Team Contributions

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Weihong Yang: 3. Training All Models | 4. Summary

Wei Chen: 5. Results Analysis | 6. Conclusion

1 Introduction

1.1 Abstract

This paper analyzes under the situation of the Heart Attack Patients discharged from the hospitals, if demographics factors and the hospital codes are given, could the researcher and the medical personnel forecast the mortality of this patients. To answer this question, we compared the performance of six classification models with Python packages, using the data of Heart Attack Patients from all of the hospitals in New York State in 1993, including sex, age, diagnosis and length of stay. These pipeline workflows start with ingesting the raw data, preprocessing, training, predicting, visualizing, analyzing, and interpreting the findings. Our result shows that the performance of decision trees model is the best among these classification models. Results also revealed that given the data groups in the training dataset are unbalanced (9:91), some predictive results from the models might lose their validations. From a safety perspective, we suggest relative personnel should use SMOTE algorithm (Synthetic Minority Oversampling Technique) to equalize the samples groups before traning the data.

1.2 Background

Heart disease is the leading cause of death for both men and women. More than half of the deaths due to heart disease were men in 2015. Patients who are suffering a heart attack, but did not have surgery might face a higher likelihood of death. According to the clinical data on Heart Attack Patients discharged from all of the hospitals in New York State in 1993, where the admitting diagnosis was an Acute Myocardial Infarction (AMI), also called a heart attack, who did not have surgery, there are several factors that would influent patients' death. It would be interesting to see if the factors are given, could medical staff predict the patients' death reversely. This paper uses different models to compare and discuss which model's predicted result is more realiable and accuratly, and comes to recommended forecasting for future clinical trial.

1.3 Data Analysis - Material and Method

The work methodology aims at understanding the factors related to demographics (sex, age) and hospital codes (diagnosis and length of stay) affecting the dying in the hospital. The statistical analysis was based on Python and R libraries using existing algorithms and methods of the machine-based data analysis (Cielen & Meysman, 2016; Halterman, 2011; Harrington, 2015; R Development Core Team, 2014). In this paper, a combination of various approaches has been used in the methodology workflow. The Python language was applied for importing and manipulating the variable data and training different models, combined with using several python packages to visualize the final result.

2.Data Preprocess

2.1 Collecting data

This dataset is provided by Health Process Management, Doylestown, PA. It contains variables related to demographics (sex, age), variables related to hospital codes (diagnosis, length of stay), variables related to cost (charges) and variables related to mortality (died, DRG). In this experience, we use the training dataset that contains 150 observations and 4 numeric variables. We select dying in the hospital (DIED) as our outcome variable, as it captures the correlation between patients' death and other possible factors that would cause the dying.

2.2 Exploring and preparing the data

After being preprocessing this data set by Python, 12000 data have been shown and they are divided into 8000 training data set and 4000 testing data set randomly for the purpose of traning the models.

```
from google.colab import drive
drive.mount('/content/drive')
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call
```

```
import pandas as pd

# Read the CSV file
heart_attack_data = pd.read_csv("/content/drive/MyDrive/WeihongYang/whole_table.csv

# Assign the data to the 'data' variable
data = heart_attack_data
```

```
import pandas as pd
import numpy as np

data["DIAGNOSIS"] = data["DIAGNOSIS"] - 41001
data["SEX"].replace("F",1,inplace = True)
data["SEX"].replace("M",2,inplace = True)
data = data.drop(["Patient","DRG","CHARGES"],axis = 1)
print(data)
```

```
       DIAGNOSIS  SEX  DIED  LOS  AGE
0             40    1     0   10   79
1             40    1     0    6   34
2             90    1     0    5   76
3             80    1     0    2   80
4             90    2     0    1   55
...          ...  ...   ...  ...  ...
12839         40    1     0   14   79
12840         90    1     0    7   91
12841         90    1     0    9   79
12842         50    2     0    5   70
12843         90    2     1    1   81

[12844 rows x 5 columns]
```

```
print(data.describe())
```

```
            DIAGNOSIS           SEX          DIED           LOS           AGE
count  12844.000000  12844.000000  12844.000000  12844.000000  12844.000000
mean      58.962161      1.605652      0.109779      7.568670     66.290330
std       31.740089      0.488729      0.312626      5.114986     13.654382
min        0.000000      1.000000      0.000000      0.000000     20.000000
25%       40.000000      1.000000      0.000000      4.000000     57.000000
50%       70.000000      2.000000      0.000000      7.000000     67.000000
75%       90.000000      2.000000      0.000000     10.000000     77.000000
max       90.000000      2.000000      1.000000     38.000000    103.000000
```

```
train_samples = 1200
train = data[:train_samples]
test= data[train_samples:]
```

Then, we take out the column DIED from the training data and keep the rest of the features as train_data variable; we also assign train_died_y variable as the value of column DIED. Therefore, the train_data is the input feature of the training dataset, and the train_died_y is the predict labels of the training dataset. It works as the same as the test_data and the test_died_y, where the test_data is the input feature of the testing dataset and the test_died_y is the predict labels of the testing dataset.

```
train_data = train.drop('DIED', axis = 1)
train_died_y = np.array(train.loc[:, 'DIED'].values)
test_data = test.drop('DIED', axis = 1)
test_died_y = test.loc[:, 'DIED'].values
```

3. Traing Models

Approchs Include:

3.1 Naive Bayes | 3.2 k-Nearest Neighbors | 3.3 Decision Tree | 3.4 Logistic Regression | 3.5 Support Vector Machine | 3.6 Neural Network(MLP)

3.1 Naive Bayes Method:

Naive Bayes Approach

- Naive Bayes is a family of probabilistic supervised learning algorithms based on Bayes' theorem.
- It is particularly useful for classification tasks and can handle both binary and multi-class problems.
- Naive Bayes models are simple and efficient, making them well-suited for high-dimensional datasets or when a quick solution is needed.

Why to use:

- They work well when the independence assumption holds between the features, although this assumption may not always hold in practice.
- Naive Bayes models are also less prone to overfitting compared to other more complex models.

Implementation Specifics:

The code first trains a Gaussian Naive Bayes model using the training dataset and computes the accuracy on the testing dataset. It also computes the recall (sensitivity) for both the 'Died' and 'Not Died' classes using the confusion matrix.

```
from sklearn.neural_network import MLPClassifier
from sklearn.neighbors import  KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.naive_bayes import GaussianNB
from sklearn.svm import SVC
import numpy as np
from sklearn import metrics
```

```
print("** Naive Bayes **")

NB = GaussianNB()
NB.fit(train_data,train_died_y)

predict_y = NB.predict(test_data)
acc = NB.score(test_data, test_died_y)
m = metrics.confusion_matrix(test_died_y, predict_y)

D_recall = m[1][1]/(m[1][0] + m[1][1])
ND_recall = m[0][0]/(m[0][0] + m[0][1])
Precision = m[1][1] / (m[1][1] + m[0][1])
F1_score = 2 * (Precision * D_recall) / (Precision + D_recall)

print("Test accuracy", acc)
print("DIED recall:",D_recall)
print("No DIED recall:",ND_recall)
```

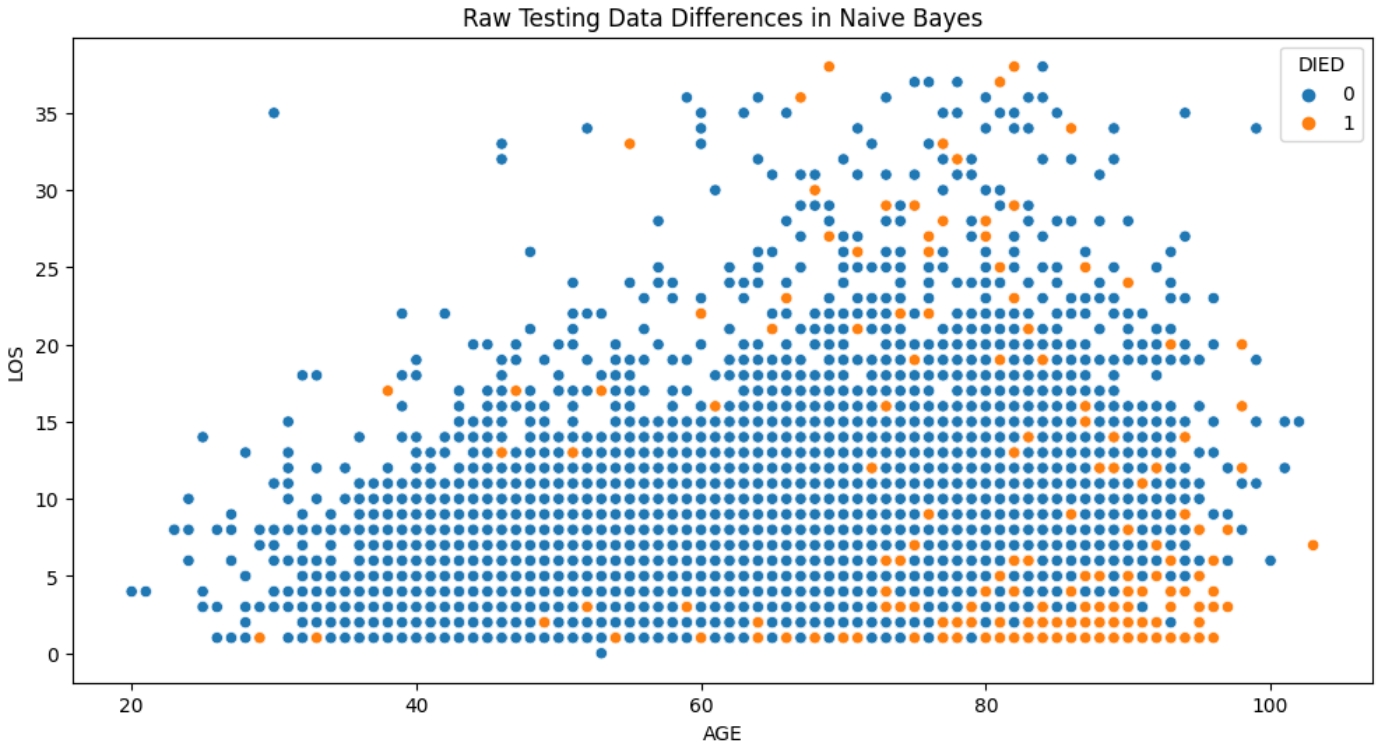
```
** Naive Bayes **
Test accuracy 0.8945379594641016
DIED recall: 0.051261829652996846
No DIED recall: 0.9975905936777179
```

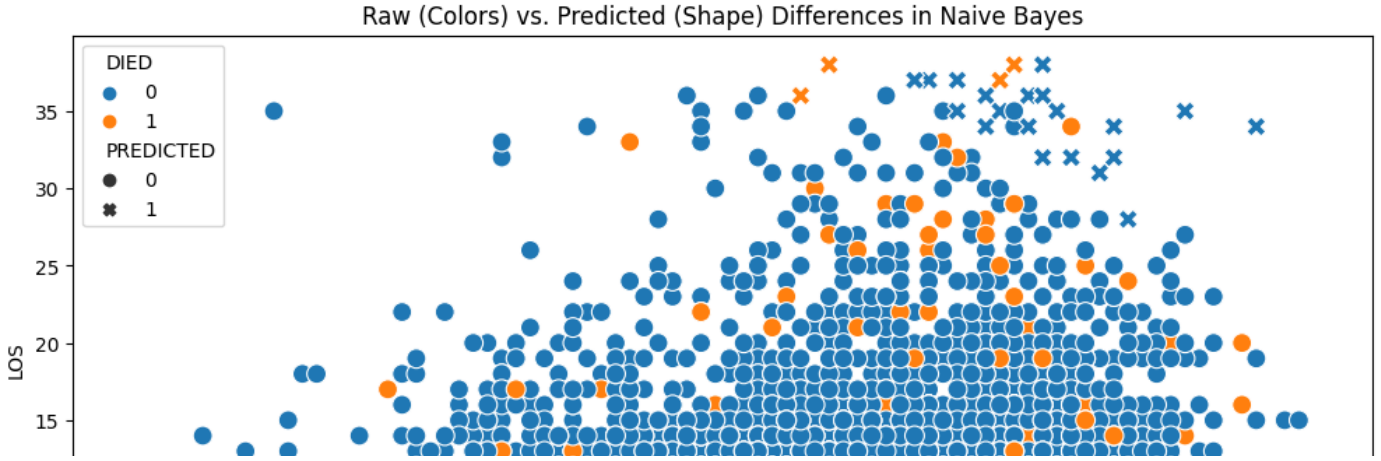
```
print("** Naive Bayes **")

D_precision = m[1][1] / (m[1][1] + m[0][1]) if (m[1][1] + m[0][1]) != 0 else 0
ND_precision = m[0][0] / (m[0][0] + m[1][0])
D_f1 = 2 * (D_precision * D_recall) / (D_precision + D_recall) if (D_precision + D_
ND_f1 = 2 * (ND_precision * ND_recall) / (ND_precision + ND_recall)

print("Died Precision:", D_precision)
print("Not Died Precision:", ND_precision)
print("Died F1-score:", D_f1)
print("Not Died F1-score:", ND_f1)
```

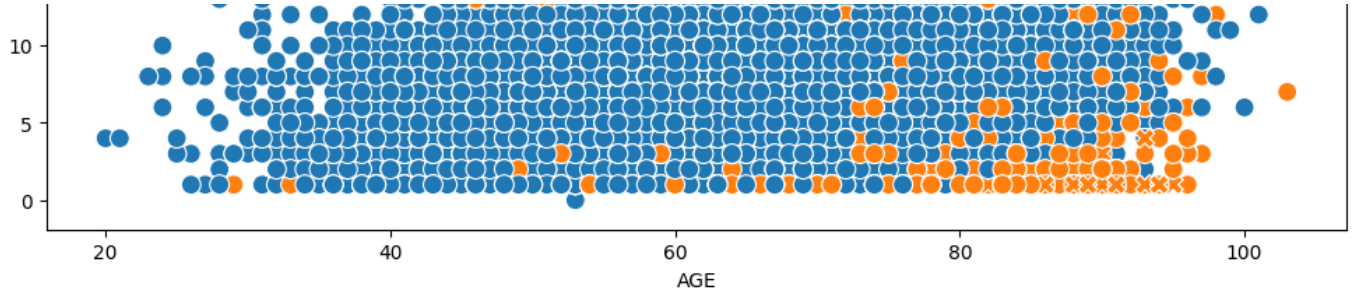
```
** Naive Bayes **
Died Precision: 0.7222222222222222
Not Died Precision: 0.895880214644279
Died F1-score: 0.09572901325478646
Not Died F1-score: 0.9440036479708162
```

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


test_data_with_died = test_data.copy()
test_data_with_died['DIED'] = test_died_y
```

```
# Create the first plot (Raw Testing Data Differences in Naive Bayes)
plt.figure(figsize=(12, 6))
sns.scatterplot(data=test_data_with_died, x='AGE', y='LOS', hue='DIED')
plt.title("Raw Testing Data Differences in Naive Bayes")
plt.legend(title='DIED')

test_data_with_predicted = test_data.copy()
test_data_with_predicted['DIED'] = test_died_y
test_data_with_predicted['PREDICTED'] = predict_y

# Create the second plot (Raw (Colors) vs. Predicted (Shape) Differences in Naive E
plt.figure(figsize=(12, 6))
sns.scatterplot(data=test_data_with_predicted, x='AGE', y='LOS', hue='DIED', style=
plt.title("Raw (Colors) vs. Predicted (Shape) Differences in Naive Bayes")
plt.show()
```





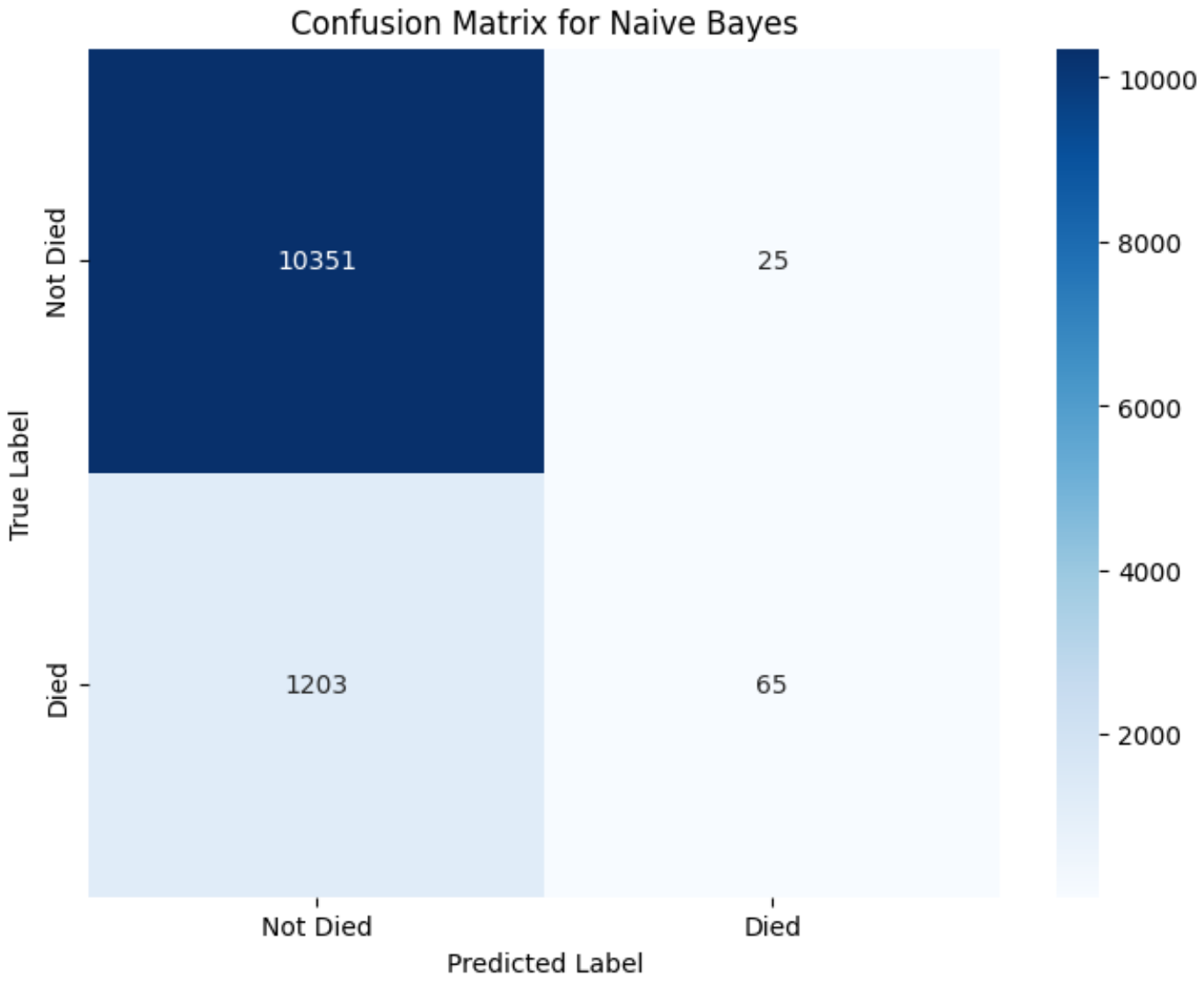


It then creates two plots:

1. A scatter plot showing the raw testing data differences with:
    - 'AGE' on the x-axis.
    - 'LOS' on the y-axis,
    - 'DIED' attribute as the color-coding.
2. A scatter plot showing the raw (colors) vs. predicted (shape) differences with 'AGE' on the x

- Yellow dots: Patients acutally died.
- Blue dots: Patients who still alive.
- Blue circle | Yellow cross: means the model’s prediction is correct.
- Yellow circle and Blue cross: means the model’s prediction is wrong.

```
# Plot the confusion matrix as a heatmap
plt.figure(figsize=(8, 6))
sns.heatmap(m, annot=True, fmt='d', cmap='Blues', xticklabels=['Not Died', 'Died'],
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('Confusion Matrix for Naive Bayes')
plt.show()
```



Under the Naive Bayes Method prediction:

- The graph shows that there are 65 True Positive, which mean this methods successfully predict 65 paitent's death while make error on 1203 False Negative on the alive patient group, which mean this methods's prediction on paitent's death is not reliabile but it can still successfully predict one paient is alive.

3.2 KNN Method

k-Nearest Neighbors Approach

- The k-Nearest Neighbors (k-NN) model is a non-parametric supervised learning algorithm used for both classification and regression tasks.
- The algorithm uses a distance metric (such as Euclidean, Manhattan, or Minkowski distance) to calculate the similarity between data points.
- In classification, the algorithm assigns the majority class label among the k nearest neighbors to the test data point.
- In regression, the algorithm assigns the average of the k nearest neighbors' target values as the predicted value.

Why to use:

- k-NN is a simple and easy-to-understand algorithm that does not require training and can work well when the data is low-dimensional.

Implementation Specifics:

The code first trains a k-Nearest Neighbors model using the training dataset and computes the accuracy on the testing dataset. It also computes the recall (sensitivity) for both the 'Died' and 'Not Died' classes using the confusion matrix.

```
print("** KNN Method **")

knn=KNeighborsClassifier()
knn.fit(train_data,train_died_y)

predict_y = knn.predict(test_data)
acc = knn.score(test_data, test_died_y)
m = metrics.confusion_matrix(test_died_y, predict_y)
D_recall = m[1][1]/(m[1][0] + m[1][1])
ND_recall = m[0][0]/(m[0][0] + m[0][1])

print("Test accuracy", acc)
print("DIED recall:",D_recall)
print("No DIED recall:",ND_recall)
```

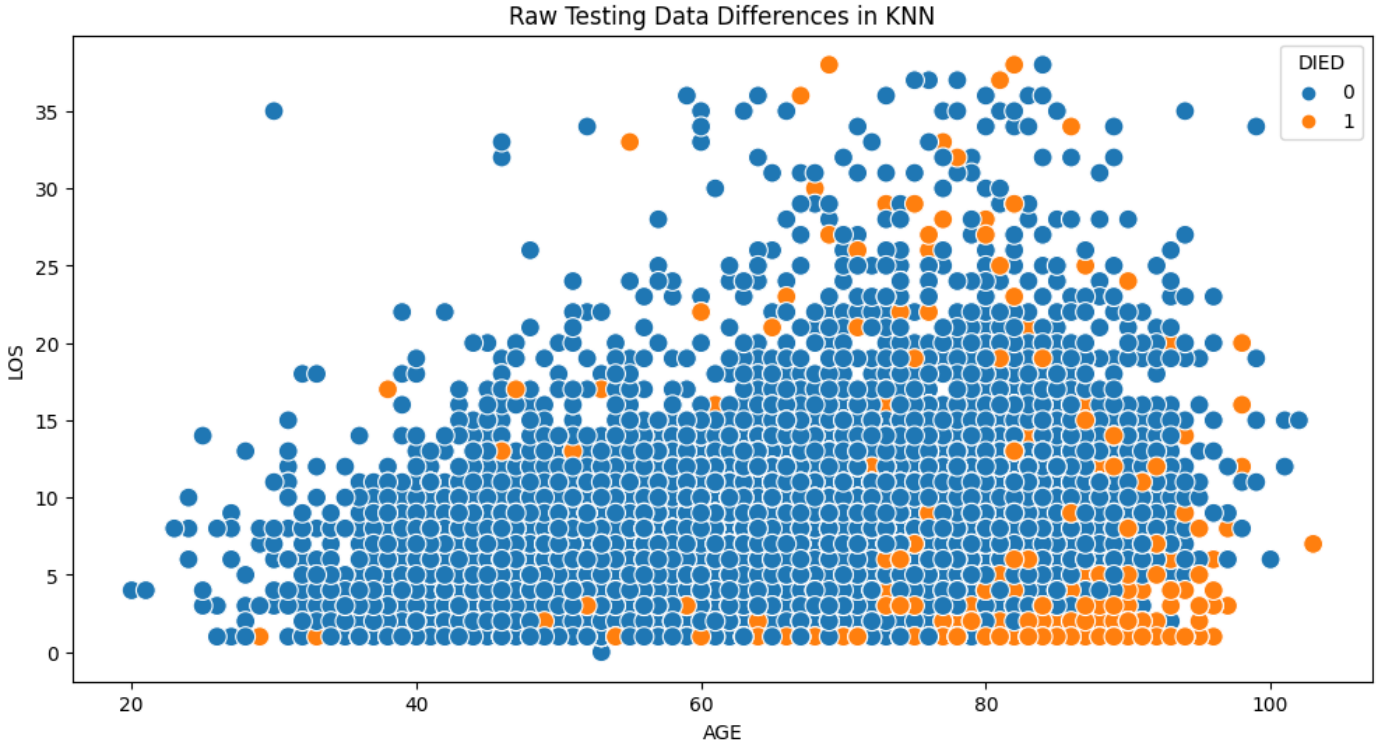
```
** KNN Method **
Test accuracy 0.8996049467536928
DIED recall: 0.35410094637223977
No DIED recall: 0.9662683114880494
```

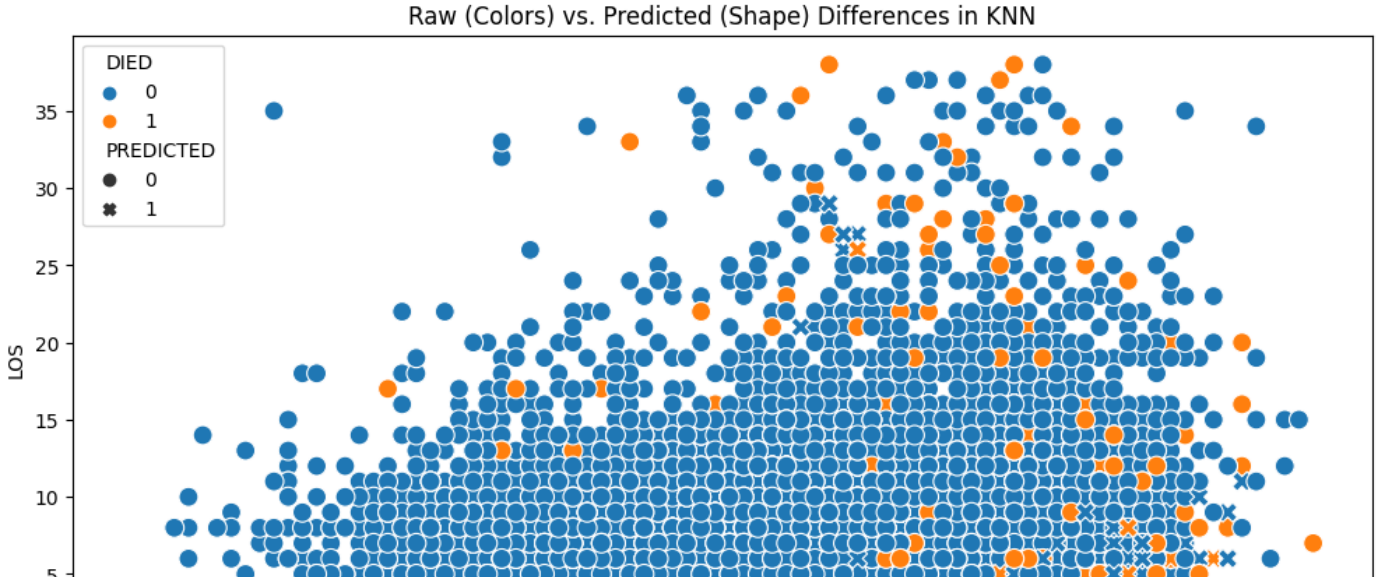
```
print("** KNN Method **")

D_precision = m[1][1] / (m[1][1] + m[0][1]) if (m[1][1] + m[0][1]) != 0 else 0
ND_precision = m[0][0] / (m[0][0] + m[1][0])
D_f1 = 2 * (D_precision * D_recall) / (D_precision + D_recall) if (D_precision + D_
ND_f1 = 2 * (ND_precision * ND_recall) / (ND_precision + ND_recall)

print("Died Precision:", D_precision)
print("Not Died Precision:", ND_precision)
print("Died F1-score:", D_f1)
print("Not Died F1-score:", ND_f1)
```

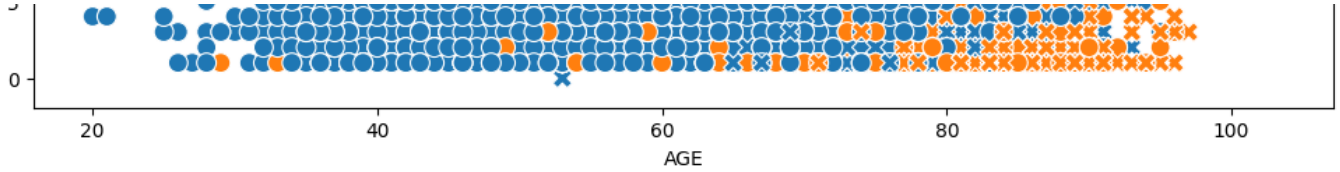
```
** KNN Method **
Died Precision: 0.5619524405506884
Not Died Precision: 0.9244813278008299
Died F1-score: 0.43444605708756656
Not Died F1-score: 0.944913057820084
```

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

def plot_raw_vs_predicted(title, test_data, test_died_y, predict_y):
    test_data_with_died = test_data.copy()
    test_data_with_died['DIED'] = test_died_y

    plt.figure(figsize=(12, 6))
    sns.scatterplot(data=test_data_with_died, x='AGE', y='LOS', hue='DIED', s=100 )
```

```
    plt.title(f"Raw Testing Data Differences in {title}")
    plt.legend(title='DIED')

    test_data_with_predicted = test_data.copy()
    test_data_with_predicted['DIED'] = test_died_y
    test_data_with_predicted['PREDICTED'] = predict_y

    plt.figure(figsize=(12, 6))
    sns.scatterplot(data=test_data_with_predicted, x='AGE', y='LOS', hue='DIED', st
    plt.title(f"Raw (Colors) vs. Predicted (Shape) Differences in {title}")
    plt.show()

plot_raw_vs_predicted('KNN', test, test_died_y, predict_y)
```



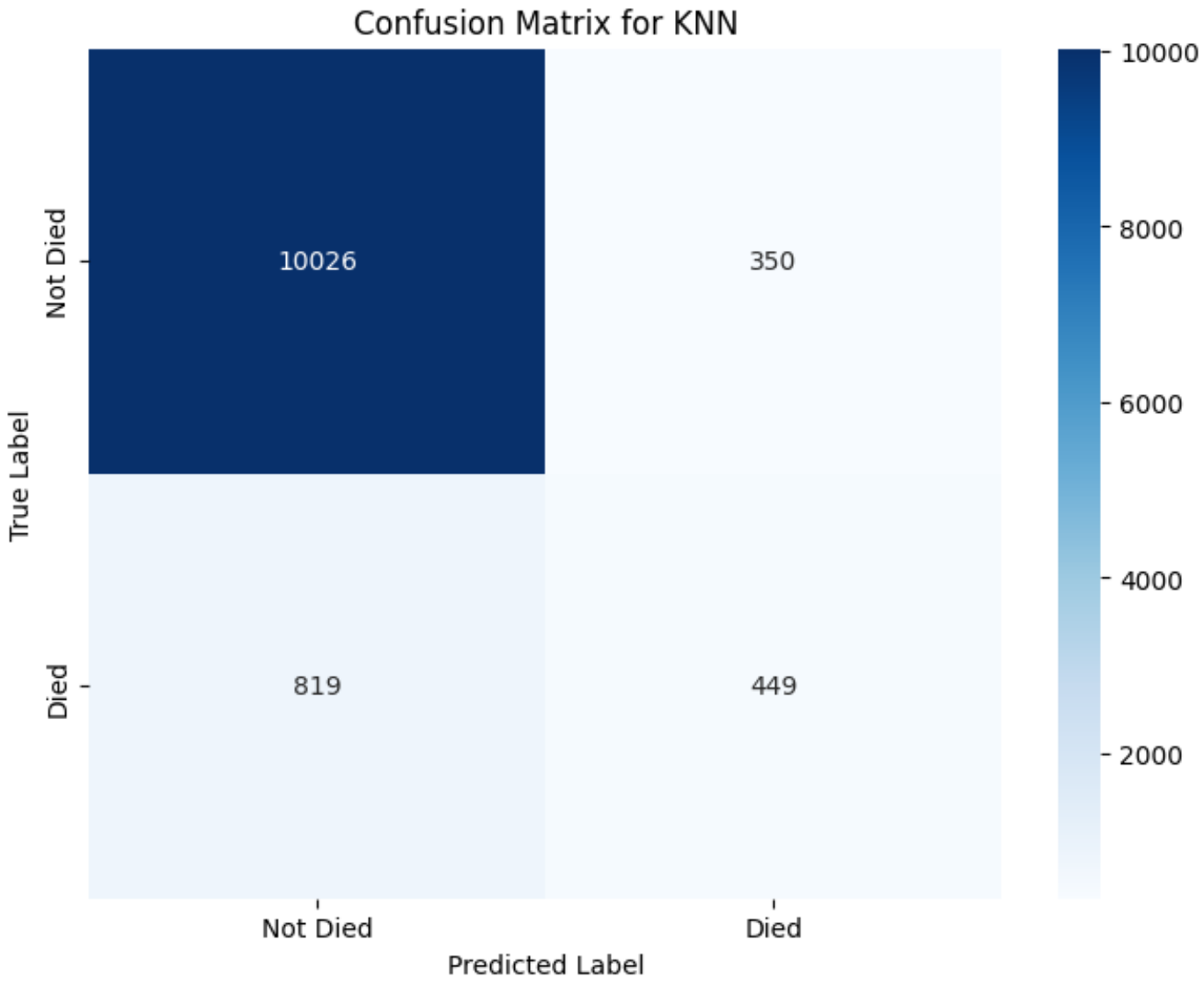




It then creates two plots:

1. A scatter plot showing the raw testing data differences with:
    - 'AGE' on the x-axis.
    - 'LOS' on the y-axis,
    - 'DIED' attribute as the color-coding.
2. A scatter plot showing the raw (colors) vs. predicted (shape) differences with 'AGE' on the x
    - Yellow dots: Patients acutally died.
    - Blue dots: Patients who still alive.
    - Blue circle | Yellow cross: means the model's prediction is correct.
    - Yellow circle and Blue cross: means the model's prediction is wrong.

```
# Plot the confusion matrix as a heatmap
plt.figure(figsize=(8, 6))
sns.heatmap(m, annot=True, fmt='d', cmap='Blues', xticklabels=['Not Died', 'Died'],
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('Confusion Matrix for KNN')
plt.show()
```



Under the KNN prediction:

- The graph shows that there are 449 True Positive, which mean this methods successfully predict 449 paitent's death while make error on 819 False Negative on the alive patient group, which mean this methods's prediction on paitent's death is not reliabile but it can still successfully predict one paient is alive.

3.3 Decision Tree Method

Decision Tree Approach

- A Decision Tree is a supervised learning model used for both classification and regression tasks.
- It is a tree-like structure where each internal node represents a feature or attribute, each branch represents a decision rule based on the feature value, and each leaf node represents the outcome or a class label (in classification) or a continuous value (in regression).

Why to use:

- Decision Trees are easy to understand and interpret, and can handle both categorical and numerical data.
- They can also handle missing values and outliers.
- However, decision trees can be prone to overfitting and may not generalize well to new data.

Implementation Specifics:

The code first trains a Decision Tree model using the training dataset and computes the accuracy on the testing dataset. It also computes the recall (sensitivity) for both the 'Died' and 'Not Died' classes using the confusion matrix.

```
print("** DecisionTree Method ** ")

tree = DecisionTreeClassifier(random_state=0)
tree.fit(train_data,train_died_y)

predict_y = tree.predict(test_data)
acc = tree.score(test_data, test_died_y)
m = metrics.confusion_matrix(test_died_y, predict_y)
D_recall = m[1][1]/(m[1][0] + m[1][1])
ND_recall = m[0][0]/(m[0][0] + m[0][1])

print("Test accuracy", acc)
print("DIED samples recall:",D_recall)
print("No DIED samples recall:",ND_recall)
```

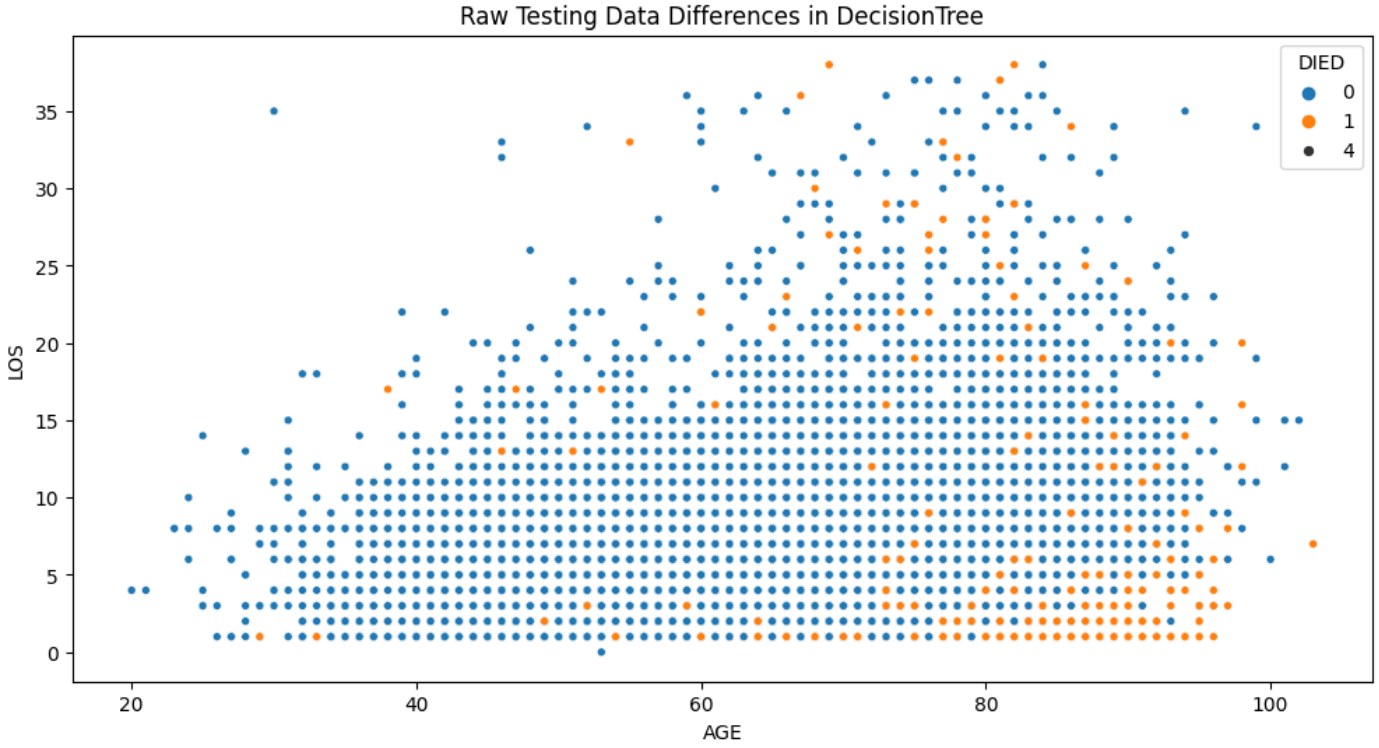
```
** DecisionTree Method **
Test accuracy 0.8549467536928891
DIED samples recall: 0.40930599369085174
No DIED samples recall: 0.9094063222821896
```

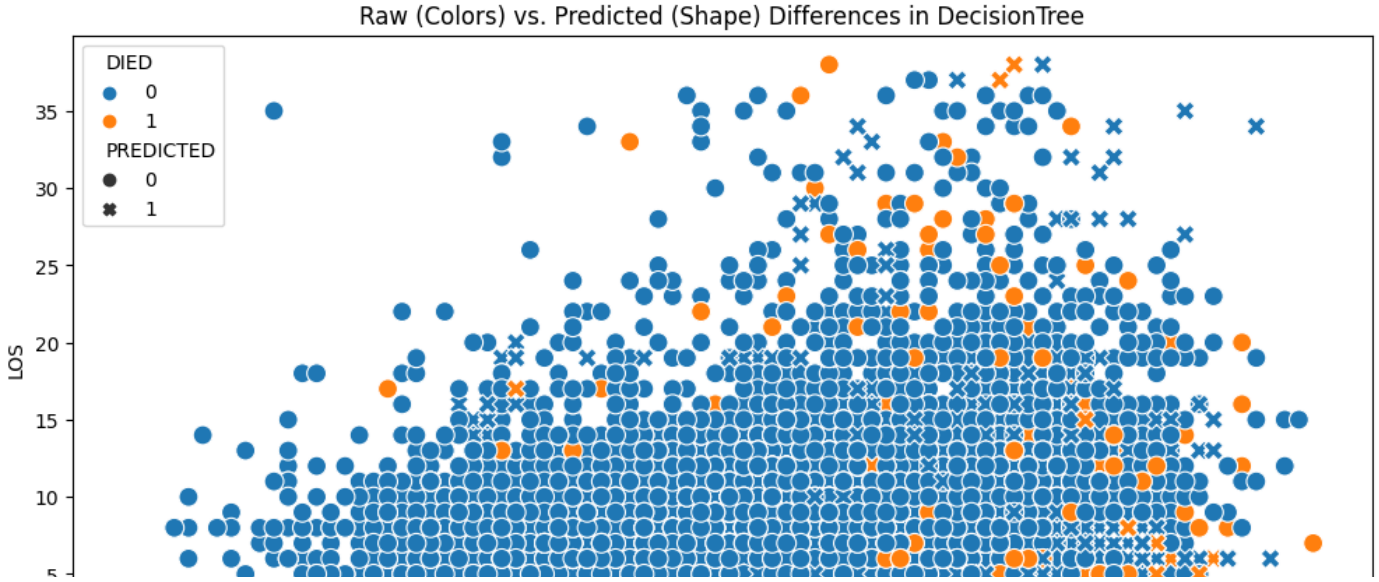
```
print("** DecisionTree Method ** ")

D_precision = m[1][1] / (m[1][1] + m[0][1]) if (m[1][1] + m[0][1]) != 0 else 0
ND_precision = m[0][0] / (m[0][0] + m[1][0])
D_f1 = 2 * (D_precision * D_recall) / (D_precision + D_recall) if (D_precision + D_
ND_f1 = 2 * (ND_precision * ND_recall) / (ND_precision + ND_recall)

print("Died Precision:", D_precision)
print("Not Died Precision:", ND_precision)
print("Died F1-score:", D_f1)
print("Not Died F1-score:", ND_f1)
```

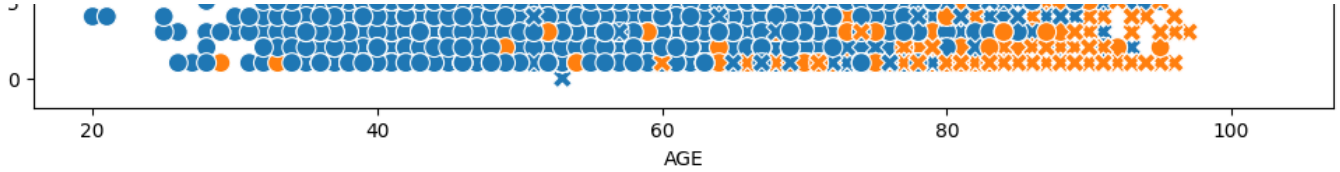
```
** DecisionTree Method **
Died Precision: 0.3557230980123372
Not Died Precision: 0.9264604810996564
Died F1-score: 0.3806380638063806
Not Died F1-score: 0.9178541899713049
```

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

def plot_raw_vs_predicted(title, test_data, test_died_y, predict_y):
    test_data_with_died = test_data.copy()
    test_data_with_died['DIED'] = test_died_y

    plt.figure(figsize=(12, 6))
    sns.scatterplot(data=test_data_with_died, x='AGE', y='LOS', hue='DIED', size=4)
```

```
    plt.title(f"Raw Testing Data Differences in {title}")
    plt.legend(title='DIED')

    test_data_with_predicted = test_data.copy()
    test_data_with_predicted['DIED'] = test_died_y
    test_data_with_predicted['PREDICTED'] = predict_y

    plt.figure(figsize=(12, 6))
    sns.scatterplot(data=test_data_with_predicted, x='AGE', y='LOS', hue='DIED', st
    plt.title(f"Raw (Colors) vs. Predicted (Shape) Differences in {title}")
    plt.show()

plot_raw_vs_predicted('DecisionTree', test, test_died_y, predict_y)
```





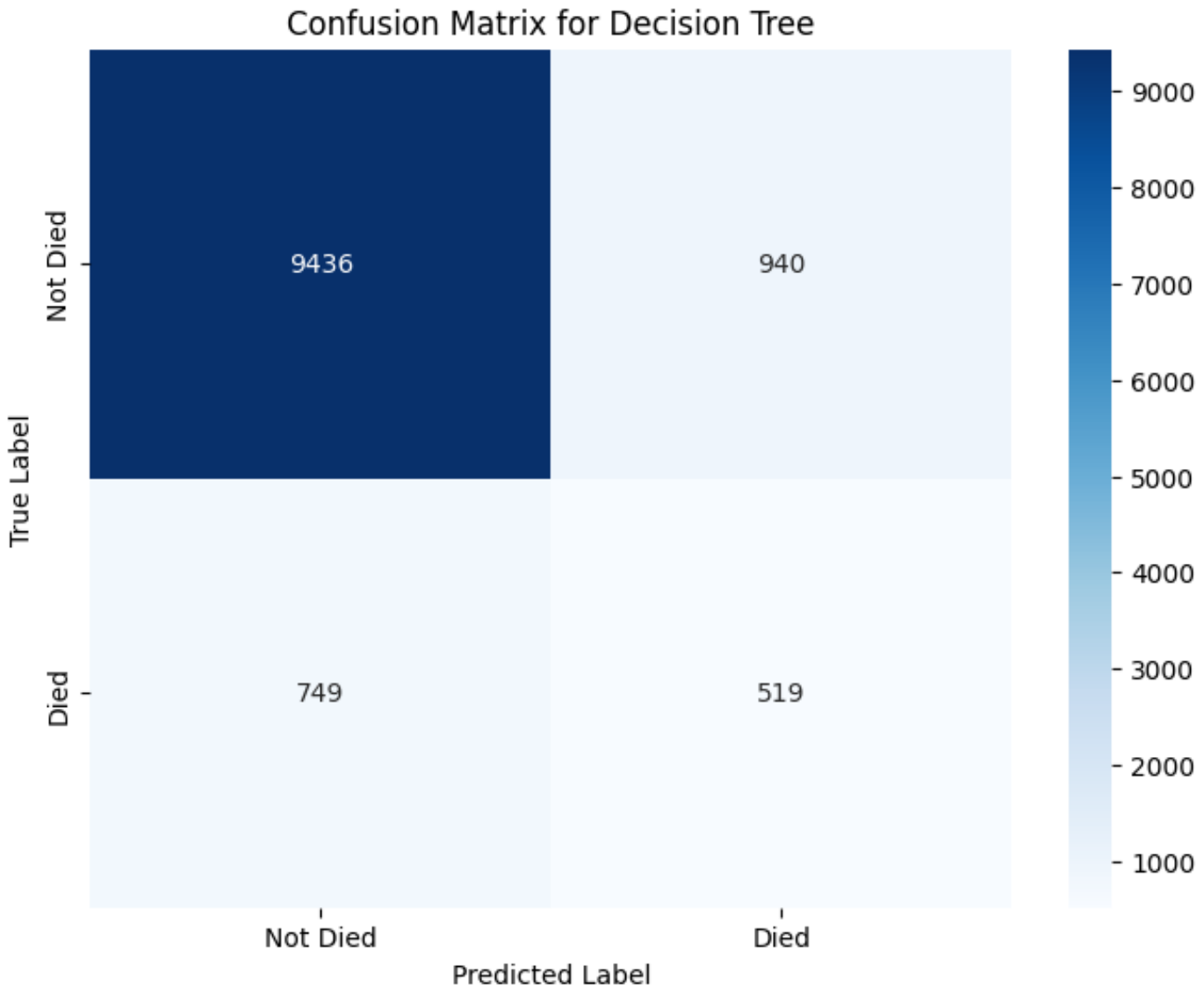


It then creates two plots:

1. A scatter plot showing the raw testing data differences with:
    - 'AGE' on the x-axis.
    - 'LOS' on the y-axis,
    - 'DIED' attribute as the color-coding.
2. A scatter plot showing the raw (colors) vs. predicted (shape) differences with 'AGE' on the x

- Yellow dots: Patients acutally died.
- Blue dots: Patients who still alive.
- Blue circle | Yellow cross: means the model’s prediction is correct.
- Yellow circle and Blue cross: means the model’s prediction is wrong.

```
# Plot the confusion matrix as a heatmap
plt.figure(figsize=(8, 6))
sns.heatmap(m, annot=True, fmt='d', cmap='Blues', xticklabels=['Not Died', 'Died'],
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('Confusion Matrix for Decision Tree')
plt.show()
```



- The graph shows that under the Decision Tree Method prediction, there are 519 True Positive, which mean this methods successfully predict 519 paitent's death while make error on 749 False Negative on the alive patient group.

3.4 Logistics Regression Method

Logistic Regression Approach

- Logistic Regression is a statistical and machine learning model used for binary classification tasks.
- It models the relationship between a continuous dependent variable and one or more independent variables.

Why to use:

- Logistic Regression models are simple and easy to interpret, and can handle both categorical and numerical data.
- They can also provide probabilistic predictions, which can be useful for decision making.
- However, logistic regression assumes a linear relationship between the input features and the output, which may not hold in practice.

Implementation Specifics:

The code first trains a Logistic Regression model using the training dataset and computes the accuracy on the testing dataset. It also computes the recall (sensitivity) for both the 'Died' and 'Not Died' classes using the confusion matrix.

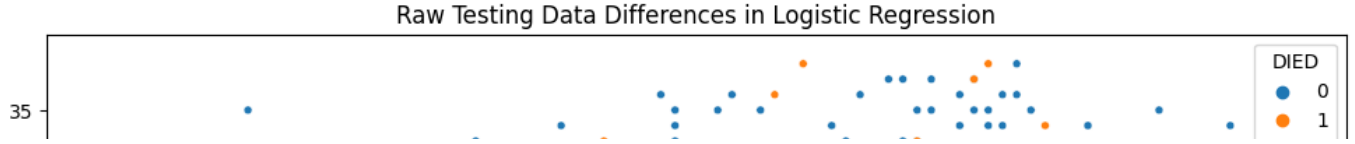
```
print("** Logistic Regression **")

lr=LogisticRegression()
lr.fit(train_data,train_died_y)

predict_y = lr.predict(test_data)
acc = lr.score(test_data, test_died_y)
m = metrics.confusion_matrix(test_died_y, predict_y)
D_recall = m[1][1]/(m[1][0] + m[1][1])
ND_recall = m[0][0]/(m[0][0] + m[0][1])

print("Test accuracy", acc)
print("Died Recall:", D_recall)
print("Not Died Recall:", ND_recall)
```

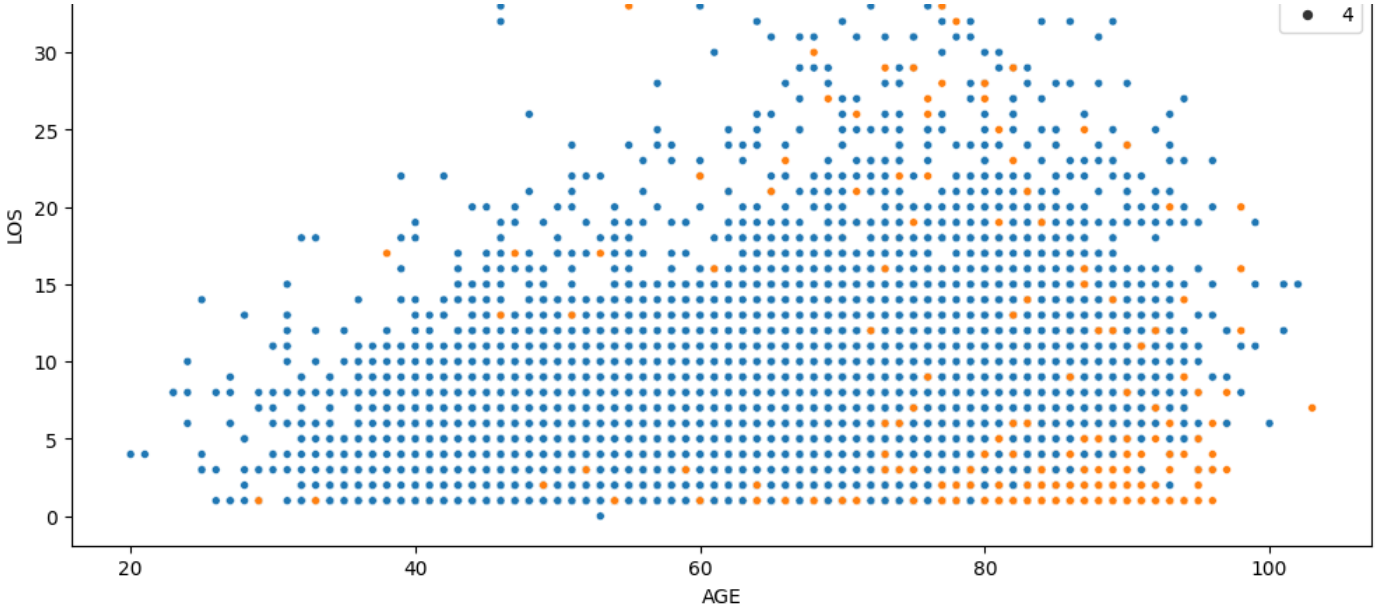
```
** Logistic Regression **
Test accuracy 0.9074201305393336
Died Recall: 0.20110410094637224
Not Died Recall: 0.9937355435620663
```

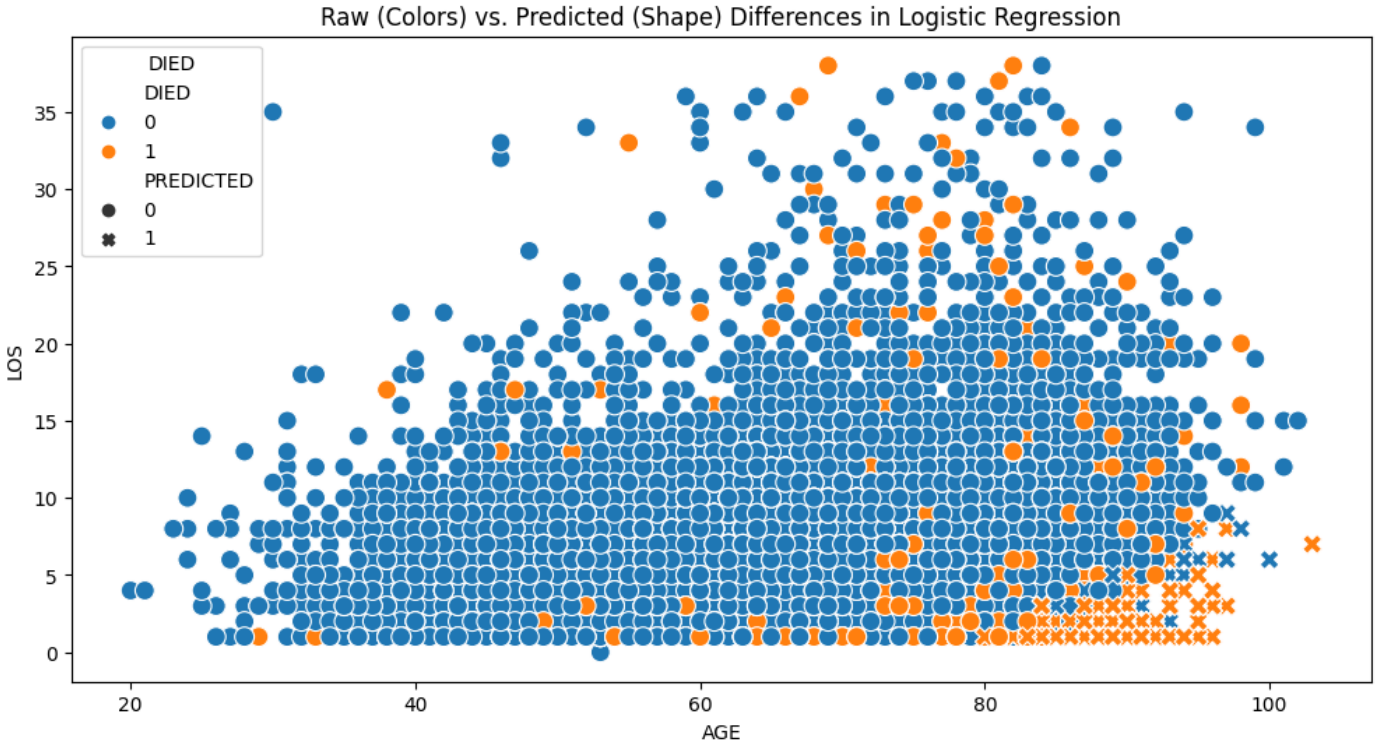
```
print("** Logistic Regression **")

D_precision = m[1][1] / (m[1][1] + m[0][1]) if (m[1][1] + m[0][1]) != 0 else 0
ND_precision = m[0][0] / (m[0][0] + m[1][0])
D_f1 = 2 * (D_precision * D_recall) / (D_precision + D_recall) if (D_precision + D_
ND_f1 = 2 * (ND_precision * ND_recall) / (ND_precision + ND_recall)

print("Died Precision:", D_precision)
print("Not Died Precision:", ND_precision)
print("Died F1-score:", D_f1)
print("Not Died F1-score:", ND_f1)
```

```
** Logistic Regression **
Died Precision: 0.796875
Not Died Precision: 0.9105439773931473
Died F1-score: 0.3211586901763224
Not Died F1-score: 0.9503225806451613
```

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

def plot_raw_vs_predicted(title, test_data, test_died_y, predict_y):
    test_data_with_died = test_data.copy()
    test_data_with_died['DIED'] = test_died_y

    plt.figure(figsize=(12, 6))
    sns.scatterplot(data=test_data_with_died, x='AGE', y='LOS', hue='DIED', size=4)
    plt.title(f"Raw Testing Data Differences in {title}")
    plt.legend(title='DIED')

    test_data_with_predicted = test_data.copy()
    test_data_with_predicted['DIED'] = test_died_y
    test_data_with_predicted['PREDICTED'] = predict_y

    plt.figure(figsize=(12, 6))
    sns.scatterplot(data=test_data_with_predicted, x='AGE', y='LOS', hue='DIED', st
    plt.title(f"Raw (Colors) vs. Predicted (Shape) Differences in {title}")
    plt.legend(title='DIED')

    plt.show()

plot_raw_vs_predicted('Logistic Regression', test, test_died_y, predict_y)
```




4
LOS
AGE
0
5
10
15
20
25
30
20
40
60
80
100

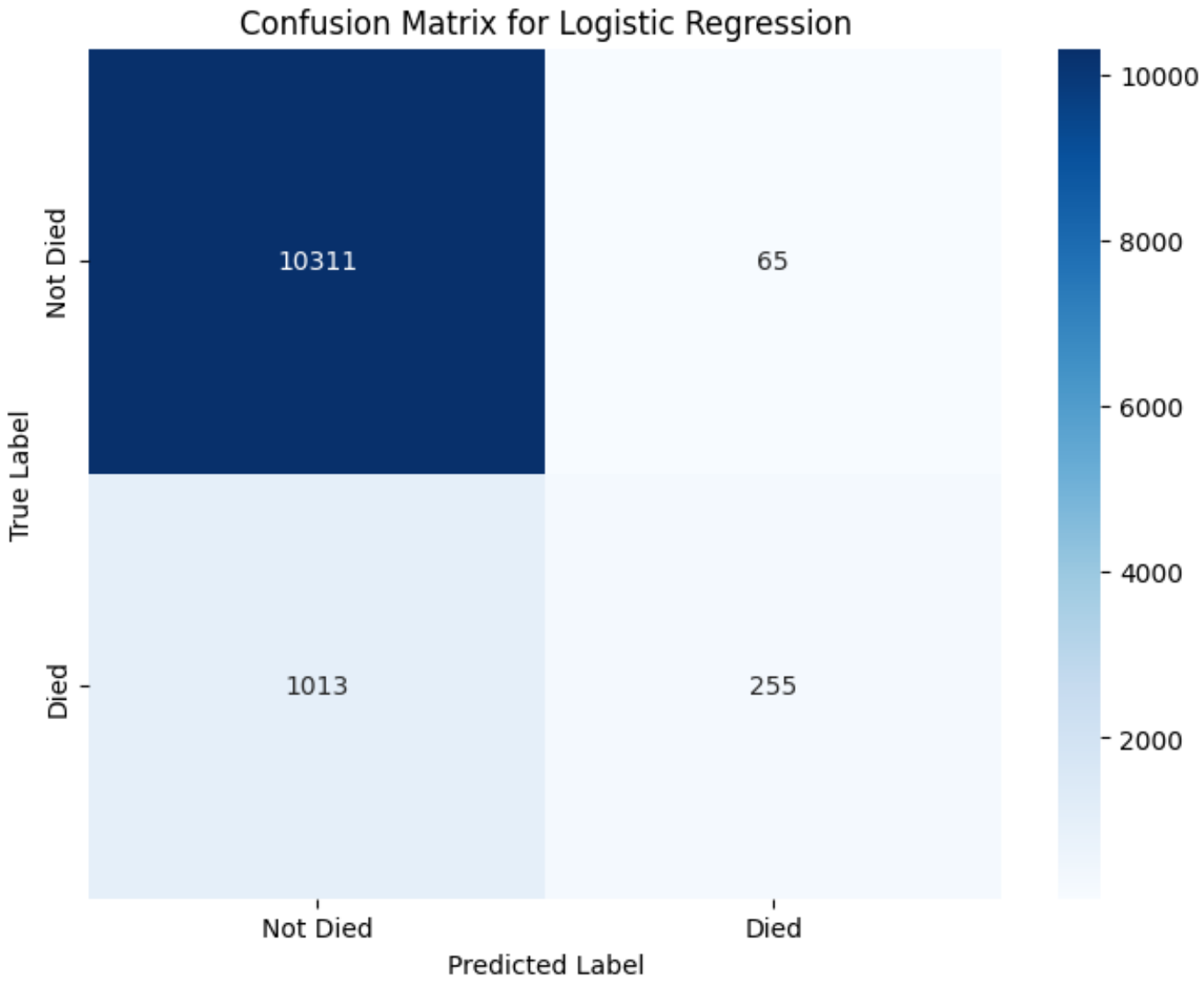

Raw (Colors) vs. Predicted (Shape) Differences in Logistic Regression
DIED
DIED
0
1
PREDICTED
0
1
LOS
AGE
0
5
10
15
20
25
30
35
20
40
60
80
100

It then creates two plots:

1. A scatter plot showing the raw testing data differences with:
    - 'AGE' on the x-axis.
    - 'LOS' on the y-axis,
    - 'DIED' attribute as the color-coding.
2. A scatter plot showing the raw (colors) vs. predicted (shape) differences with 'AGE' on the x

- Yellow dots: Patients acutally died.
- Blue dots: Patients who still alive.
- Blue circle | Yellow cross: means the model’s prediction is correct.
- Yellow circle and Blue cross: means the model’s prediction is wrong.

```
# Plot the confusion matrix as a heatmap
plt.figure(figsize=(8, 6))
sns.heatmap(m, annot=True, fmt='d', cmap='Blues', xticklabels=['Not Died', 'Died'],
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('Confusion Matrix for Logistic Regression')
plt.show()
```



- The graph shows that there are 255 True Positive, which mean this methods successfully predict 255 paitent's death while make error on 1013 False Negative on the alive patient group.

3.5 Support Vector Machine Method

Support Vector Machine Approach

- A Support Vector Machine (SVM) is a supervised machine learning algorithm used for classification and regression tasks.
- In the context of classification, an SVM classifier works by finding the optimal hyperplane that separates the classes in the feature space.
- The hyperplane is chosen in a way that maximizes the margin between the classes, which is the distance between the hyperplane and the closest data points from each class.
- These closest data points are called support vectors, as they "support" the definition of the hyperplane.

Why to use:

- SVMs can handle both linear and non-linear decision boundaries using different kernel functions.
- They are particularly useful when the data is high-dimensional and the number of features is larger than the number of samples.
- However, SVMs can be sensitive to the choice of kernel function and the tuning of hyperparameters.

Implementation Specifics:

The code first trains a Support Vector model using the training dataset and computes the accuracy on the testing dataset. It also computes the recall (sensitivity) for both the 'Died' and 'Not Died' classes using the confusion matrix.

```
print("** SVM Method **")

svm=SVC()
svm.fit(train_data,train_died_y)

predict_y = svm.predict(test_data)
acc = svm.score(test_data, test_died_y)
m = metrics.confusion_matrix(test_died_y, predict_y)
D_recall = m[1][1]/(m[1][0] + m[1][1])
ND_recall = m[0][0]/(m[0][0] + m[0][1])

print("Test accuracy", acc)
print("DIED recall:",D_recall)
print("No DIED recall:",ND_recall)
```

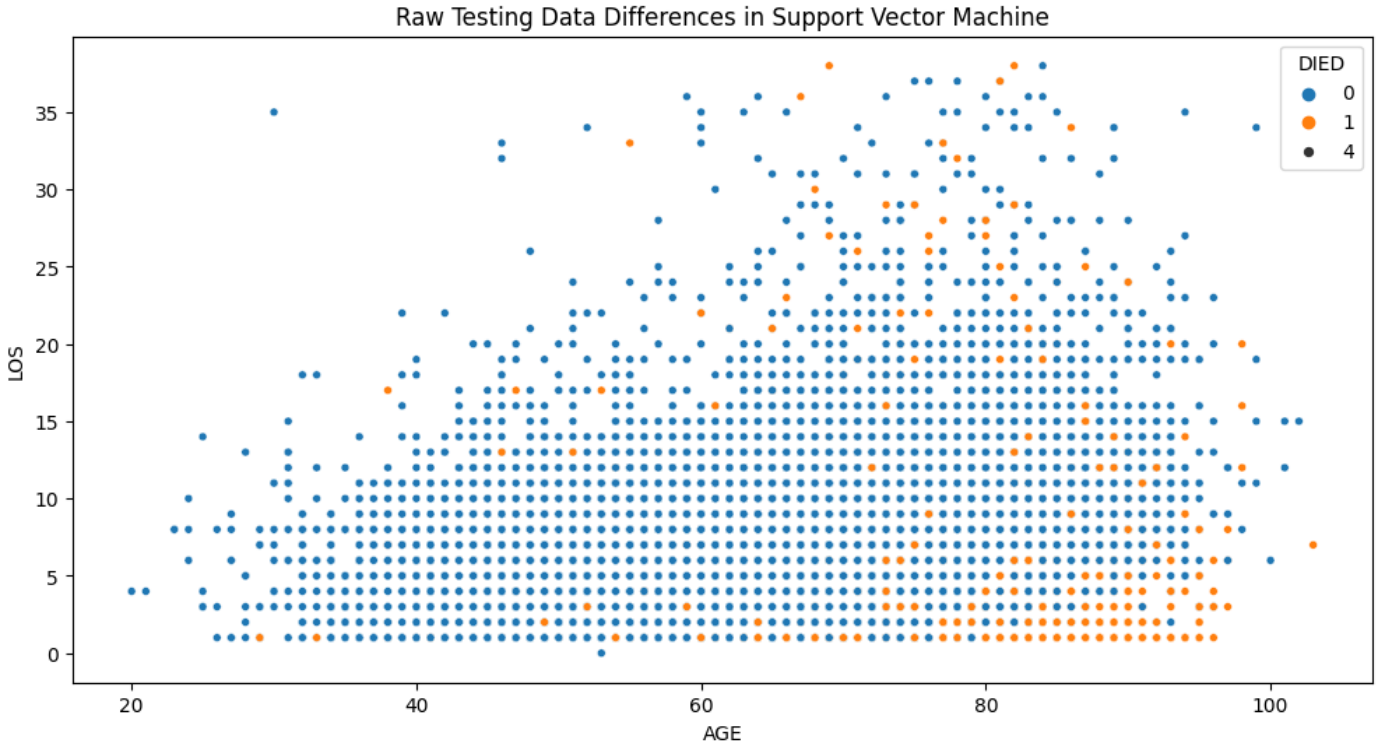
```
** SVM Method **
Test accuracy 0.8911027138440398
DIED recall: 0.0
No DIED recall: 1.0
```

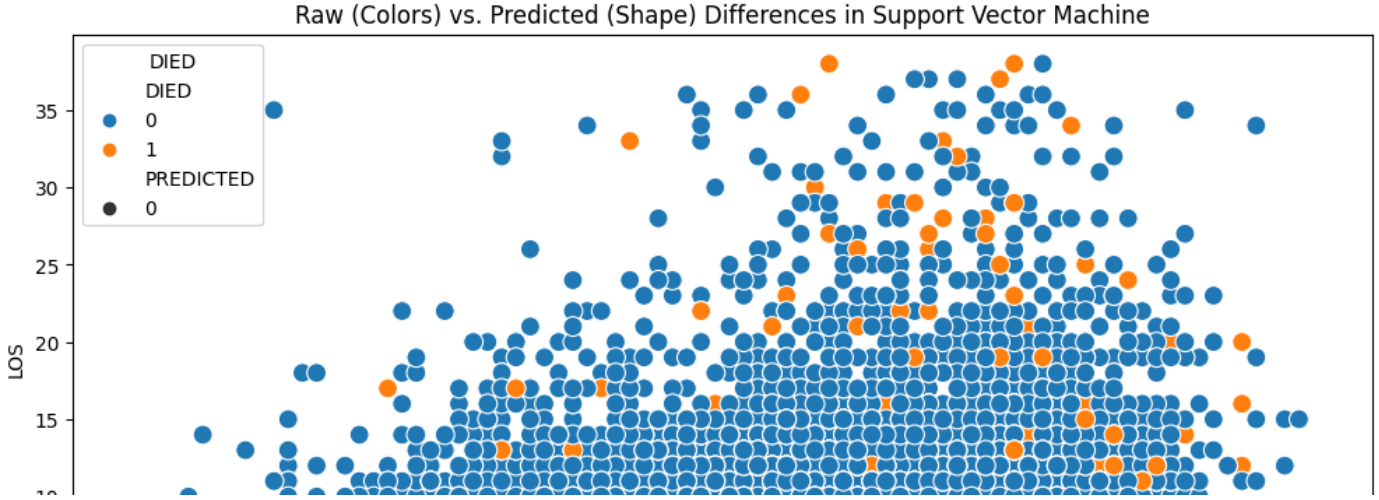
```
print("** SVM Method **")

D_precision = m[1][1] / (m[1][1] + m[0][1]) if (m[1][1] + m[0][1]) != 0 else 0
ND_precision = m[0][0] / (m[0][0] + m[1][0])
D_f1 = 2 * (D_precision * D_recall) / (D_precision + D_recall) if (D_precision + D_
ND_f1 = 2 * (ND_precision * ND_recall) / (ND_precision + ND_recall)

print("Died Precision:", D_precision)
print("Not Died Precision:", ND_precision)
print("Died F1-score:", D_f1)
print("Not Died F1-score:", ND_f1)
```

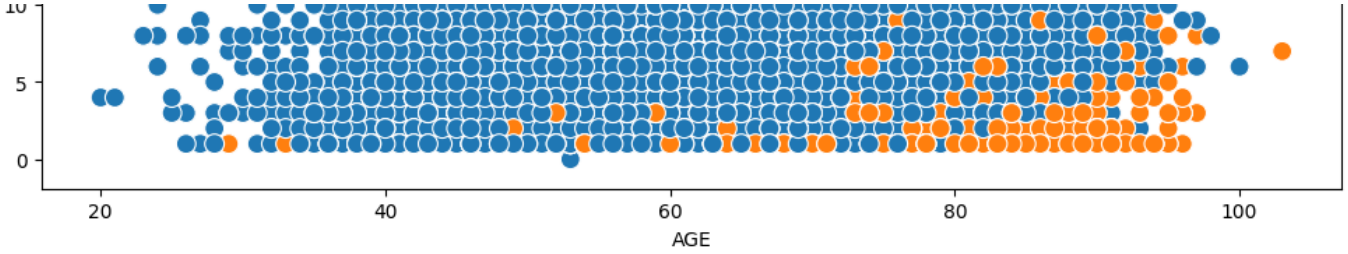
```
** SVM Method **
Died Precision: 0
Not Died Precision: 0.8911027138440398
Died F1-score: 0
Not Died F1-score: 0.9424159854677565
```

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

def plot_raw_vs_predicted(title, test_data, test_died_y, predict_y):
    test_data_with_died = test_data.copy()
    test_data_with_died['DIED'] = test_died_y

    plt.figure(figsize=(12, 6))
    sns.scatterplot(data=test_data_with_died, x='AGE', y='LOS', hue='DIED', size=4)
```

```
    plt.title(f"Raw Testing Data Differences in {title}")
    plt.legend(title='DIED')

    test_data_with_predicted = test_data.copy()
    test_data_with_predicted['DIED'] = test_died_y
    test_data_with_predicted['PREDICTED'] = predict_y

    plt.figure(figsize=(12, 6))
    sns.scatterplot(data=test_data_with_predicted, x='AGE', y='LOS', hue='DIED', st
    plt.title(f"Raw (Colors) vs. Predicted (Shape) Differences in {title}")
    plt.legend(title='DIED')

    plt.show()

plot_raw_vs_predicted('Support Vector Machine', test, test_died_y, predict_y)
```





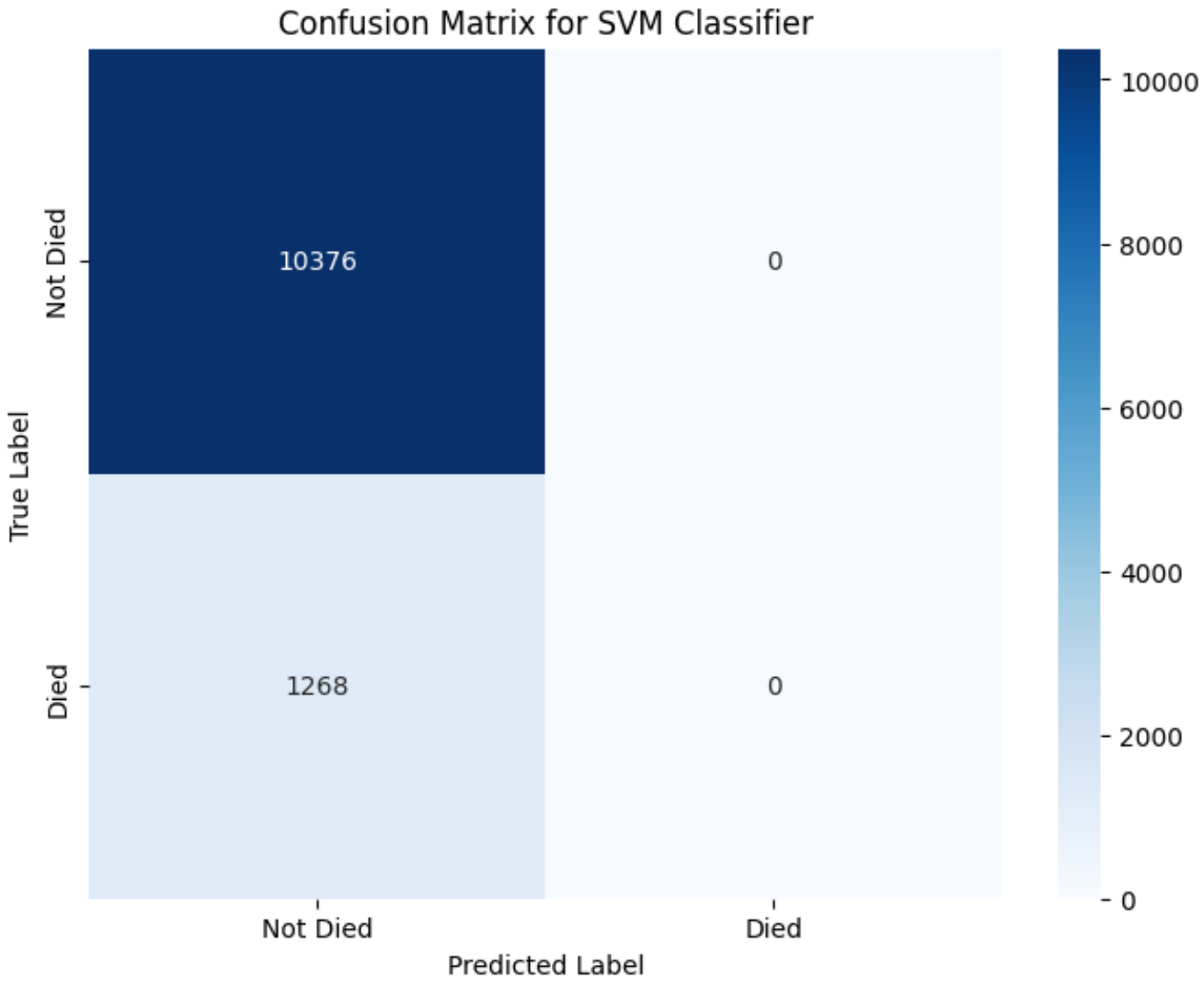


It then creates two plots:

1. A scatter plot showing the raw testing data differences with:
    - 'AGE' on the x-axis.
    - 'LOS' on the y-axis,
    - 'DIED' attribute as the color-coding.
2. A scatter plot showing the raw (colors) vs. predicted (shape) differences with 'AGE' on the x

- Yellow dots: Patients acutally died.
- Blue dots: Patients who still alive.
- Blue circle | Yellow cross: means the model’s prediction is correct.
- Yellow circle and Blue cross: means the model’s prediction is wrong.

```
# Plot the confusion matrix as a heatmap
plt.figure(figsize=(8, 6))
sns.heatmap(m, annot=True, fmt='d', cmap='Blues', xticklabels=['Not Died', 'Died'],
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('Confusion Matrix for SVM Classifier')
plt.show()
```



Under the Support Vector Machine Method prediction:

- The graph shows that there are 0 True Positive, which mean this methods successfully predict 0 paitent's death while make error on 1268 False Negative on the alive patient group, which means all the patients are alive.
- Since the dead recall rate is 0, It doesn't successfully predict how many people died. It indicates this model is not reliable.

3.6 Neural Network

Neural Network(MLP) Approach

- An MLP (Multi-Layer Perceptron) neural network classifier is a type of artificial neural network that consists of multiple layers of neurons connected in a feedforward manner.
- It is a supervised learning algorithm used for classification tasks where the goal is to predict the class label of input data.

Why to use neural network

- They are able to learn complex nonlinear relationships between the input features and the output and can capture high-level abstract features from raw data.
- Neural networks can handle both categorical and numerical data, and are able to automatically extract relevant features from the input data, reducing the need for feature engineering. They are also able to generalize well to new data and can handle noisy or incomplete data.
- However, neural networks can be computationally expensive to train, particularly for large datasets, and can be difficult to interpret. Additionally, they require a significant amount of data to train effectively.

Implementation Specifics:

The code first trains a (MLP) Neural Network model using the training dataset and computes the accuracy on the testing dataset. It also computes the recall (sensitivity) for both the 'Died' and 'Not Died' classes using the confusion matrix.

```
from sklearn.preprocessing import StandardScaler

print("** Neural Network(MLP) ** ")

scaler = StandardScaler()
train_data_scaled = scaler.fit_transform(train_data)
test_data_scaled = scaler.transform(test_data)

mlp = MLPClassifier(solver='lbfgs',
                    alpha=1e-5, hidden_layer_sizes=(10,), max_iter=500)

mlp.fit(train_data_scaled, train_died_y)
predict_y = mlp.predict(test_data_scaled)
acc = mlp.score(test_data_scaled, test_died_y)
m = metrics.confusion_matrix(test_died_y, predict_y)
D_recall = m[1][1]/(m[1][0] + m[1][1])
ND_recall = m[0][0]/(m[0][0] + m[0][1])

print("Test accuracy", acc)
print("DIED samples recall:",D_recall)
print("No DIED samples recall:",ND_recall)
```

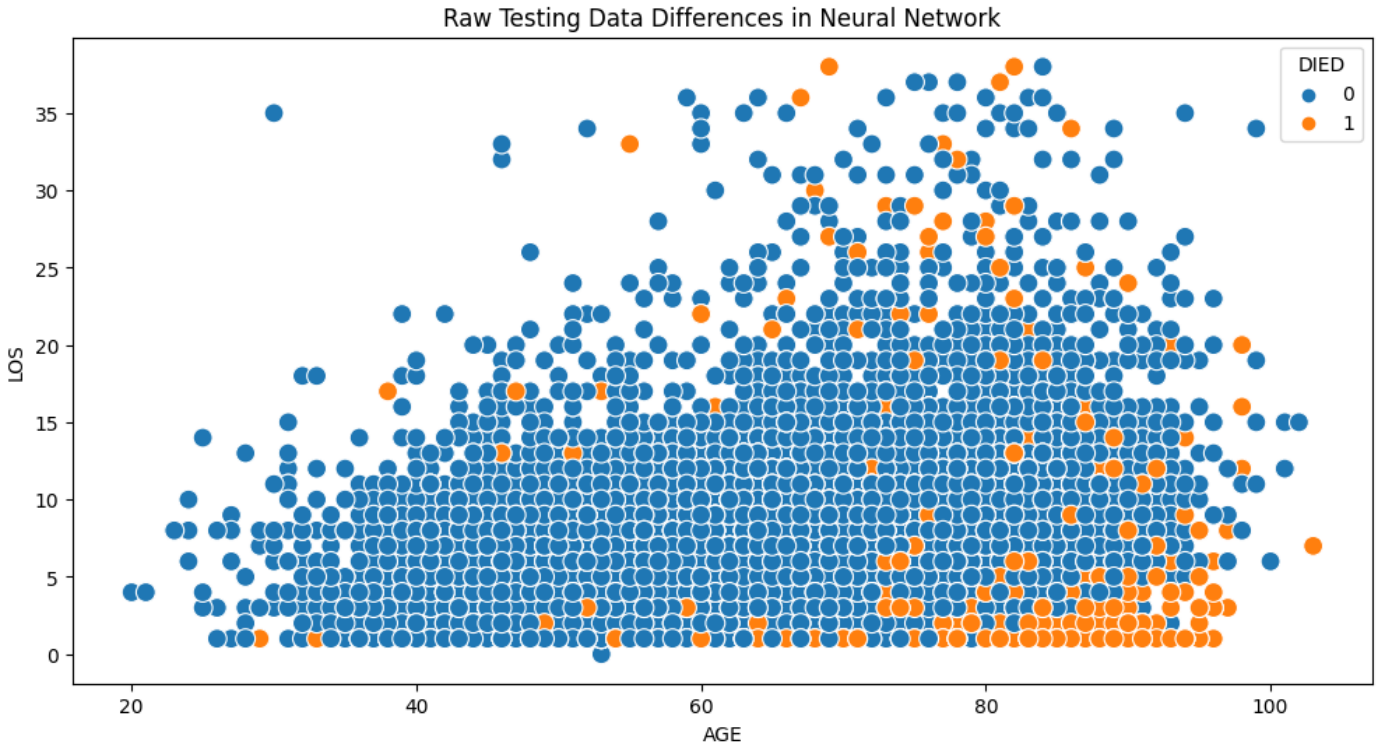
```
** Neural Network(MLP) **
Test accuracy 0.9133459292339402
DIED samples recall: 0.3943217665615142
No DIED samples recall: 0.9767733230531996
```

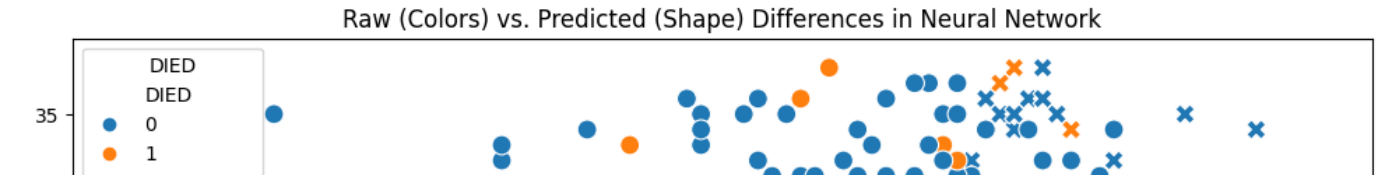
```
print("** Neural Network(MLP) ** ")
D_precision = m[1][1] / (m[1][1] + m[0][1]) if (m[1][1] + m[0][1]) != 0 else 0
ND_precision = m[0][0] / (m[0][0] + m[1][0])

D_f1 = 2 * (D_precision * D_recall) / (D_precision + D_recall) if (D_precision + D_
ND_f1 = 2 * (ND_precision * ND_recall) / (ND_precision + ND_recall)

print("Died Precision:", D_precision)
print("Not Died Precision:", ND_precision)

print("Died F1-score:", D_f1)
print("Not Died F1-score:", ND_f1)
```

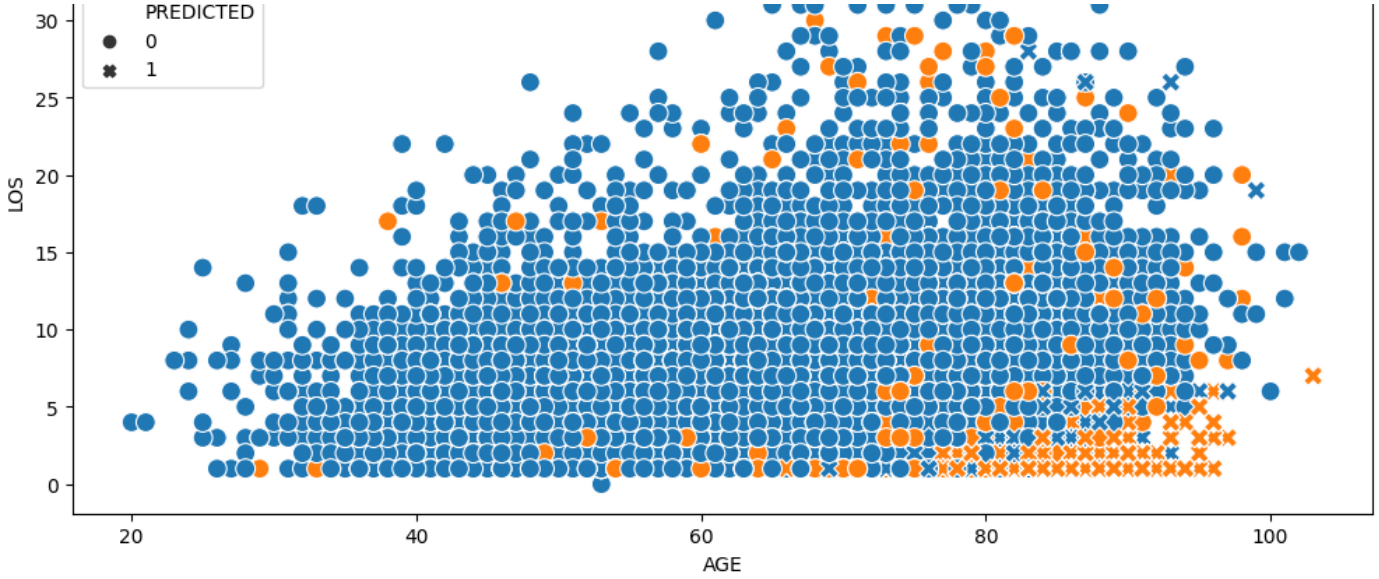
```
** Neural Network(MLP) **
Died Precision: 0.6747638326585695
Not Died Precision: 0.929560671374851
Died F1-score: 0.49776007964161273
Not Died F1-score: 0.9525823581935241
```

```
import matplotlib.pyplot as plt
```

```
import seaborn as sns

def plot_raw_vs_predicted(title, test_data, test_died_y, predict_y):
    test_data_with_died = test_data.copy()
    test_data_with_died['DIED'] = test_died_y

    plt.figure(figsize=(12, 6))
    sns.scatterplot(data=test_data_with_died, x='AGE', y='LOS', hue='DIED', s=100)
    plt.title(f"Raw Testing Data Differences in {title}")
    plt.legend(title='DIED')

    test_data_with_predicted = test_data.copy()
    test_data_with_predicted['DIED'] = test_died_y
    test_data_with_predicted['PREDICTED'] = predict_y

    plt.figure(figsize=(12, 6))
    sns.scatterplot(data=test_data_with_predicted, x='AGE', y='LOS', hue='DIED', st
    plt.title(f"Raw (Colors) vs. Predicted (Shape) Differences in {title}")
    plt.legend(title='DIED')

    plt.show()

plot_raw_vs_predicted('Neural Network', test, test_died_y, predict_y)
```





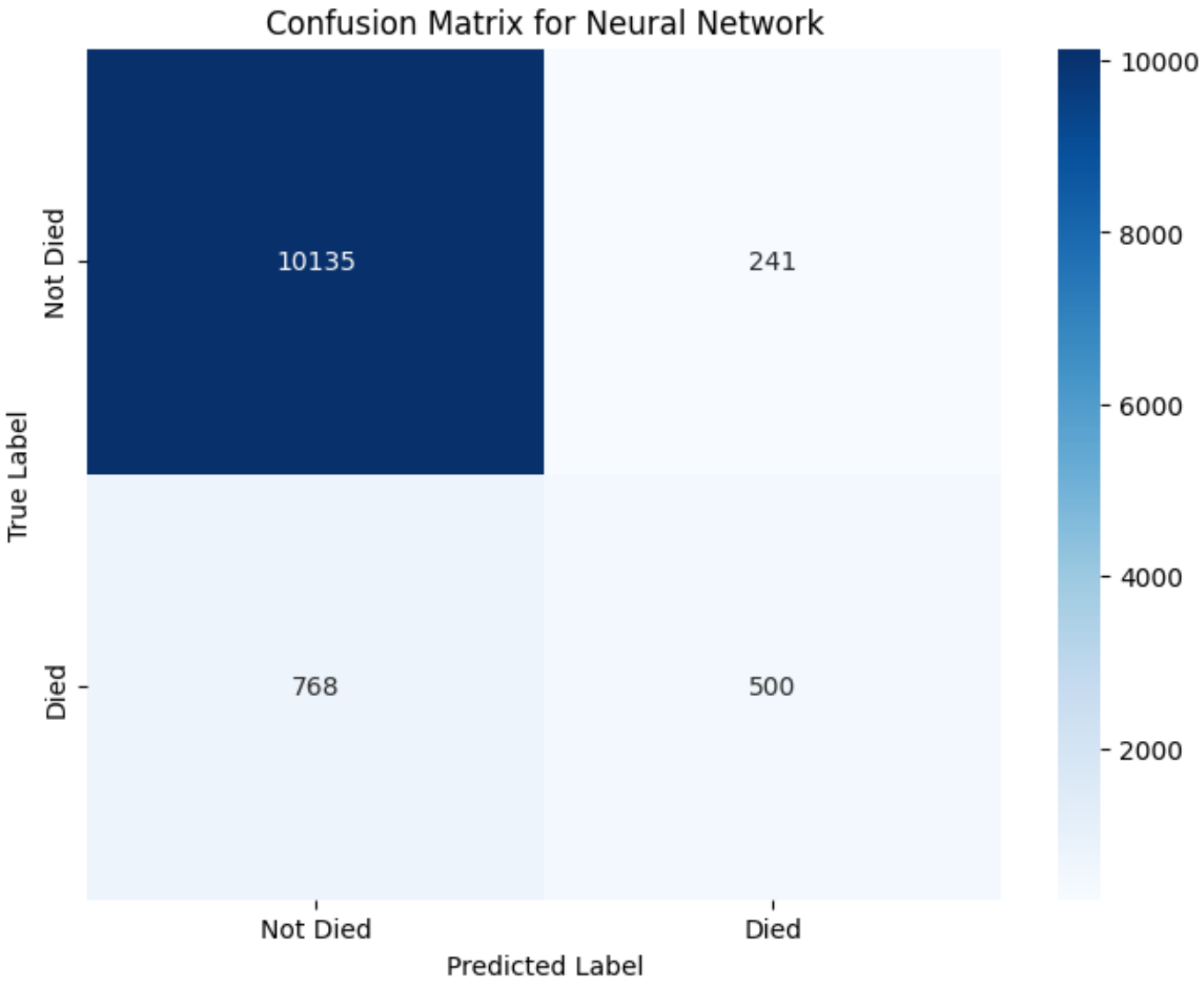


It then creates two plots:

1. A scatter plot showing the raw testing data differences with:
    - 'AGE' on the x-axis.
    - 'LOS' on the y-axis,
    - 'DIED' attribute as the color-coding.
2. A scatter plot showing the raw (colors) vs. predicted (shape) differences with 'AGE' on the x

- Yellow dots: Patients acutally died.
- Blue dots: Patients who still alive.
- Blue circle | Yellow cross: means the model's prediction is correct.
- Yellow circle and Blue cross: means the model's prediction is wrong.

```
# Plot the confusion matrix as a heatmap
plt.figure(figsize=(8, 6))
sns.heatmap(m, annot=True, fmt='d', cmap='Blues', xticklabels=['Not Died', 'Died'],
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('Confusion Matrix for Neural Network')
plt.show()
```



Under the Neural Network Method prediction:

- The graph shows that there are 455 True Positive, which mean this methods successfully predict 455 paitent's death while make error on 813 False Negative on the alive patient group, which means all the patients are alive.

3.7 Summary Table - (Original Traing Models)

Models	Test Accuracy	Death sample recall rate	Non-death sample recall rate	Death Precision	Death F
Naive Bayes	89.45%	5.12%	99.76%	72.22%	9.57%
KNN	89.96%	35.41%	96.63%	56.20%	43.44%
Decision Trees	85.49%	40.93%	90.94%	35.57%	38.06%
Logistics Regression	90.74%	20.11%	99.37%	79.69%	32.12%
Support Vector Machine	89.11%	0.00%	100.00%	0.00%	0.0%
Neural Networks	91.33%	39.43%	97.68%	67.48%	49.78%

4 Swote Improvments

SMOTE Algo Approach:

SMOTE (Synthetic Minority Over-sampling Technique) is an oversampling technique used in machine learning to address class imbalance. Class imbalance refers to the situation where one class (the minority class) has significantly fewer samples than the other class(es) (the majority class(es)) in a binary or multi-class classification problem.

Why Use SMOTE Algo For Improvements:

The reason why some of the non-death sample recall rate is exist bias is previously in the training dataset, the ratio of death to non-death is unbalanced. Therefore, in order to make the sample blanced so that the result could be validated, we use the SMOTE (stands for Synthetic Minority Oversampling Technique) algorithm to equalize the positive and negative samples.

```
from google.colab import drive
drive.mount('/content/drive')
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call
```

```
from sklearn.neural_network import MLPClassifier
from sklearn.neighbors import  KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.naive_bayes import GaussianNB
from imblearn.over_sampling import SMOTE
from sklearn.svm import SVC
import numpy as np
from sklearn import metrics
import pandas as pd
from sklearn.preprocessing import StandardScaler
```

```
file_path = "/content/drive/MyDrive/WeihongYang/whole_table.csv"

DIAGNOSIS_dict = {}
data = []
label_died = []

with open(file_path, "r", encoding='utf-8') as f:
    next(f)  # Skip the header line
    for line in f:
        one_record = line.split(",")
        diagnosis = int(one_record[1]) - 41011
        sex = 1 if one_record[2] == "F" else 2
        died = int(one_record[4])
        los = int(one_record[6])
        age = int(one_record[7])
        data.append([diagnosis, sex, los, age])
        label_died.append(died)

train_samples = 12000
train_data = np.array(data[:train_samples])
train_died_y = np.array(label_died[:train_samples])

print("** SMOTE algorithm for balancing data **")

model_smote = SMOTE()
train_data, train_died_y = model_smote.fit_resample(train_data, train_died_y)
test_data = np.array(data[train_samples:])
test_died_y = np.array(label_died[train_samples:])
train_data = np.array(train_data)
train_died_y = np.array(train_died_y)

print("train data shape :  " + str(train_data.shape))
print("test data shape : " + str(test_data.shape))
```

```
** SMOTE algorithm for balancing data **
train data shape :  (21352, 4)
test data shape : (844, 4)
```

4.1 Naive Bayes(SMOTE)

```
print("** Naive Bayes **")

NB = GaussianNB()
NB.fit(train_data, train_died_y)
predict_y = NB.predict(test_data)

print("Training Accuracy:", NB.score(train_data, train_died_y))
print("Test Accuracy:", NB.score(test_data, test_died_y))
print("Confusion matrix:")
print(metrics.confusion_matrix(test_died_y, predict_y))

m = metrics.confusion_matrix(test_died_y, predict_y)
D_recall = m[1][1] / (m[1][0] + m[1][1])
ND_recall = m[0][0] / (m[0][0] + m[0][1])

print("No DIED recall:", ND_recall)
print("DIED recall:", D_recall)
```

```
** Naive Bayes **
Training Accuracy: 0.7525758711127764
Test Accuracy: 0.7144549763033176
Confusion matrix:
[[542 216]
 [ 25  61]]
No DIED recall: 0.7150395778364116
DIED recall: 0.7093023255813954
```

4.2 KNN(SMOTE)

```
print("** KNN Method **")

knn = KNeighborsClassifier()
knn.fit(train_data, train_died_y)
predict_y = knn.predict(test_data)

print("Training Accuracy:", knn.score(train_data, train_died_y))
print("Test Accuracy:", knn.score(test_data, test_died_y))
print("Confusion matrix:")
print(metrics.confusion_matrix(test_died_y, predict_y))

m = metrics.confusion_matrix(test_died_y, predict_y)
D_recall = m[1][1] / (m[1][0] + m[1][1])
ND_recall = m[0][0] / (m[0][0] + m[0][1])

print("No DIED recall:", ND_recall)
print("DIED recall:", D_recall)
```

```
** KNN Method **
Training Accuracy: 0.8640408392656426
Test Accuracy: 0.8578199052132701
Confusion matrix:
[[669  89]
 [ 31  55]]
No DIED recall: 0.8825857519788918
DIED recall: 0.6395348837209303
```

4.3 Decision Tree(SMOTE)

```
print("** DecisionTree Method ** ")

tree = DecisionTreeClassifier(random_state=0)
tree.fit(train_data, train_died_y)
feat_importance = tree.tree_.compute_feature_importances(normalize=False)
predict_y = tree.predict(test_data)

print("feat importance = " + str(feat_importance))
print("Training Accuracye:", tree.score(train_data, train_died_y))
print("Test Accuracy:", tree.score(test_data, test_died_y))
print("Confusion matrix:")
print(metrics.confusion_matrix(test_died_y, predict_y))

m = metrics.confusion_matrix(test_died_y, predict_y)
D_recall = m[1][1] / (m[1][0] + m[1][1])
ND_recall = m[0][0] / (m[0][0] + m[0][1])

print("No DIED recall:", ND_recall)
print("DIED recall:", D_recall)
```

```
** DecisionTree Method **
feat importance = [0.04752558 0.03444687 0.1872836  0.11609529]
Training Accuracye: 0.9154645934807044
Test Accuracy: 0.8187203791469194
Confusion matrix:
[[640 118]
 [ 35  51]]
No DIED recall: 0.8443271767810027
DIED recall: 0.5930232558139535
```

4.4 Logistic Regression(SMOTE)

```
print("** Logistic Regression **")

lr = LogisticRegression(class_weight='balanced')
lr.fit(train_data, train_died_y)
predict_y = lr.predict(test_data)

print("Training Accuracy:", lr.score(train_data, train_died_y))
print("Test Accuracy:", lr.score(test_data, test_died_y))
print("Confusion matrix:")
print(metrics.confusion_matrix(test_died_y, predict_y))

m = metrics.confusion_matrix(test_died_y, predict_y)
D_recall = m[1][1] / (m[1][0] + m[1][1])
ND_recall = m[0][0] / (m[0][0] + m[0][1])

print("No DIED recall:", ND_recall)
print("DIED recall:", D_recall)
```

```
** Logistic Regression **
Training Accuracy: 0.7671880854252529
Test Accuracy: 0.7665876777251185
Confusion matrix:
[[582 176]
 [ 21  65]]
No DIED recall: 0.7678100263852242
DIED recall: 0.7558139534883721
```

4.5 SVM(SMOTE)

```
print("** SVM Method **")

svm = SVC(class_weight='balanced')
svm.fit(train_data, train_died_y)
predict_y = svm.predict(test_data)

print("Training Accuracy:", svm.score(train_data, train_died_y))
print("Test Accuracy:", svm.score(test_data, test_died_y))
print("Confusion matrix:")
print(metrics.confusion_matrix(test_died_y, predict_y))

m = metrics.confusion_matrix(test_died_y, predict_y)
D_recall = m[1][1] / (m[1][0] + m[1][1])
ND_recall = m[0][0] / (m[0][0] + m[0][1])

print("No DIED recall:", ND_recall)
print("DIED recall:", D_recall)
```

```
** SVM Method **
Training Accuracy: 0.788029224428625
Test Accuracy: 0.8436018957345972
Confusion matrix:
[[648 110]
 [ 22  64]]
No DIED recall: 0.8548812664907651
DIED recall: 0.7441860465116279
```

4.1 Neural Network(SMOTE)

```
print("** Neural Network(MLP) ** ")

scaler = StandardScaler()
train_data_scaled = scaler.fit_transform(train_data)
test_data_scaled = scaler.transform(test_data)
mlp = MLPClassifier(solver='lbfgs', alpha=1e-5, hidden_layer_sizes=(10,), max_iter=
mlp.fit(train_data_scaled, train_died_y)
predict_y = mlp.predict(test_data_scaled)

print("Training Accuracy:", mlp.score(train_data, train_died_y))
print("Test Accuracy:", mlp.score(test_data, test_died_y))
print("Confusion matrix:")
print(metrics.confusion_matrix(test_died_y, predict_y))

m = metrics.confusion_matrix(test_died_y, predict_y)
D_recall = m[1][1] / (m[1][0] + m[1][1])
ND_recall = m[0][0] / (m[0][0] + m[0][1])

print("No DIED recall:", ND_recall)
print("DIED recall:", D_recall)
```

```
** Neural Network(MLP) **
Training Accuracy: 0.5
Test Accuracy: 0.1018957345971564
Confusion matrix:
[[652 106]
 [ 21  65]]
No DIED recall: 0.8601583113456465
DIED recall: 0.7558139534883721
```

The printed data shows the results of 6 different classification models.

4.2 Summary - (SMOTE)

Models (SMOTE)	Training Accuracy	Test Accuracy	No DIED Recall rate	DIED Recall rate
Naive Bayes	75.26%	71.45%	71.50%	70.93%
KNN	86.40%	85.78%	88.26%	63.95%
Decision Trees	91.55%	81.87%	84.43%	59.30%
Logistic Regression	76.72%	76.66%	76.78%	75.58%
SVM	78.80%	84.36%	85.49%	74.42%
Neural Network (MLP)	50.00%	10.19%	86.02%	75.58%

5 Results Analysis

5.1 Results Table - (Original Traing Models) Data Analysis

Summarizing all the model's performance by comparing 2 results tables:

Models	Test Accuracy	Death sample recall rate	Non-death sample recall rate	Death Precision	Death F
Naive Bayes	89.45%	5.12%	99.76%	72.22%	9.57%
KNN	89.96%	35.41%	96.63%	56.20%	43.44%
Decision Trees	85.49%	40.93%	90.94%	35.57%	38.06%
Logistics Regression	90.74%	20.11%	99.37%	79.69%	32.12%
Support Vector Machine	89.11%	0.00%	100.00%	0.00%	0.0%
Neural Networks	91.33%	39.43%	97.68%	67.48%	49.78%

Based on the Summary Table(6 Original Traing Models), we can analyze the performance of the six machine learning models as follows:

Naive Bayes:

- Naive Bayes has a high test accuracy and an excellent non-death sample recall rate but struggles with identifying death samples, as indicated by the low death sample recall rate and F1-score.

KNN:

- KNN has good test accuracy and a decent non-death sample recall rate. While it performs better than Naive Bayes for death samples, it still has a relatively low death sample recall rate and F1-score.

Decision Trees:

- Decision Trees have the lowest test accuracy among the models but a higher death sample recall rate compared to Naive Bayes and KNN. However, the death precision and F1-score are lower than KNN.

Logistic Regression:

- Logistic Regression has the second-highest test accuracy and a great non-death sample recall rate. Although it has a low death sample recall rate, it achieves the highest death precision among the models, resulting in a moderate F1-score.

Support Vector Machine:

- Support Vector Machine has a good test accuracy and a perfect non-death sample recall rate. However, it fails to identify any death samples, resulting in the lowest death precision and F1-score.

Neural Networks:

- Neural Networks have the highest test accuracy and a good non-death sample recall rate. They perform the best among the models in identifying death samples, with the highest death sample recall rate and F1-score.

Summary:

> For 6 Original Traing Models, Neural Networks perform the best in terms of test accuracy and death sample identification, with the highest death sample recall rate and F1-score. Logistic Regression has the highest death precision but a lower death sample recall rate. Support Vector Machine fails to identify any death samples, while Naive Bayes struggles with identifying them. KNN and Decision Trees have moderate performance in identifying death samples.

> Depending on the application and the importance of specific metrics, different models might be preferred. For instance, if the focus is on correctly identifying death samples (higher death recall rate), Decision Trees might be a better choice, despite their lower overall accuracy. On the other hand, if overall performance is more important, Logistic Regression seems to be the best choice among these models.

5.2 Results Table (SMOTE)

Here is an analysis of the SMOTE algo's performance:

Models (SMOTE)	Training Accuracy	Test Accuracy	No DIED Recall rate	DIED Recall rate
Naive Bayes	75.26%	71.45%	71.50%	70.93%
KNN	86.40%	85.78%	88.26%	63.95%
Decision Trees	91.55%	81.87%	84.43%	59.30%
Logistic Regression	76.72%	76.66%	76.78%	75.58%
SVM	78.80%	84.36%	85.49%	74.42%
Neural Network (MLP)	50.00%	10.19%	86.02%	75.58%

Based on the Summary Table(SMOTE Traing Models), we can analyze the performance of the six machine learning models in the classification task as follows:

Training Accuracy:

- The highest training accuracy is achieved by the Decision Trees model at 91.55%, followed by KNN at 86.40%. The lowest training accuracy is observed in the Neural Network (MLP) model at 50.00%.
- It's important to note that a high training accuracy may indicate overfitting, so it's crucial to also consider the test accuracy.

Test Accuracy:

- The highest test accuracy is obtained by the KNN model at 85.78%, followed closely by SVM at 84.36%.
- The lowest test accuracy is observed in the Neural Network (MLP) model at 10.19%, which suggests that the model may not be performing well and needs further optimization or adjustments.

No DIED Recall rate:

- The highest recall rate for the No DIED class is achieved by the KNN model at 88.26%. The Neural Network (MLP) model follows closely with a recall rate of 86.02%.
- The lowest recall rate for this class is observed in the Naive Bayes model at 71.50%.

DIED Recall rate:

- The highest recall rate for the DIED class is achieved by the Neural Network (MLP) and Logistic Regression models, both at 75.58%.
- The lowest recall rate for this class is observed in the Decision Trees model at 59.30%.

Summary:

> When selecting a model, it's important to consider the balance between test accuracy and recall rates for both classes, especially if the goal is to minimize false negatives or false positives. In this case, KNN seems to perform the best overall, with the highest test accuracy and the highest recall rate for the No DIED class. However, if the DIED class is more important, Logistic Regression or Neural Network (MLP) may be more suitable due to their higher recall rates. Note that the Neural Network (MLP) model has a very low test accuracy, and it needs further optimization or adjustments before it can be considered for practical use.

5.3 Performance for SWOTE algo + 6 Models:

Based on the Summary Table(SMOTE Traing Models), we can analyze the performance of the six machine learning models as follows:

Neural Network (MLP): Training set score: 50.00% | Test set score: 10.19% | No DIED recall: 86.02% | DIED recall: 75.58% |

- MLP shows poor performance on both training and test sets, which indicates possible issues with the model configuration or the input data.

KNN: Training set score: 86.27% | Test set score: 84.60% | No DIED recall: 86.94% | DIED recall: 63.95% |

- KNN has the second-highest test set score, suggesting good generalization. However, its DIED recall is relatively lower compared to other models.

Decision Tree: Training set score: 91.38% | Test set score: 81.40% | No DIED recall: 83.51% | DIED recall: 62.79% |

- Decision Trees show good performance on the training set but lower performance on the test set, which may indicate overfitting. The DIED recall is also relatively low.

Logistic Regression: Training set score: 76.44% | Test set score: 76.30% | No DIED recall: 76.52% | DIED recall: 74.42% |

- Logistic Regression has a balanced performance between training and test sets, and it has one of the highest DIED recall rates.

Naive Bayes: Training set score: 74.91% | Test set score: 71.68% | No DIED recall: 71.77% | DIED recall: 70.93% |

- Naive Bayes shows lower test set scores but maintains a relatively high DIED recall rate.

SVM: Training set score: 78.75% | Test set score: 83.18% | No DIED recall: 84.17% | DIED recall: 74.42% |

- SVM performs well on both training and test sets and has one of the highest DIED recall rates.

To Summarize:

> For 6 SWOTE Traing Models, KNN and SVM models appear to perform the best in terms of test set scores, suggesting good generalization. However, the DIED recall rate for KNN is relatively low compared to other models. If the priority is to have a high DIED recall rate, Logistic Regression and SVM models are the most suitable. The Neural Network (MLP) model has poor performance on both training and test sets, indicating issues with the model configuration or input data that need to be addressed.

6 Conclusions

This data mining project uses clinic trial data to test 6 models predictive performance, and SMOTE algo improvments.

- Models Includes: Naive Bayes, KNN, Decision Trees, Logistics Regression, Support Vector Machine, Neural Networks and SMOTE algo version.
- In Conclusion, according to the experimental results, KNN has the highest test set score but a lower DIED recall rate. Logistic Regression and SVM have balanced performance and relatively high DIED recall rates.
- If the goal is to maximize the DIED recall rate, Logistic Regression or SVM might be the preferred choice.
- If the overall test set performance is more important, KNN might be a better option. However, it is crucial to consider the specific requirements of the application when selecting the best model.

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