## diabetesclassification

## September 27, 2024

```
[32]: # This Python 3 environment comes with many helpful analytics libraries
       \hookrightarrow installed
      # It is defined by the kaggle/python Docker image: https://github.com/kaggle/
       →docker-python
      # For example, here's several helpful packages to load
      import numpy as np # linear algebra
      import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
      # Input data files are available in the read-only "../input/" directory
      # For example, running this (by clicking run or pressing Shift+Enter) will list _{\sqcup}
       ⇔all files under the input directory
      import os
      for dirname, _, filenames in os.walk('/kaggle/input'):
          for filename in filenames:
              print(os.path.join(dirname, filename))
      # You can write up to 20GB to the current directory (/kaggle/working/) that ⊔
       →gets preserved as output when you create a version using "Save & Run All"
      # You can also write temporary files to /kaqqle/temp/, but they won't be saved
       ⇔outside of the current session
```

## /kaggle/input/diabetes/diabetes.csv

```
[33]: import pandas as pd
import warnings
warnings.filterwarnings("ignore", category=FutureWarning)
warnings.filterwarnings("ignore", category=UserWarning)
df = pd.read_csv("/kaggle/input/diabetes/diabetes.csv")
```

## [34]: df.info()

```
768 non-null
                                     int64
 0
     Pregnancies
 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
                    768 non-null
                                     float64
 6
     Pedigree
 7
                    768 non-null
                                     int64
     Age
     Outcome
                    768 non-null
                                     int64
dtypes: float64(2), int64(7)
```

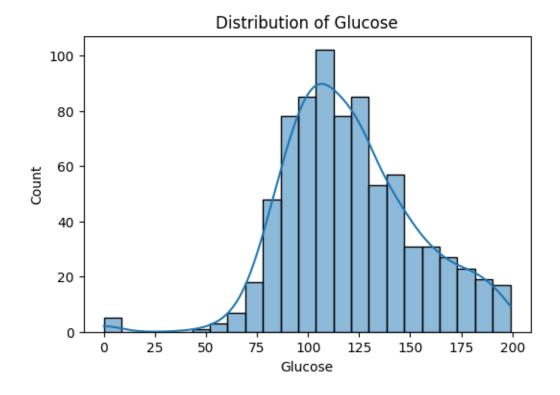
dtypes. 110at04(2), 111t04

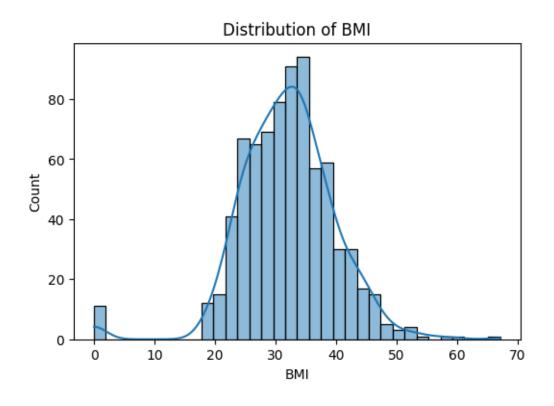
memory usage: 54.1 KB

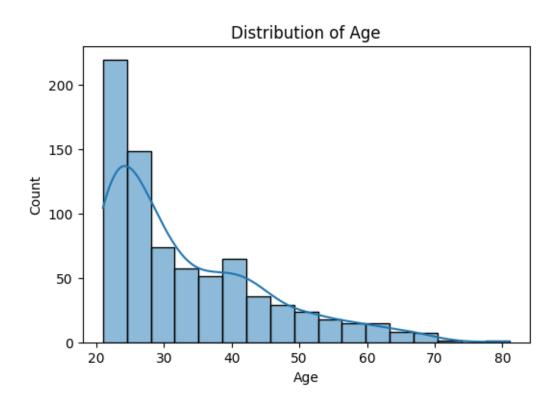
```
[35]: import matplotlib.pyplot as plt import seaborn as sns
```

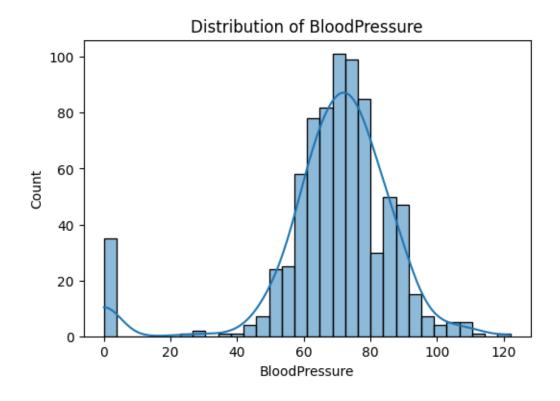
```
[36]: # Features to visualize
features = ['Glucose', 'BMI', 'Age', 'BloodPressure', 'Insulin']

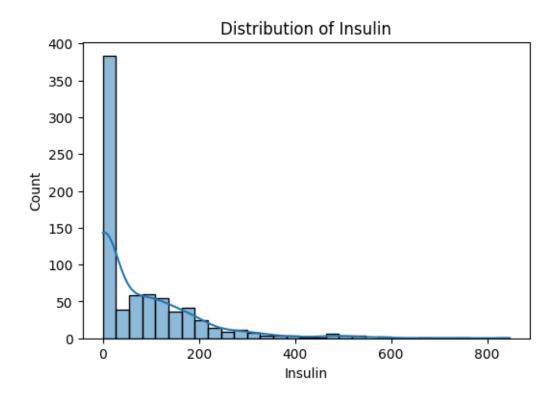
# Plotting distributions
for feature in features:
    plt.figure(figsize=(6,4))
    sns.histplot(df[feature], kde=True)
    plt.title(f'Distribution of {feature}')
    plt.show()
```



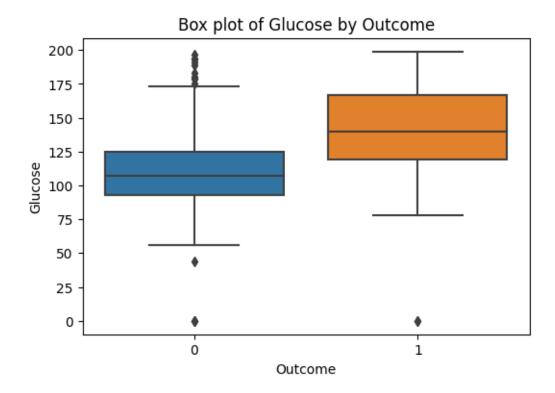


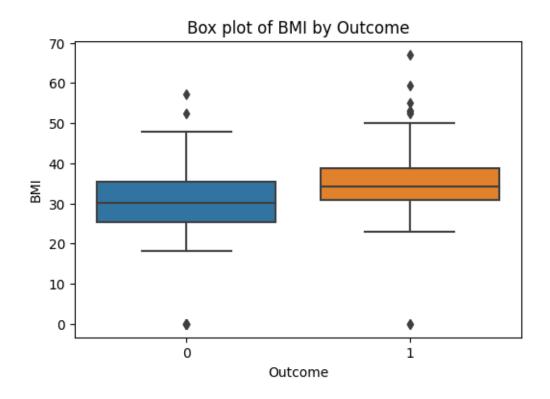


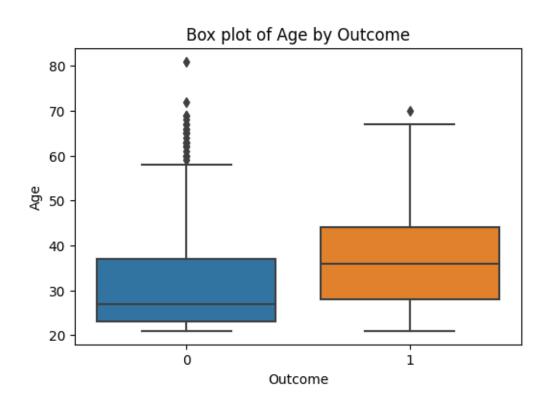


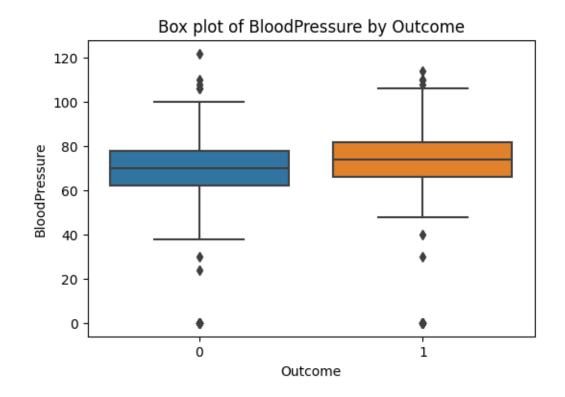


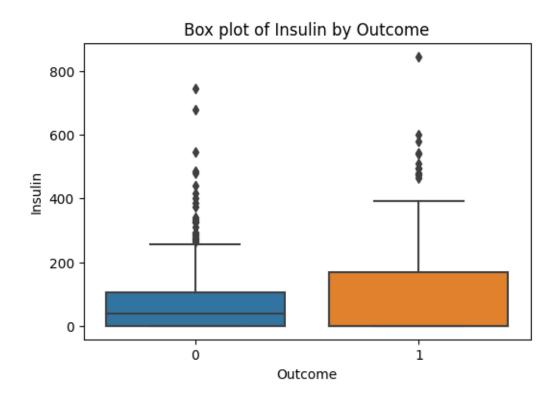
```
[37]: for feature in features:
    plt.figure(figsize=(6,4))
    sns.boxplot(data=df, x='Outcome', y=feature)
    plt.title(f'Box plot of {feature} by Outcome')
    plt.show()
```





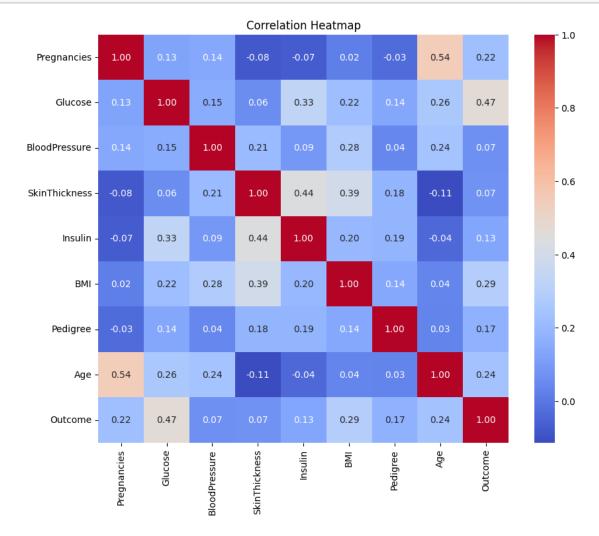




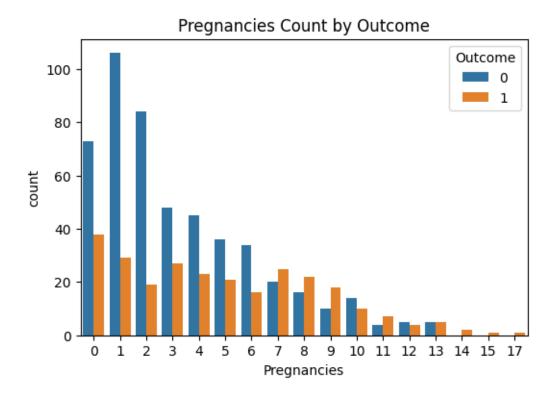


```
[38]: corr_matrix = df.corr()

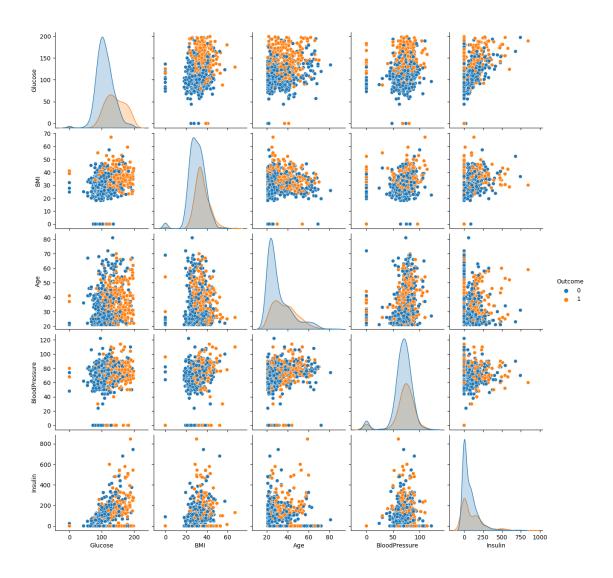
# Plot the heatmap
plt.figure(figsize=(10,8))
sns.heatmap(corr_matrix, annot=True, cmap='coolwarm', fmt='.2f')
plt.title('Correlation Heatmap')
plt.show()
```



```
[39]: plt.figure(figsize=(6,4))
    sns.countplot(data=df, x='Pregnancies', hue='Outcome')
    plt.title('Pregnancies Count by Outcome')
    plt.show()
```

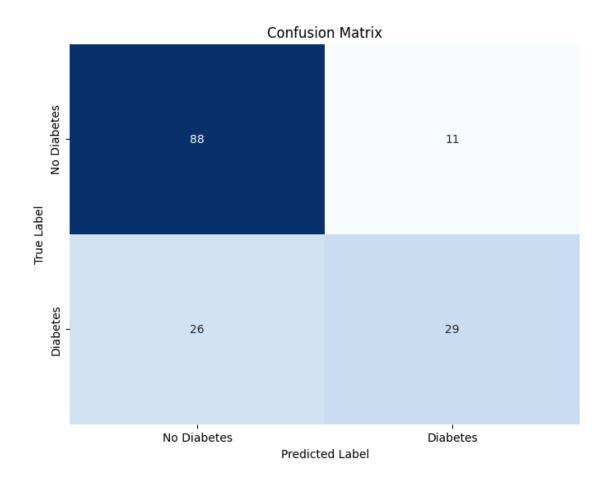


```
[40]: sns.pairplot(df, hue='Outcome', vars=['Glucose', 'BMI', 'Age', 'BloodPressure', \( \times'\) plt.show()
```



X\_test = scaler.transform(X\_test)

```
[44]: knn = KNeighborsClassifier(n_neighbors=18)
      knn.fit(X_train, y_train)
[44]: KNeighborsClassifier(n_neighbors=18)
[45]: y_pred = knn.predict(X_test)
[46]: error_rates = []
      for k in range(1, 21):
          knn = KNeighborsClassifier(n neighbors=k)
          knn.fit(X_train, y_train)
          y_pred_k = knn.predict(X_test)
          error_rates.append(np.mean(y_pred_k != y_test))
      print('Error rates for different k:', error_rates)
     Error rates for different k: [0.37662337662337664, 0.34415584415, 0.34415584416,
     0.2922077922077922, 0.2987012987012987, 0.3051948051948052, 0.2987012987012987,
     0.31818181818182, 0.2922077922077922, 0.3181818181818182, 0.3116883116883117,
     0.2922077922077922, 0.2792207792207792, 0.2922077922077922, 0.27272727272727,
     0.2792207792207792, 0.2532467532467532, 0.24675324675324675,
     0.24025974025974026, 0.24025974025974026, 0.24025974025974026]
[47]: import seaborn as sns
      import matplotlib.pyplot as plt
      from sklearn.metrics import confusion_matrix
      # Compute confusion matrix
      conf_matrix = confusion_matrix(y_test, y_pred)
      # Plot the confusion matrix using a heatmap
      plt.figure(figsize=(8,6))
      sns.heatmap(conf matrix, annot=True, fmt='d', cmap='Blues', cbar=False,
                  xticklabels=['No Diabetes', 'Diabetes'],
                  yticklabels=['No Diabetes', 'Diabetes'])
      plt.title('Confusion Matrix')
      plt.xlabel('Predicted Label')
      plt.ylabel('True Label')
      plt.show()
```



```
[48]: accuracy = accuracy_score(y_test, y_pred)
error_rate = 1 - accuracy
print('Accuracy:', accuracy)
print('Error Rate:', error_rate)
```

Accuracy: 0.7597402597402597 Error Rate: 0.24025974025974028

```
[49]: precision = precision_score(y_test, y_pred)
recall = recall_score(y_test, y_pred)
print('Precision:', precision)
print('Recall:', recall)
```

Precision: 0.725

Recall: 0.5272727272727272