ASSIGNMENT : 1

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MovieLens 1M Dataset GroupLens Research provides a number of collections of movie ratings data collected from users of MovieLens in the late 1990s and early 2000s. The data provide movie ratings, movie metadata (genres and year), and demographic data about the users (age, zip code, gender identification, and occupation). Such data is often of interest in the development of recommendation systems based on machine learning algorithms. While we do not explore machine learning techniques in detail in this book, I will show you how to slice and dice datasets like these into the exact form you need. The MovieLens 1M dataset contains 1 million ratings collected from 6,000 users on 4,000 movies. It's spread across three tables: ratings, user information, and movie information. After extracting the data from the ZIP file, we can load each table into a pandas DataFrame object using pandas.read_table and perform the following task.

1. Perform null values identification in the given dataset.

In [16]:
```
import pandas as pd
```

In [3]:
```
df = pd.read_csv('C:/Users/user/OneDrive/Desktop/diabetes.csv')
```

In [4]:
```
df
```

Out[4]:

	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
...	...	...	...	...	...	...	...	...	...
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

768 rows × 9 columns

In [5]:
```
null_values = df.isnull().sum()
print(null_values)
```

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

2. Identify types of attributes in the dataset.

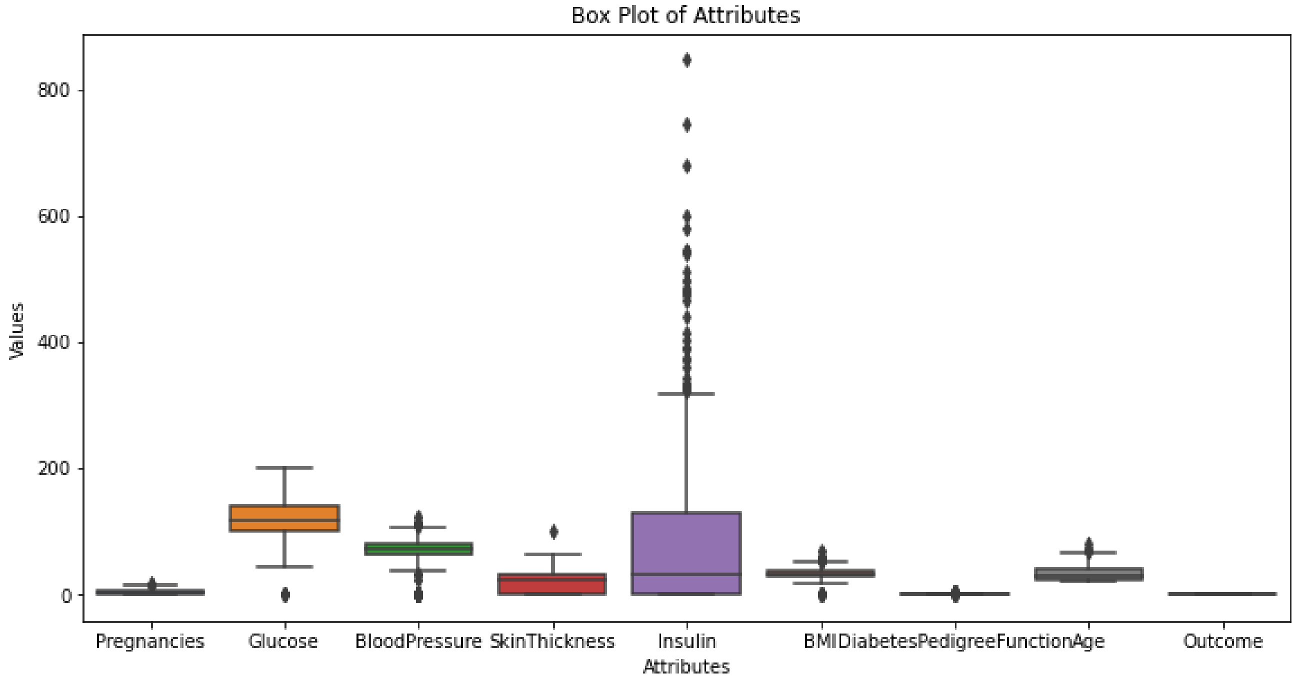
In [6]:
```
attribute_types = df.dtypes
print(attribute_types)
```

```
Pregnancies                   int64
Glucose                       int64
BloodPressure                 int64
SkinThickness                 int64
Insulin                       int64
BMI                         float64
DiabetesPedigreeFunction    float64
Age                           int64
Outcome                       int64
dtype: object
```

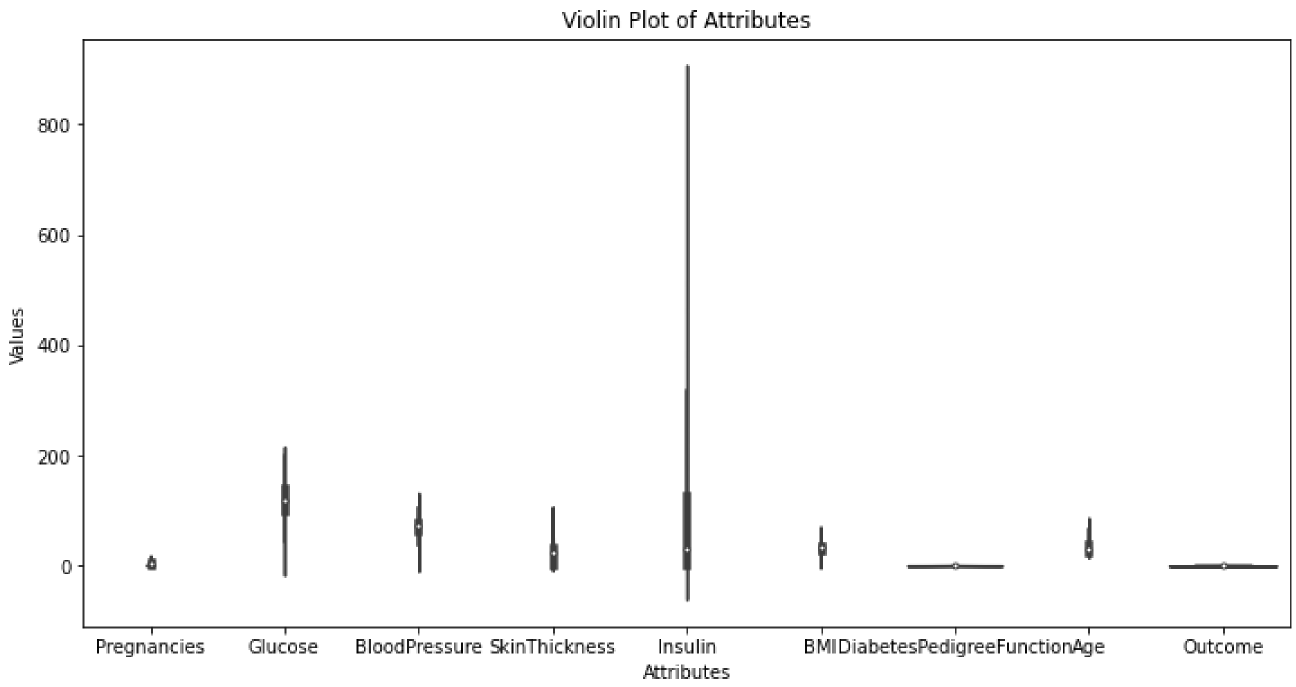
3. Plot Box plot and violin plot. (also state the inference of each attribute and also find the outlier in the attribute)

In [8]:
```
import matplotlib.pyplot as plt
import seaborn as sns

# CREATE BOX PLOTS
plt.figure(figsize=(12, 6))
sns.boxplot(data=df)
plt.title('Box Plot of Attributes')
plt.xlabel('Attributes')
plt.ylabel('Values')
plt.show()
```



In [9]:
```python
# CREATE VIOLIN PLOTS
plt.figure(figsize=(12, 6))
sns.violinplot(data=df)
plt.title('Violin Plot of Attributes')
plt.xlabel('Attributes')
plt.ylabel('Values')
plt.show()
```



In [10]:
```python
# IDENTIFY OUTLIER USING BOX PLOTS
for column in df.columns:
    if df[column].dtype != 'object':  # Exclude non-numeric attributes
        q1 = df[column].quantile(0.25)
        q3 = df[column].quantile(0.75)
        iqr = q3 - q1
        lower_bound = q1 - 1.5 * iqr
        upper_bound = q3 + 1.5 * iqr
        outliers = df[(df[column] < lower_bound) | (df[column] > upper_bound)]
        if outliers.shape[0] > 0:
            print(f"Outliers in attribute '{column}':")
            print(outliers)
```

```
502          6       0            68            41       0  39.0

     DiabetesPedigreeFunction  Age  Outcome
75                      0.140   22        0
182                     0.299   21        0
342                     0.389   22        0
349                     0.346   37        1
502                     0.727   41        1
Outliers in attribute 'BloodPressure':
     Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
7             10      115              0              0        0  35.3
15             7      100              0              0        0  30.0
18             1      103             30             38       83  43.3
43             9      171            110             24      240  45.4
49             7      105              0              0        0   0.0
60             2       84              0              0        0   0.0
78             0      131              0              0        0  43.2
81             2       74              0              0        0   0.0
84             5      137            108              0        0  48.8
106            1       96            122              0        0  22.4
```

In [11]:
```python
# IDENTIFY INFERENCE FOR EACH ATTRIBUTE
for column in df.columns:
    if df[column].dtype == 'object':  # CATEGORICAL ATTRIBUTES
        print(f"Attribute '{column}' is a categorical attribute.")
        print(f"Unique values: {df[column].unique()}")
    else:  # NUMERIC ATTRIBUTES
        print(f"Attribute '{column}' is a numeric attribute.")
        print(f"Summary statistics: {df[column].describe()}")
```

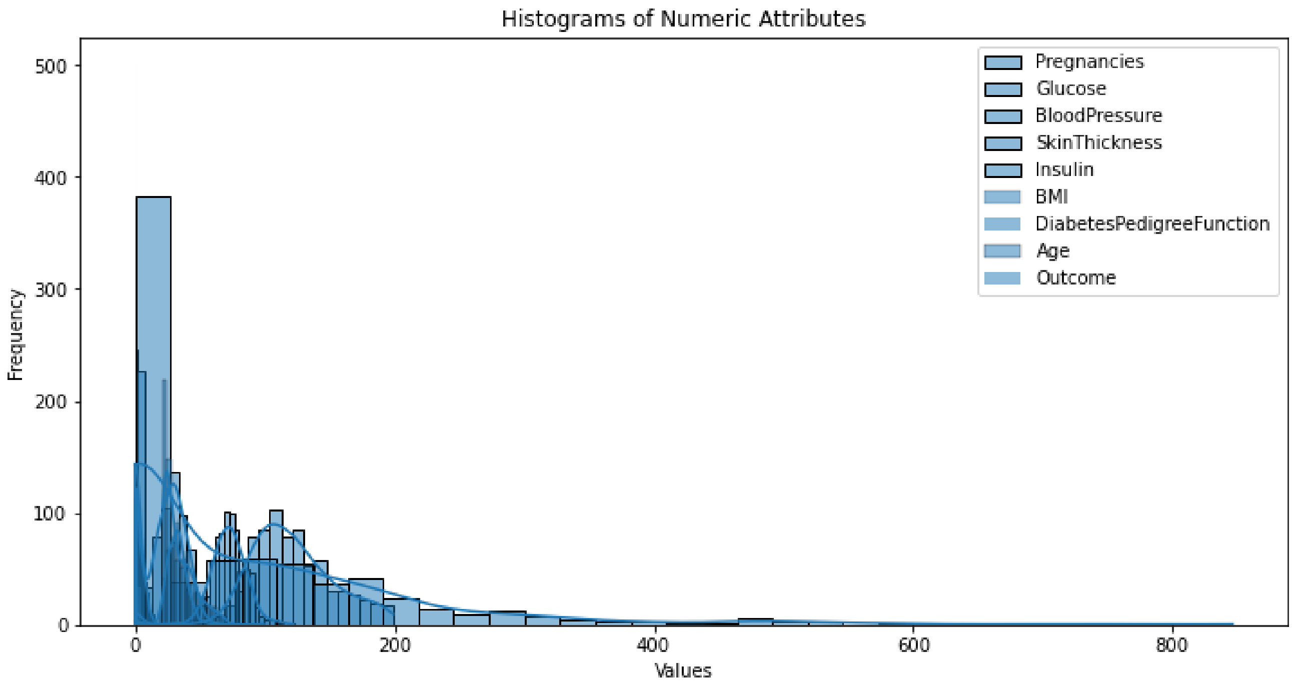
```
Attribute 'Pregnancies' is a numeric attribute.
Summary statistics: count    768.000000
mean       3.845052
std        3.369578
min        0.000000
25%        1.000000
50%        3.000000
75%        6.000000
max       17.000000
Name: Pregnancies, dtype: float64
Attribute 'Glucose' is a numeric attribute.
Summary statistics: count    768.000000
mean     120.894531
std       31.972618
min        0.000000
25%       99.000000
50%      117.000000
75%      140.250000
max      199.000000
Name: Glucose, dtype: float64
Attribute 'BloodPressure' is a numeric attribute.
Summary statistics: count    768.000000
mean      69.105469
std       19.355807
min        0.000000
25%       62.000000
50%       72.000000
75%       80.000000
max      122.000000
Name: BloodPressure, dtype: float64
Attribute 'SkinThickness' is a numeric attribute.
Summary statistics: count    768.000000
mean      20.536458
std       15.952218
min        0.000000
25%        0.000000
50%       23.000000
75%       32.000000
max       99.000000
Name: SkinThickness, dtype: float64
Attribute 'Insulin' is a numeric attribute.
Summary statistics: count    768.000000
mean      79.799479
std      115.244002
min        0.000000
25%        0.000000
50%       30.500000
75%      127.250000
max      846.000000
Name: Insulin, dtype: float64
Attribute 'BMI' is a numeric attribute.
Summary statistics: count    768.000000
mean      31.992578
std        7.884160
min        0.000000
25%       27.300000
50%       32.000000
75%       36.600000
max       67.100000
Name: BMI, dtype: float64
Attribute 'DiabetesPedigreeFunction' is a numeric attribute.
Summary statistics: count    768.000000
mean       0.471876
std        0.331329
min        0.078000
25%        0.243750
50%        0.372500
75%        0.626250
max        2.420000
Name: DiabetesPedigreeFunction, dtype: float64
Attribute 'Age' is a numeric attribute.
Summary statistics: count    768.000000
```

```
mean         33.240885
std          11.760232
min          21.000000
25%          24.000000
50%          29.000000
75%          41.000000
max          81.000000
Name: Age, dtype: float64
Attribute 'Outcome' is a numeric attribute.
Summary statistics: count    768.000000
mean          0.348958
std           0.476951
min           0.000000
25%           0.000000
50%           0.000000
75%           1.000000
max           1.000000
Name: Outcome, dtype: float64
```

4. Histogram and identification of overlapping.(also state the inference for each attribute.)

In [14]:

```
# CREATE HISTOGRAM
plt.figure(figsize=(12, 6))
for column in df.columns:
    if df[column].dtype != 'object':  # Exclude non-numeric attributes
        sns.histplot(df[column], kde=True, label=column)
plt.title('Histograms of Numeric Attributes')
plt.xlabel('Values')
plt.ylabel('Frequency')
plt.legend()
plt.show()
```



In [13]:

```
# IDENTIFY OVERLAPPING
for column1 in df.columns:
    for column2 in df.columns:
        if column1 != column2 and df[column1].dtype != 'object' and df[column2].dtype != 'object'
            overlap = df[(df[column1] > df[column2].min()) & (df[column1] < df[column2].max())]
            if overlap.shape[0] > 0:
                print(f"Overlapping between '{column1}' and '{column2}':")
                print(overlap)
```

```
     DiabetesPedigreeFunction  Age  Outcome
0                       0.627   50        1
1                       0.351   31        0
2                       0.672   32        1
3                       0.167   21        0
5                       0.201   30        0
..                        ...  ...      ...
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

[657 rows x 9 columns]
Overlapping between 'Pregnancies' and 'DiabetesPedigreeFunction':
     Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
1              1       85             66             29        0  26.6
3              1       89             66             23       94  28.1
8              2      197             70             45      543  30.5
```

In [15]:

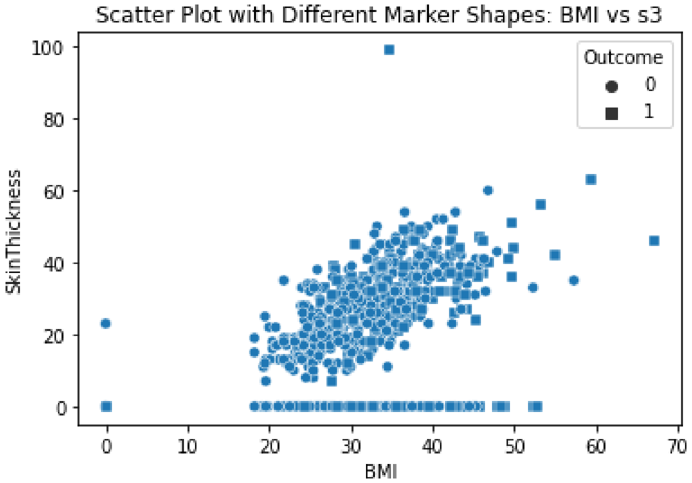
```
# IDENTIFY INFERENCE FOR EACH ATTRIBUTE
for column in df.columns:
    if df[column].dtype == 'object':  # CATEGORICAL ATTRIBUTES
        print(f"Attribute '{column}' is a categorical attribute.")
        print(f"Unique values: {df[column].unique()}")
    else:  # NUMERIC ATTRIBUTES
        print(f"Attribute '{column}' is a numeric attribute.")
        print(f"Summary statistics: {df[column].describe()}")
```

```
Attribute 'Pregnancies' is a numeric attribute.
Summary statistics: count    768.000000
mean       3.845052
std        3.369578
min        0.000000
25%        1.000000
50%        3.000000
75%        6.000000
max       17.000000
Name: Pregnancies, dtype: float64
Attribute 'Glucose' is a numeric attribute.
Summary statistics: count    768.000000
mean     120.894531
std       31.972618
min        0.000000
25%       99.000000
50%      117.000000
75%      140.250000
max      199.000000
Name: Glucose, dtype: float64
Attribute 'BloodPressure' is a numeric attribute.
Summary statistics: count    768.000000
mean      69.105469
std       19.355807
min        0.000000
25%       62.000000
50%       72.000000
75%       80.000000
max      122.000000
Name: BloodPressure, dtype: float64
Attribute 'SkinThickness' is a numeric attribute.
Summary statistics: count    768.000000
mean      20.536458
std       15.952218
min        0.000000
25%        0.000000
50%       23.000000
75%       32.000000
max       99.000000
Name: SkinThickness, dtype: float64
Attribute 'Insulin' is a numeric attribute.
Summary statistics: count    768.000000
mean      79.799479
std      115.244002
min        0.000000
25%        0.000000
50%       30.500000
75%      127.250000
max      846.000000
Name: Insulin, dtype: float64
Attribute 'BMI' is a numeric attribute.
Summary statistics: count    768.000000
mean      31.992578
std        7.884160
min        0.000000
25%       27.300000
50%       32.000000
75%       36.600000
max       67.100000
Name: BMI, dtype: float64
Attribute 'DiabetesPedigreeFunction' is a numeric attribute.
Summary statistics: count    768.000000
mean       0.471876
std        0.331329
min        0.078000
25%        0.243750
50%        0.372500
75%        0.626250
max        2.420000
Name: DiabetesPedigreeFunction, dtype: float64
Attribute 'Age' is a numeric attribute.
Summary statistics: count    768.000000
```

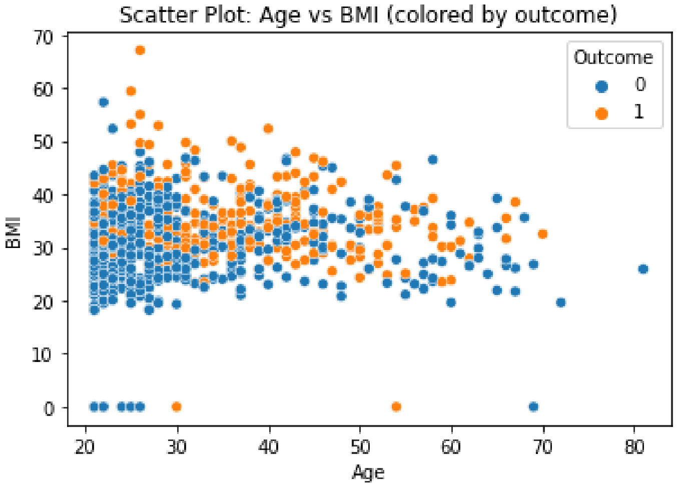
```
mean       33.240885
std        11.760232
min        21.000000
25%        24.000000
50%        29.000000
75%        41.000000
max        81.000000
Name: Age, dtype: float64
Attribute 'Outcome' is a numeric attribute.
Summary statistics: count    768.000000
mean         0.348958
std          0.476951
min          0.000000
25%          0.000000
50%          0.000000
75%          1.000000
max          1.000000
Name: Outcome, dtype: float64
```

5. Draw different types of scatter plot.(using seaborn library)

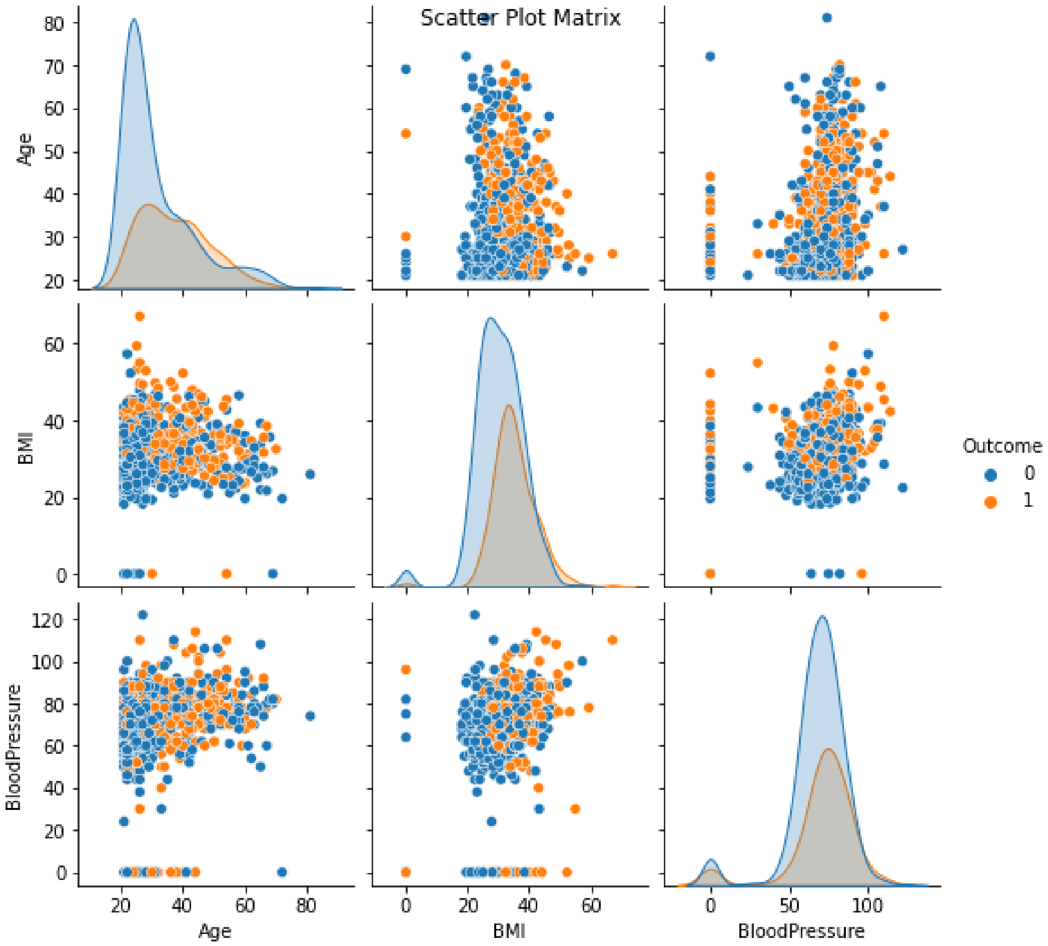
In [29]:
```python
# SCATTER PLOT WITH SINGLE VARIABLES(UNIVARIATE SCATTER PLOT)
sns.scatterplot(x='Age', y='BMI', data=df)
plt.title('Scatter Plot: Age vs BMI')
plt.xlabel('Age')
plt.ylabel('BMI')
plt.show()
```



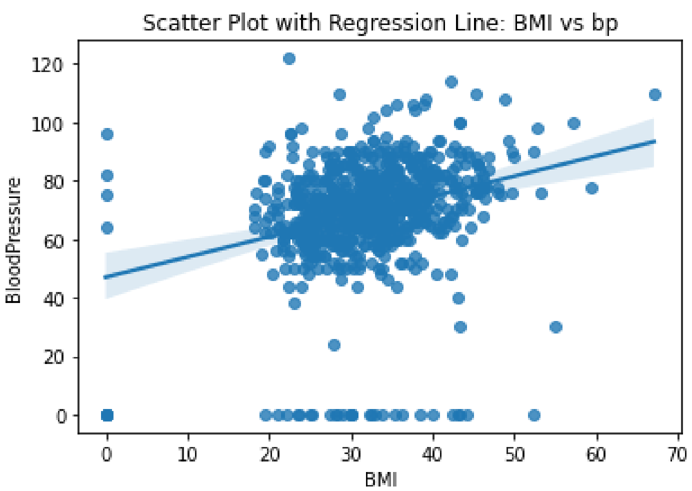
In [30]:
```python
# SCATTER PLOT WITH TWO VARIABLES(BIVARIATE SCATTER PLOT)
sns.scatterplot(x='Age', y='BMI', hue='Outcome', data=df)
plt.title('Scatter Plot: Age vs BMI (colored by outcome)')
plt.xlabel('Age')
plt.ylabel('BMI')
plt.show()
```



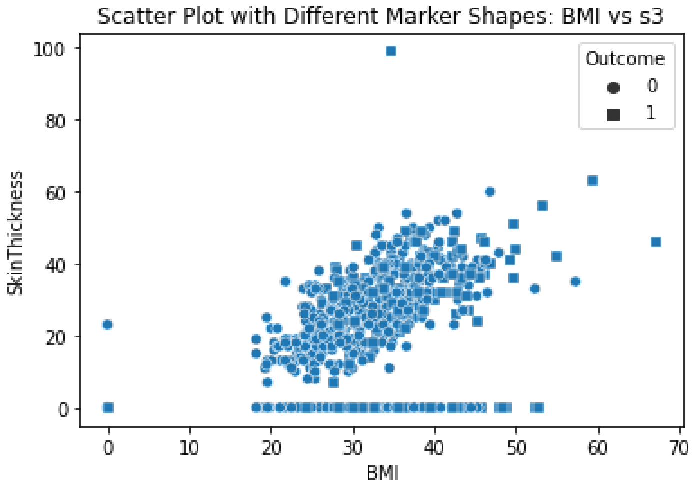
In [31]:
```
# SCATTER PLOT MATRIX(PAIRPLOT)
sns.pairplot(data=df, vars=['Age', 'BMI', 'BloodPressure'], hue='Outcome')
plt.suptitle('Scatter Plot Matrix')
plt.show()
```



In [32]:
```
# SCATTER PLOT WITH REGRESSION LINE(REGRESSION PLOT)
sns.regplot(x='BMI', y='BloodPressure', data=df)
plt.title('Scatter Plot with Regression Line: BMI vs bp')
plt.xlabel('BMI')
plt.ylabel('BloodPressure')
plt.show()
```

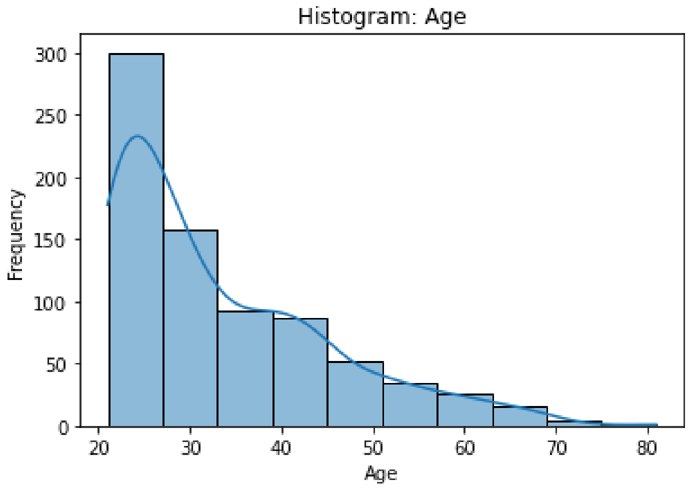


In [33]:
```
# SCATTER PLOT WITH DIFFERENT MARKER SHAPES(SCATTER PLOT WITH MARKER PARAMETER)
sns.scatterplot(x='BMI', y='SkinThickness', data=df, style='Outcome', markers=['o', 's'])
plt.title('Scatter Plot with Different Marker Shapes: BMI vs SkinThickness')
plt.xlabel('BMI')
plt.ylabel('SkinThickness')
plt.show()
```

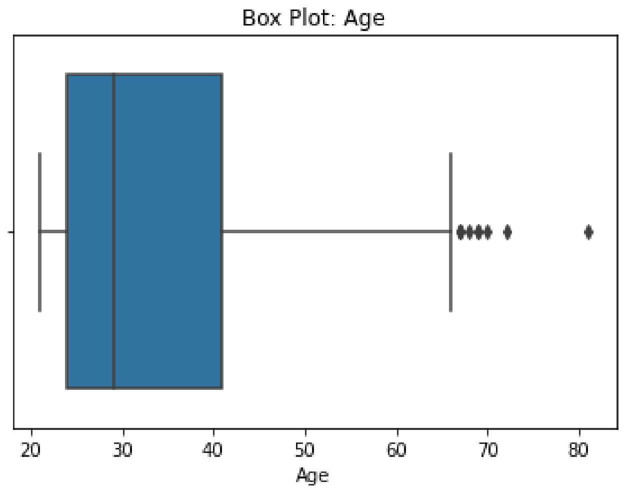


6. Univariate and multivariate analysis.

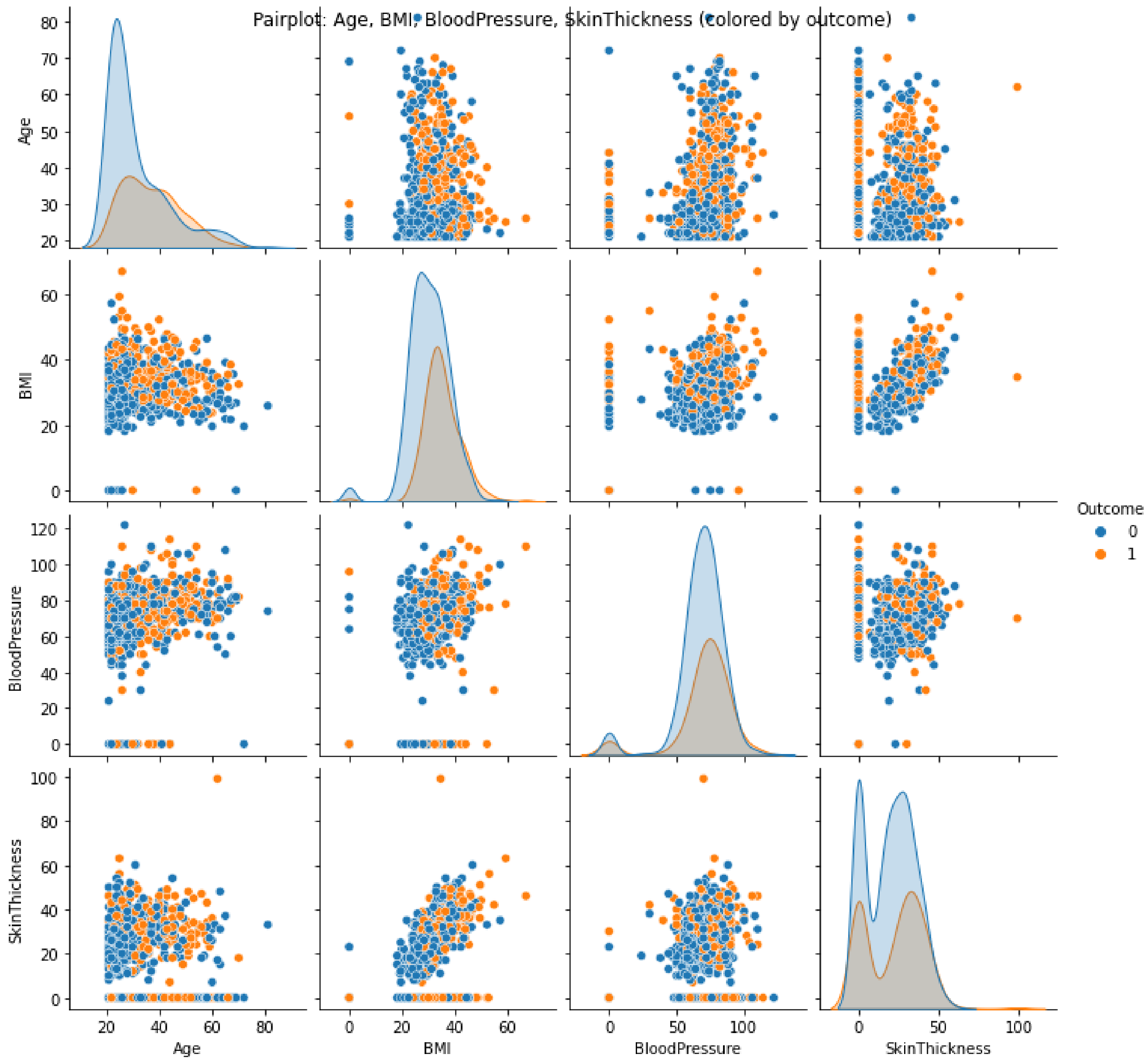
In [41]:
```
# UNIVARIATE ANALYSIS: HISTOGRAM
sns.histplot(df['Age'], bins=10, kde=True)
plt.title('Histogram: Age')
plt.xlabel('Age')
plt.ylabel('Frequency')
plt.show()
```



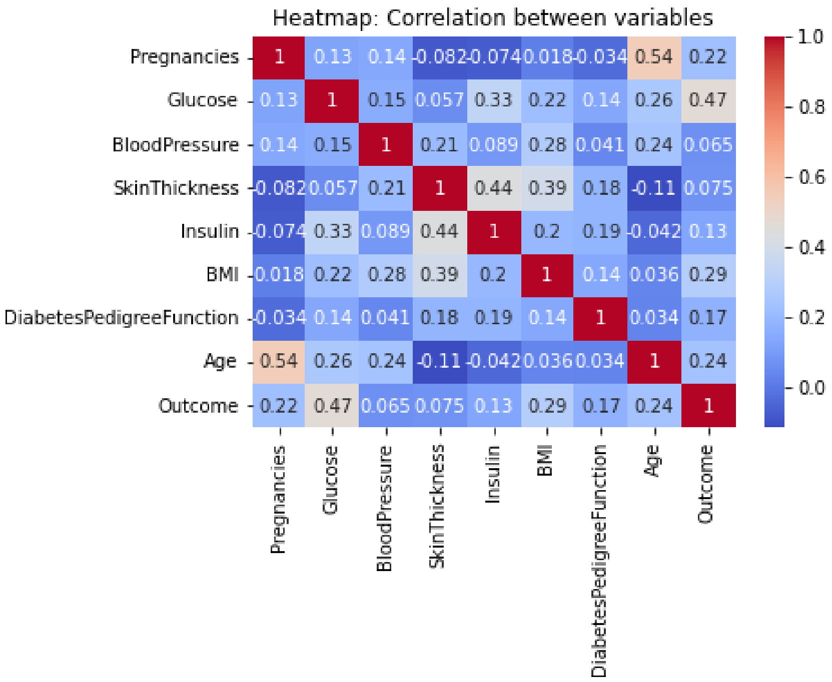
In [40]:
```
# UNIVARIATE ANALYSIS: BOX PLOT
sns.boxplot(x='Age', data=df)
plt.title('Box Plot: Age')
plt.xlabel('Age')
plt.show()
```



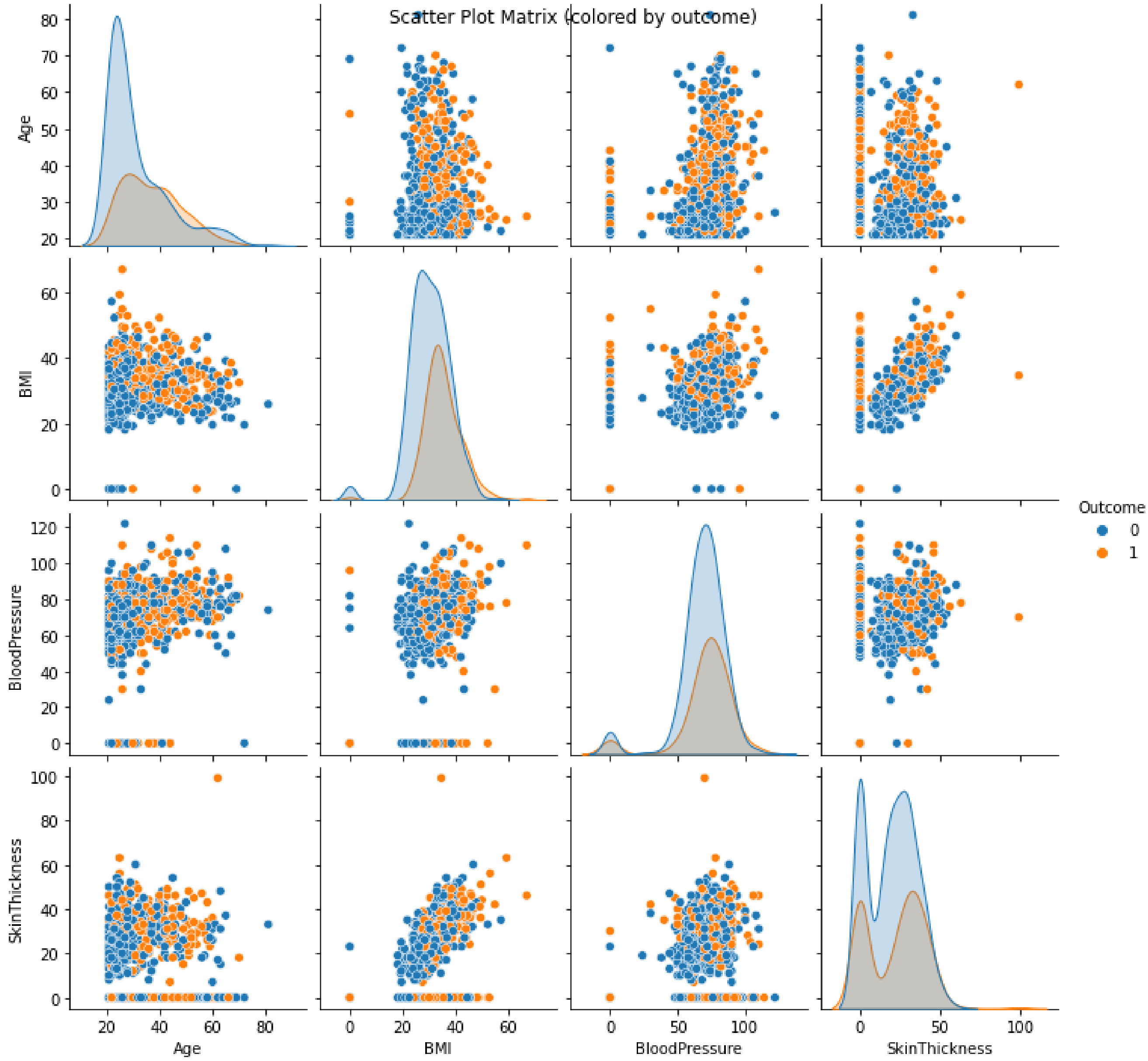
In [42]:
```
# MULTIVARIATE ANALYSIS: PAIRPLOT
sns.pairplot(data=df, hue='Outcome', vars=['Age', 'BMI', 'BloodPressure', 'SkinThickness'])
plt.suptitle('Pairplot: Age, BMI, BloodPressure, SkinThickness (colored by outcome)')
plt.show()
```



In [43]:
```
# MULTIVARIATE ANALYSIS: HEATMAP
corr_matrix = df.corr()
sns.heatmap(corr_matrix, annot=True, cmap='coolwarm')
plt.title('Heatmap: Correlation between variables')
plt.show()
```



In [44]:
```python
# MULTIVARIATE ANALYSIS: SCATTER PLOT MATRIX
sns.pairplot(data=df, vars=['Age', 'BMI', 'BloodPressure', 'SkinThickness'], hue='Outcome')
plt.suptitle('Scatter Plot Matrix (colored by outcome)')
plt.show()
```



2. Diabetics datasets :

Data Exploration: This includes inspecting the data, visualizing the data, and cleaning the data. Some of the steps used are as follows:

1. Viewing the data statistics.

In [52]:
```
# VIEW THE FIRST FEW ROWS OF THE DATA
print("Head of the data:")
print(df.head())
```

```
Head of the data:
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            6      148             72             35        0  33.6
1            1       85             66             29        0  26.6
2            8      183             64              0        0  23.3
3            1       89             66             23       94  28.1
4            0      137             40             35      168  43.1

   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
1                     0.351   31        0
2                     0.672   32        1
3                     0.167   21        0
4                     2.288   33        1
```

In [47]:
```
# VIEW THE DATA STATISTICS
print("Data statistics:")
print(df.describe())
```

```
Data statistics:
       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
```

In [48]:
```
# View the data types of each column
print("Data types:")
print(df.dtypes)
```

```
Data types:
Pregnancies                   int64
Glucose                       int64
BloodPressure                 int64
SkinThickness                 int64
Insulin                       int64
BMI                         float64
DiabetesPedigreeFunction    float64
Age                           int64
Outcome                       int64
dtype: object
```

In [49]:
```
# VIEW THE SHAPE OF THE DATA (NUMBER OF ROWS AND COLUMNS)
print("Data shape:")
print(df.shape)
```

```
Data shape:
(768, 9)
```

In [50]:
```
# VIEW THE COLUMN NAMES
print("Column names:")
print(df.columns)
```

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

In [51]:
```
# VIEW THE NUMBER OF MISSING VALUES IN EACH COLUMN
print("Missing values:")
print(df.isnull().sum())
```

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

2. Finding out the dimensions of the dataset, the variable names, the data types, etc.

In [59]:
```
# VIEW THE SHAPE OF THE DATA (NUMBER OF ROWS AND COLUMNS)
print("Data shape:")
print(df.shape)
```

```
Data shape:
(768, 9)
```

In [57]:
```
# VIEW THE COLUMN NAMES
print("Column names:")
print(df.columns)
```

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

In [58]:
```
# VIEW THE DATA TYPES OF EACH COLUMN
print("Data types:")
print(df.dtypes)
```

```
Data types:
Pregnancies                   int64
Glucose                       int64
BloodPressure                 int64
SkinThickness                 int64
Insulin                       int64
BMI                         float64
DiabetesPedigreeFunction    float64
Age                           int64
Outcome                       int64
dtype: object
```

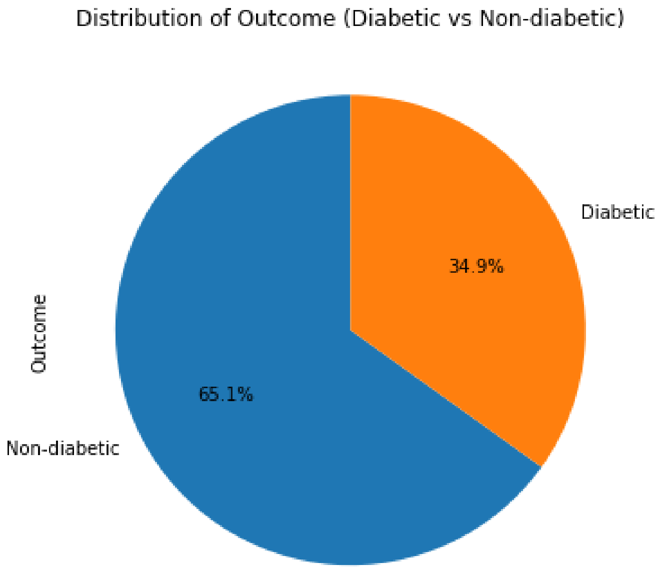
3. Checking for null values.

In [62]:
```
# CHECK FOR MISSING VALUES IN EACH COLUMN
print("Missing values:")
print(df.isnull().sum())
```

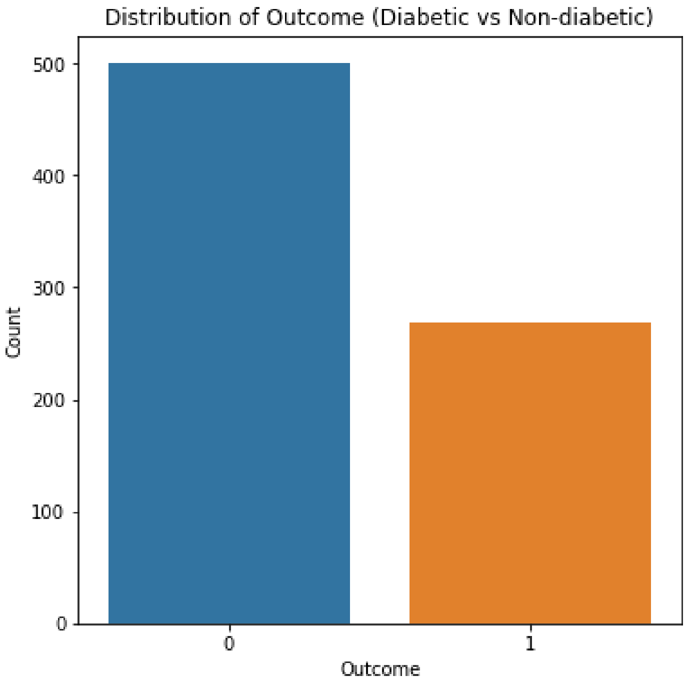
```
Missing values:
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64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

4. Inspecting the target variable using pie plot and count plot.

In [65]:
```
# INSPECT THE TARGET VARIABLE (e.g., 'Outcome') USING A PIE PLOT
plt.figure(figsize=(6, 6))
df['Outcome'].value_counts().plot.pie(labels=['Non-diabetic', 'Diabetic'], autopct='%1.1f%%', sta
plt.title('Distribution of Outcome (Diabetic vs Non-diabetic)')
plt.show()
```



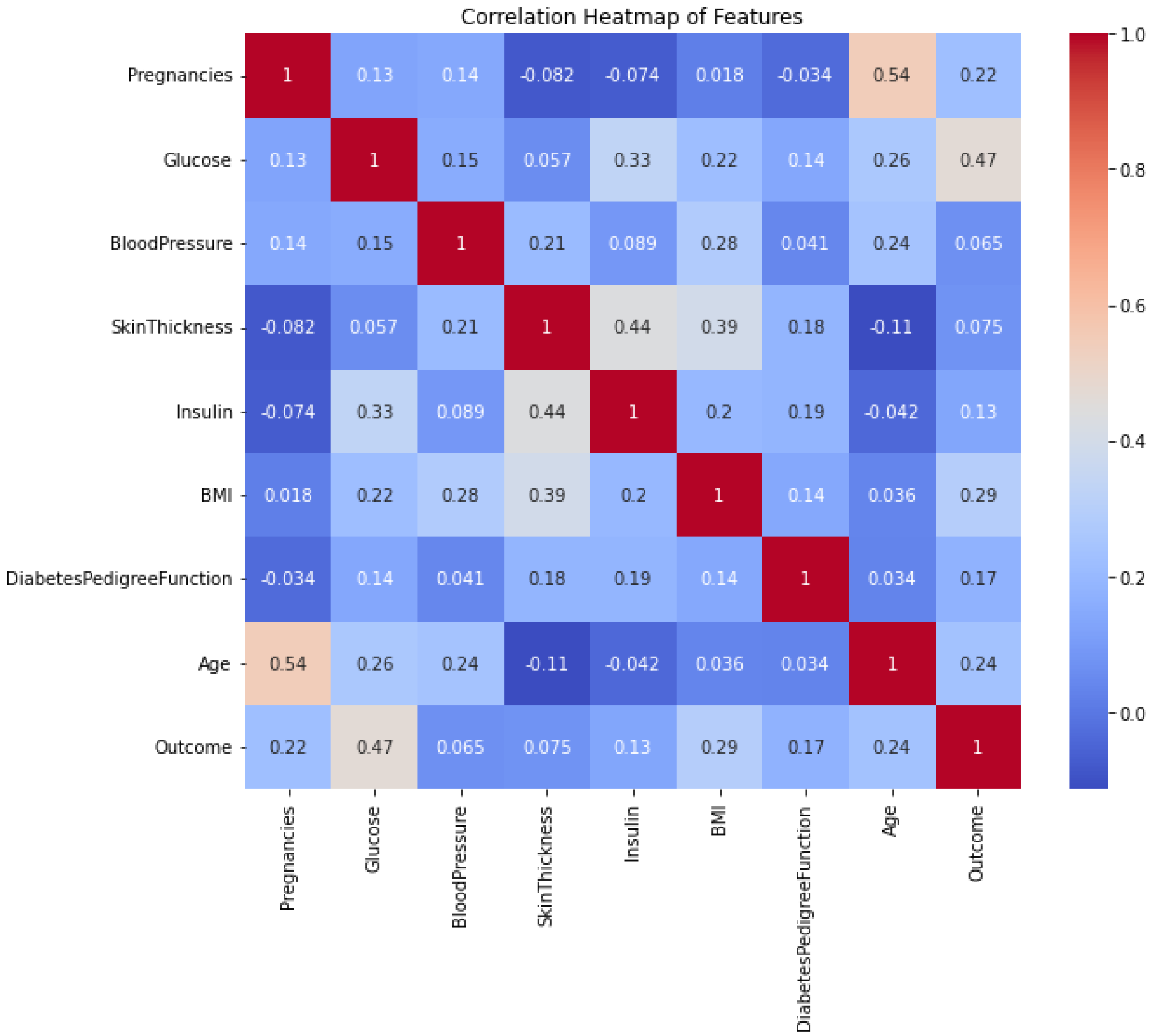
In [66]:
```
# INSPECT THE TARGET VARIABLE USING A COUNT PLOT
plt.figure(figsize=(6, 6))
sns.countplot(x='Outcome', data=df)
plt.xlabel('Outcome')
plt.ylabel('Count')
plt.title('Distribution of Outcome (Diabetic vs Non-diabetic)')
plt.show()
```



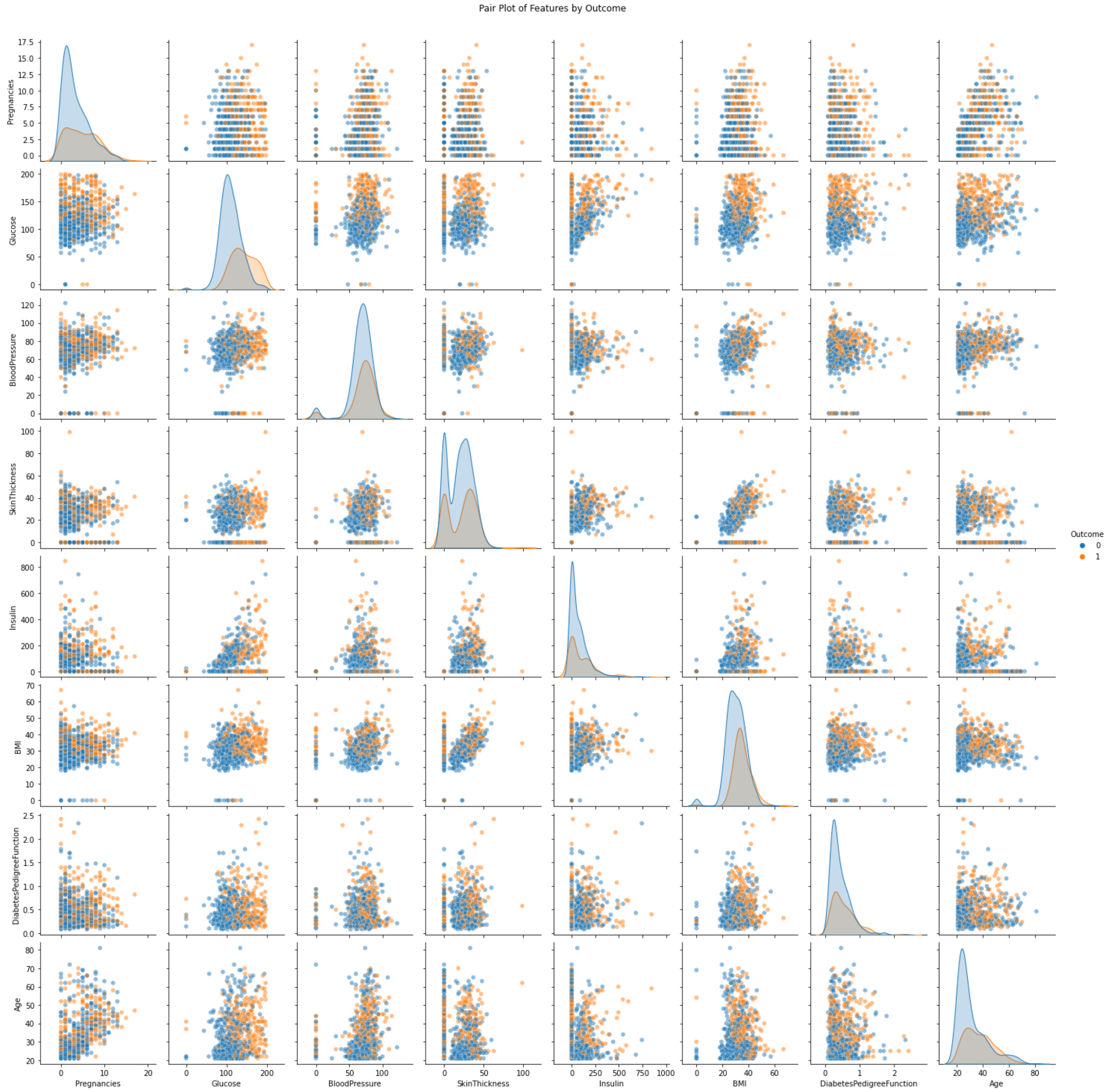
5. Finding out the correlation among different features using heatmap and the bivariate relation between each pair of features using pair plot.

In [70]:
```
# COMPUTE THE CORRELATION MATRIX AMONG FEATURES
corr_matrix = df.corr()

# CREATE A HEATMAP TO VISUALIZE THE CORRELATION MATRIX
plt.figure(figsize=(10, 8))
sns.heatmap(corr_matrix, annot=True, cmap='coolwarm')
plt.title('Correlation Heatmap of Features')
plt.show()
```



In [71]:
```
# CREATE A PAIR PLOT TO VISUALIZE THE BIVARIATE RELATION BETWEEN FEATURES
sns.pairplot(df, diag_kind='kde', hue='Outcome', markers='o', plot_kws={'alpha':0.5})
plt.suptitle('Pair Plot of Features by Outcome', y=1.02)
plt.show()
```



Model Training: 5 Classification Algorithms have been used to find out the best one. These are Logistic Regression, Support Vector Machine, Random Forest, K-Nearest Neighbours, and Naive Bayes.

In each of the algorithms, the steps followed are as follows:

1. Importing the library for the algorithm.

In [77]:
```
# Import libraries for Logistic Regression
from sklearn.linear_model import LogisticRegression
```

In [73]:
```
# Import libraries for Support Vector Machine
from sklearn.svm import SVC
```

In [74]:
```
# Import libraries for Random Forest
from sklearn.ensemble import RandomForestClassifier
```

In [75]:
```
# Import libraries for K-Nearest Neighbors
from sklearn.neighbors import KNeighborsClassifier
```

In [76]:
```
# Import libraries for Naive Bayes
from sklearn.naive_bayes import GaussianNB
```

2. Creating an instance of the Classifier (with default values of parameters or by specifying certain values in certain cases).

In [83]:
```
# Create an instance of Logistic Regression with default parameters
logistic_regression = LogisticRegression()
```

In [79]:
```
# Create an instance of Support Vector Machine with specified parameters
svm = SVC(kernel='linear', C=1.0)
```

In [80]:
```
# Create an instance of Random Forest with default parameters
random_forest = RandomForestClassifier()
```

In [81]:
```
# Create an instance of K-Nearest Neighbors with specified parameters
knn = KNeighborsClassifier(n_neighbors=5)
```

In [82]:
```
# Create an instance of Naive Bayes with default parameters
naive_bayes = GaussianNB()
```

3. Training the model on the train set.

In [96]:
```
X = df.drop('Outcome', axis=1)  # Drop the 'Outcome' column as features (X)
y = df['Outcome']

# Split the dataset into training and testing sets
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Create instances of classifiers with default parameter values
logreg = LogisticRegression()
svm = SVC()
rf = RandomForestClassifier()
knn = KNeighborsClassifier()
nb = GaussianNB()

# Train the classifiers on the training set
logreg.fit(X_train, y_train)
svm.fit(X_train, y_train)
rf.fit(X_train, y_train)
knn.fit(X_train, y_train)
nb.fit(X_train, y_train)
```

```
C:\Users\user\anaconda\lib\site-packages\sklearn\linear_model\_logistic.py:814: ConvergenceWarn
ing: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html (https://scikit-learn.org/stabl
e/modules/preprocessing.html)
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression (https://scik
it-learn.org/stable/modules/linear_model.html#logistic-regression)
  n_iter_i = _check_optimize_result(
```

Out[96]:
```
GaussianNB()
```

4. Prediction on the test set using the trained model.

In [95]:
```python
# Import necessary libraries
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score
# Assuming the classifiers (logreg, svm, rf, knn, nb) are already trained on the training set
# Make predictions on the test set
y_pred_logreg = logreg.predict(X_test)
y_pred_svm = svm.predict(X_test)
y_pred_rf = rf.predict(X_test)
y_pred_knn = knn.predict(X_test)
y_pred_nb = nb.predict(X_test)

# Evaluate the performance of the classifiers
print('Logistic Regression Accuracy:', accuracy_score(y_test, y_pred_logreg))
print('Support Vector Machine Accuracy:', accuracy_score(y_test, y_pred_svm))
print('Random Forest Accuracy:', accuracy_score(y_test, y_pred_rf))
print('K-Nearest Neighbors Accuracy:', accuracy_score(y_test, y_pred_knn))
print('Naive Bayes Accuracy:', accuracy_score(y_test, y_pred_nb))
print('---')
print('Logistic Regression Precision:', precision_score(y_test, y_pred_logreg))
print('Support Vector Machine Precision:', precision_score(y_test, y_pred_svm))
print('Random Forest Precision:', precision_score(y_test, y_pred_rf))
print('K-Nearest Neighbors Precision:', precision_score(y_test, y_pred_knn))
print('Naive Bayes Precision:', precision_score(y_test, y_pred_nb))
print('---')
print('Logistic Regression Recall:', recall_score(y_test, y_pred_logreg))
print('Support Vector Machine Recall:', recall_score(y_test, y_pred_svm))
print('Random Forest Recall:', recall_score(y_test, y_pred_rf))
print('K-Nearest Neighbors Recall:', recall_score(y_test, y_pred_knn))
print('Naive Bayes Recall:', recall_score(y_test, y_pred_nb))
print('---')
print('Logistic Regression F1 Score:', f1_score(y_test, y_pred_logreg))
print('Support Vector Machine F1 Score:', f1_score(y_test, y_pred_svm))
print('Random Forest F1 Score:', f1_score(y_test, y_pred_rf))
print('K-Nearest Neighbors F1 Score:', f1_score(y_test, y_pred_knn))
print('Naive Bayes F1 Score:', f1_score(y_test, y_pred_nb))
```

```
Logistic Regression Accuracy: 0.7532467532467533
Support Vector Machine Accuracy: 0.7662337662337663
Random Forest Accuracy: 0.7337662337662337
K-Nearest Neighbors Accuracy: 0.6623376623376623
Naive Bayes Accuracy: 0.7662337662337663
---
Logistic Regression Precision: 0.6491228070175439
Support Vector Machine Precision: 0.7209302325581395
Random Forest Precision: 0.625
K-Nearest Neighbors Precision: 0.5245901639344263
Naive Bayes Precision: 0.6610169491525424
---
Logistic Regression Recall: 0.6727272727272727
Support Vector Machine Recall: 0.5636363636363636
Random Forest Recall: 0.6363636363636364
K-Nearest Neighbors Recall: 0.5818181818181818
Naive Bayes Recall: 0.7090909090909091
---
Logistic Regression F1 Score: 0.6607142857142858
Support Vector Machine F1 Score: 0.6326530612244898
Random Forest F1 Score: 0.6306306306306306
K-Nearest Neighbors F1 Score: 0.5517241379310346
Naive Bayes F1 Score: 0.6842105263157895
```

5. Calculating the accuracy of the prediction.

In [97]:
```
from sklearn.metrics import accuracy_score

# Assuming the classifiers (logreg, svm, rf, knn, nb) are already trained on the training set
# Assuming the predictions (y_pred_logreg, y_pred_svm, y_pred_rf, y_pred_knn, y_pred_nb) are alre

# Calculate accuracy for each classifier
accuracy_logreg = accuracy_score(y_test, y_pred_logreg)
accuracy_svm = accuracy_score(y_test, y_pred_svm)
accuracy_rf = accuracy_score(y_test, y_pred_rf)
accuracy_knn = accuracy_score(y_test, y_pred_knn)
accuracy_nb = accuracy_score(y_test, y_pred_nb)

# Print accuracy for each classifier
print('Logistic Regression Accuracy:', accuracy_logreg)
print('Support Vector Machine Accuracy:', accuracy_svm)
print('Random Forest Accuracy:', accuracy_rf)
print('K-Nearest Neighbors Accuracy:', accuracy_knn)
print('Naive Bayes Accuracy:', accuracy_nb)
```

```
Logistic Regression Accuracy: 0.7532467532467533
Support Vector Machine Accuracy: 0.7662337662337663
Random Forest Accuracy: 0.7337662337662337
K-Nearest Neighbors Accuracy: 0.6623376623376623
Naive Bayes Accuracy: 0.7662337662337663
```