ML algorithms for Indians Diabetes Prediction

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1 Introduction

In this laboratory, we will

1. Import libraries
2. Import DataFrame related to heart disease diagnosis
3. Explore the Data Analysis (EDA)
4. Data preparation
5. Modeling: Decision Tree classifier vs Logistic Regression classifier

Context This dataset is originally from the National Institute of Diabetes and Digestive and Kidney Diseases (source in kaggle is here. The objective of the dataset is to diagnostically predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset. Several constraints were placed on the selection of these instances from a larger database. In particular, all patients here are females at least 21 years old of Pima Indian heritage.

Description of the dataset The datasets consist of several medical predictor (independent) variables and one target (dependent) variable, Outcome. Independent variables include the number of pregnancies the patient has had, their BMI, insulin level, age, and so on:

- `Pregnancies`: Number of times pregnant (continuous variable)
- `Glucose`: Plasma glucose concentration a 2 hours in an oral glucose tolerance test (continuous variable)
- `BloodPressure`: Diastolic blood pressure (mm Hg) (continuous variable)
- `SkinThickness`: Triceps skin fold thickness (mm) (continuous variable)
- `Insulin`: 2-Hour serum insulin (mu U/ml) (continuous variable)
- `BMI`: Body mass index (weight in kg/(height in m)^2) (continuous variable)
- `DiabetesPedigreeFunction`: Diabetes pedigree function (continuous variable)
- `age`: age (years) (continuous variable)
- `Outcome`: Class variable (0 or 1) 268 of 768 are 1, the others are 0 (0: No diabete, 1: diabete) (binary variable)

These variables are used to analyze risk factors and symptoms associated with diabete diseases.

2 Import the necessary libraries

[1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

# ML libraries for data processing
from sklearn.preprocessing import LabelEncoder, StandardScaler
from sklearn.compose import ColumnTransformer
from sklearn.model_selection import train_test_split
```

[2]:
```
import warnings
# Suppress all warnings
warnings.filterwarnings("ignore")
```

3 Import the dataframe

[3]:
```
import os
for dirname, _, filenames in os.walk('/kaggle/input'):
    for filename in filenames:
        print(os.path.join(dirname, filename))
```

```
/kaggle/input/pima-indians-diabetes-database/diabetes.csv
```

[4]:
```
data = pd.read_csv('/kaggle/input/pima-indians-diabetes-database/diabetes.csv')
```

4 Exploratory Data Analysis (EDA)

- Display the first five rows of the DataFrame to understand the variables

[5]:
```
data.head()
```

[5]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

- Display the last five rows of the DataFrame to understand the variables

[6]:
```
data.tail()
```

[6]:
```
     Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
763           10      101             76             48      180  32.9
764            2      122             70             27        0  36.8
765            5      121             72             23      112  26.2
766            1      126             60              0        0  30.1
767            1       93             70             31        0  30.4

     DiabetesPedigreeFunction  Age  Outcome
763                     0.171   63        0
764                     0.340   27        0
765                     0.245   30        0
766                     0.349   47        1
767                     0.315   23        0
```

- Explore information about the structure, data types, and memory usage of the DataFrame.

[7]:
```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   Pregnancies               768 non-null    int64
 1   Glucose                   768 non-null    int64
 2   BloodPressure             768 non-null    int64
 3   SkinThickness             768 non-null    int64
 4   Insulin                   768 non-null    int64
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64
 8   Outcome                   768 non-null    int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

- Generate descriptive statistics of a DataFrame

[8]:
```
data.describe()
```

[8]:
```
       Pregnancies     Glucose  BloodPressure  SkinThickness     Insulin  \
count   768.000000  768.000000     768.000000     768.000000  768.000000
mean      3.845052  120.894531      69.105469      20.536458   79.799479
std       3.369578   31.972618      19.355807      15.952218  115.244002
min       0.000000    0.000000       0.000000       0.000000    0.000000
25%       1.000000   99.000000      62.000000       0.000000    0.000000
```

```
50%       3.000000  117.000000       72.000000       23.000000   30.500000
75%       6.000000  140.250000       80.000000       32.000000  127.250000
max      17.000000  199.000000      122.000000       99.000000  846.000000
```

```
              BMI  DiabetesPedigreeFunction         Age     Outcome
count  768.000000                768.000000  768.000000  768.000000
mean    31.992578                  0.471876   33.240885    0.348958
std      7.884160                  0.331329   11.760232    0.476951
min      0.000000                  0.078000   21.000000    0.000000
25%     27.300000                  0.243750   24.000000    0.000000
50%     32.000000                  0.372500   29.000000    0.000000
75%     36.600000                  0.626250   41.000000    1.000000
max     67.100000                  2.420000   81.000000    1.000000
```

- Shape of the data

[9]:
```
data.shape
```

[9]:
```
(768, 9)
```

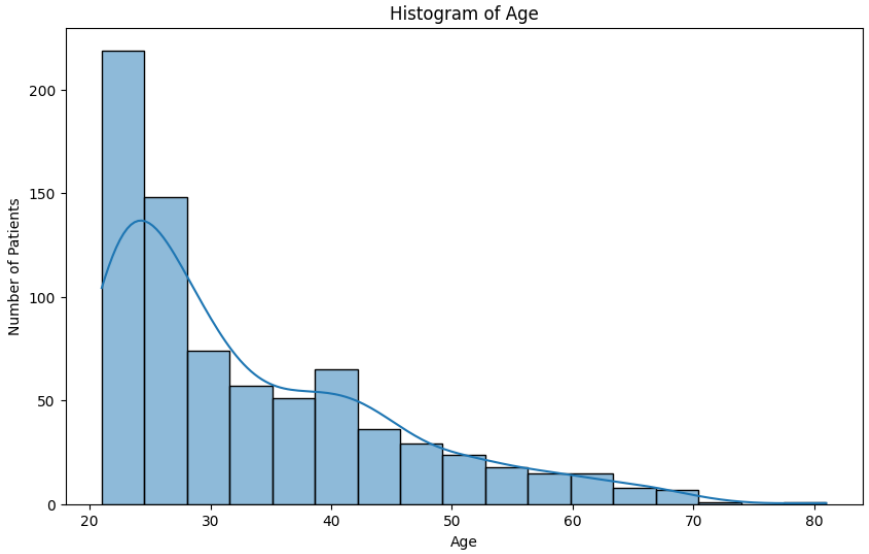
- Show columns name

[10]:
```
data.columns
```

[10]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

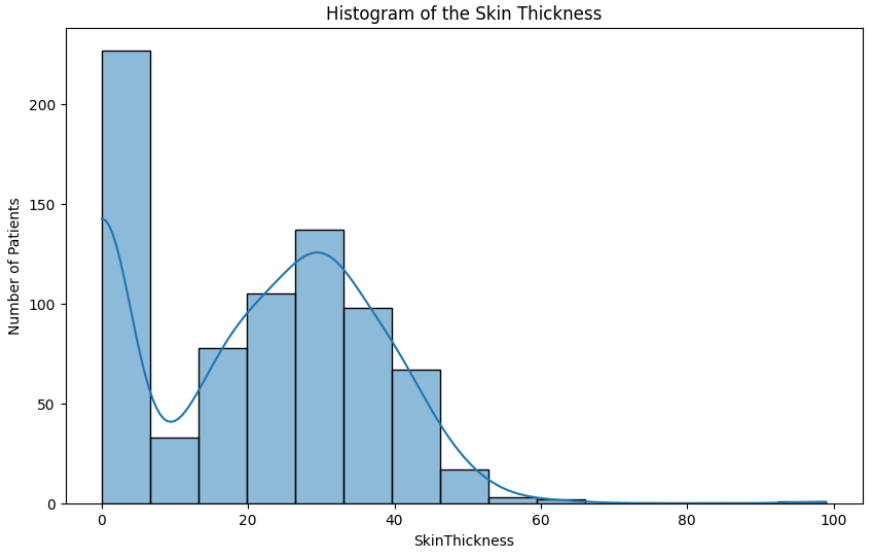
- Create a histogram of the age variable

[11]:
```
# Set the figure size
plt.figure(figsize=(10, 6))

# Create a histogram using Seaborn
sns.histplot(data['Age'], kde=True)

# Add title and labels
plt.title('Histogram of Age')
plt.xlabel('Age')
plt.ylabel('Number of Patients')

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



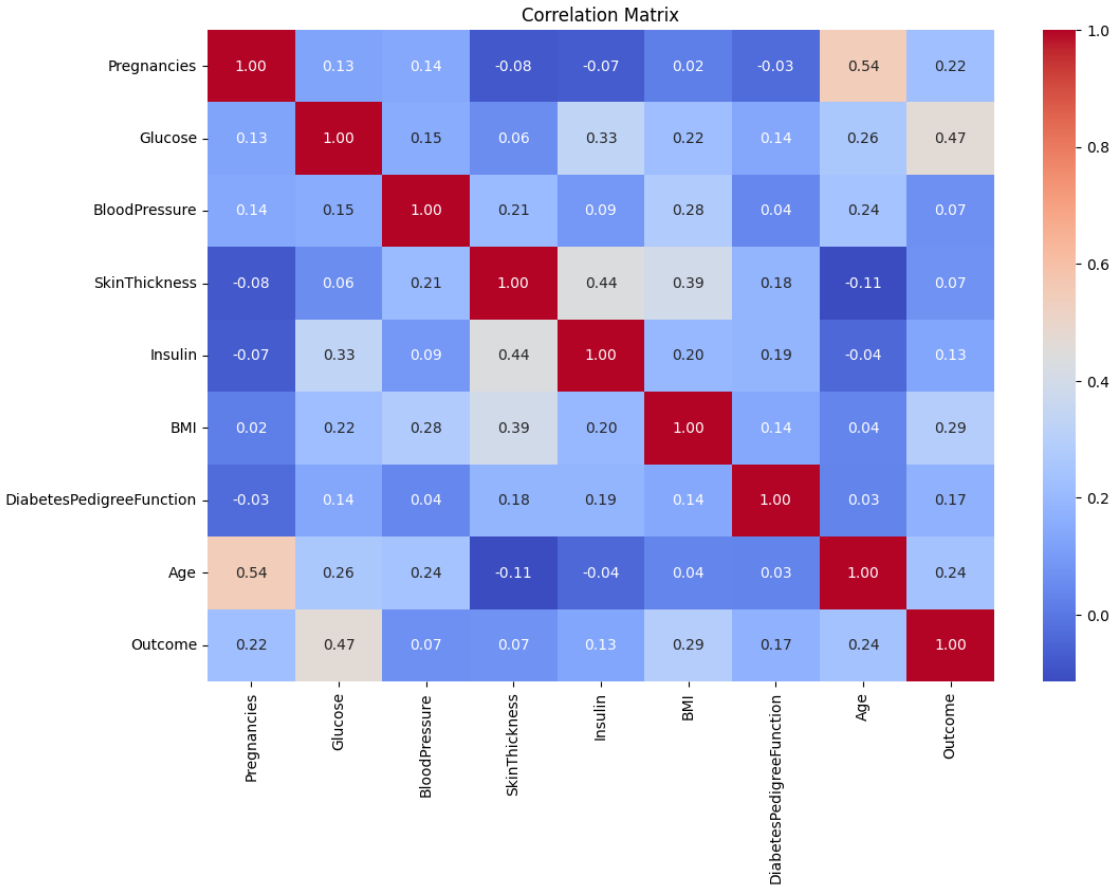
- Create a histogram of the `SkinThickness` variable

[12]:
```
plt.figure(figsize=(10, 6))
sns.histplot(data['SkinThickness'], kde=True)

plt.title('Histogram of the Skin Thickness')
plt.xlabel('SkinThickness')
plt.ylabel('Number of Patients')

plt.show()
```



- Create a heatmap of the correlation matrix to compute the correlation coefficients between all pairs of variables in the DataFrame

[13]:
```
# Set the figure size
plt.figure(figsize=(12, 8))

# Create a heatmap using Seaborn
sns.heatmap(data.corr(), annot=True, cmap='coolwarm', fmt='.2f')

# Add title
plt.title('Correlation Matrix')

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

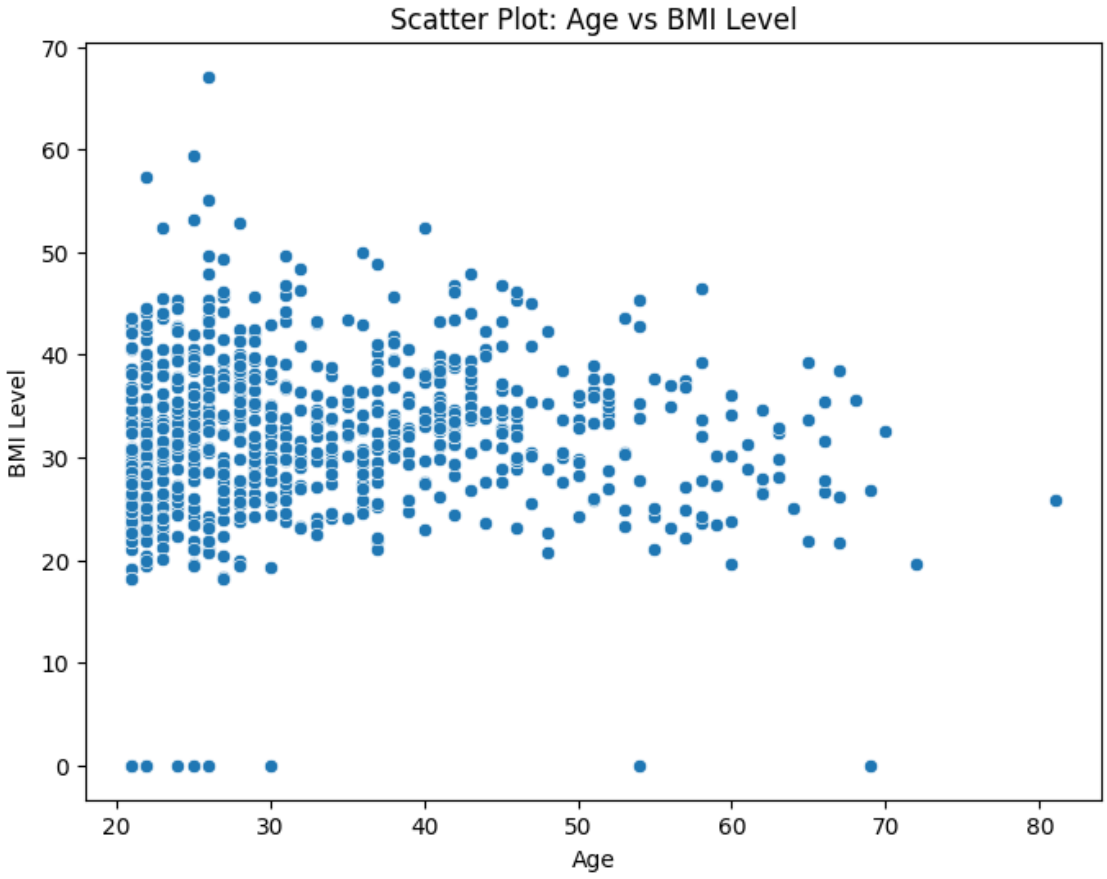


The colors represent the strength and direction of the correlation (cool colors for negative correlation, warm colors for positive correlation).

The resulting plot provides a visual representation of how each variable correlates with every other variable in the dataset

- Creating a scatter plot to visualize the relationship between age and BMI levels

[14]:
```
# Set the figure size
plt.figure(figsize=(8, 6))

# Create a scatter plot using Seaborn
sns.scatterplot(x='Age', y='BMI', data=data)

# Add title and labels
plt.title('Scatter Plot: Age vs BMI Level')
plt.xlabel('Age')
plt.ylabel('BMI Level')

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

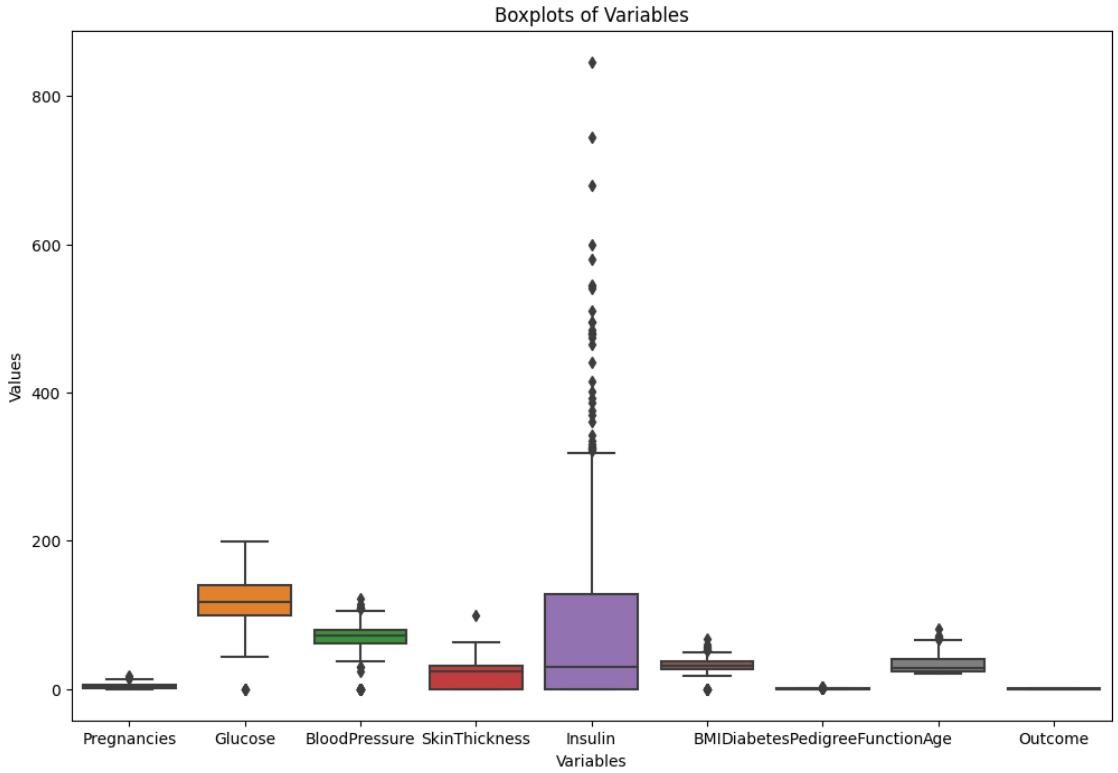


- Creating a pair plot to visualize the relationships between all the variables to generates a grid of scatter plots where each variable is plotted against every other variable. The diagonal of the grid displays histograms for each individual variable. The pair plot is useful for quickly visualizing the relationships and distributions between multiple variables in the dataset.

[15]:
```
# Create a pair plot using Seaborn
sns.pairplot(data)

# Add a title
plt.suptitle('Pair Plot of Variables')

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

- Creating boxplots to visualize the distribution and identify outliers for all the variables to generate a boxplot for each variable, providing a visual representation of the distribution, central tendency, and presence of outliers. Here, the x-axis represents the variables, and the y-axis represents the values.

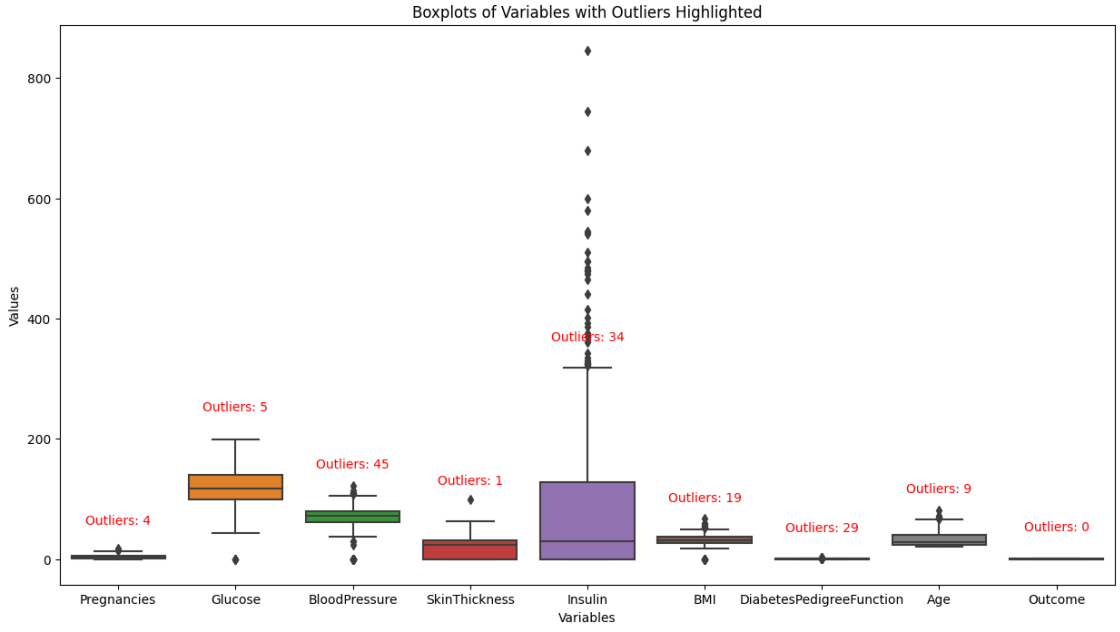
[16]:
```
# Set the figure size
plt.figure(figsize=(12, 8))

# Create boxplots using Seaborn
sns.boxplot(data=data)

# Add title and labels
plt.title('Boxplots of Variables')
plt.xlabel('Variables')
plt.ylabel('Values')

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



Tips: show the number of outliers in each column above the boxplots, we calculate and display the count of outliers for each column.

[17]:
```
# Calculate the lower and upper bounds for outliers
Q1 = data.quantile(0.25)
Q3 = data.quantile(0.75)
IQR = Q3 - Q1
```

```
lower_bound = Q1 - 1.5 * IQR
upper_bound = Q3 + 1.5 * IQR

# Identify outliers
outliers = ((data < lower_bound) | (data > upper_bound))

# Set the figure size
plt.figure(figsize=(15, 8))

# Create boxplots
sns.boxplot(data=data)

# Add title and labels
plt.title('Boxplots of Variables with Outliers Highlighted')
plt.xlabel('Variables')
plt.ylabel('Values')

# Show the number of outliers for each column above the boxplots
for col in data.columns:
    num_outliers = outliers[col].sum()
    plt.text(data.columns.get_loc(col), upper_bound[col] + 0.1 * (upper_bound.
 ↪max() - lower_bound.min()),
             f'Outliers: {num_outliers}', ha='center', va='center', color='red')

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



- check if there are any missing values in the DataFrame

[18]:
```
missing_values = data.isnull().sum()
print(missing_values)
```

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

If we get missing values in a DataFrame, we can Handle them. Here are several common strategies for handling missing values in three or four columns:

1. **Remove Rows with Missing Values:** You can remove rows that contain missing values in any of the specified columns using the `dropna()` method. This is suitable if the number of rows with missing values is small.

   ```
   data.dropna(subset=['Column1', 'Column2', 'Column3', 'Column4'], inplace=True)
   ```

2. **Replace with Default or Specific Values:** You can replace missing values with a default value or a specific value based on the characteristics of the data.

   ```
   data['Column1'].fillna(default_value, inplace=True)
   data['Column2'].fillna(another_value, inplace=True)
   data['Column3'].fillna(specific_value, inplace=True)
   data['Column4'].fillna(another_specific_value, inplace=True)
   ```

3. **Impute with Mean, Median, or Mode:** If the missing values are numerical, you can replace them with the mean, median, or mode of the respective columns.

   ```
   mean_value = data['Column1'].mean()
   data['Column1'].fillna(mean_value, inplace=True)

   median_value = data['Column2'].median()
   data['Column2'].fillna(median_value, inplace=True)

   mode_value = data['Column3'].mode().iloc[0]
   data['Column3'].fillna(mode_value, inplace=True)
   ```

4. **Interpolation:** If your data has a temporal or sequential structure, you might consider using interpolation to estimate missing values based on existing values.

   ```
   data.interpolate(method='linear', inplace=True)
   ```

5 Data Preparation

- Handle outliers using the mean. We calculate the lower and upper bounds based on the interquartile range (IQR) and replaces any values outside this range with the mean of the respective column.

Note: We compute for each variable:

- Q1: The first quantile (25%)
- Q3: The third quantile (75%)
- $IQR = Q3 - Q1$
- The $lower_{bound} = Q1 - 1.5 * IQR$
- The $upper_{bound} = Q3 + 1.5 * IQR$

After that, we replace the outliers by lower and upper bounds

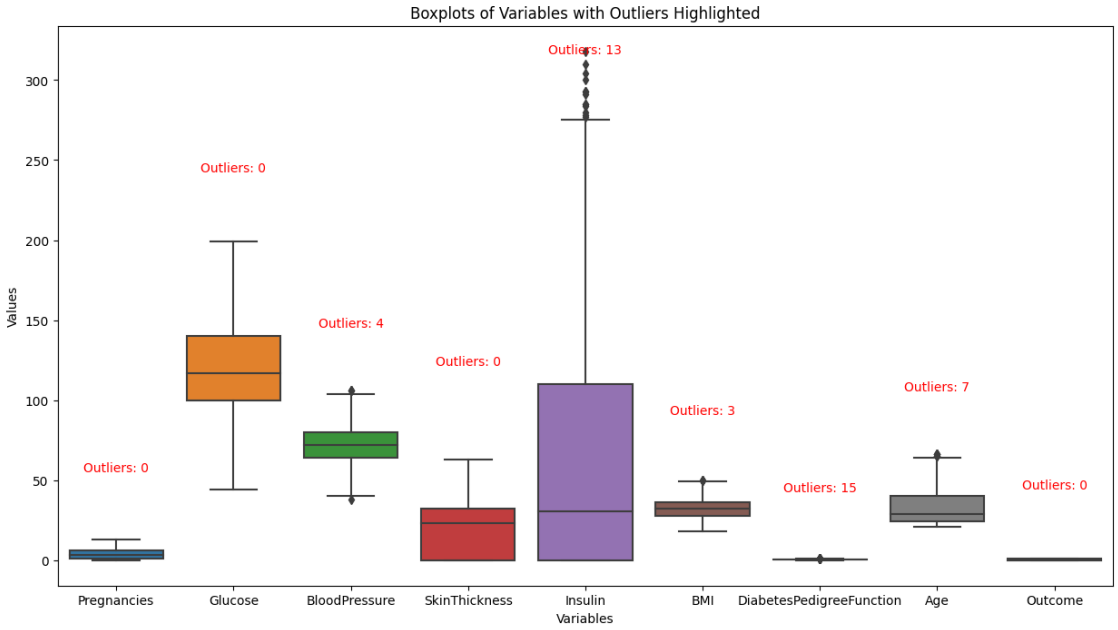
[19]:
```
for col in data.columns:
    Q1 = data[col].quantile(0.25)
    Q3 = data[col].quantile(0.75)
    iqr = Q3 - Q1
    lower_bound = Q1 - 1.5 * iqr
    upper_bound = Q3 + 1.5 * iqr
    data[col] = np.where((data[col] < lower_bound) | (data[col] > upper_bound),␣
↪data[col].mean(), data[col])
```

Tips: I run the cell above three times to handle the outliers by the mean

- Check if there are still any outliers or not

[20]:
```
# Calculate the lower and upper bounds for outliers
Q1 = data.quantile(0.25)
Q3 = data.quantile(0.75)
IQR = Q3 - Q1

lower_bound = Q1 - 1.5 * IQR
upper_bound = Q3 + 1.5 * IQR

# Identify outliers
outliers = ((data < lower_bound) | (data > upper_bound))

# Set the figure size
plt.figure(figsize=(15, 8))

# Create boxplots
sns.boxplot(data=data)

# Add title and labels
plt.title('Boxplots of Variables with Outliers Highlighted')
plt.xlabel('Variables')
plt.ylabel('Values')
```

```
# Show the number of outliers for each column above the boxplots
for col in data.columns:
    num_outliers = outliers[col].sum()
    plt.text(data.columns.get_loc(col), upper_bound[col] + 0.1 * (upper_bound.
 ↪max() - lower_bound.min()),
             f'Outliers: {num_outliers}', ha='center', va='center', color='red')

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



Split the de data in to parts or sets; features and target. - Target is the column `Outcome` - Features are all the columns except the target

[21]:
```
X = data.drop('Outcome', axis=1)
y = data['Outcome']
```

- show the number of observations for each class (1 and 0) in the 'Outcome' column

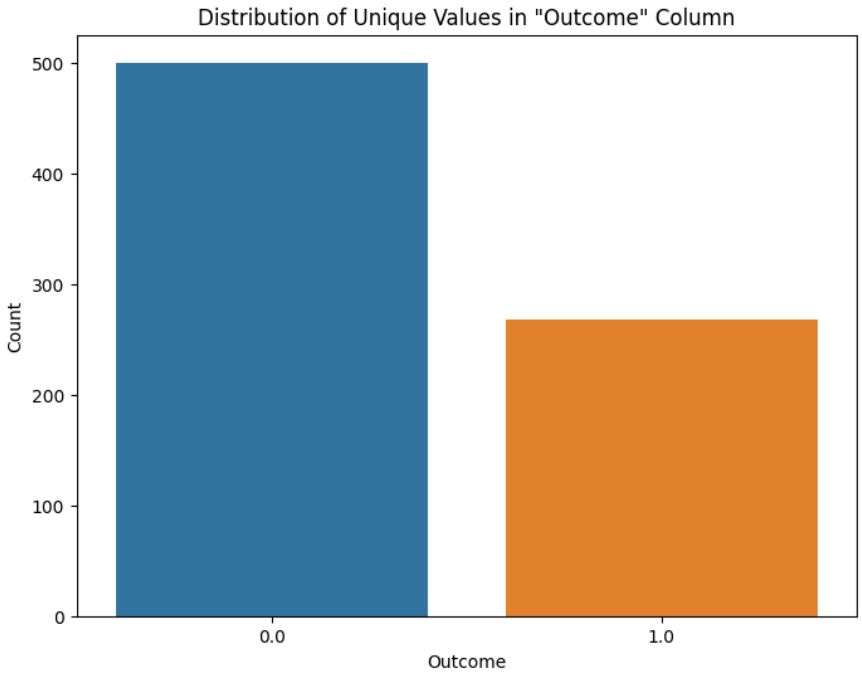
[22]:
```
print(f"Unique values in 'Outcome' column: {y.unique()}")
print(f"Number of unique values in 'Outcome' column: {y.nunique()}")
print(f'Count the number of observations for each class \n: {y.value_counts()}')
```

```
Unique values in 'Outcome' column: [1. 0.]
Number of unique values in 'Outcome' column: 2
Count the number of observations for each class
: Outcome
0.0    500
```

```
1.0    268
Name: count, dtype: int64
```

- visualize the distribution of unique values in the 'Outcome' column, which contains binary values (1 and 0)

[23]:
```
# Plot the distribution
plt.figure(figsize=(8, 6))
sns.countplot(x=y)
plt.title('Distribution of Unique Values in "Outcome" Column')
plt.xlabel('Outcome')
plt.ylabel('Count')
plt.show()
```



we can also use:

```
y.value_counts().plot(kind='bar', color=['skyblue', 'lightcoral'])
```

From the statistics describtion of the data (`data.discribe()`), we can see the columns must be scaled

- Normalizing numeric variables with StandardScaler

[24]:
```
scaler = StandardScaler()
X = scaler.fit_transform(X)
```

- Sow the Normalisation result

[25]:
```
X_df = pd.DataFrame(X, columns=data.columns[:-1])
X_df.describe()
```

[25]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin
count	7.680000e+02	7.680000e+02	7.680000e+02	7.680000e+02	7.680000e+02
mean	1.434038e-16	-1.595946e-16	4.255855e-16	1.272131e-17	-7.864080e-17
std	1.000652e+00	1.000652e+00	1.000652e+00	1.000652e+00	1.000652e+00
min	-1.158789e+00	-2.553955e+00	-3.048148e+00	-1.302538e+00	-8.153544e-01
25%	-8.527940e-01	-7.210503e-01	-7.190618e-01	-1.302538e+00	-8.153544e-01
50%	-2.408039e-01	-1.539182e-01	-2.419844e-03	1.635453e-01	-4.212562e-01
75%	6.771814e-01	6.104773e-01	7.142221e-01	7.372301e-01	6.059836e-01
max	2.819147e+00	2.542014e+00	3.043308e+00	2.713255e+00	3.293605e+00

	BMI	DiabetesPedigreeFunction	Age
count	7.680000e+02	7.680000e+02	7.680000e+02
mean	2.151057e-16	-8.789266e-17	2.266705e-16
std	1.000652e+00	1.000652e+00	1.000652e+00
min	-2.185127e+00	-1.443178e+00	-1.069690e+00
25%	-7.334514e-01	-7.663432e-01	-7.979675e-01
50%	-3.102758e-02	-2.405970e-01	-3.450974e-01
75%	6.401774e-01	6.159099e-01	6.512168e-01
max	2.778668e+00	3.101720e+00	3.006141e+00

6 Modelling

In this modelling phase we use:

Supervised learning

decision tree

logistic regression

For the supervised learning our target is `Outcome`

- Split the data into training set and testing set using train_test_split

[26]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state=42)
```

- Display the shape of the splited sets: `X_train, X_test, y_train, y_test`

[27]:
```
print(f'The shape of training features is: {X_train.shape}')
print(f'The shape of training target is: {y_train.shape}')

print(f'The shape of testing features is: {X_test.shape}')
print(f'The shape of testing target is: {y_test.shape}')
```

```
The shape of training features is: (614, 8)
The shape of training target is: (614,)
```

```
The shape of testing features is: (154, 8)
The shape of testing target is: (154,)
```

6.0.1 Decision Tree classifier

Here are the steps to implement a Decision Tree classifier:

1. Import the Decision Tree classifier from scikit-learn:

```
from sklearn.tree import DecisionTreeClassifier
```

2. Create an instance of the Decision Tree classifier:

```
# we adjust hyperparameters like max_depth, min_samples_split, etc.
tree = DecisionTreeClassifier(max_depth=..., min_samples_split=...)
```

3. Train the classifier using the training data `X_train` and `y_train`:

```
tree.fit(X_train, y_train)
```

4. Make predictions on the test data `X_test` and store the predicted labels in `y_pred`:

```
y_pred = tree.predict(X_test)
```

[28]:
```
from sklearn.tree import DecisionTreeClassifier


# Create an instance of the Decision Tree classifier
tree = DecisionTreeClassifier()

# Train the classifier using the training data
tree.fit(X_train, y_train)

# Make predictions on the test data
y_pred = tree.predict(X_test)
```

Calculating various performance metrics for a classification model using couple of metrics:

- accuracy_score: The accuracy score is a measure of the overall correctness of a classification model. It is calculated as the ratio of correctly predicted instances to the total number of instances. The mathematical formula for accuracy score is:

$$\text{Accuracy} = \frac{\text{Number of Correct Predictions}}{\text{Total Number of Predictions}}$$

Mathematically, if we have: - (TP) (True Positives): the number of instances correctly predicted as positive, - (TN) (True Negatives): the number of instances correctly predicted as negative, - (FP) (False Positives): the number of instances incorrectly predicted as positive, - (FN) (False Negatives): the number of instances incorrectly predicted as negative, then the accuracy can be expressed as:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

- precision_score: Precision is a metric used in classification to measure the accuracy of the positive predictions made by a model. It is calculated as the ratio of true positive predictions

to the total number of positive predictions (both true positives and false positives). The precision formula is given by:

$$\text{Precision} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Positives}}$$

- recall_score: Recall, also known as sensitivity or true positive rate, is a metric in classification that measures the ability of a model to identify all relevant instances of a class. It is calculated as the ratio of true positive predictions to the total number of actual positive instances (true positives and false negatives). The recall formula is given by:

$$\text{Recall} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}}$$

- f1_score: The F1 score is a metric in classification that combines precision and recall into a single measure. It is the harmonic mean of precision and recall and is particularly useful when there is an uneven class distribution (imbalanced datasets). The F1 score is calculated using the following formula:

$$\text{F1 Score} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

the F1 score can be expressed as:

$$\text{F1 Score} = \frac{2 \times \frac{\text{True Positives}}{\text{True Positives} + \text{False Positives}} \times \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}}}{\frac{\text{True Positives}}{\text{True Positives} + \text{False Positives}} + \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}}}$$

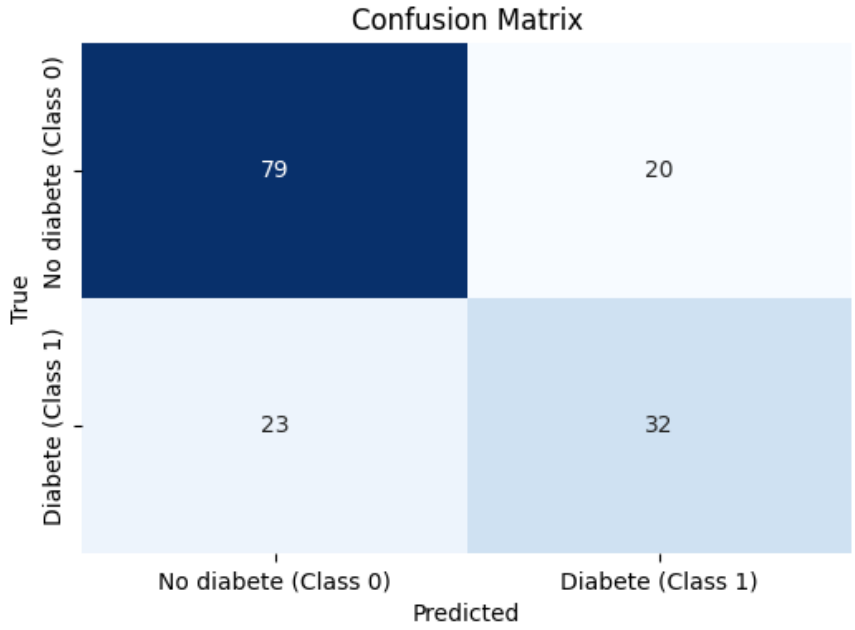
[29]:
```
from sklearn.metrics import accuracy_score, precision_score, recall_score,␣
↪f1_score

# Calculation of accuracy
accuracy = accuracy_score(y_test, y_pred)

# Calculation of precision
precision = precision_score(y_test, y_pred)

# Calculation of recall
recall = recall_score(y_test, y_pred)

# Calculation of F1 score
f1 = f1_score(y_test, y_pred)

# Displaying the results
print("Accuracy: {:.2f}%".format(accuracy * 100))
print("Precision: {:.2f}%".format(precision * 100))
print("Recall: {:.2f}%".format(recall * 100))
print("F1 Score: {:.2f}%".format(f1 * 100))
```

```
Accuracy: 72.08%
Precision: 61.54%
```

```
Recall: 58.18%
F1 Score: 59.81%
```

- plot the confusion matrix for the Decision Tree classifier

[30]:
```
from sklearn.metrics import confusion_matrix


# Calculate the confusion matrix
cm = confusion_matrix(y_test, y_pred)

# Plot the confusion matrix
plt.figure(figsize=(6, 4))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', cbar=False,
            xticklabels=['No diabete (Class 0)', 'Diabete (Class 1)'],
            yticklabels=['No diabete (Class 0)', 'Diabete (Class 1)'])
plt.xlabel('Predicted')
plt.ylabel('True')
plt.title('Confusion Matrix')
plt.show()
```



In a confusion matrix, the elements represent the counts of True Positives (TP), True Negatives (TN), False Positives (FP), and False Negatives (FN).

The following table represents the four cases in a confusion matrix:

	Predicted Positive	Predicted Negative
Actual Positive	True Positives (TP)	False Negatives (FN)
Actual Negative	False Positives (FP)	True Negatives (TN)

- find the optimal hyperparameters for a Decision Tree classifier using Grid Search

[31]:
```
from sklearn.model_selection import GridSearchCV

# Define the parameter grid
param_grid = {
    'max_depth': [2, 3, 5, 7, None],  # Maximum depth of the tree
    'min_samples_split': [1, 2, 5, 10]  # Minimum samples required to split an␣
 ↪internal node
}

tree = DecisionTreeClassifier()

# Create GridSearchCV instance
grid_search = GridSearchCV(tree, param_grid, cv=5, scoring='accuracy')

# Perform grid search on the training data
grid_search.fit(X_train, y_train)

# Print the best hyperparameters
print("Best Hyperparameters:", grid_search.best_params_)

# Make predictions on the test data using the best model
best_model = grid_search.best_estimator_
y_pred = best_model.predict(X_test)

# Calculate accuracy
accuracy = accuracy_score(y_test, y_pred)
print(f'Accuracy with Best Model: {accuracy * 100:.2f}%')
```

```
Best Hyperparameters: {'max_depth': 3, 'min_samples_split': 2}
Accuracy with Best Model: 75.97%
```

[32]:
```
best_model
```

[32]:
```
DecisionTreeClassifier(max_depth=3)
```

6.0.2 Logistic Regression classifier

Here are the steps to implement a Logistic Regression classifier:

1. Import the Logistic Regression classifier from scikit-learn:

```
from sklearn.linear_model import LogisticRegression
```

2. Create an instance of the Logistic Regression classifier:

```
# We can adjust hyperparameters like C (inverse of regularization strength), solver, etc.
logistic_regression = LogisticRegression(C=..., solver=...)
```

3. Train the classifier using the training data `X_train` and `y_train`:

```
logistic_regression.fit(X_train, y_train)
```

4. Make predictions on the test data `X_test` and store the predicted labels in `y_pred`:

```
y_pred = logistic_regression.predict(X_test)
```

[33]:
```
from sklearn.linear_model import LogisticRegression


# Create a Logistic Regression classifier
logistic_regression = LogisticRegression()

# Train the classifier using the training data
logistic_regression.fit(X_train, y_train)

# Make predictions on the test data
y_pred = logistic_regression.predict(X_test)

# Calculate accuracy
accuracy = accuracy_score(y_test, y_pred)
print(f'Accuracy: {accuracy * 100:.2f}%')
```

```
Accuracy: 75.32%
```

- find the optimal hyperparameters for a Logistic Regression classifier using Grid Search

[34]:
```
# Define the parameter grid
param_grid = {
    'C': [0.001, 0.01, 0.1, 1, 10, 100],  # Inverse of regularization strength
    'solver': ['liblinear', 'lbfgs', 'newton-cg', 'sag', 'saga']  # Solver␣
 ↪algorithm
}

# Create a Logistic Regression classifier
logistic_regression = LogisticRegression()

# Create GridSearchCV instance
grid_search_lr = GridSearchCV(logistic_regression, param_grid, cv=5,␣
 ↪scoring='accuracy')

# Perform grid search on the training data
grid_search_lr.fit(X_train, y_train)

# Print the best hyperparameters
```

```
print("Best Hyperparameters:", grid_search_lr.best_params_)

# Make predictions on the test data using the best model
best_model_lr = grid_search_lr.best_estimator_
y_pred = best_model_lr.predict(X_test)

# Calculate accuracy
accuracy = accuracy_score(y_test, y_pred)
print(f'Accuracy with Best Model: {accuracy * 100:.2f}%')
```

```
Best Hyperparameters: {'C': 0.1, 'solver': 'lbfgs'}
Accuracy with Best Model: 75.97%
```

[35]:
```
best_model_lr
```

[35]:
```
LogisticRegression(C=0.1)
```

[ ]:
```

```