```
import pandas as pd
import numpy as np
import plotly.express as px
from sklearn.preprocessing import StandardScaler, MinMaxScaler
from sklearn.utils import resample
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn import metrics
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay
from tqdm.notebook import tqdm
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings("ignore")

df = pd.read_csv("diabetes.csv")

df
```

```
     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

..           ...      ...            ...            ...      ...   ...

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


     Pedigree  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]
```

```
df.describe().T
```

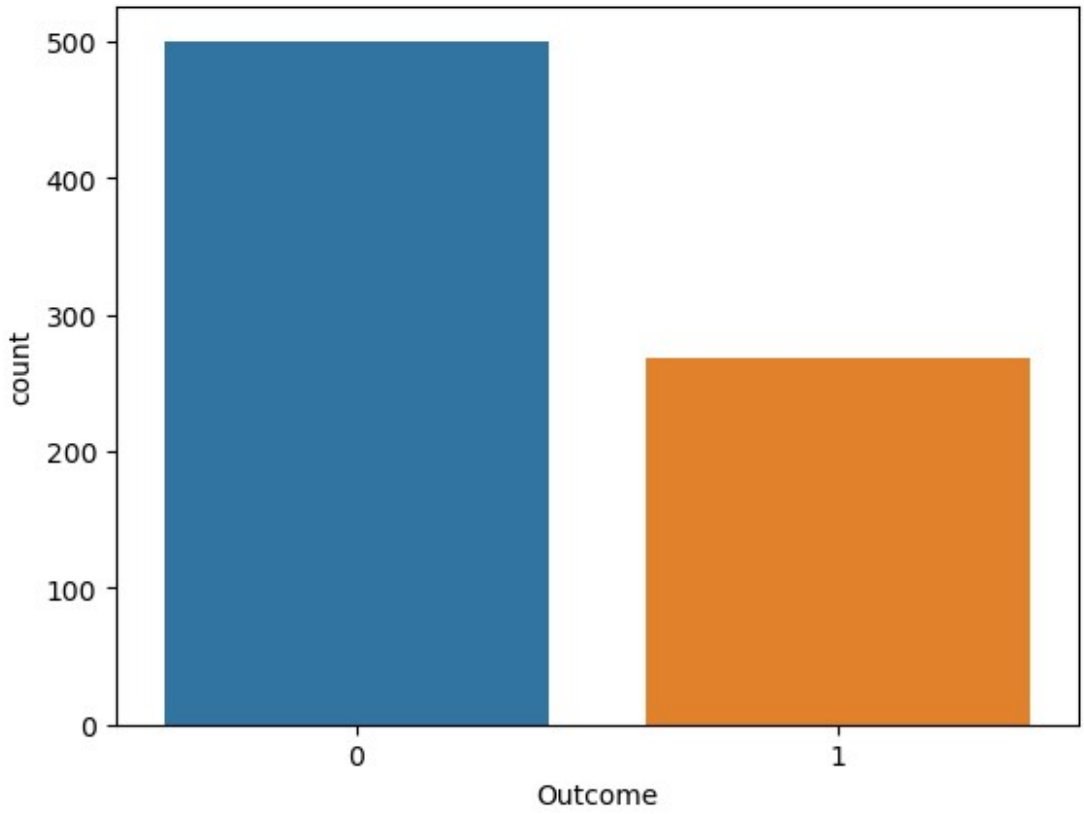
```
                count        mean         std     min       25%
50%  \
Pregnancies    768.0    3.845052    3.369578   0.000   1.00000
3.0000
Glucose        768.0  120.894531   31.972618   0.000  99.00000
117.0000
BloodPressure  768.0   69.105469   19.355807   0.000  62.00000
72.0000
SkinThickness  768.0   20.536458   15.952218   0.000   0.00000
23.0000
Insulin        768.0   79.799479  115.244002   0.000   0.00000
30.5000
BMI            768.0   31.992578    7.884160   0.000  27.30000
32.0000
Pedigree       768.0    0.471876    0.331329   0.078   0.24375
0.3725
Age            768.0   33.240885   11.760232  21.000  24.00000
29.0000
Outcome        768.0    0.348958    0.476951   0.000   0.00000
0.0000

                     75%     max
Pregnancies      6.00000   17.00
Glucose        140.25000  199.00
BloodPressure   80.00000  122.00
SkinThickness   32.00000   99.00
Insulin        127.25000  846.00
BMI             36.60000   67.10
Pedigree         0.62625    2.42
Age             41.00000   81.00
Outcome          1.00000    1.00
```

```
df["Outcome"].value_counts()
```

```
0    500
1    268
Name: Outcome, dtype: int64
```

```
sns.countplot(data=df, x=df["Outcome"])
plt.show()
```




```
negative_data = df[df["Outcome"] == 0]
positive_data = df[df["Outcome"] == 1]

positive_upsample = resample(
    positive_data,
    replace=True,
    n_samples=int(0.9 * len(negative_data)),
    random_state=42,
)

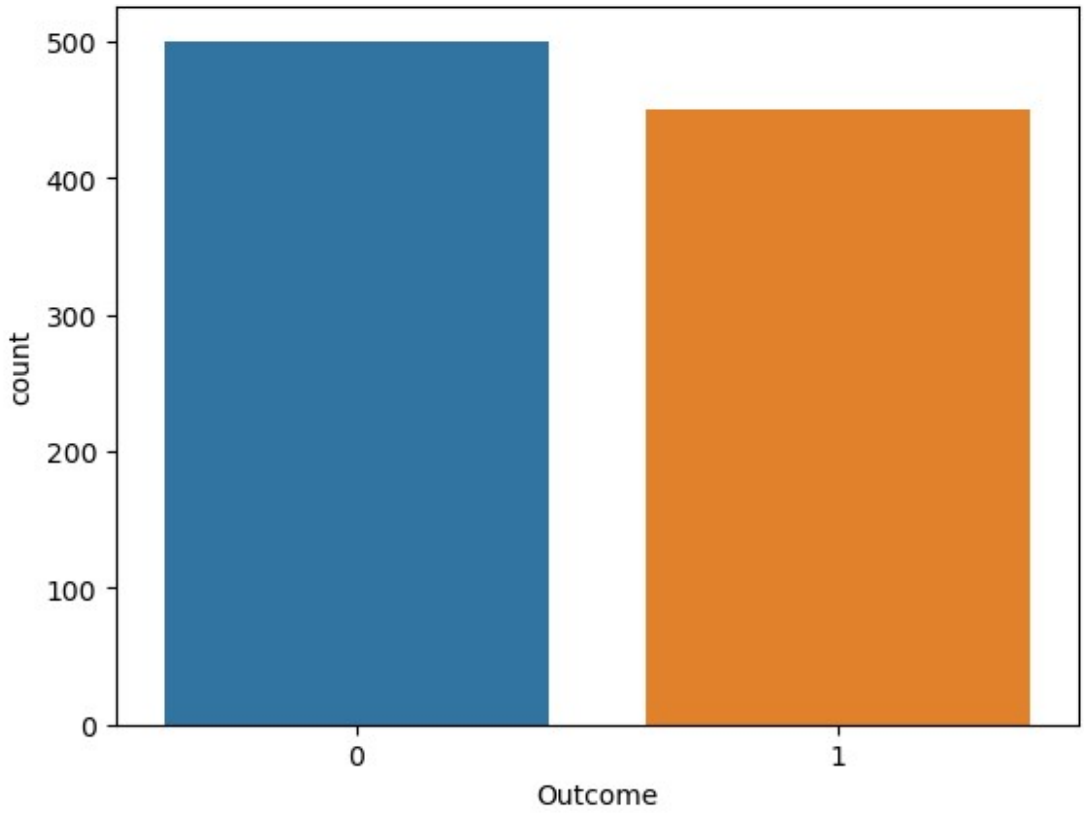
new_df = negative_data
new_df = pd.concat([new_df, positive_upsample], ignore_index=True)

new_df.shape
```

```
(950, 9)
```

```
new_df = new_df.sample(frac=1)

sns.countplot(data=new_df, x=new_df["Outcome"])
plt.show()
```




```
x = new_df.drop("Outcome", axis=1)
y = new_df[["Outcome"]]

scaler = MinMaxScaler()
scaled_values = scaler.fit_transform(x)

x_train, x_test, y_train, y_test = train_test_split(
    scaled_values, y, test_size=0.2, random_state=42
)

k_values = [1, 3, 5, 7, 9,  11, 13, 15, 17, 19, 21, 23, 25, 27, 29,
31, 33, 35, 37,  39, 41, 43, 45, 47, 49]
accuracy_values = []

for i in tqdm(range(len(k_values))):
    model = KNeighborsClassifier(n_neighbors=k_values[i])
    model.fit(x_train, y_train)
    y_pred = model.predict(x_test)
    accuracy = metrics.accuracy_score(y_test, y_pred)
    accuracy_values.append(accuracy)
```

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```
px.line(x=k_values, y=accuracy_values)
```

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```


```
optimal_k = -1
optimal_accuracy = -1
for i in list(zip(k_values, accuracy_values)):
    if i[1] > optimal_accuracy:
```

```
        optimal_k = i[0]
        optimal_accuracy = i[1]

knn_model = KNeighborsClassifier(n_neighbors=optimal_k)

knn_model.fit(x_train, y_train)

KNeighborsClassifier(n_neighbors=1)

y_pred = knn_model.predict(x_test)

print(metrics.classification_report(y_test, y_pred))

              precision    recall  f1-score   support

           0       0.90      0.86      0.88       105
           1       0.83      0.88      0.86        85

    accuracy                           0.87       190
   macro avg       0.87      0.87      0.87       190
weighted avg       0.87      0.87      0.87       190


cm = metrics.confusion_matrix(y_test, y_pred)
plot_confusion_matrix(cm)
plt.show()

---------------------------------------------------------------------------
-----
NameError                                 Traceback (most recent call
last)
Cell In[26], line 2
      1 cm = metrics.confusion_matrix(y_test, y_pred)
----> 2 plot_confusion_matrix(cm)
      3 plt.show()

NameError: name 'plot_confusion_matrix' is not defined

y_score = model.predict_proba(x_test)[:, 1]

false_positive_rate, true_positive_rate, threshold =
metrics.roc_curve(y_test, y_score)

print("roc_auc_score for DecisionTree: ",
metrics.roc_auc_score(y_test, y_score))

roc_auc_score for DecisionTree:  0.8794397759103642

plt.subplots(1, figsize=(10, 7))
plt.title("Receiver Operating Characteristic - KNN")
plt.plot(false_positive_rate, true_positive_rate)
plt.plot([0, 1], ls="--")
plt.plot([0, 0], [1, 0], c=".7"), plt.plot([1, 1], c=".7")
```

```
plt.ylabel("True Positive Rate")
plt.xlabel("False Positive Rate")
plt.show()
```