Diabetes Patients Prediction Project

MeriSKILL 2nd Project

Objective: The objective of the dataset is to diagnostically predict whether a patient has diabetes based on certain diagnostic measurements included in the dataset.

Importing Necessary Libraries

In [ ]:
```
# Data Analysis
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

# Machine Learning
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import confusion_matrix, classification_report, ConfusionMatri
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier

# Other Libraries
import warnings
warnings.filterwarnings('ignore')
```

Import dataset

In [ ]:
```
diabetes_df = pd.read_csv('diabetes.csv')
diabetes_df.head()
```

Out[ ]:

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

In [ ]:
```
diabetes_df.shape
```

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

EDA

Inspect the structure of the dataset

In [ ]:
```
diabetes_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
```

There are two data types; int and float. There are no null values in the columns.

Check null values in the columns

In [ ]:
```
diabetes_df.isna().sum()
```

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

Check null values in the dataset

In [ ]:
```
diabetes_df.duplicated().sum()
```

Out[ ]:
```
0
```

There are no duplicate rows in the dataset

Check dataset statistics

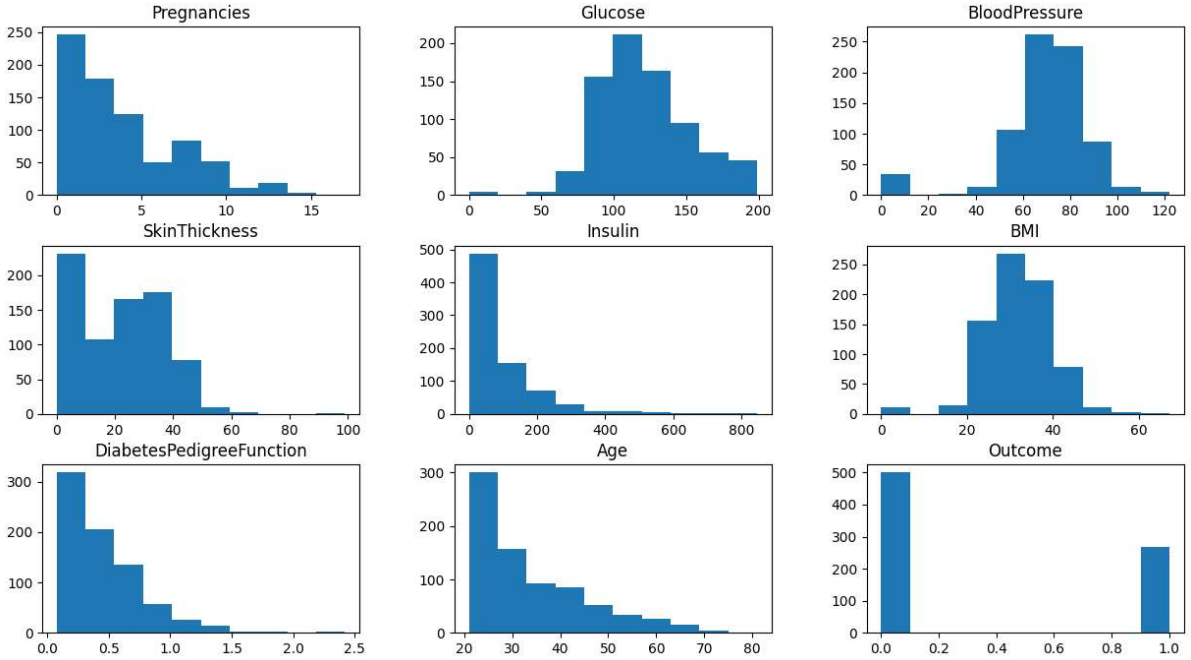
In [ ]:
```
diabetes_df.describe().T
```

Out[ ]:

	count	mean	std	min	25%	50%	75%	
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000	1
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000	1
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.00000	
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.25000	8
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.60000	
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000	

Glucose, BloodPressure, SkinThickness, Insulin and BMI all have minimum value to be zero which is not possible. We go ahead to fill the zeros in these columns with the median of the said columns.

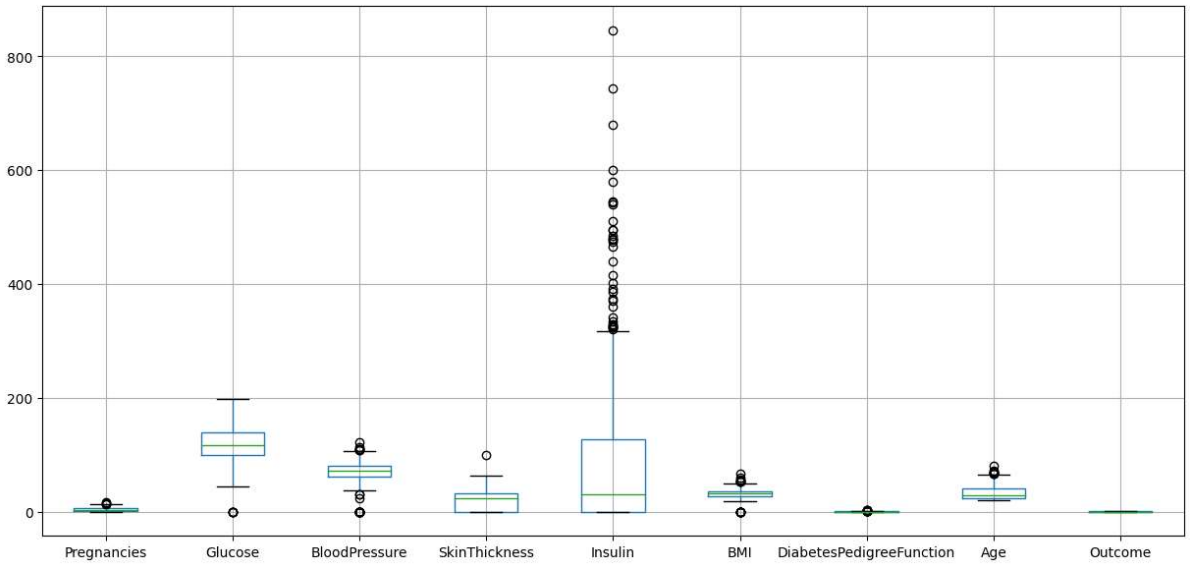
In [ ]:
```
diabetes_df.hist(figsize=(15, 8), grid=False);
```



We see the distribution of our columns.

In [ ]:
```
diabetes_df.boxplot(figsize=(15, 7))
```

Out[ ]:
```
<Axes: >
```



Glucose, BloodPressure, SkinThickness, Insulin, and BMI's zero values are filled with their respective averages since the values for these columns cannot be zero, for example you can check the link attached. Insulin values

Data Preparation

Data Cleaning

In [ ]:
```
mean_insulin = diabetes_df.where(diabetes_df['Insulin'] > 0)['Insulin'].mean()

diabetes_df.loc[diabetes_df['Insulin'] == 0, 'Insulin'] = mean_insulin
```

In [ ]:
```
mean_glucose = diabetes_df.where(diabetes_df['Glucose'] > 0)['Glucose'].mean()

diabetes_df.loc[diabetes_df['Glucose'] == 0, 'Glucose'] = mean_glucose
```

In [ ]:
```
mean_bloodpressure = diabetes_df.where(diabetes_df['BloodPressure'] > 0)['BloodPres

diabetes_df.loc[diabetes_df['BloodPressure'] == 0, 'BloodPressure'] = mean_bloodpre
```

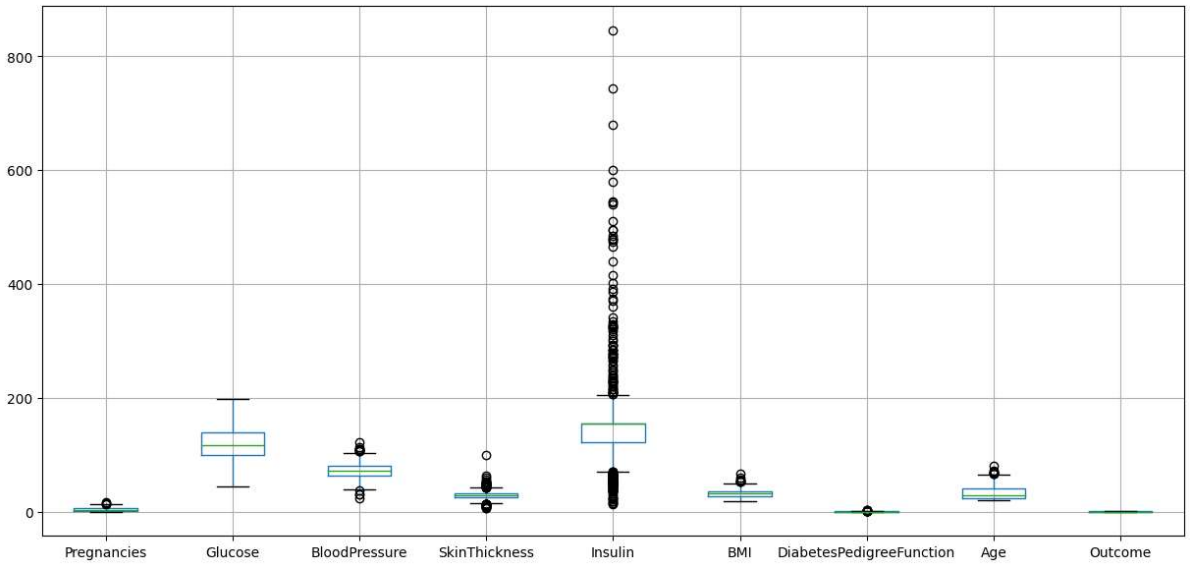
In [ ]:
```
mean_BMI = diabetes_df.where(diabetes_df['BMI'] > 0)['BMI'].mean()

diabetes_df.loc[diabetes_df['BMI'] == 0, 'BMI'] = mean_BMI
```

In [ ]:
```
mean_skinthinkness = diabetes_df.where(diabetes_df['SkinThickness'] > 0)['SkinThick

diabetes_df.loc[diabetes_df['SkinThickness'] == 0, 'SkinThickness'] = mean_skinthir
```

In [ ]:
```
diabetes_df.boxplot(figsize=(15, 7));
```



Considering the factors which contributes to a person being diabetic or not, we can't consider the extreme values as outlies but instead it is an indication that our values are widely spread.

In [ ]:
```
diabetes_df.describe().T
```

Out[ ]:

	count	mean	std	min	25%	50%	75%
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.000000	6.000000
Glucose	768.0	121.686763	30.435949	44.000	99.75000	117.000000	140.250000
BloodPressure	768.0	72.405184	12.096346	24.000	64.00000	72.202592	80.000000
SkinThickness	768.0	29.153420	8.790942	7.000	25.00000	29.153420	32.000000
Insulin	768.0	155.548223	85.021108	14.000	121.50000	155.548223	155.548223
BMI	768.0	32.457464	6.875151	18.200	27.50000	32.400000	36.600000
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.372500	0.626250
Age	768.0	33.240885	11.760232	21.000	24.00000	29.000000	41.000000
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.000000	1.000000

Inspect the describe table again to ensure the changes have been implemented

In [ ]:
```
diabetes_df.corr().tail(1)
```

Out[ ]:

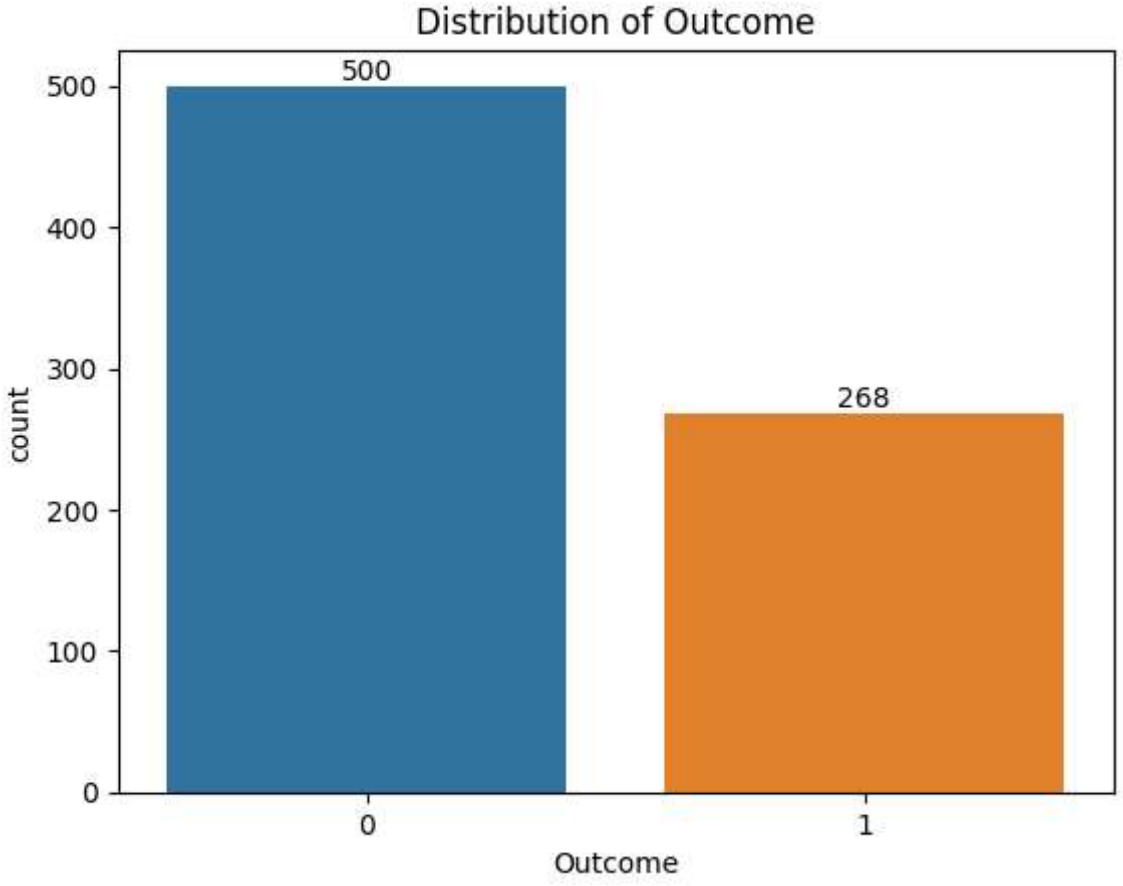
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigr
Outcome	0.221898	0.492928	0.166074	0.215299	0.214411	0.311924	

We inspect the relationship between each column and the outcome.

View the count of values in the outcome column

In [ ]:
```
ax = sns.countplot(data=diabetes_df, x='Outcome')
for bars in ax.containers:
    ax.bar_label(bars)
```

```
plt.title('Distribution of Outcome')
plt.show()
```



0 - represents `Non-diabetic` , 1 - represents `Diabetic`

Given the critical nature of early diabetes detection and its impact on patient outcomes, our objective is to develop a highly accurate predictive model with a minimum overall accuracy of 90% and a macro average of at least 85%. This emphasis on accuracy stems from the urgency of timely diagnosis and intervention to ensure the best possible health outcomes for individuals affected by diabetes.

Divide data into training and testing data

In [ ]:
```
X = diabetes_df.drop(['Outcome'], axis=1)
X.head()
```

Out[ ]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctior
0	6	148.0	72.0	35.00000	155.548223	33.6	0.62
1	1	85.0	66.0	29.00000	155.548223	26.6	0.35
2	8	183.0	64.0	29.15342	155.548223	23.3	0.67
3	1	89.0	66.0	23.00000	94.000000	28.1	0.16
4	0	137.0	40.0	35.00000	168.000000	43.1	2.28

In [ ]:
```
y = diabetes_df['Outcome']
y
```

Out[ ]:
```
0      1
1      0
2      1
3      0
4      1
      ..
763    0
764    0
765    0
766    1
767    0
Name: Outcome, Length: 768, dtype: int64
```

In [ ]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=.20, random_sta
```

In [ ]:
```
X_train.shape
```

Out[ ]:
```
(614, 8)
```

In [ ]:
```
y_train.shape
```

Out[ ]:
```
(614,)
```

In [ ]:
```
X_test.shape
```

Out[ ]:
```
(154, 8)
```

In [ ]:
```
y_test.shape
```

Out[ ]:
```
(154,)
```

Modeling

Random Classification

In [ ]:
```
rfc_clf =  RandomForestClassifier(random_state=42)
rfc_clf.fit(X_train, y_train)
```

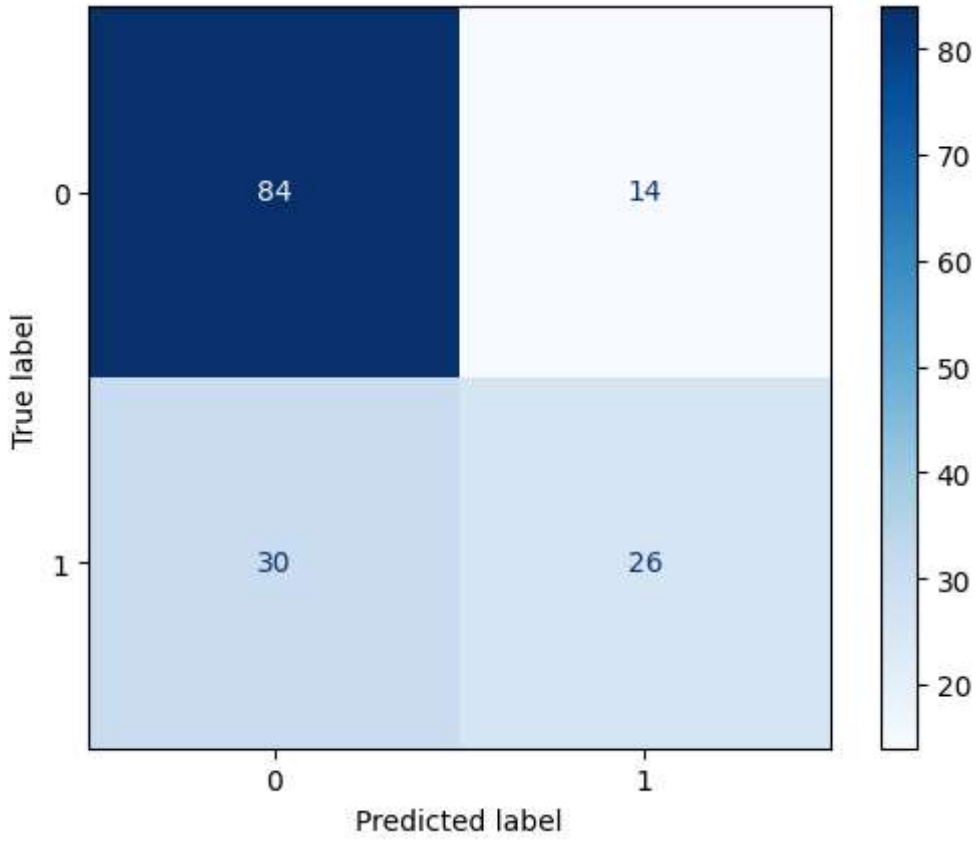
Out[ ]:
```
RandomForestClassifier(random_state=42)
```

In [ ]:
```
cr_y_pred = rfc_clf.predict(X_test)

cnf_mx = confusion_matrix(y_test, cr_y_pred)
print(cnf_mx)
```

```
[[84 14]
 [30 26]]
```

In [ ]:
```
ConfusionMatrixDisplay.from_predictions(y_test, cr_y_pred, cmap='Blues');
```



In [ ]:
```
print(classification_report(y_test, cr_y_pred))
```

```
              precision    recall  f1-score   support

           0       0.74      0.86      0.79        98
           1       0.65      0.46      0.54        56

    accuracy                           0.71       154
   macro avg       0.69      0.66      0.67       154
weighted avg       0.71      0.71      0.70       154
```

KNN Classification

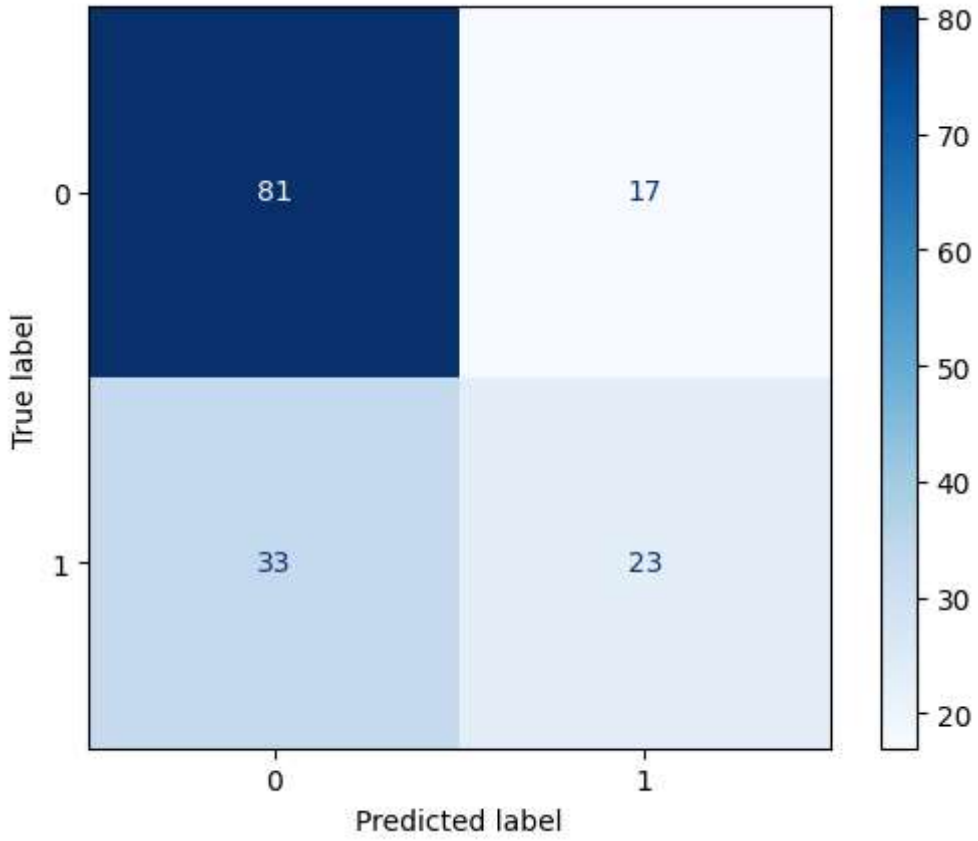
In [ ]:
```
knc = KNeighborsClassifier()
knc.fit(X_train, y_train)
```

Out[ ]:
```
▾ KNeighborsClassifier
KNeighborsClassifier()
```

In [ ]:
```
kn_y_pred = knc.predict(X_test)
cnf_mx = confusion_matrix(y_test, kn_y_pred)
print(cnf_mx)
```

```
[[81 17]
 [33 23]]
```

In [ ]:
```
ConfusionMatrixDisplay.from_predictions(y_test, kn_y_pred, cmap='Blues');
```



In [ ]:
```
print(classification_report(y_test, kn_y_pred))
```

```
              precision    recall  f1-score   support

           0       0.71      0.83      0.76        98
           1       0.57      0.41      0.48        56

    accuracy                           0.68       154
   macro avg       0.64      0.62      0.62       154
weighted avg       0.66      0.68      0.66       154
```

Decision Tree Classification

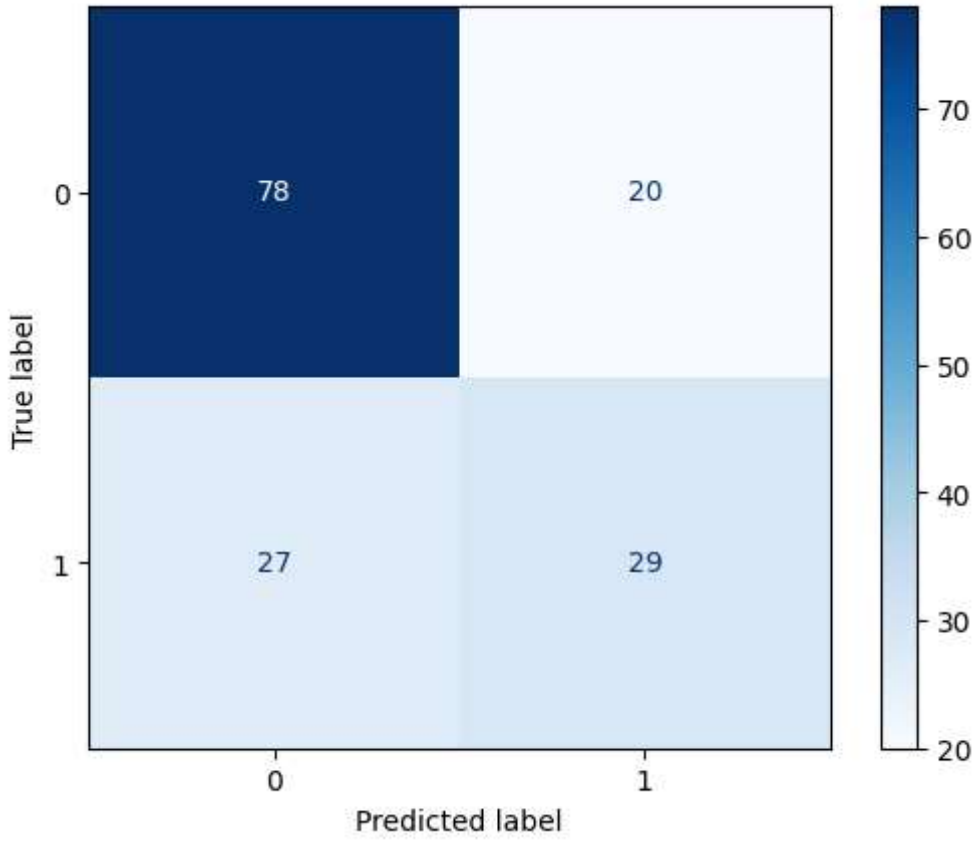
In [ ]:
```
dcf = DecisionTreeClassifier(random_state=42)
dcf.fit(X_train, y_train)
```

Out[ ]:
```
DecisionTreeClassifier(random_state=42)
```

In [ ]:
```
dcf_y_pred = dcf.predict(X_test)
cnf_mx = confusion_matrix(y_test, dcf_y_pred)
print(cnf_mx)
```

```
[[78 20]
 [27 29]]
```

In [ ]:
```
ConfusionMatrixDisplay.from_predictions(y_test, dcf_y_pred, cmap='Blues');
```



In [ ]:
```
print(classification_report(y_test, dcf_y_pred))
```

```
              precision    recall  f1-score   support

           0       0.74      0.80      0.77        98
           1       0.59      0.52      0.55        56

    accuracy                           0.69       154
   macro avg       0.67      0.66      0.66       154
weighted avg       0.69      0.69      0.69       154
```

Conclusion: Comparing the model accuracy and macro average for our models to our goal, we can't settle on choosing any of the models as a best prediction model since it doesn't meet our goal.

Recommendations:

- More data must be collected to enhance the prediction model.