matrix from dataframe
X_train_trees, X_test_trees = df_train_trees[best_features_list].values, df_test_trees[best

# Decision Tree
```

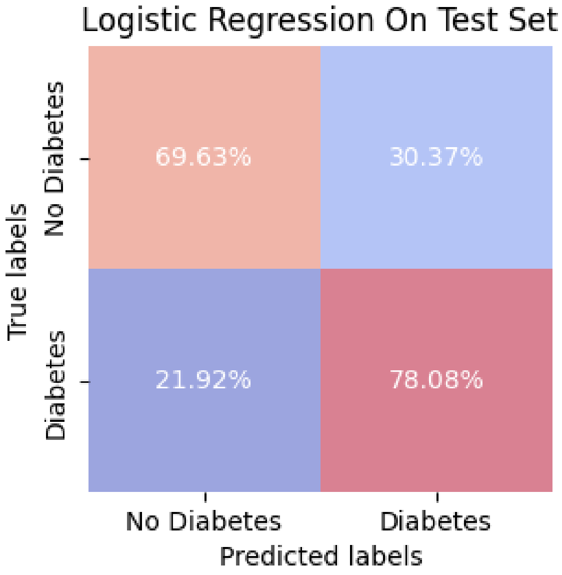
```
dt_accuracy, Y_pred_dt_test = train_and_evaluate(DecisionTreeClassifier,
                                                 best_dt_params,
                                                 X_train_trees, Y_train,
                                                 X_test_trees, Y_test)

# Random Forest
rf_accuracy, Y_pred_rf_test = train_and_evaluate(RandomForestClassifier,
                                                 best_rf_params,
                                                 X_train_trees, Y_train,
                                                 X_test_trees, Y_test)

print('Accuracy for Decision Tree on test set:\n', round(dt_accuracy, 3))

print('Accuracy for Random Forest on test set:\n', round(rf_accuracy, 3))
```

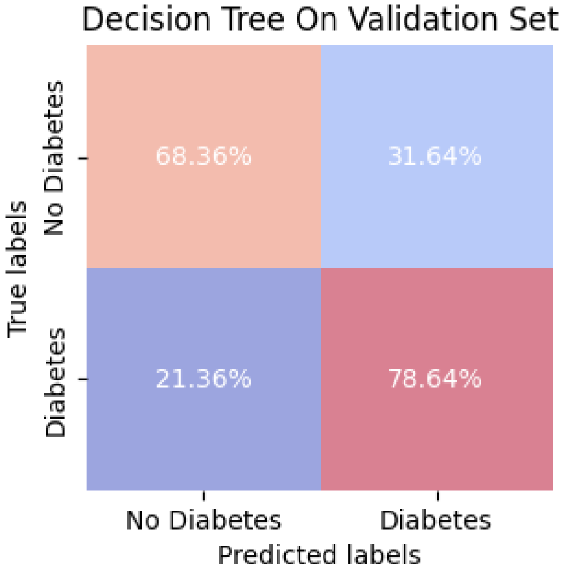
```
Accuracy for Decision Tree on test set:
 0.731
Accuracy for Random Forest on test set:
 0.735
```

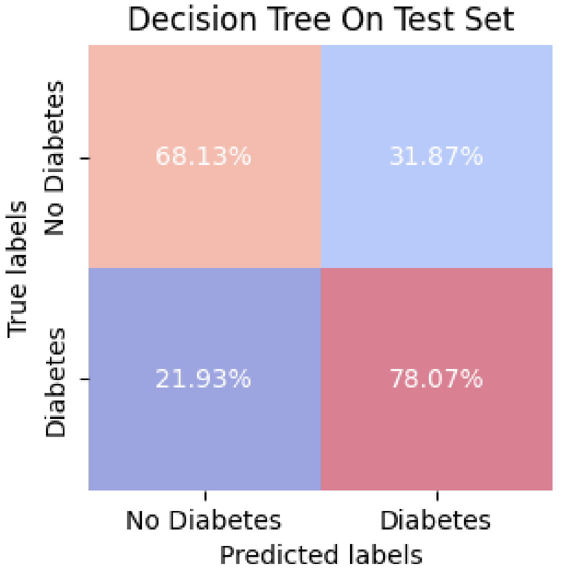
In [ ]:

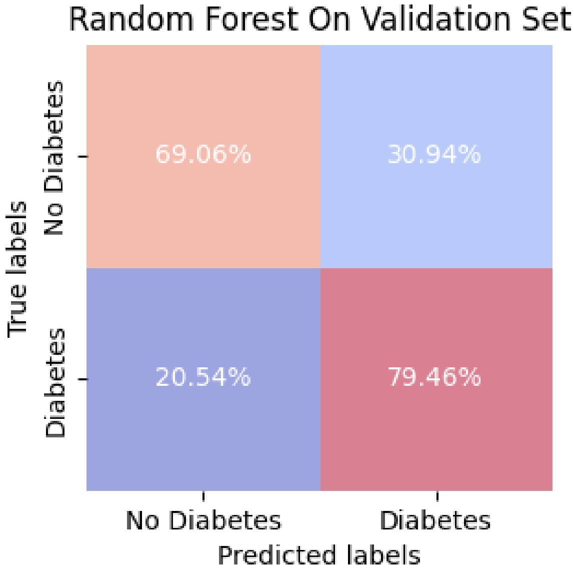
```
# predictions on validation set with best features set
Y_pred_lr_val = Y_pred_lr_best
Y_pred_dt_val = Y_pred_dt_best
Y_pred_rf_val = Y_pred_rf_best

predictions = {
    "Logistic Regression On Validation Set": (Y_val, Y_pred_lr_val),
    "Logistic Regression On Test Set": (Y_test, Y_pred_lr_test),
    "Decision Tree On Validation Set": (Y_val, Y_pred_dt_val),
    "Decision Tree On Test Set": (Y_test, Y_pred_dt_test),
    "Random Forest On Validation Set": (Y_val, Y_pred_rf_val),
    "Random Forest On Test Set": (Y_test, Y_pred_rf_test)
}

fig, axes = plt.subplots(3, 2, figsize=(8, 12))

for ax, (title,  (Y_true, Y_pred)) in zip(axes.ravel(), predictions.items()):
        plot_confusion_matrix(Y_true, Y_pred, title, ax, xy_legends=['No Diabetes', 'Diabet

plt.tight_layout(pad=5.0)
plt.show()
```

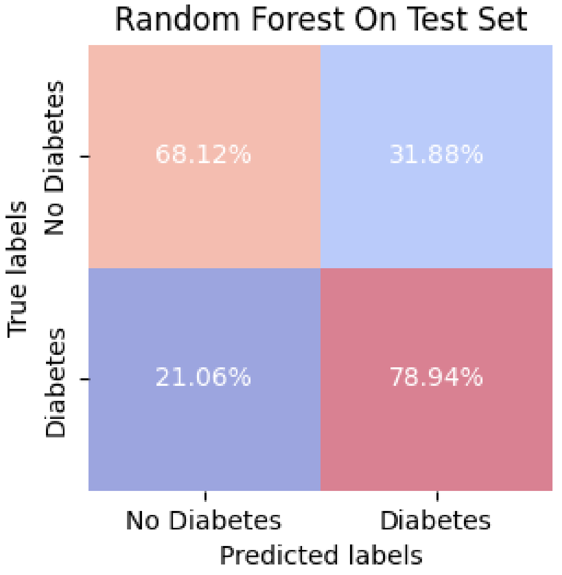

Logistic Regression On Validation Set


Logistic Regression On Test Set


Decision Tree On Validation Set


Decision Tree On Test Set


Random Forest On Validation Set


Random Forest On Test Set

Each model shows a level of consistency between the validation set and test set, with only slight variations in the percentages of true positives (individuals correctly predicted with diabetes) and true negatives (individuals correctly predicted without diabetes), as well as false positives and false negatives. This suggests that the models are likely generalizing well and not overfitting to the validation data.

Also, we can note that the Random Forest model shows a high recall with a slight advantage in minimizing false positives (incorrectly predicts diabetes in an individual), it could be considered the most stable model among the three, especially if the priority is to minimize false negatives.

4. Conclusions

From the exploratory data analysis (EDA), we identified the possibility of dropping some redundant features from the dataset out of the initial 22, leading to two subsets: the 'small feature set' (with features agreed upon by all correlation metrics) and the 'large feature set' (a union of features selected by both Mutual Information and Pearson Correlation).

In the Model Training and Validation section we showed that both feature sets produced similar outcomes across Logistic Regression, Decision Tree, and Random Forest models, with only slight variances in accuracy and other metrics such as F1 Score, Precision, Recall, and AUC. The Features selected by the models shows to be a even smaller set of feature, with only five features, that demonstrates also a high predictive power with only a marginal difference from the other features set.

The challenge in reducing the false negative rate (individuals wrongly classified with diabetes) from the different models may be due the possible class imbalances of the features **CholCHeck**, **Stroke**, **HeartDiseaseorAttack**, **Vaggies**, **HvyAlcoholConsump**, **AnyHealthcare**, **NoDocbcCost**, as noted previously in the EDA. One idea for improvement for the dataset in a future work may be focus on adding another tables from Kaggle that can be used complementary to the one used here.

A important information from our analysis is the indicative that the features **BMI**, **GenHlth**, **Age**, **HighBP**, and **HighChol** are the most predictive risk factors for diabetes, consistent with established clinical insights. Our project successfully reduce the feature space from 22 possible risk factors to just a subset of five, facilitating a simplified predictive model without compromising accuracy.

The Random Forest model, utilizing just these five risk factors, show to be the most balanced option in terms of complexity and predictive capacity, and was selected for the final model deployment.

5. Prepare For Deployment

In [ ]:

```python
# libraries for saving the model and requesting data from the API
from joblib import dump
import requests
```

5.1 Train and Save Random Forest Model

In [ ]:

```python
# Make copies of the dataframes
df_train_trees = df_train.copy()
df_val_trees = df_val.copy()
df_test_trees = df_test.copy()

# preprocess
dtype_dict_trees = {
    'int32': categorical_features + boolean_features
}

df_train_trees = convert_dtypes(df_train_trees, dtype_dict_trees)
df_test_trees = convert_dtypes(df_test_trees, dtype_dict_trees)
df_val_trees = convert_dtypes(df_val_trees, dtype_dict_trees)

# Save trained Model
X_train_trees = df_train_trees[best_features_list].values
print('\nRandom Forest Best Parameters:\n', best_rf_params)
```

```
rf_model = RandomForestClassifier(**best_rf_params)
rf_model.fit(X_train_trees, Y_train)

# Save trained Model as a joblib file
dump(rf_model, '../models/random_forest_model.joblib')

# Additionally, save trained Model as a binary file
with open('../models/random_forest_model.bin', 'wb') as f_out:
    dump(rf_model, f_out)

# Add the target variable back to the dataframes
df_train_trees['Diabetes'] = Y_train
df_val_trees['Diabetes'] = Y_val
df_test_trees['Diabetes'] = Y_test

#  Save DataFrames with the target variable
target_feature_list = best_features_list + ['Diabetes']
df_train_trees[target_feature_list].to_csv('../data/processed/train_data.csv')
df_test_trees[target_feature_list].to_csv('../data/processed/test_data.csv')
df_val_trees[target_feature_list].to_csv('../data/processed/val_data.csv')
```

```
Random Forest Best Parameters:
 {'criterion': 'gini', 'max_depth': 10, 'min_samples_leaf': 15, 'min_samples_split': 5, 'n_
estimators': 60, 'random_state': 42}
```

5.2 Testing Web Service

Once the container is running with Flask application inside the container set up to handle POST requests at the /predict endpoint, we can then make a POST request to that endpoint from your notebook or any other client capable of sending HTTP requests.

In [ ]:

```
url_local = "http://127.0.0.1:9696/predict"
# Single prediction of diabetes for a individual
diabetes_indicators = {'GenHlth':2, "BMI" :29.0,'Age': 1, 'HighChol':0, 'HighBP':0 }
requests.post(url_local, json = diabetes_indicators).json()

# {'Diabetes Prediction': 'Low Chance Of Diabetes'}
```

Out[ ]:

```
{'Diabetes Prediction': 'Low Chance Of Diabetes'}
```

In [ ]:

```
# Clound URL
url_clound = "https://diabetes-indicators.onrender.com/predict"
diabetes_indicators = {'GenHlth':2, "BMI" :29.0,'Age': 1, 'HighChol':0, 'HighBP':0 }
requests.post(url_clound, json = diabetes_indicators).json()

# {'Diabetes Prediction': 'Low Chance Of Diabetes'}
```

Out[ ]:

```
{'Diabetes Prediction': 'Low Chance Of Diabetes'}
```