DIABETES PREDICTION USING PERCEPTRON

Importing necessary Libraries

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

In [2]:
```
data=pd.read_csv("C:/Users/LEGION/Documents/diabetes.csv")
data
```

Out[2]:

	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 [3]:
```
data.dtypes
```

Out[3]:
```
Pregnancies                   int64
Glucose                       int64
BloodPressure                 int64
SkinThickness                 int64
Insulin                       int64
BMI                         float64
DiabetesPedigreeFunction    float64
Age                           int64
Outcome                       int64
dtype: object
```

In [4]:
```
#Intial summary of dataset
data.describe()
```

Out[4]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction
count	768.000000	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	0.471876
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329

min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000

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

Out[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

In [6]:
```
#Check the NA data in the table
data.isna().sum()
```

Out[6]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

Important Observation(s):

.It seems like null values are present in the form of zeros.

.It's impossible to have Glucose, BloodPressure, SkinThickness, Insulin, BMI to be zero. So, we have to handle this.

.Let's get a sense of how many zero value are present in each column.

In [7]:
```
zero_not_present = ["Glucose", "BloodPressure", "SkinThickness",
                    "Insulin", "BMI"]
for col in zero_not_present:
    data[col].replace(0,np.nan,inplace=True)


#checkf if zeros were replaced in required columns
data.head(n=10)
```

Out[7]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148.0	72.0	35.0	NaN	33.6	0.627	50	1
1	1	85.0	66.0	29.0	NaN	26.6	0.351	31	0
2	8	183.0	64.0	NaN	NaN	23.3	0.672	32	1

3	1	89.0	66.0	23.0	94.0	28.1	0.167	21	0
4	0	137.0	40.0	35.0	168.0	43.1	2.288	33	1
5	5	116.0	74.0	NaN	NaN	25.6	0.201	30	0
6	3	78.0	50.0	32.0	88.0	31.0	0.248	26	1
7	10	115.0	NaN	NaN	NaN	35.3	0.134	29	0
8	2	197.0	70.0	45.0	543.0	30.5	0.158	53	1
9	8	125.0	96.0	NaN	NaN	NaN	0.232	54	1

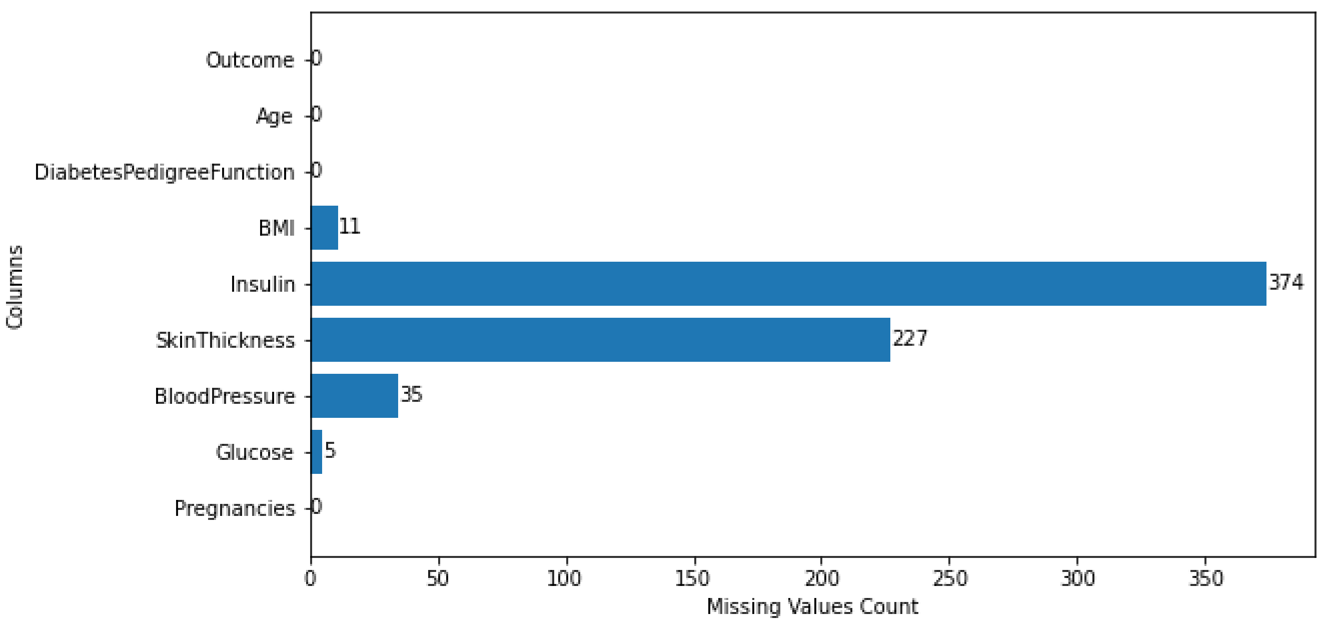
In [8]:

```
missing_values_count = data.isna().sum()

# Create a bar plot
plt.figure(figsize=(9, 5))
plt.barh(missing_values_count.index, missing_values_count)
plt.xlabel('Missing Values Count')
plt.ylabel('Columns')
plt.grid(False)

# Add labels to the bars
for index, value in enumerate(missing_values_count):
    plt.text(value, index, f'{value:.0f}', va='center')

plt.show()
```



Performing Mean Imputation on the Columns with NA

In [9]:

```
data.fillna(data.mean(), inplace=True)
```

In [10]:

```
data.describe()
```

Out[10]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction
count	768.000000	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	0.471876
std	3.369578	30.435949	12.096346	8.790942	85.021108	6.875151	0.331329
min	0.000000	44.000000	24.000000	7.000000	14.000000	18.200000	0.078000

25%	1.000000	99.750000	64.000000	25.000000	121.500000	27.500000	0.243750
50%	3.000000	117.000000	72.202592	29.153420	155.548223	32.400000	0.372500
75%	6.000000	140.250000	80.000000	32.000000	155.548223	36.600000	0.626250
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000

We can see the Mean values for Glucose, BloodPressure, SkinThickness, Insulin, BMI has changed

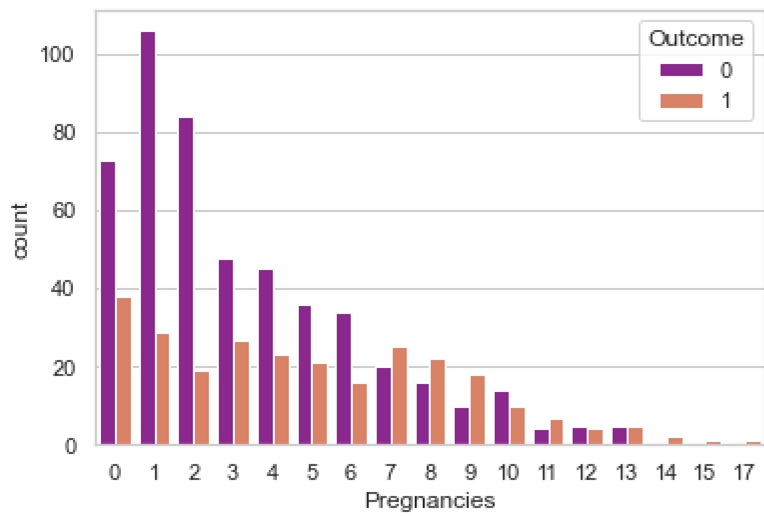
Pregnancies with outcome

In [111…

```
import random
pallete = ['Accent_r', 'Blues', 'BrBG', 'BrBG_r', 'BuPu', 'CMRmap', 'CMRmap_r', 'Dark2',
sns.countplot(x="Pregnancies", hue = "Outcome", data=data, palette=random.choice(pallete
```

Out[111]:

```
<AxesSubplot:xlabel='Pregnancies', ylabel='count'>
```

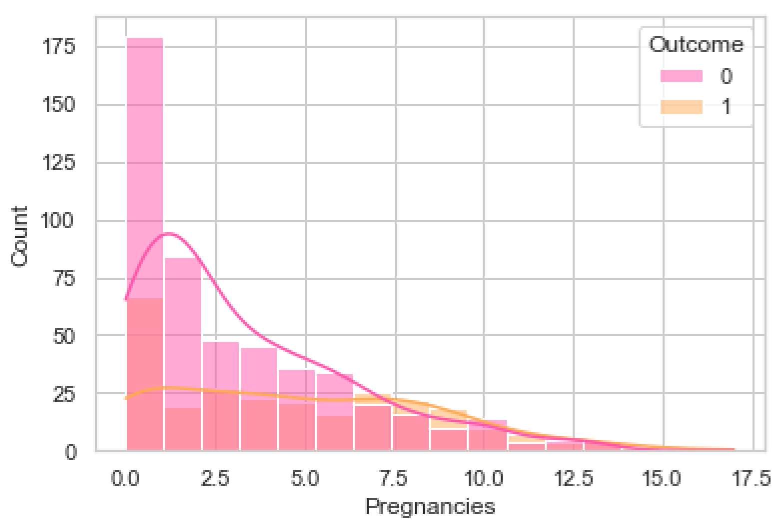


In [112…

```
sns.histplot(x="Pregnancies", hue="Outcome", data=data, kde=True, palette=random.choice(
```

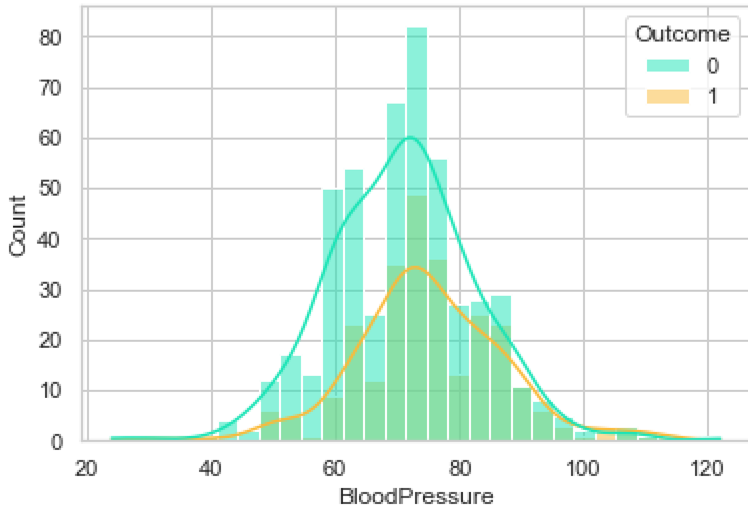
Out[112]:

```
<AxesSubplot:xlabel='Pregnancies', ylabel='Count'>
```



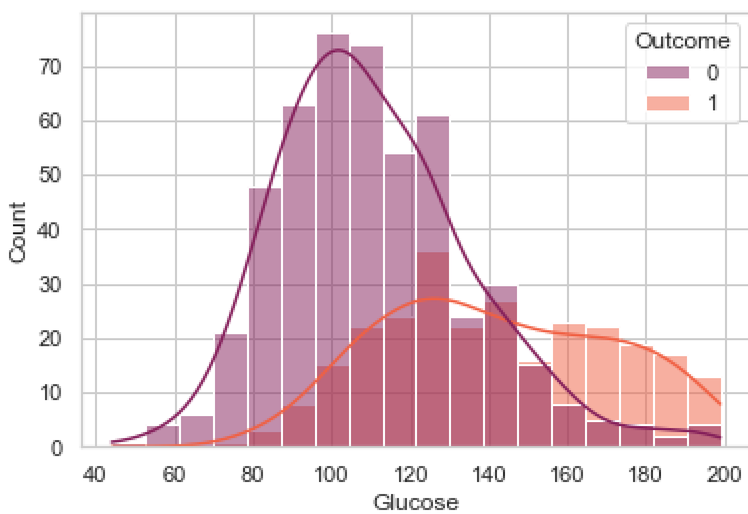
We can see as number of pregnacies increase, more chance of being diabetic

Blood Pressure with Outcome

In [113…
```
sns.histplot(x="BloodPressure", hue="Outcome", data=data, kde=True, palette=random.choic
```
Out[113]:
```
<AxesSubplot:xlabel='BloodPressure', ylabel='Count'>
```


we can see that blood pressure levels of diabetic people are high

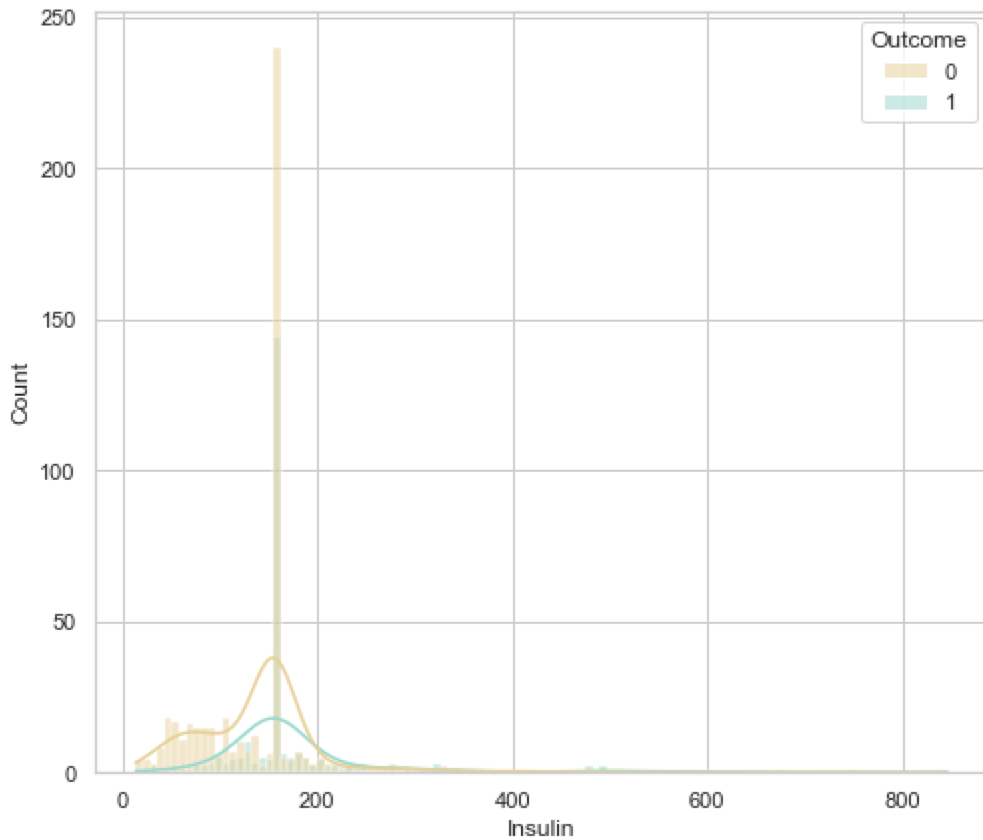
Glucose with Outcome

In [115…
```
sns.histplot(x="Glucose", hue="Outcome", data=data, kde=True, palette=random.choice(pall
```
Out[115]:
```
<AxesSubplot:xlabel='Glucose', ylabel='Count'>
```


Glucose levels of diabetic people are very high

Insulin with Outcome

In [117…
```
plt.figure(figsize=(8,7))
sns.histplot(x="Insulin", hue="Outcome", data=data, kde=True, palette=random.choice(pall
```
Out[117]:
```
<AxesSubplot:xlabel='Insulin', ylabel='Count'>
```



Diabetic people have a little more insulin.

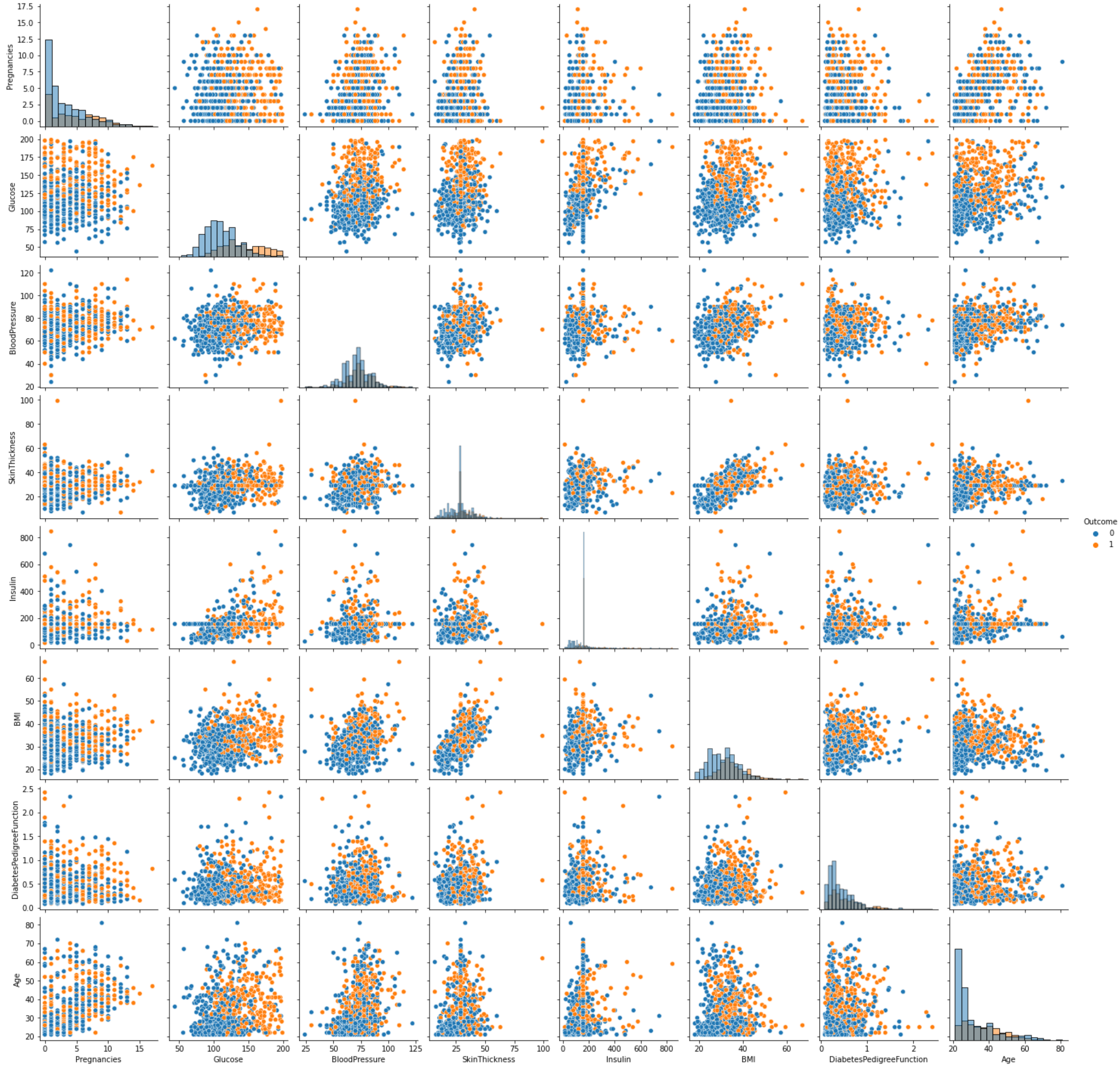
Ploting Pairwise relationship in the dataset

In [11]:

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

# Plot pairwise relationships in a dataset
plt.figure(figsize=(20, 20))
pairplot = sns.pairplot(data=data, hue="Outcome", diag_kind="hist")
plt.show()
```

```
<Figure size 1440x1440 with 0 Axes>
```



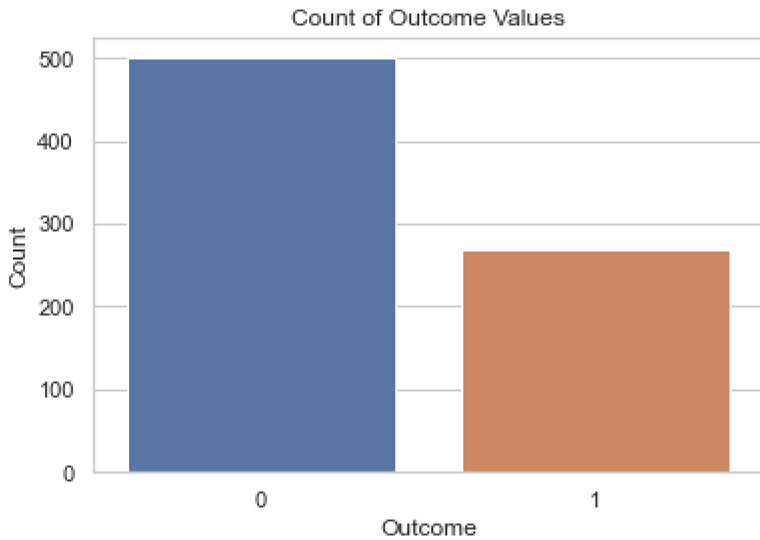
Representing a bar plot based on the outcome

In [39]:

```
sns.set(style='whitegrid')

sns.countplot(x='Outcome', data=data) #Counts all the values for you and create a bar pl
plt.title('Count of Outcome Values')
plt.xlabel('Outcome')
plt.ylabel('Count')

plt.show()
```



Conculsions from Data-set

1.There are no NaN values in the data. 2.As number of pregnacies increase, more chance of being diabetic 3.The blood pressure levels of diabetic people are high 4.Glucose levels of diabetic people are very high. 5.Diabetic people have a little more insulin. 6.The distribution curve of insulin and DiabetesPedidgreeFunction(DPF) is right skewed(from plotting the pairwise relationship). 7.The BloodPressure lies between 40 and 100, and there are less number of people with diabetes in this range (from plotting the pairwise relationship).

From plotting the Pairwise relationship we can understand that:-

1>Females with high glucose levels who are over the pregnancy threshold have diabetes.

2>Diabetes risk increases with both insulin and glucose levels.

3>The likelihood of developing diabetes increases with both BMI and glucose levels.

4>Age alone does not necessarily indicate diabetes.

5>It makes sense that middle-aged adults with high blood pressure and high glucose levels have a higher risk of developing diabetes.

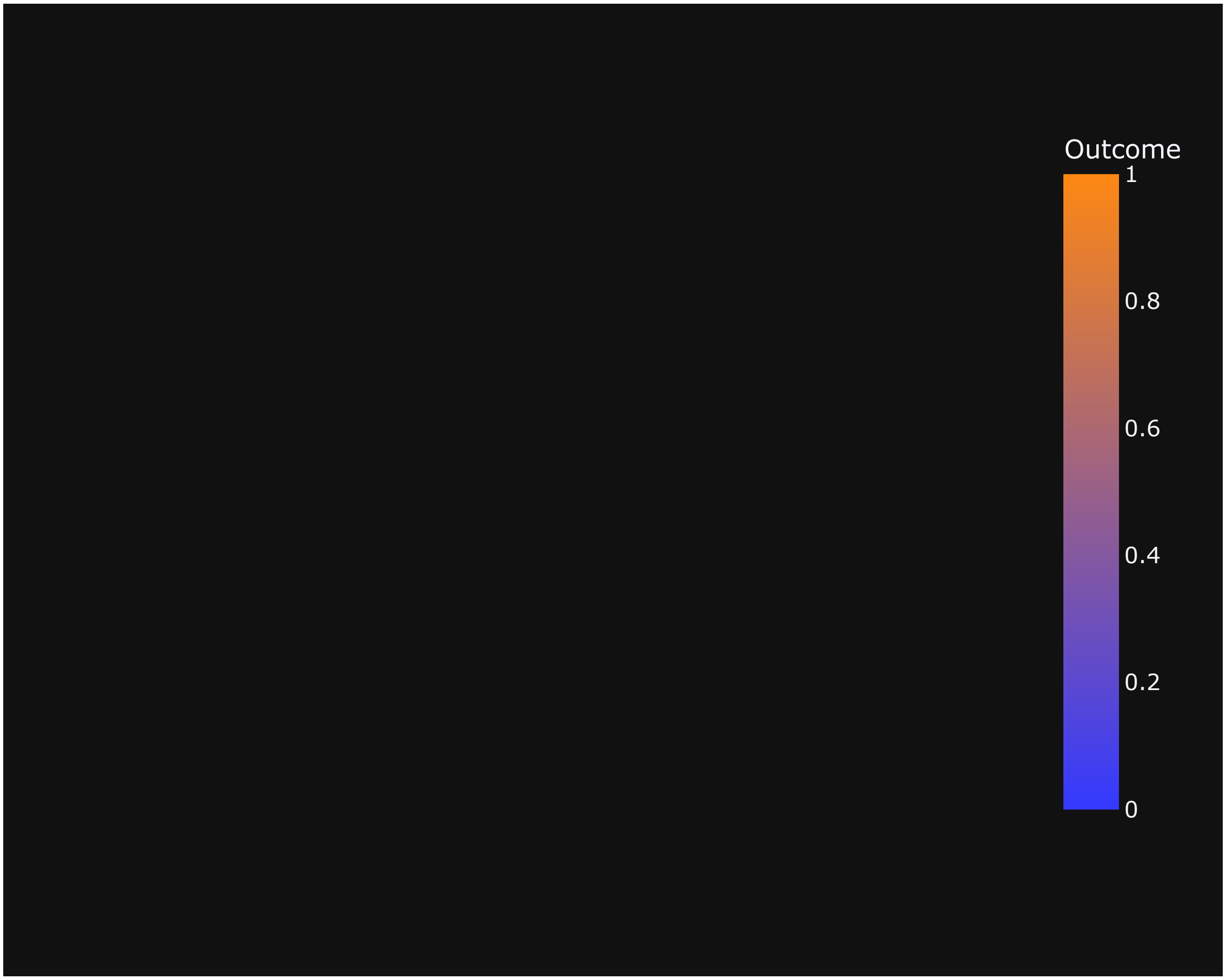
Scatter plot of Glucose vs Insulin with respect to Outcome

In [43]:
```
pip install plotly
```

```
Collecting plotly
  Downloading plotly-5.17.0-py2.py3-none-any.whl (15.6 MB)
     ---------------------------------------- 15.6/15.6 MB 8.4 MB/s eta 0:00:00
Collecting tenacity>=6.2.0
  Downloading tenacity-8.2.3-py3-none-any.whl (24 kB)
Requirement already satisfied: packaging in c:\users\legion\appdata\local\programs\pytho
n\python38\lib\site-packages (from plotly) (21.3)
Requirement already satisfied: pyparsing!=3.0.5,>=2.0.2 in c:\users\legion\appdata\local
\programs\python\python38\lib\site-packages (from packaging->plotly) (3.0.9)
Installing collected packages: tenacity, plotly
Successfully installed plotly-5.17.0 tenacity-8.2.3
Note: you may need to restart the kernel to use updated packages.
[notice] A new release of pip is available: 23.0.1 -> 23.2.1
```

```
[notice] To update, run: python.exe -m pip install --upgrade pip
```

In [45]:
```
import plotly.express as px
fig = px.scatter_3d(data, x='Glucose', y='Insulin', z='Outcome',
              color='Outcome',size_max=18,color_continuous_scale=["#3339FF", "#ff8811"])
fig.update_layout({"template":"plotly_dark"})
fig.show()
```



The Perceptron Algorithm

Using Hyperparameter Tuning specifaclly RandomSearchCV was able to get a basic idea of the best parameters which was needed to tune/optimize the model

In [95]:
```
import numpy as np
from sklearn.model_selection import RandomizedSearchCV
from sklearn.neural_network import MLPClassifier

# Define the hyperparameter search space
param_dist = {
    'hidden_layer_sizes': [(64, 32), (128, 64), (256, 128)],
    'activation': ['logistic', 'relu'],
    'alpha': [0.0001, 0.001, 0.01],
    'learning_rate_init': [0.001, 0.01, 0.1,0.0001],
    'max_iter': [500, 1000, 1500]
}

# Create an MLP classifier
mlp = MLPClassifier(random_state=42)
```

```
# Perform random search
random_search = RandomizedSearchCV(estimator=mlp, param_distributions=param_dist, n_iter

# Fit random search to your data
random_search.fit(X_train, y_train)

# Print the best hyperparameters and the best score
print("Best Hyperparameters:", random_search.best_params_)
print("Best Score (Accuracy):", random_search.best_score_)
```

```
Best Hyperparameters: {'max_iter': 1500, 'learning_rate_init': 0.001, 'hidden_layer_size
s': (256, 128), 'alpha': 0.01, 'activation': 'logistic'}
Best Score (Accuracy): 0.7687724910035986
```

Multi Layer Perceptron Algorithm

In [110…

```
import torch
import torch.nn as nn
import torch.optim as optim
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score

#Random Seed
torch.manual_seed(42)

# Assuming you have loaded and preprocessed your data

# Standardize features
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)

# Convert data to PyTorch tensors
X_train_tensor = torch.FloatTensor(X_train)
y_train_tensor = torch.LongTensor(y_train)
X_test_tensor = torch.FloatTensor(X_test)
y_test_tensor = torch.LongTensor(y_test)

# Define a custom MLP model with batch normalization and dropout
class CustomMLP(nn.Module):
    def __init__(self):
        super(CustomMLP, self).__init__()
        self.fc1 = nn.Linear(in_features=X_train.shape[1], out_features=64)
        self.bn1 = nn.BatchNorm1d(64)  # Batch normalization
        self.relu1 = nn.Sigmoid()
        self.dropout1 = nn.Dropout(0.5)  # Dropout with 50% probability
        self.fc2 = nn.Linear(in_features=64, out_features=32)
        self.bn2 = nn.BatchNorm1d(32)  # Batch normalization
        self.relu2 = nn.Sigmoid()
        self.dropout2 = nn.Dropout(0.5)  # Dropout with 50% probability
        self.fc3 = nn.Linear(in_features=32, out_features=2)

    def forward(self, x):
        x = self.fc1(x)
        x = self.bn1(x)
        x = self.relu1(x)
        x = self.dropout1(x)
        x = self.fc2(x)
        x = self.bn2(x)
        x = self.relu2(x)
        x = self.dropout2(x)
        x = self.fc3(x)
        return x
```

```python
# Initialize the model
model = CustomMLP()

# Define loss function and optimizer
criterion = nn.CrossEntropyLoss()
optimizer = optim.Adam(model.parameters(), lr=0.001)

# Training loop
epochs = 100
for epoch in range(epochs):
    optimizer.zero_grad()
    outputs = model(X_train_tensor)
    loss = criterion(outputs, y_train_tensor)
    loss.backward()
    optimizer.step()

# Evaluation on the test set
model.eval()
with torch.no_grad():
    outputs = model(X_test_tensor)
    _, predicted = torch.max(outputs, 1)
    test_accuracy = accuracy_score(y_test, predicted.numpy())

print(f'Test Accuracy: {test_accuracy:.2f}')
with torch.no_grad():
    train_outputs = model(X_train_tensor)
    _, train_predicted = torch.max(train_outputs, 1)

# Calculate the accuracy score for training data
train_accuracy = accuracy_score(y_train, train_predicted.numpy())
print(f'Training Accuracy: {train_accuracy:.2f}')
```

```
Test Accuracy: 0.75
Training Accuracy: 0.78
```

In [105…

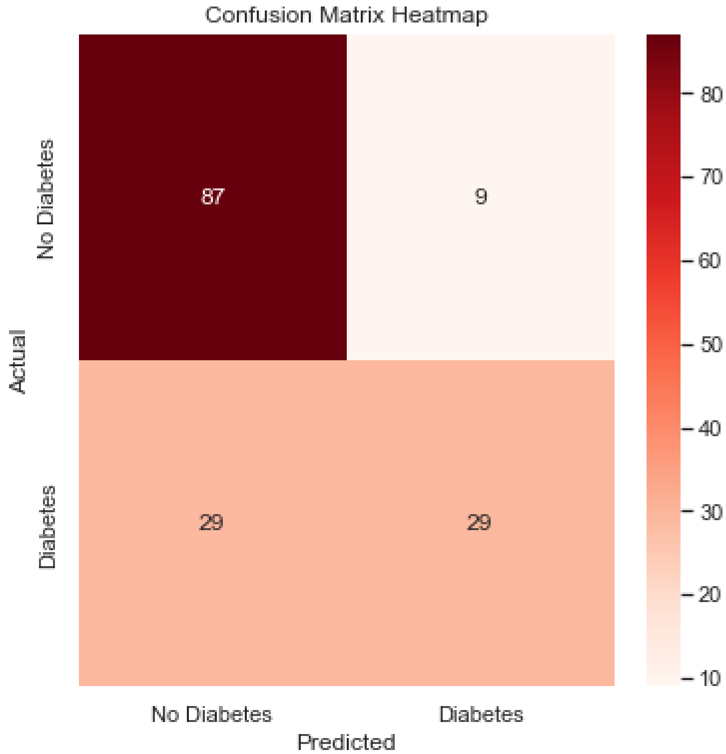
```python
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.metrics import confusion_matrix

# Assuming you have trained your model as shown in your code

# Evaluate the model on the test set
model.eval()
with torch.no_grad():
    outputs = model(X_test_tensor)
    _, predicted = torch.max(outputs, 1)

# Generate the confusion matrix
conf_matrix = confusion_matrix(y_test, predicted.numpy())

# Create a heatmap for the confusion matrix
plt.figure(figsize=(6, 6))
sns.heatmap(conf_matrix, annot=True, fmt='d', cmap="Reds", cbar=True,
            xticklabels=['No Diabetes', 'Diabetes'],
            yticklabels=['No Diabetes', 'Diabetes'])
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix Heatmap')
plt.show()
print(f'Test Accuracy: {test_accuracy:.2f}')
```




```
Test Accuracy: 0.75
```

In [106…

```python
from sklearn.metrics import accuracy_score, precision_score, recall_score

# Assuming you have already trained your MLPClassifier and obtained predictions

# Calculate accuracy
accuracy = accuracy_score(y_test, predicted)

# Calculate precision
precision = precision_score(y_test, predicted)

# Calculate recall
recall = recall_score(y_test, predicted)

print(f'Accuracy: {accuracy:.2f}')
print(f'Precision: {precision:.2f}')
print(f'Recall: {recall:.2f}')
```

```
Accuracy: 0.75
Precision: 0.76
Recall: 0.50
```