ML Assignment 4

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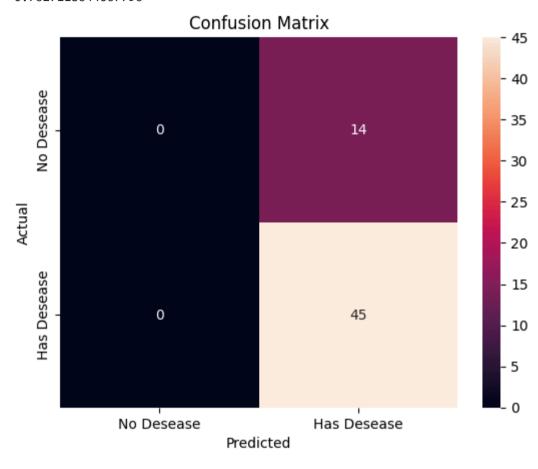
```
In [2]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
```

```
In [3]: df = pd.read csv('liver patient.csv')
        df.head()
            Age Gender Total_Bilirubin Direct_Bilirubin Alkaline_Phosphotase Alamine_Aminotransferase Aspartate_Aminotransferase Total_Protic
Out[3]:
                                                                                                                              18
             65
                 Female
                                    0.7
                                                   0.1
                                                                        187
                                                                                                   16
             62
                   Male
                                   10.9
                                                   5.5
                                                                        699
                                                                                                   64
                                                                                                                             100
             62
                                    7.3
                                                   4.1
                                                                        490
                                                                                                   60
                                                                                                                              68
                   Male
             58
                   Male
                                                   0.4
                                                                        182
                                                                                                   14
                                                                                                                              20
                                    1.0
                                                   2.0
                                                                        195
                                                                                                   27
                                                                                                                              59
             72
                   Male
                                    3.9
In [4]: df.columns
```

```
Out[4]: Index(['Age', 'Gender', 'Total Bilirubin', 'Direct Bilirubin',
                 'Alkaline Phosphotase', 'Alamine Aminotransferase',
                 'Aspartate Aminotransferase', 'Total Protiens', 'Albumin',
                 'Albumin and Globulin Ratio', 'liver disease'],
                dtvpe='object')
In [5]: df.drop(['Age', 'Gender'], axis=1, inplace=True)
 In [6]: from sklearn.preprocessing import MinMaxScaler
         scaler = MinMaxScaler()
         df scaled = scaler.fit transform(df)
         print(df scaled)
                         0.06057645 ... 0.52173913 0.24
        [[0.00402145 0.
                                                                     1.
         [0.14075067 0.2755102 0.31069858 ... 0.5
                                                          0.176
                                                                     1.
         [0.0924933  0.20408163  0.20859795  ...  0.52173913  0.236
         [0.00536193 0.00510204 0.0889106 ... 0.5
                                                          0.28
                                                                     1.
         [0.01206434 0.02040816 0.05911089 ... 0.54347826 0.28
                                                                     1.
                                                                               11
         [0.0080429  0.01020408  0.07474353  ...  0.76086957  0.48
In [7]: X = df scaled[:, :-1]
         y = df scaled[:, -1]
 In [9]: from sklearn.model selection import train test split
         X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.1, random_state=0)
In [10]: from sklearn.linear model import LogisticRegression
         LR = LogisticRegression()
         LR.fit(X train, y train)
         y pred = LR.predict(X test)
In [12]: from sklearn.metrics import accuracy score, confusion matrix
         import seaborn as sns
         cm = confusion matrix(y test, y pred)
         print(accuracy score(y test, y pred))
         plt.title("Confusion Matrix")
         sns.heatmap(cm, annot=True, xticklabels=['No Desease', 'Has Desease'], yticklabels=['No Desease', 'Has Desease'])
```

```
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.show()
```

0.7627118644067796

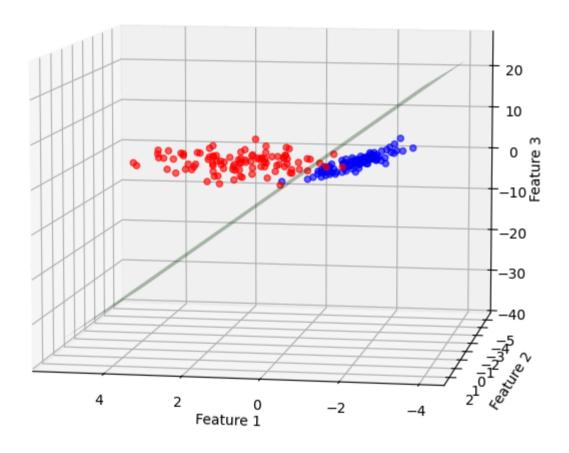


```
n informative = 3,
             n redundant = 0,
             n clusters per class = 1,
             class sep=1.5,
             random state = 42
In [15]: X train, X test, y train, y test = train test split(X, y, test size=0.1, random state=0)
In [16]: LR2 = LogisticRegression()
         LR2.fit(X train, y train)
Out[16]:
          ▼ LogisticRegression
         LogisticRegression()
In [17]: y pred = LR2.predict(X test)
         accuracy = accuracy score(y test, y pred)
         print(f'Accuracy: {accuracy}')
        Accuracy: 0.9
In [18]: coef = LR2.coef [0]
         intercept = LR2.intercept [0]
         print(f'Coefficient: {coef}')
         print(f'Intercept: {intercept}')
        Coefficient: [ 3.44786906 -0.15460582 0.54363775]
        Intercept: 0.9906768241834434
In [20]: fig = plt.figure(figsize = (12, 8))
         ax = fig.add subplot(111, projection='3d')
         ax.scatter(X[y == 0, 0], X[y == 0, 1], X[y == 0, 2], color='blue', label='Class 0', alpha=0.6)
         ax.scatter(X[y == 1, 0], X[y == 1, 1], X[y == 1, 2], color='red', label='Class 1', alpha=0.6)
         x \min, x \max = X[:, 0].\min() - 1, X[:, 0].\max() + 1
         y_{min}, y_{max} = X[:, 1].min() - 1, X[:, 1].max() + 1
         xx, yy = np.meshgrid(np.linspace(x_min, x_max, 50), np.linspace(y_min, y_max, 50))
         zz = -(coef[0]*xx + coef[1]*yy + intercept) / coef[2]
         ax.plot surface(xx, yy, zz, color='green', alpha=0.3, edgecolor = 'none')
```

```
ax.set_xlabel('Feature 1')
ax.set_ylabel('Feature 2')
ax.set_zlabel('Feature 3')
ax.set_title('3D Logistic Regression Decision Boundary')
ax.legend()
ax.view_init(elev=8, azim=100)
plt.show()
```

3D Logistic Regression Decision Boundary





```
In [21]: data = df[['Total_Bilirubin', 'Direct_Bilirubin', 'liver_disease']]
     data.head(20)
```

Out[21]:		Total_Bilirubin	Direct_Bilirubin	liver_disease
	0	0.7	0.1	1
	1	10.9	5.5	1
	2	7.3	4.1	1
	3	1.0	0.4	1
	4	3.9	2.0	1
	5	1.8	0.7	1
	6	0.9	0.2	1
	7	0.9	0.3	1
	8	0.9	0.3	0
	9	0.7	0.2	1
	10	0.6	0.1	1
	11	2.7	1.3	1
	12	0.9	0.3	0
	13	1.1	0.4	1
	14	0.7	0.2	1
	15	0.6	0.1	0
	16	1.8	0.8	1
	17	1.6	0.5	0
	18	0.9	0.3	1
	19	0.9	0.3	1

In [22]: scaled_data = scaler.fit_transform(data)

```
print(scaled data)
        [[0.00402145 0.
                                1.
         [0.14075067 0.2755102 1.
         [0.0924933 0.20408163 1.
         [0.00536193 0.00510204 1.
         [0.01206434 0.02040816 1.
                                          11
         [0.0080429 0.01020408 0.
In [24]: X = scaled data[:, :-1]
         y = scaled data[:, -1]
In [26]: LR3 = LogisticRegression()
         LR3.fit(X train, y train)
         y pred = LR3.predict(X test)
         acc score = accuracy score(y test, y pred)
         print(f'Accuracy: {acc score}')
        Accuracy: 0.9
In [27]: coef = LR3.coef [0]
         intercept = LR3.intercept
         print(f'Coefficient: {coef}')
         print(f'Intercept: {intercept}')
        Coefficient: [ 3.44786906 -0.15460582 0.54363775]
        Intercept: [0.99067682]
In [52]: plt.figure(figsize=(7, 4))
         plt.scatter(data['Total Bilirubin'][data['liver disease'] == 0]+10,
                     data['Direct Bilirubin'][data['liver disease'] == 0]+10,
                     color='blue', label='No Liver Disease')
         plt.scatter(data['Total Bilirubin'][data['liver disease'] == 1],
                     data['Direct_Bilirubin'][data['liver_disease'] == 1],
                     color='red', label='Liver Disease')
         x min, x max = data['Total Bilirubin'].min() - 1, data['Total Bilirubin'].max() + 1
```

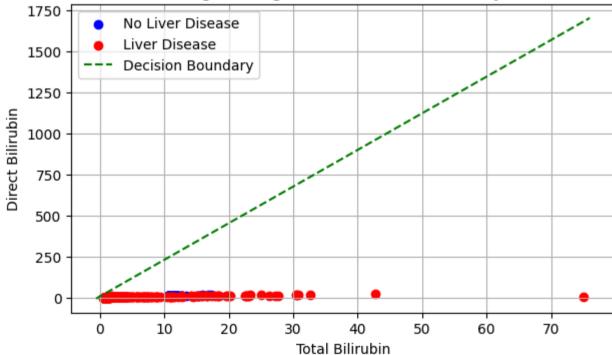
```
x_values = np.linspace(x_min, x_max, 100)
y_values = -(coef[0] * x_values + intercept) / coef[1]

plt.plot(x_values, y_values, color='green', linestyle='--', label='Decision Boundary')

plt.xlabel('Total Bilirubin')
plt.ylabel('Direct Bilirubin')
plt.title('Logistic Regression Decision Boundary')

plt.legend()
plt.grid()
```





```
In [39]: df = df = pd.read csv('liver patient.csv')
         df.head()
Out[39]:
            Age Gender Total_Bilirubin Direct_Bilirubin Alkaline_Phosphotase Alamine_Aminotransferase Aspartate_Aminotransferase Total_Protic
          0
              65
                  Female
                                    0.7
                                                   0.1
                                                                        187
                                                                                                  16
                                                                                                                             18
              62
                                   10.9
                                                                                                                            100
         1
                    Male
                                                    5.5
                                                                        699
                                                                                                  64
          2
              62
                    Male
                                    7.3
                                                    4.1
                                                                        490
                                                                                                  60
                                                                                                                             68
              58
                                    1.0
                                                   0.4
                                                                        182
                                                                                                                             20
                    Male
                                                                                                  14
                                                                                                  27
                                                                                                                             59
              72
                    Male
                                    3.9
                                                    2.0
                                                                        195
In [40]: df = df.drop(columns=['Age', 'Gender'])
         missing values = df.isnull().sum()
         df = df.fillna(df.median())
         X = df.drop(columns=['liver disease']).values
         y = df['liver_disease'].values
In [41]: # Normalize the feature values (Min-Max Scaling)
         X = (X - X.min(axis=0)) / (X.max(axis=0) - X.min(axis=0))
         # Add bias term (column of ones)
         X = np.c_{np.ones}(X.shape[0]), X] # Adding x0 = 1 for bias
         # Convert y to 0 and 1 (if not already binary)
         y = (y > 0).astype(int)
In [42]: X.shape, y.shape
```

```
Out[42]: ((583, 9), (583,))
In [44]: def sigmoid(z):
             return 1 / (1 + np.exp(-z))
         def compute cost(X, y, theta):
             m = len(y)
             h = sigmoid(X @ theta)
             cost = (-1/m) * np.sum(y * np.log(h) + (1 - y) * np.log(1 - h))
             return cost
         # Gradient Descent Algorithm
         def gradient descent(X, y, theta, alpha, epochs):
             m = len(y)
             cost history = []
             for _ in range(epochs):
                 gradient = (1/m) * (X.T @ (sigmoid(X @ theta) - y))
                 theta -= alpha * gradient
                 cost history.append(compute cost(X, y, theta))
             return theta, cost_history
In [45]: theta = np.zeros(X.shape[1])
         alpha = 0.01
         epochs = 1000
         # Train the model
         theta optimal, cost history = gradient descent(X, y, theta, alpha, epochs)
         final cost = compute cost(X, y, theta optimal)
         final cost
Out[45]: np.float64(0.5964520453207424)
```

Make Preiction

```
In [48]: # Convert probabilities to binary values (0 or 1)
predictions = sigmoid(X @ theta_optimal) >= 0.5

# Compute accuracy
accuracy = np.mean(predictions == y) * 100
accuracy

Out[48]: np.float64(71.35506003430532)

In [49]: # Convert probabilities to binary values (0 or 1)
predictions = sigmoid(X @ theta_optimal) >= 0.5

# Compute accuracy
accuracy = np.mean(predictions == y) * 100
print(f"Model Accuracy: {accuracy: .2f}%")
Model Accuracy: 71.36%
In []:
```