UO Predictive Analytics

Practical Activity: Data Manipulation and Feature Selection

This notebook is an excercise for performing data preprocessing and manipulation, including the following tasks:

- Handling missing values
- Performing feature selection and feature filtering

We apply the concepts discussed in Data Exploration and Data Preprocessing

We will use the following python libraries for this practical.

- numpy: https://numpy.org/
- Pandas: https://pandas.pydata.org/
- scikit-learn: https://scikit-learn.org/stable/

Diabetes Dataset

Our aim is to build a classification model to predict diabetes. We will be using the diabetes dataset which contains 768 observations and 9 variables, as below:

- **Pregnancies:** Number of times pregnant.
- **Glucose Plasma:** glucose concentration a 2 hours in an oral glucose tolerance test].
- **BloodPressure:** Diastolic blood pressure (mm Hg).
- **SkinThickness:** Triceps Skinfold thickness (mm).
- **Insulin:** 2-Hour serum insulin (mu U/ml).
- **BMI:** Body mass index (weight in kg/(height in m)^2).
- **DiabetesPedigreeFunction:** Diabetes pedigree function.
- **Age:** Age in years.
- **Outcome:** “1” represents the presence of diabetes while “0” represents the absence of it.

The dataset was downloaded from https://www.kaggle.com/uciml/pima-indians-diabetes-database

Task 1. Handling missing values

Missing values are one of the main obstacles in building predictive models. It is important to explore various approaches to imputing missing values and understand the reasons for selecting a specific method. By doing so, you can ensure your data is as complete and accurate as possible before training and evaluating your predictive models.

Step 1 - Loading the required libraries and modules.

In [7]:
```
#import the required libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.impute import SimpleImputer
```

In [8]:
```
from sklearn.experimental import enable_iterative_imputer
from sklearn.impute import IterativeImputer
from sklearn.feature_selection import SelectKBest
from sklearn.feature_selection import mutual_info_classif
#function that renders the figure in a notebook
%matplotlib inline
```

In [9]:
```
# Load the dataset
df = pd.read_csv('diabetes.csv')
```

Step 2 - Describing and Summarising the dataset

In [11]:
```
# return the number of rows and columns in the dataframe
df.shape
```

Out[11]: (768, 9)

In [12]:
```
# return the first 5 rows in the dataset
df.head()
```

Out[12]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Ag
0	6	148	72	35	0	33.6	0.627	5
1	1	85	66	29	0	26.6	0.351	3
2	8	183	64	0	0	23.3	0.672	3
3	1	89	66	23	94	28.1	0.167	2
4	0	137	40	35	168	43.1	2.288	3

In [13]:
```
# return a concise summary of the dataset
df.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
```

In [14]:
```
# return a descriptive statistics of the dataset
df.describe()
```

Out[14]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedi
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	

Step 3 - Handling missing values

In this step, we explore three common techniques for dealing with missing values in datasets. Proper handling of missing data is essential to ensure the reliability and accuracy of models.

1. Removing Rows with Missing Values

- This method involves deleting rows that contain missing values.
- It is simple but can lead to loss of valuable data, especially if missing values are widespread.

2. Imputing Missing Values with a Summary Statistic (Mean, Median, or Mode)
Instead of removing missing values, they can be replaced with a representative value:

- **Mean**: Suitable for normally distributed data.
- **Median**: More robust for skewed data or when outliers are present.
- **Mode**: Works well for categorical data by filling in the most frequent value.

3. Imputing Missing Values Using an Estimator

- A more advanced method where a predictive model (e.g., regression, k-NN, or decision trees) is used to estimate and fill missing values based on existing data patterns.

Based on the descriptive analysis, it is evident that the following columns may **have invalid zero values**, which should be treated as missing data:

- **Glucose**: Plasma glucose concentration
- **BloodPressure**: Diastolic blood pressure
- **SkinThickness**: Triceps skinfold thickness
- **Insulin**: 2-hour serum insulin
- **BMI**: Body mass index

These zero values are likely invalid and should be addressed using one of the methods above to improve the quality of the dataset.

In [17]:

```
# Columns where zeros should be replaced with NaN
columns_to_replace = ["Glucose", "BloodPressure", "SkinThickness", "Insulin", "BMI"]

# Replace zeros with NaN in the specified columns
df[columns_to_replace] = df[columns_to_replace].replace(0, np.nan)
```

In [18]:
```
print("\nDataFrame after replacing zeros with NaN:")
print(df)
```

```
DataFrame after replacing zeros with NaN:
     Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0              6    148.0           72.0           35.0      NaN  33.6
1              1     85.0           66.0           29.0      NaN  26.6
2              8    183.0           64.0            NaN      NaN  23.3
3              1     89.0           66.0           23.0     94.0  28.1
4              0    137.0           40.0           35.0    168.0  43.1
..           ...      ...            ...            ...      ...   ...
763           10    101.0           76.0           48.0    180.0  32.9
764            2    122.0           70.0           27.0      NaN  36.8
765            5    121.0           72.0           23.0    112.0  26.2
766            1    126.0           60.0            NaN      NaN  30.1
767            1     93.0           70.0           31.0      NaN  30.4

     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
..                        ...  ...      ...
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

[768 rows x 9 columns]
```

Approach 1: Removing rows with missing values

In [20]:
```
# make a copy of the dataset
df_dropna = df.copy()
```

In [21]:
```
# drop rows with missing values
df_dropna.dropna(inplace=True)
```

In [22]:
```
#how many data are left
df_dropna.shape
```

Out[22]: (392, 9)

In [23]:
```
df_dropna.describe()
```

Out[23]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedi
count	392.000000	392.000000	392.000000	392.000000	392.000000	392.000000	
mean	3.301020	122.627551	70.663265	29.145408	156.056122	33.086224	
std	3.211424	30.860781	12.496092	10.516424	118.841690	7.027659	
min	0.000000	56.000000	24.000000	7.000000	14.000000	18.200000	
25%	1.000000	99.000000	62.000000	21.000000	76.750000	28.400000	
50%	2.000000	119.000000	70.000000	29.000000	125.500000	33.200000	
75%	5.000000	143.000000	78.000000	37.000000	190.000000	37.100000	
max	17.000000	198.000000	110.000000	63.000000	846.000000	67.100000	

In [24]:
```
# check if there are still missing values in the dataset
df_dropna.isnull().sum()
```

Out[24]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

Approach 2: Imputing missing values with the mean

We can impute missing values with the mean using two different approaches. One way is to use **Pandas** `fillna()` function.

In [27]:
```
# make two copies of the dataset
df_mean_a1 = df.copy()
df_mean_a2 = df.copy()
```

In [28]:
```
## fill missing values with mean column values
df_mean_a1.fillna(df_mean_a1.mean(), inplace=True)
```

In [29]:
```
df_mean_a1.describe()
```

Out[29]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedi
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	
mean	3.845052	121.686763	72.405184	29.153420	155.548223	32.457464	
std	3.369578	30.435949	12.096346	8.790942	85.021108	6.875151	
min	0.000000	44.000000	24.000000	7.000000	14.000000	18.200000	
25%	1.000000	99.750000	64.000000	25.000000	121.500000	27.500000	
50%	3.000000	117.000000	72.202592	29.153420	155.548223	32.400000	
75%	6.000000	140.250000	80.000000	32.000000	155.548223	36.600000	
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	

In [30]:
```
# check if there are still missing values in the dataset
df_mean_a1.isnull().sum()
```

Out[30]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

One other way is to use scikit-learn `SimpleImputer` object. The `SimpleImputer` class provides straightforward strategies for handling missing values in a dataset. Missing values can be replaced with a specified constant or with a statistical measure such as the **mean**, **median**, or **most frequent** value from each column containing missing data. For comparison purposes, we use the **mean** in this example.

Keep in mind that `SimpleImputer` class supports different encodings for missing values, making it flexible for various datasets and data cleaning scenarios.

In [32]:
```
# retrieve the numpy array as the SimpleImputer object operates
# directly on the numpy array instead of pandas dataframe
values_mean = df_mean_a2.values
# initialise the simple imputer and specify the replacing value
# as the column mean
imputer = SimpleImputer(missing_values=np.nan, strategy='mean')
# transform the dataset
transformed_mean = imputer.fit_transform(values_mean)
```

In [33]:
```
# count the number of nan values using np.isnan in each column
print('Missing: %d' % np.isnan(transformed_mean.sum()))
```

```
Missing: 0
```

In [34]:
```
transformed_mean
```

Out[34]:
```
array([[  6.   , 148.   ,  72.   , ...,   0.627,  50.   ,   1.   ],
       [  1.   ,  85.   ,  66.   , ...,   0.351,  31.   ,   0.   ],
       [  8.   , 183.   ,  64.   , ...,   0.672,  32.   ,   1.   ],
       ...,
       [  5.   , 121.   ,  72.   , ...,   0.245,  30.   ,   0.   ],
       [  1.   , 126.   ,  60.   , ...,   0.349,  47.   ,   1.   ],
       [  1.   ,  93.   ,  70.   , ...,   0.315,  23.   ,   0.   ]])
```

In [35]:
```
transformed_mean.mean(axis=0)
```

Out[35]:
```
array([  3.84505208, 121.68676278,  72.40518417,  29.15341959,
       155.54822335,  32.45746367,   0.4718763 ,  33.24088542,
         0.34895833])
```

If you're curious to learn more about how to handle missing data effectively, check out this additional resource:

👉 **Statistical Imputation for Missing Values in Machine Learning**

Approach 3: Imputing missing values using an estimator

In [38]:
```
# we make another copy of the dataset for the sake of comparison
df_estimator = df.copy()
```

In [39]:
```
# Impute missing values in df_estimator using IterativeImputer with 50 iterations
values_estimator = df_estimator.values
imputer_iterative = IterativeImputer(max_iter=50, random_state=1)
transformed_estimator = imputer.fit_transform(values_estimator)
```

In [40]:
```
# count the number of nan values using np.isnan in each column
print('Missing: %d' % np.isnan(transformed_estimator.sum()))
```

```
Missing: 0
```

In [41]:
```
transformed_estimator
```

Out[41]:
```
array([[  6.   , 148.   ,  72.   , ...,   0.627,  50.   ,   1.   ],
       [  1.   ,  85.   ,  66.   , ...,   0.351,  31.   ,   0.   ],
       [  8.   , 183.   ,  64.   , ...,   0.672,  32.   ,   1.   ],
       ...,
       [  5.   , 121.   ,  72.   , ...,   0.245,  30.   ,   0.   ],
       [  1.   , 126.   ,  60.   , ...,   0.349,  47.   ,   1.   ],
       [  1.   ,  93.   ,  70.   , ...,   0.315,  23.   ,   0.   ]])
```

In [42]:
```
transformed_estimator.mean(axis=0)
```

Out[42]:
```
array([  3.84505208, 121.68676278,  72.40518417,  29.15341959,
       155.54822335,  32.45746367,   0.4718763 ,  33.24088542,
         0.34895833])
```

To explore more about imputation methods in scikit-learn, check out this official documentation:

👉 **Imputation of Missing Values**

It provides a comprehensive guide on different imputation strategies and how to apply them in your machine learning workflows!

Task 2: Performing feature selection and feature filtering

When working with datasets, you'll often encounter a large number of features (or dimensions). Selecting only the most relevant ones is crucial for improving model performance. This process, known as **feature selection**, helps remove redundant or irrelevant features, making the model easier to interpret, speeding up the learning process, and often boosting predictive accuracy.

There are several common approaches to feature selection:

- **Brute-force approach** – Tries all possible feature subsets to determine the best combination.
- **Embedded methods** – Feature selection happens naturally as part of the learning algorithm.
- **Filter methods** – Features are ranked based on statistical scores before training the model.
- **Wrapper methods** – The model itself is used to evaluate and select the best subset of features.

For this task, we'll focus on **filter methods**, which rank features based on importance scores. Specifically, we'll use scikit-learn's `mutual_info_classif` and `SelectKBest` to select the most relevant features.

📌 **Learn more about these methods here:**

- mutual_info_classif
- SelectKBest

Step 1 - Visualsing the dataset

In [47]:
```
# return counts of the unique values in each column
df.value_counts()
```

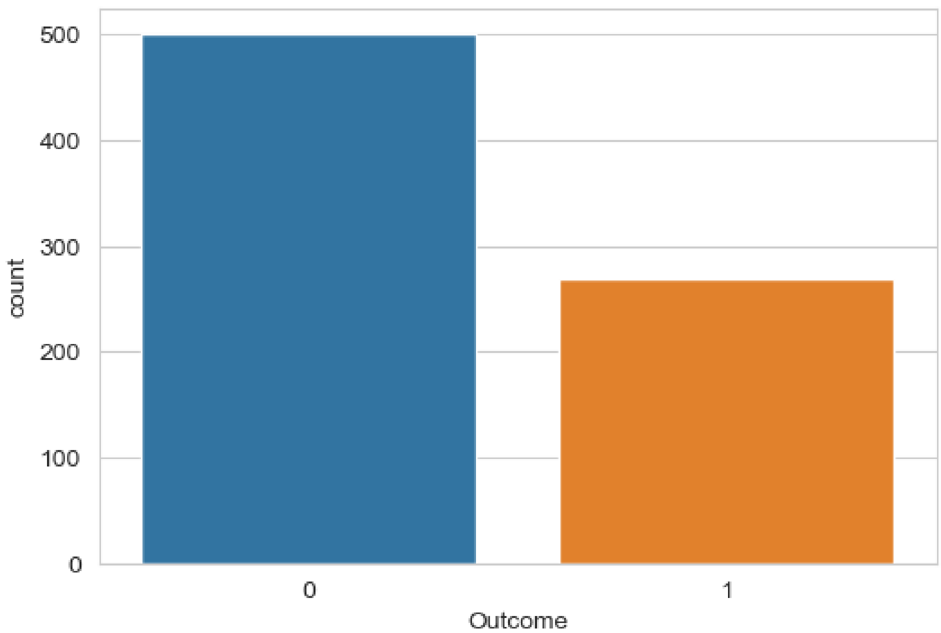
Out[47]:

```
Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin  BMI   DiabetesPedigreeFunctio
n  Age  Outcome
0            74.0     52.0           10.0           36.0     27.8  0.269
22   0        1
4            117.0    64.0           27.0           120.0    33.2  0.230
24   0        1
             111.0    72.0           47.0           207.0    37.1  1.390
56   1        1
             110.0    76.0           20.0           100.0    28.4  0.118
27   0        1
             109.0    64.0           44.0           99.0     34.8  0.905
26   1        1

..
1            131.0    64.0           14.0           415.0    23.7  0.389
21   0        1
             130.0    70.0           13.0           105.0    25.9  0.472
22   0        1
                      60.0           23.0           170.0    28.6  0.692
21   0        1
             128.0    98.0           41.0           58.0     32.0  1.321
33   1        1
17           163.0    72.0           41.0           114.0    40.9  0.817
47   1        1
Name: count, Length: 392, dtype: int64
```

> **Try it yourself: Why the above value_counts() function returns only 392 records?**

In [97]:

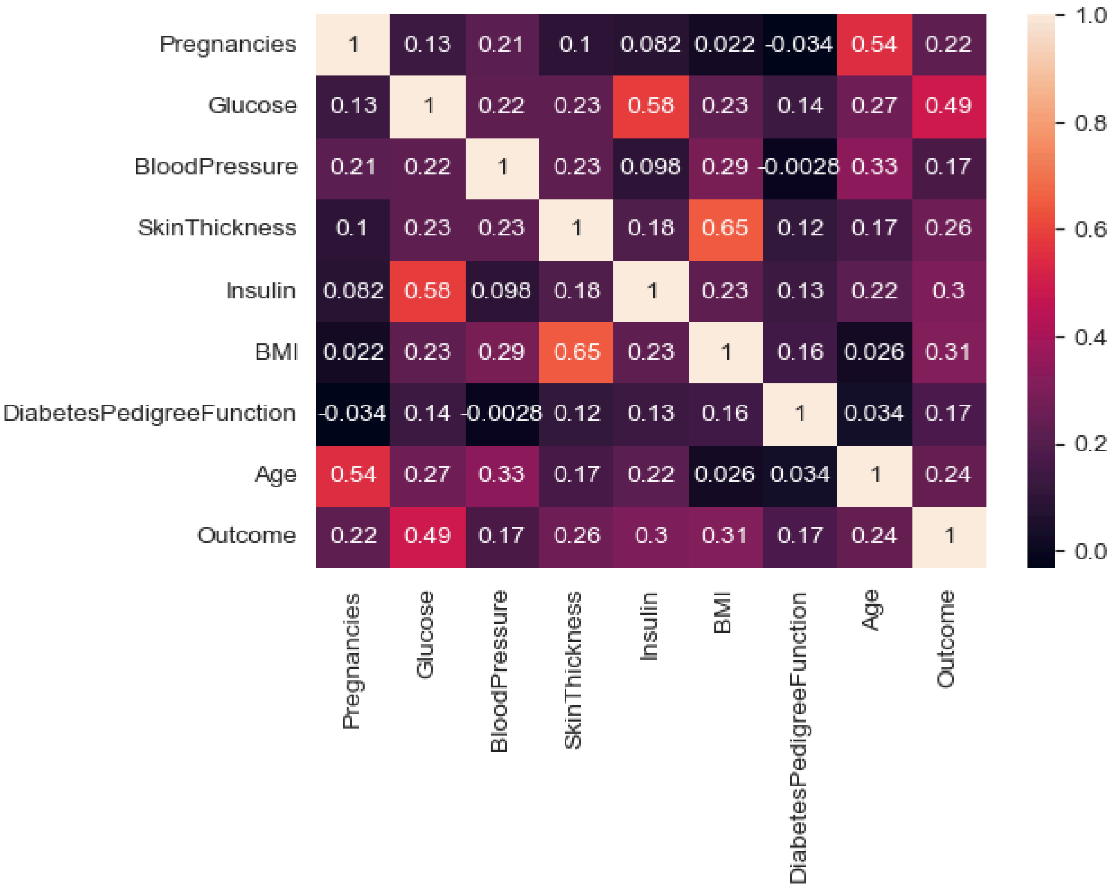
```python
# distribution of the target variable
sns.set_style('whitegrid')
plt.figure(figsize=(6, 4))
sns.countplot(x="Outcome", data=df);
```



In [99]:

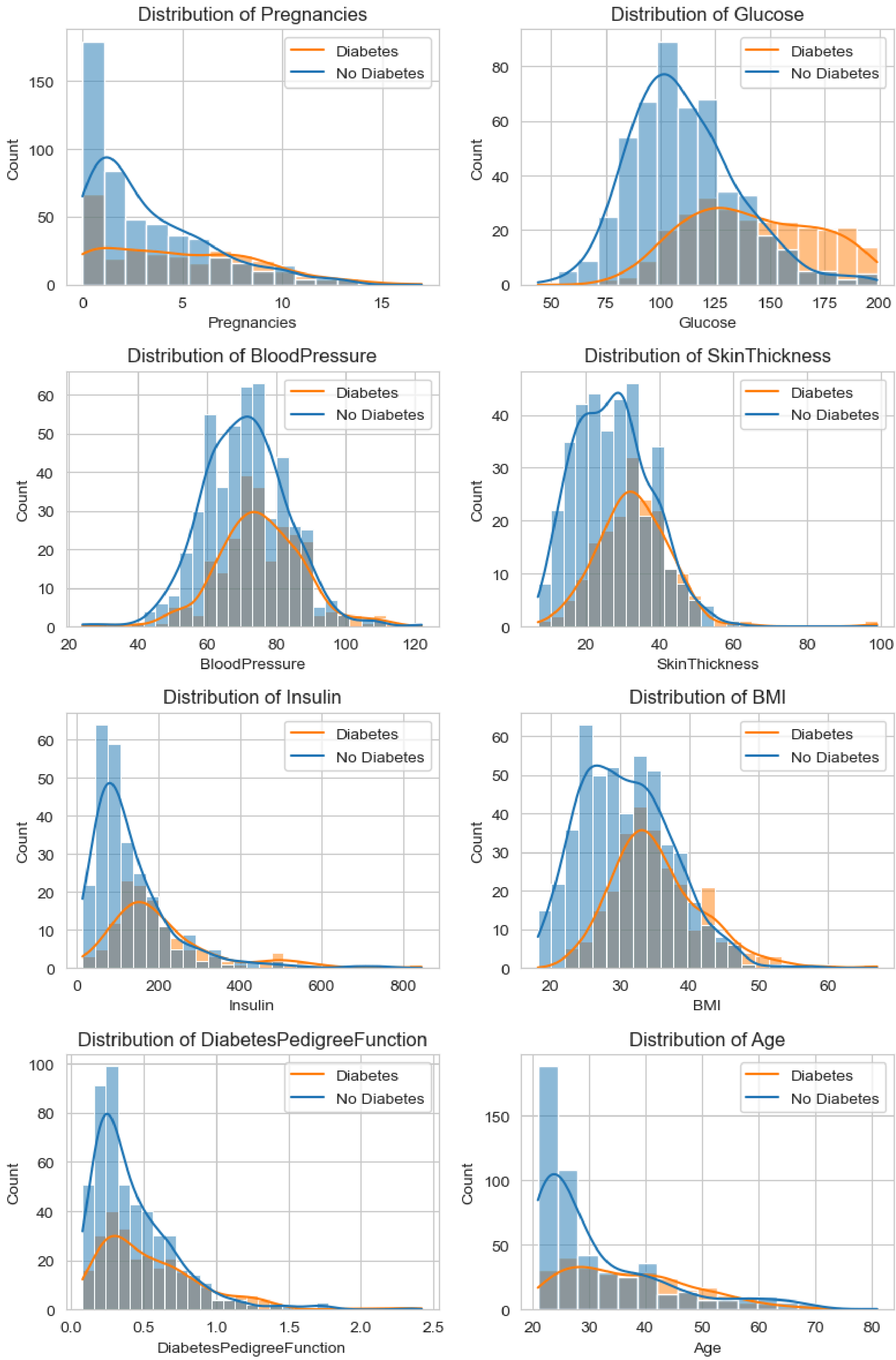
```python
# correlation among variables
plt.figure(figsize = (6,4))
sns.heatmap(df.corr(), annot =True)
```

Out[99]: <Axes: >



In [105…

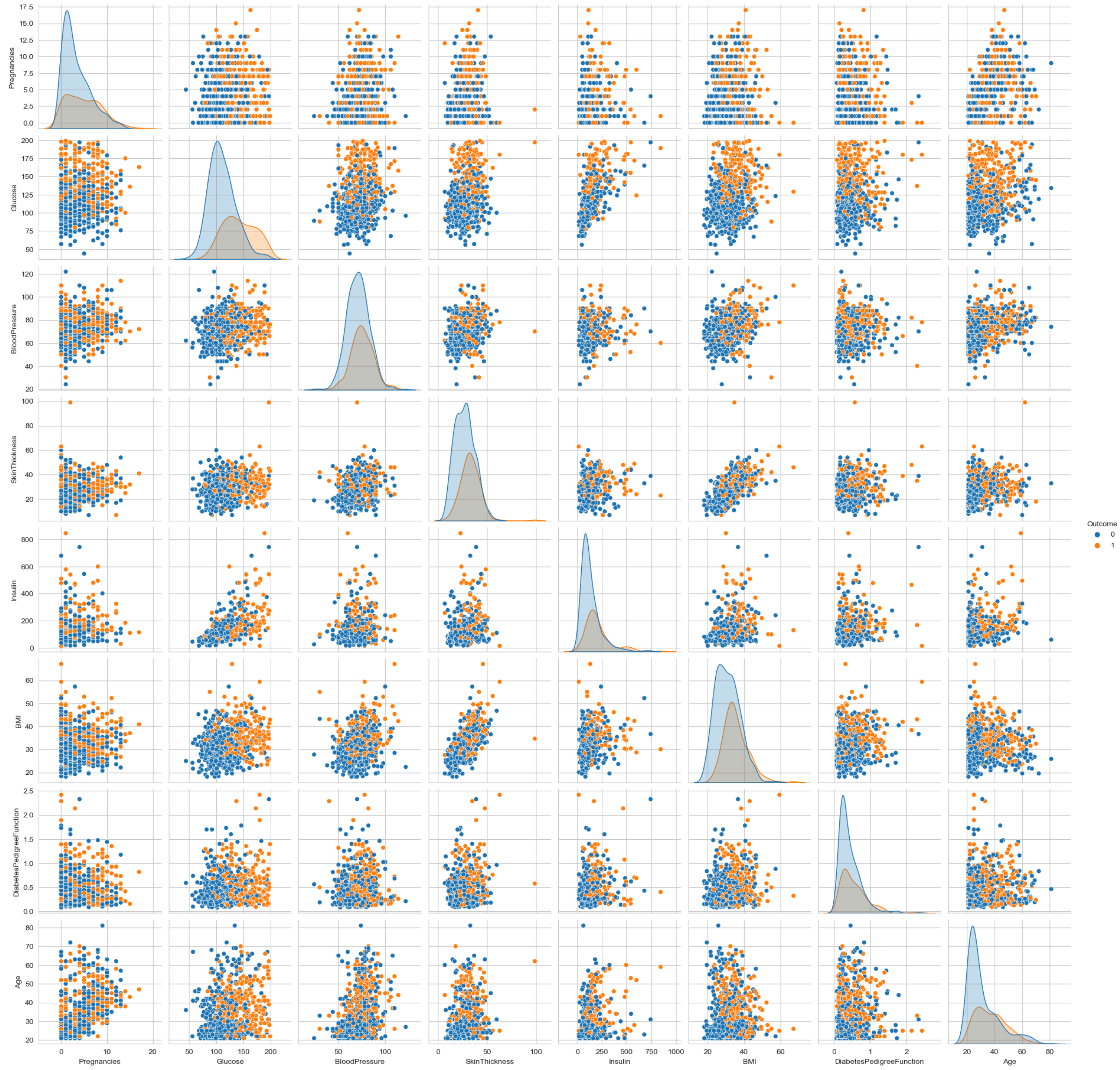
```
# Function to plot distributions with 2 per row
def plot_distribution2(df):
    columns = [col for col in df.columns if col != 'Outcome']
    num_cols = len(columns)

    # Set up subplots: 2 plots per row
    rows = (num_cols // 2) + (num_cols % 2)  # Dynamic row count
    fig, axes = plt.subplots(rows, 2, figsize=(8, 3 * rows))  # Adjust spacing

    # Flatten the axes array for easy iteration
    axes = axes.flatten()

    for i, column in enumerate(columns):
        sns.histplot(data=df, x=column, hue=df['Outcome'], kde=True, ax=axes[i])
        axes[i].set_title(f"Distribution of {column}")
        axes[i].legend(['Diabetes', 'No Diabetes'])

    # Hide empty subplots (if any)
    for j in range(i + 1, len(axes)):
        fig.delaxes(axes[j])

    plt.tight_layout()
    plt.show()

# Call the function
plot_distribution2(df)
```



In [52]:
```python
# pairplot of the dataset
sns.pairplot(df, hue='Outcome')
```

```
C:\Users\cifuenam\AppData\Local\anaconda3\Lib\site-packages\seaborn\axisgrid.py:118: UserWar
ning: The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```

Out[52]: <seaborn.axisgrid.PairGrid at 0x1ea97b03bd0>



Step 2 - Selecting the best k features using mutual information

In [54]:

```
# Separate features from the target variable.
# Using df_dropna since SelectKBest does not work with NaN values.

feature_columns = [
    "Pregnancies", "Glucose", "BloodPressure", "SkinThickness",
    "Insulin", "BMI", "DiabetesPedigreeFunction", "Age"
]

features = df_dropna[feature_columns].values
target = df_dropna["Outcome"].values
```

In [55]:

```
features
```

Out[55]:

```
array([[  1.   ,  89.   ,  66.   , ...,  28.1  ,   0.167,  21.   ],
       [  0.   , 137.   ,  40.   , ...,  43.1  ,   2.288,  33.   ],
       [  3.   ,  78.   ,  50.   , ...,  31.   ,   0.248,  26.   ],
       ...,
       [  2.   ,  88.   ,  58.   , ...,  28.4  ,   0.766,  22.   ],
       [ 10.   , 101.   ,  76.   , ...,  32.9  ,   0.171,  63.   ],
       [  5.   , 121.   ,  72.   , ...,  26.2  ,   0.245,  30.   ]])
```

In [56]:

```
target
```

```
Out[56]: array([0, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0,
       0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0,
       1, 0, 0, 0, 0, 1, 1, 1, 0, 1, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1, 0,
       1, 1, 1, 1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 1, 1, 1, 0, 1, 0, 0, 0,
       0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 1, 0, 0, 0, 1, 1, 1, 0, 1, 0, 1, 1, 0, 0, 1, 0, 1, 1,
       0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0,
       1, 0, 1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1,
       0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 1, 1, 1, 0, 0, 0, 1, 1, 1, 0,
       1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0,
       1, 0, 0, 1, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1,
       1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 0, 0, 1, 1, 0, 0, 0, 0,
       0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0,
       0, 1, 1, 0, 0, 0, 0, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0,
       1, 1, 1, 0, 0, 0, 0, 1, 0, 0, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 1, 0, 1, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 1, 0, 0, 1, 0, 0,
       1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 0], dtype=int64)
```

```
In [57]: # Define the number of most relevant features
threshold = 5

# Initialize SelectKBest with mutual information as the scoring function
skb = SelectKBest(score_func=mutual_info_classif, k=threshold)

# Fit the selector to the data
sel_skb = skb.fit(features, target)

# Get the boolean mask of selected features
sel_skb_index = sel_skb.get_support()

# Extract the selected features
df_skb = features[:, sel_skb_index]

# Print feature scores and selected features
print("Feature Scores:", sel_skb.scores_)
print("Selected Features:\n", df_skb)
# Selected: "Pregnancies"(0), "Glucose"(1), "Insulin"(4), "BMI"(5), "Age"(7)
```

```
Feature Scores: [0.05495772 0.16908132 0.01867657 0.         0.08643687 0.06049918
 0.         0.06532759]
Selected Features:
 [[  1.    89.    94.    28.1   21. ]
 [  0.   137.   168.    43.1   33. ]
 [  3.    78.    88.    31.    26. ]
 ...
 [  2.    88.    16.    28.4   22. ]
 [ 10.   101.   180.    32.9   63. ]
 [  5.   121.   112.    26.2   30. ]]
```

Additional Reference on Feature Selection

If you're interested in exploring more feature selection techniques, check out the official scikit-learn documentation:

👉 **Feature Selection in Scikit-Learn**
