# experiment4

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## 1 Experiment 4

1.1 22 january

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3.1 Q1. Today we will implement logistic regression to fit a model in connection with the dataset "liver patient.csv" available for you to download in moodle.

Download the dataset 'liver patient.csv' from moodle. This dataset has information regarding whether a person has liver disease or not based on some medical parameters (features) of a person. Open the CSV file and see the different features and the target variable Y also. 1 specifies yes and 0 specifies no in this last column of your dataset, which gives information regarding whether the person has or not liver disease.

#### 3.1.1 Load the dataset to a dataframe.

[115]:		Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	\
	0	65	Female	0.7	0.1	187	
	1	62	Male	10.9	5.5	699	
	2	62	Male	7.3	4.1	490	
	3	58	Male	1.0	0.4	182	
	4	72	Male	3.9	2.0	195	
			•••	•••	•••	•••	
	578	60	Male	0.5	0.1	500	
	579	40	Male	0.6	0.1	98	
	580	52	Male	0.8	0.2	245	
	581	31	Male	1.3	0.5	184	
	582	38	Male	1.0	0.3	216	

	Alamine_	Aminotransferase	Aspartate_	Aminotransferase	Total_Protiens	\
0		16		18	6.8	
1		64		100	7.5	
2		60		68	7.0	
3		14		20	6.8	
4		27		59	7.3	
 578		 20		34	 5.9	
579		35		31	6.0	
580		48		49	6.4	
581		29		32	6.8	
582		21		24	7.3	
	Albumin	Albumin_and_Glob	ulin_Ratio	liver_disease		
0	3.3		0.90	1		
1	3.2		0.74	1		
2	3.3		0.89	1		
3	3.4		1.00	1		
4	2.4		0.40	1		
			0.10			
 578	1.6		0.37			
579	3.2		1.10	1		
580	3.2		1.00	1		
581	3.4		1.00	1		
582	4.4		1.50	0		
[583	3 rows x 1	1 columns]				
df['	'liver dis	ease'].value_coun	ts()			
	er_disease					
1	416					
0	167					
Name	e: count,	dtype: int64				
df.i	info()					
<clas< td=""><td>ss 'pandas</td><td>s.core.frame.DataB</td><td>Frame'&gt;</td><td></td><td></td><td></td></clas<>	ss 'pandas	s.core.frame.DataB	Frame'>			
	-	33 entries, 0 to 5				
_		(total 11 columns)				
#	Column	(	Non-Null	Count Dtype		
0	A co		593 non	null int64		
0	Age		583 non-1			
1	Gender		583 non-1	3		
2	Total_Bil		583 non-			
3	Direct_B		583 non-			
4	Alkaline	_Phosphotase	583 non-	null int64		

[116]

[116]

[117]

int64

583 non-null

Alamine\_Aminotransferase

```
int64
6
    Aspartate_Aminotransferase 583 non-null
7
   Total_Protiens
                                583 non-null
                                                float64
8
   Albumin
                                583 non-null
                                                float64
9
   Albumin_and_Globulin_Ratio 583 non-null
                                                float64
                                583 non-null
10 liver disease
                                                int64
```

dtypes: float64(5), int64(5), object(1)

memory usage: 50.2+ KB

### 3.1.2 Drop the 'Age', 'Gender' columns in your dataframe

```
[118]: df.drop(['Age', 'Gender'], axis=1, inplace = True)
       df
[118]:
             Total_Bilirubin Direct_Bilirubin Alkaline_Phosphotase
                          0.7
                                              0.1
                                                                       187
       1
                         10.9
                                              5.5
                                                                      699
       2
                          7.3
                                              4.1
                                                                      490
       3
                                                                       182
                          1.0
                                              0.4
       4
                          3.9
                                              2.0
                                                                       195
       . .
                                                                      500
       578
                          0.5
                                              0.1
       579
                          0.6
                                              0.1
                                                                       98
       580
                          0.8
                                              0.2
                                                                      245
       581
                          1.3
                                              0.5
                                                                      184
       582
                          1.0
                                              0.3
                                                                      216
             Alamine_Aminotransferase
                                         Aspartate_Aminotransferase Total_Protiens \
       0
                                                                                     6.8
                                     16
                                                                    18
                                     64
                                                                   100
                                                                                     7.5
       1
       2
                                     60
                                                                    68
                                                                                     7.0
       3
                                     14
                                                                    20
                                                                                     6.8
       4
                                     27
                                                                    59
                                                                                     7.3
                                                                                     5.9
       578
                                     20
                                                                    34
       579
                                     35
                                                                    31
                                                                                     6.0
       580
                                     48
                                                                    49
                                                                                     6.4
                                     29
       581
                                                                    32
                                                                                     6.8
       582
                                     21
                                                                    24
                                                                                     7.3
             Albumin
                      Albumin_and_Globulin_Ratio
                                                     liver_disease
                 3.3
       0
                                               0.90
                                                                   1
                 3.2
       1
                                               0.74
                                                                   1
       2
                 3.3
                                               0.89
                                                                   1
                 3.4
       3
                                               1.00
                                                                   1
       4
                 2.4
                                               0.40
                                                                   1
       578
                 1.6
                                               0.37
                                                                   0
```

579	3.2	1.10	1
580	3.2	1.00	1
581	3.4	1.00	1
582	4.4	1.50	0

[583 rows x 9 columns]

3.1.3 USe MinMaxScaler() to scale the data in the range of 0 to 1

```
[119]: from sklearn.preprocessing import MinMaxScaler

MM = MinMaxScaler()
    x = MM.fit_transform(df)
```

3.1.4 Split the data into training and testing sets using appropriate functions. Use a 80:20 split and prepare your x train,x test,y train,y test data.

3.1.5 Now, import the inbuilt LogisticRegression class and create an object of this class and fit the model using training data as you have done in the linear and multiple linear regression case like last lab

```
[124]: from sklearn.linear_model import LogisticRegression
    logisticR = LogisticRegression()
    logisticR.fit(x_train,y_train)
    y_pred = logisticR.predict(x_test)
```

```
[125]: from sklearn.metrics import accuracy_score
accuracy1 = accuracy_score(y_test,y_pred)*100
print("Accuracy score of the model is:",accuracy1 ,"%")
```

Accuracy score of the model is: 74.35897435897436 %

3.1.6 Q2. Since its difficult to visualize the decision boundary in the above case we will take case where we will generate some dummy data with three features and the respective classes and implement logistic regression and visualize the decision boundary

```
[18]: import numpy as np
  import matplotlib.pyplot as plt
  from sklearn.datasets import make_classification
  from sklearn.linear_model import LogisticRegression
  from sklearn.model_selection import train_test_split
  from sklearn.metrics import accuracy_score
```

```
[22]: # generating a fake data first
x, y = make_classification(
    n_samples=200, # total number of samples in the dataset
    n_features=3, #total number of features in each sample
    n_informative=3, #number of informative features relevant for classification
    n_redundant=0, #cane be used for generating new features as linear_
    combinition
    n_clusters_per_class=1, # number of cluster per class
    class_sep = 3, #seperation between classes higher means easier_
    classification
    random_state=42)
```

```
[23]: # Splitting the data into test and train
      x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.2,_
       →random_state=0)
      # Train the logistic regression model
      logisticR = LogisticRegression()
      logisticR.fit(x_train, y_train)
      # Predict and calculate accuracy
      y pred = logisticR.predict(x test)
      accuracy = accuracy_score(y_test, y_pred)
      print("Accuracy score:", accuracy * 100, "%")
      # Get the model coefficients and intercept
      coef = logisticR.coef_[0]
      intercept = logisticR.intercept_[0]
      print("Coefficients:", coef)
      print("Intercept:", intercept)
      # Create a 3D plot for the decision boundary
      fig = plt.figure(figsize=(12, 8))
      ax = fig.add_subplot(111, projection='3d')
```

```
# Plot the datapoints
ax.scatter(x[y == 0, 0], x[y == 0, 1], x[y == 0, 2], color='blue', label='class_\square
\hookrightarrow0', alpha=0.7)
ax.scatter(x[y == 1, 0], x[y == 1, 1], x[y == 1, 2], color='red', label='class_u'
 \hookrightarrow 1', alpha=0.7)
# Create a grid for decision boundary
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))
# Calculate the z value (decision boundary plane)
zz = -(coef[0] * xx + coef[1] * yy + intercept) / coef[2]
# Plot the decision boundary plane
ax.plot_surface(xx, yy, zz, color='green', alpha=0.8, edgecolor='none')
# Set plot labels and title
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=90)
# Show the plot
plt.show()
```

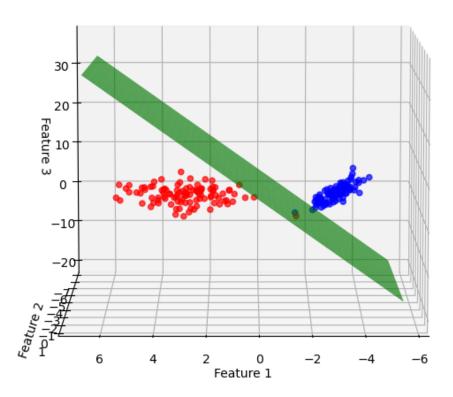
Accuracy score: 100.0 %

Coefficients: [ 2.17203369 0.19178324 -0.5114248 ]

Intercept: 3.3230582995486557

## 3D Logistic Regression Decision Boundary

class 0class 1



- 3.1.7 Q3. Now use any two features (except the age and gender) from the liver patient.csv dataset and implement logistic regression to predict whether a person has liver disease or not and in this case find the accuracy of the model and plot the decision boundary
- [24]: df = pd.read\_csv(r"D:\study material\VIT\_Data\_Science\Winter\_Sem\Data Mining\_

  →and Machine Learning Lab\Class\_notes\ML\_exp4\liver\_patient.csv")

  df.head()
- [24]: Age Gender Total\_Bilirubin Direct\_Bilirubin Alkaline\_Phosphotase 0 65 Female 0.7 0.1 187 1 10.9 5.5 62 Male 699

```
7.3
                                                       4.1
                                                                              490
      2
          62
                Male
      3
          58
                Male
                                    1.0
                                                       0.4
                                                                              182
                                                       2.0
      4
          72
                Male
                                    3.9
                                                                              195
         Alamine_Aminotransferase Aspartate_Aminotransferase Total_Protiens
      0
                                16
                                                              18
                                                                              6.8
                                                             100
      1
                                64
                                                                              7.5
      2
                                60
                                                                              7.0
                                                              68
      3
                                                              20
                                14
                                                                              6.8
      4
                                27
                                                              59
                                                                              7.3
         Albumin Albumin_and_Globulin_Ratio liver_disease
             3.3
      0
                                          0.90
             3.2
                                          0.74
                                                             1
      1
      2
             3.3
                                          0.89
                                                             1
      3
             3.4
                                          1.00
                                                             1
      4
                                          0.40
             2.4
                                                             1
[25]: df.drop(['Age', 'Gender'], axis=1, inplace = True)
     3.1.8 We randomly select 2 features and check its accuracy
[95]: features = df.columns[:-1]
      selected_features = np.random.choice(features, 2, replace=False)
      print("Selected features:", selected_features)
     Selected features: ['Alamine_Aminotransferase' 'Albumin']
[96]: x = df[selected_features]
[97]: x
[97]:
           Alamine_Aminotransferase
                                      Albumin
                                           3.3
                                   16
      0
      1
                                   64
                                           3.2
      2
                                   60
                                           3.3
      3
                                   14
                                           3.4
      4
                                   27
                                           2.4
      . .
      578
                                   20
                                           1.6
      579
                                           3.2
                                   35
      580
                                           3.2
                                   48
      581
                                   29
                                           3.4
      582
                                           4.4
                                   21
      [583 rows x 2 columns]
[98]: y = df['liver_disease']
```

```
[99]: y
 [99]: 0
              1
       1
              1
       2
              1
       3
              1
              1
       578
              0
       579
              1
       580
              1
       581
              1
       582
              0
       Name: liver_disease, Length: 583, dtype: int64
[100]: from sklearn.model_selection import train_test_split
       x_train,x_test,y_train,y_test = train_test_split(x,y,test_size=0.
        →2,random_state=42)
[101]: from sklearn.linear_model import LogisticRegression
       logisticR = LogisticRegression()
       logisticR.fit(x_train,y_train)
       y_pred = logisticR.predict(x_test)
       from sklearn.metrics import accuracy_score
       print("Accuracy score of the model is:", accuracy_score(y_test,y_pred)*100,"%")
      Accuracy score of the model is: 76.92307692307693 %
      3.1.9 Q4. Using the liver patient.csv dataset, drop the features age and gender in
            that dataframe and write down a gradient descent algorithm to implement the
            same. find the predictions of your model and the accuracy of the same. compare
            with Q1 results
[126]: df = pd.read csv(r"D:\study material\VIT Data Science\Winter Sem\Data Mining,
        →and Machine Learning Lab\Class_notes\ML_exp4\liver_patient.csv")
       df.drop(['Age','Gender'],axis=1,inplace = True)
[130]: X = df.drop(columns=['liver_disease']).values
       y = df['liver_disease'].values
       #scaling to the range of 0 and 1
       scaler = MinMaxScaler()
       X = scaler.fit transform(X)
       X = np.c_[np.ones(X.shape[0]), X]
       # Split the data into training and test sets
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,_
 →random_state=42)
# Sigmoid function
def sigmoid(z):
    return 1 / (1 + np.exp(-z))
# Gradient Descent function
def gradient_descent(X, y, parameters, alpha, iterations):
    m = len(y)
    for i in range(iterations):
        predictions = sigmoid(X @ parameters)
        error = predictions - y # (h(x) - y)
        gradients = (1 / m) * (X.T @ error)
        # Update the parameters
        parameters -= alpha * gradients
    return parameters
# Initialize parameters with zeros
parameters = np.zeros(X_train.shape[1])
# Setting learning rate (alpha) and number of iterations
alpha = 0.01
iterations = 1000
# Perform gradient descent
parameters = gradient_descent(X_train, y_train, parameters, alpha, iterations)
# Final model parameters
print("Optimized parameters:", parameters)
# Predict function
def predict(X, parameters):
    predictions = sigmoid(X @ parameters)
    return [1 if p \ge 0.5 else 0 for p in predictions]
# Predict on the test set
y_pred = predict(X_test, parameters)
# Evaluate accuracy
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy through gradient descent algorithm: {accuracy * 100}%")
print(f"Accuracy in Q1(through sklearn logistic regression):{accuracy1}%")
Optimized parameters: [0.5549485 0.10303017 0.1923647 0.1585347 0.09027214
0.05447359
```

Accuracy through gradient descent algorithm: 74.35897435897436%

0.27471853 0.13911428 0.05708392

Accuracy in Q1(through sklearn logistic regression):74.35897435897436%