Github --> https://github.com/Somto-Dera/ECGR5090-Machine-Learning.git

# Homework 2

In this homework, we will use the Diabetes dataset. (Note: You can use the built-in function from ML libraries for gradient descent, training, and validation.)

## Problem 1

Using the diabetes dataset, build a logistic regression binary classifier for positive diabetes. Please use 80% and 20% split between training and evaluation (test). Make sure to perform proper scaling and standardization before your training. Report your results, including accuracy, precision, and recall. Also, plot the confusion matrix representing your binary classifier.

#### **STEPS**

- -- Import Library
- -- Load dataset
- -- Process data
- -- Create model
- -- Evaluate Model

# Import Library

```
In [1]:
         # pandas is used for data manipulation and analysis
         import pandas as pd
         # numpy is used for array and matrics manipulation
         import numpy as np
         # matplotlib is used for data visualisation
         import matplotlib.pyplot as plt
         # seaborn is used for data visualization (heat map)
         import seaborn as sns
         # sklearn-metrics is used for measuring classification peformance
         from sklearn import metrics
         from sklearn import model selection
         # sklearn-logreg is used for creating logreg model
         from sklearn.linear model import LogisticRegression
         # sklearn-traintestsplit is used for spliting dataset
         from sklearn.model_selection import train_test_split, KFold
         # sklearn-scaler is used for scaling dataset
         from sklearn.preprocessing import StandardScaler
         # sklearn-naive_bayes is used for creating GNB model
         from sklearn.naive bayes import GaussianNB
         #%matplotlib inline
```

### Import and Display the first 5 rows of the dataset

```
In [2]: # load dataset into diabetes variable
diabetes = pd.read_csv('diabetes.csv')

# To get first five rows from the dataset default value
diabetes.head()
```

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

# Data Preprocessing and Analysis

Make a new dataframe which is a conviol the dataset so that our original dataset remains

```
In [3]: # load dataset into a new variable(df)
    df = diabetes

# display first five rows of the dataset
    df.head()
```

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

#### Find the size of the dataframe

```
In [4]: # prints shape of dataset so we can know it's dimensions
    df.shape

Out[4]: (768, 9)
```

#### Check if our data contains any missing values

```
In [5]:
         # Check for number of empty(NaN) cells in dataset
         df.isnull().sum().sort_values(ascending=False)[:10]
                                     0
        Pregnancies
Out[5]:
                                     0
        Glucose
        BloodPressure
                                     0
        SkinThickness
                                     0
        Insulin
                                     0
        BMI
        DiabetesPedigreeFunction
                                     0
        Age
                                     0
        Outcome
                                      0
        dtype: int64
```

#### Checking the data datatypes of each columns in the dataset

Out[7

```
In [6]:
         # ".dtypes" returns a Series with the data type of each column
         df.dtypes
Out[6]: Pregnancies
                                       int64
        Glucose
                                       int64
        BloodPressure
                                       int64
        SkinThickness
                                       int64
        Insulin
                                       int64
        BMI
                                     float64
        DiabetesPedigreeFunction
                                     float64
                                       int64
                                       int64
        Outcome
        dtype: object
In [7]:
         # Shows descriptive statistics on the dataset
         df.describe()
```

7]:		Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	ВМІ	DiabetesP€
	count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	
	mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	
	std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	
	min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	
	25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	
	50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	
	75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	
	max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	

#### Split datasets into feature and target datasets

```
In [8]: # Split dataset in features and target sets
feature_cols = ['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness','I

# Features, '[]' is used because X is a matrix
X = df[feature_cols]

# Target variable, '.Outcome' is used because y is a vector
y = df.Outcome

# Print out first five rows of the X set
X.head()
```

Out[8]:		Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	ВМІ	DiabetesPedigreeFunction	Δ
	0	6	148	72	35	0	33.6	0.627	
	1	1	85	66	29	0	26.6	0.351	
	2	8	183	64	0	0	23.3	0.672	

```
Pregnancies Glucose BloodPressure SkinThickness Insulin BMI DiabetesPedigreeFunction A

1 89 66 23 94 28.1 0.167
```

#### Split X and y datasets into train and test datasets

Split datasets into 80-20 ratio.

```
In [9]:
# split X and y into training, testing sets and print out it's shape
X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.20,random_stat
print('X_train dimension= ', X_train.shape)
print('X_test dimension= ', X_test.shape)
print('y_train dimension= ', y_train.shape)
print('y_test dimension= ', y_test.shape)

X_train dimension= (614, 8)
X_test dimension= (154, 8)
y_train dimension= (614,)
y_test dimension= (154,)
```

#### Scale and standardize features

```
In [10]:
          # create an instance of StandardScaler
          sc = StandardScaler()
          # Scale the test and train data set.
          X_train = sc.fit_transform(X_train)
          X test = sc.transform(X test)
          # print out scaled datasets
          print("Scaled training features:\n", X_train)
          print("\nScaled testing features:\n", X_test)
         Scaled training features:
          [[-0.52639686 -1.15139792 -3.75268255 ... -4.13525578 -0.49073479
           -1.03594038]
          [ 1.58804586 -0.27664283  0.68034485 ... -0.48916881  2.41502991
            1.48710085]
          [-0.82846011 0.56687102 -1.2658623 ... -0.42452187 0.54916055
           -0.94893896]
          [ 1.8901091 -0.62029661 0.89659009 ... 1.76054443 1.981245
            0.44308379]
          [-1.13052335  0.62935353  -3.75268255  ...  1.34680407  -0.78487662
           -0.33992901]
          [-1.13052335  0.12949347  1.43720319  ... -1.22614383  -0.61552223
           -1.03594038]]
         Scaled testing features:
          [[ 0.68185612 -0.71402038 -0.61712658 ... 0.26073561 -0.11637247
            0.87809089]
          [-0.52639686 -0.27664283 0.30191569 ... 0.48053518 -0.954231
           -1.03594038]
```

```
[-0.52639686 -0.40160784 -0.29275872 ... -0.15300476 -0.9245197 -1.03594038]
...
[1.28598261 -0.80774414 0.13973176 ... 0.62275843 0.04703966 2.0961108 ]
[-0.52639686 0.78555979 0.03160914 ... -0.51502758 -0.39268751 -0.33992901]
[1.28598261 -1.46381046 0.03160914 ... 0.42881763 0.70068816
```

**Side Note:** From cell(In[4]) we can observe that there are a total of 768 rows and 9 columns. The feature variables are 'Pregnancies', 'Glucose',

'BloodPressure', 'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age' and the target variables are 'Outcome'. We also observed that there are no empty cells(In[5]) in the dataset. The dataset has been scaled and splitted accordingly.

### Binary Logistic Regression Model

**Side Note:** From the output of cell([]) you see that Training score is more than the Test score. This is misleading. Which is why we use seperate datasets for testing when creating models, if not it won't generalise well and may give inaccurate predictions.

### Model Evaluation

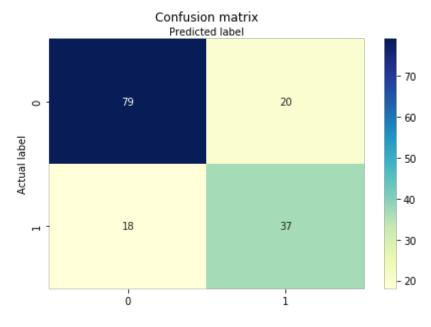
Confusion Matrix

```
In [12]: # Create confusion matrix
    cnf_matrix = metrics.confusion_matrix(y_test, y_pred)

class_names=[0,1] # name of classes
    fig, ax = plt.subplots()
    tick_marks = np.arange(len(class_names))
    plt.xticks(tick_marks, class_names)
    plt.yticks(tick_marks, class_names)

# create heatmap
    sns.heatmap(pd.DataFrame(cnf_matrix), annot=True, cmap="YlGnBu" ,fmt='g')
    ax.xaxis.set_label_position("top")
    plt.tight_layout()
    plt.title('Confusion matrix', y=1.1)
    plt.ylabel('Actual label')
    plt.xlabel('Predicted label')
```

Out[12]: Text(0.5, 257.44, 'Predicted label')



#### Side Note:

True Positives (TP): we correctly predicted that they do have diabetes.

• 37

True Negatives (TN): we correctly predicted that they don't have diabetes.

• 79

False Positives (FP): we incorrectly predicted that they do have diabetes (a "Type I error")

- 20
- Falsely predict positive

• Type I error

False Negatives (FN): we incorrectly predicted that they don't have diabetes (a "Type II error")

- 18
- Falsely predict negative
- Type II error

0: negative class 1: positive class

#### **Performance Metrics of Model**

- -- Accuracy is the percentage of correct predictions ((TP + TN)/(TP+FP+TN+FN)).
- -- Precision is the accuracy of positive predictions (TP/(TP + FP)).
- -- Recall is the fraction of positives that were correctly identified (TP/(TP+FN)).
- -- *F1-score* is the percent of positive predictions were correct (2(*Recall* Precision) / (Recall + Precision)).
- -- Support is the number of occurances of a given class.
- -- Null Accuracy\* is reading gotten by predicting the most frequent class.

```
In [13]:
          # print classification report
          print(metrics.classification_report(y_test, y_pred))
          # prints accuracy of the model
          print("\n\nAccuracy:",metrics.accuracy_score(y_test, y_pred))
          # prints classification error of the model
          print("Classification Error:",1 - metrics.accuracy score(y test, y pred))
          # prints precision of the model
          print("Precision:", metrics.precision score(y test, y pred))
          # prints recall of the model
          print("Recall/Sensitivity:",metrics.recall_score(y_test, y_pred))
          # prints specitivity of the model
          print("Specificity:",(cnf_matrix[0, 0] / (cnf_matrix[0, 0] + cnf_matrix[0, 1]
          # Calculate Null Accuracy to test our model
          # calculate the percentage of ones
          #percentage_ones = y_test.mean()
          # calculate the percentage of zeros
          #percentage_zero = 1 - y_test.mean()
          # calculate null accuracy
          #print("Null accuracy:", max(percentage ones, percentage zero))
          # examine the class distribution of the testing set (using a Pandas Series me
          print("Class Distribution:\n")
          print(y_test.value_counts())
```

	precision	recall	fl-score	support
0 1	0.81 0.65	0.80 0.67	0.81 0.66	99 55
accuracy macro avg weighted avg	0.73 0.76	0.74 0.75	0.75 0.73 0.75	154 154 154

Accuracy: 0.7532467532467533

Classification Error: 0.24675324675324672

Precision: 0.6491228070175439

Recall/Sensitivity: 0.6727272727272727

Specificity: 0.7979797979798

Class Distribution:

0 99 1 55

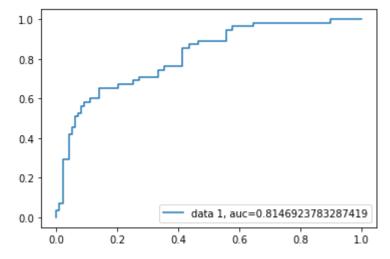
Name: Outcome, dtype: int64

**Side Note:** We have a null accuracy of 0.64 compared to the accuracy of our model which is 0.75, which means our model is decent(our model isn't dumb).

#### **ROC Curve**

Receiver Operating Characteristic(ROC) curve is a plot of the true positive rate against the false positive rate. It shows the tradeoff between sensitivity and specificity. Ideally the curve should be close to the top left corner, we'll want a high recall with and low fpr. AUC is useful when there is high class imbalance.

```
In [14]:
    y_pred_prob = lm.predict_proba(X_test)[::,1]
    fpr, tpr, thresholds = metrics.roc_curve(y_test, y_pred_prob)
    auc = metrics.roc_auc_score(y_test, y_pred_prob)
    plt.plot(fpr,tpr,label="data 1, auc="+str(auc), )
    plt.legend(loc=4)
    plt.show()
```



AUC score for the case is 0.81. AUC score 1 represents perfect classifier.

Problem 2

Using the diabetes dataset, build a Naïve Bayes binary classifier for positive diabetes. Please use 80% and 20% split between training and evaluation (test). Make sure to perform proper scaling and standardization before your training. Report your results, including accuracy, precision, and recall. Also, plot the confusion matrix representing your binary classifier. Compare and analyze your results against problem 1.

### Gaussian Naive-Bayes Model

#### **Performance Metrics of Model**

- -- Accuracy is the percentage of correct predictions ((TP + TN)/(TP+FP+TN+FN)).
- -- Precision is the accuracy of positive predictions (TP/(TP + FP)).
- -- Recall is the fraction of positives that were correctly identified (TP/(TP+FN)).
- -- *F1-score* is the percent of positive predictions were correct (2(*Recall* Precision) / (Recall + Precision)).
- -- Support is the number of occurances of a given class.
- -- Null Accuracy\* is reading gotten by predicting the most frequent class.

```
In [16]:
          # print classification report
          print(metrics.classification report(y test, y pred))
          # prints accuracy of the model
          print("\n\nAccuracy:",metrics.accuracy_score(y_test, y_pred))
          # prints classification error of the model
          print("Classif Error:",1 - metrics.accuracy score(y test, y pred))
          # prints precision of the model
          print("Precision:", metrics.precision score(y test, y pred))
          # prints recall of the model
          print("Recall/Sensitivity:",metrics.recall_score(y_test, y_pred))
          # prints specitivity of the model
          print("Specificity:",(cnf_matrix[0, 0] / (cnf_matrix[0, 0] + cnf_matrix[0, 1]
          # Calculate Null Accuracy to test our model
          # calculate the percentage of ones
          #percentage_ones = y_test.mean()
          # calculate the percentage of zeros
          #percentage_zero = 1 - y_test.mean()
          # calculate null accuracy
          #print("Null accuracy:", max(percentage ones, percentage zero))
          # examine the class distribution of the testing set (using a Pandas Series me
          print("Class Distribution:\n")
          print(y test.value counts())
```

	precision	recall	f1-score	support
0 1	0.83 0.66	0.80 0.71	0.81 0.68	99 55
accuracy macro avg weighted avg	0.75 0.77	0.75 0.77	0.77 0.75 0.77	154 154 154

Accuracy: 0.7662337662337663

Classif Error: 0.23376623376623373 Precision: 0.6610169491525424

Recall/Sensitivity: 0.7090909090909091

Specificity: 0.7979797979798

Class Distribution:

9955

Name: Outcome, dtype: int64

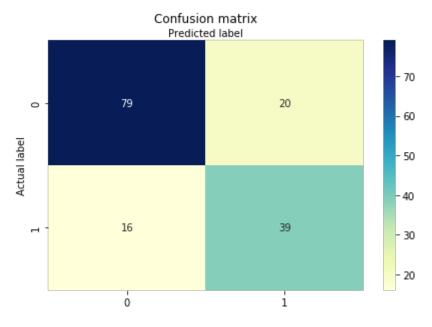
#### Confusion Matrix

```
In [17]: # Create confusion matrix
    cnf_matrix = metrics.confusion_matrix(y_test, y_pred)

class_names=[0,1] # name of classes
    fig, ax = plt.subplots()
    tick_marks = np.arange(len(class_names))
    plt.xticks(tick_marks, class_names)
    plt.yticks(tick_marks, class_names)

# create heatmap
    sns.heatmap(pd.DataFrame(cnf_matrix), annot=True, cmap="YlGnBu" ,fmt='g')
    ax.xaxis.set_label_position("top")
    plt.tight_layout()
    plt.title('Confusion matrix', y=1.1)
    plt.ylabel('Actual label')
    plt.xlabel('Predicted label')
```

Out[17]: Text(0.5, 257.44, 'Predicted label')



#### Side Note:

True Positives (TP): we correctly predicted that they do have diabetes.

• 39

True Negatives (TN): we correctly predicted that they don't have diabetes.

• 79

False Positives (FP): we incorrectly predicted that they do have diabetes (a "Type I error")

- 20
- Falsely predict positive

• Type I error

False Negatives (FN): we incorrectly predicted that they don't have diabetes (a "Type II error")

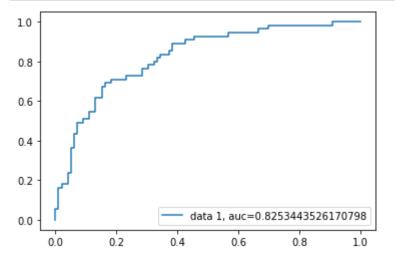
- 16
- Falsely predict negative
- Type II error

0: negative class 1: positive class

#### **ROC Curve**

Receiver Operating Characteristic(ROC) curve is a plot of the true positive rate against the false positive rate. It shows the tradeoff between sensitivity and specificity. Ideally the curve should be close to the top left corner, we'll want a high recall with and low fpr. AUC is useful when there is high class imbalance.

```
In [18]:
    y_pred_prob = gnb_model.predict_proba(X_test)[::,1]
    fpr, tpr, thresholds = metrics.roc_curve(y_test, y_pred_prob)
    auc = metrics.roc_auc_score(y_test, y_pred_prob)
    plt.plot(fpr,tpr,label="data 1, auc="+str(auc), )
    plt.legend(loc=4)
    plt.show()
```



### Problem 3

Repeat problem 1, and this time use K-fold cross-validation for your training and validation. Perform the training two times for K=5 and K=10. Analyze and compare your results against

Perform k=10 kfold (Logistic Regression): I am not here.

```
In [19]:
          # Applying 10-Fold Cross Validation
          kfold = KFold(n_splits=10, random_state=100, shuffle= True)
          # create instance of log regression object
          lr kfold = LogisticRegression(solver='lbfgs', max iter=1000)
          # create kfold Logistic Regression model
          #results kfold = model selection.cross val score(lr kfold, X = X train, y= y
          results kfold = model selection.cross val score(lr kfold, X = X, y= y, cv=kfo
          # convert scores to percent
          lst results kfold = [val * 100.0 for val in results kfold]
          lst results kfold = ['%.5f' % val for val in lst results kfold]
          # print out model metrics
          print("Average Accuracy: %.5f%" % (results kfold.mean()*100.0))
          print("Standard Deviation: %.5f%" % (results kfold.std()*100.0))
          print("Accuracy of Each Fold(Splits = 10): ",(lst_results_kfold))
         Average Accuracy: 77.33766%
         Standard Deviation: 4.50468%
         Accuracy of Each Fold(Splits = 10): ['77.92208', '68.83117', '77.92208', '7
         6.62338', '77.92208', '75.32468', '84.41558', '84.41558', '72.36842', '77.631
         58']
```

**Perform k=5 kfold (Logistic Regression):** I am not here.

```
In [20]: # Applying 5-Fold Cross Validation
kfold = KFold(n_splits=5, random_state=100, shuffle= True)

# create instance of log regression object
lr_kfold = LogisticRegression(solver='lbfgs', max_iter=1000)

# create kfold Logistic Regression model
# results_kfold = model_selection.cross_val_score(lr_kfold, X = X_train, y= y)
results_kfold = model_selection.cross_val_score(lr_kfold, X = X, y= y, cv=kfo)

# convert scores to percent
lst_results_kfold = [val * 100.0 for val in results_kfold]
lst_results_kfold = ['%.5f' % val for val in lst_results_kfold]

# print out model metrics
print("Accuracy: %.5f%" % (results_kfold.mean()*100.0))
print("Standard Deviation: %.5f%" % (results_kfold.std()*100.0))
print("Accuracy of Each Fold(Splits = 5): ",(lst_results_kfold))
```

```
Accuracy: 77.86945%

Standard Deviation: 3.56733%

Accuracy of Each Fold(Splits = 5): ['74.02597', '77.92208', '77.92208', '84.

31373', '75.16340']
```

## Problem 4

Repeat problem 2, and this time use K-fold cross-validation for your training and validation. Does this make sense? Elaborate on your answer.

Perform k=10 kfold (Gassian Naive-Bayes)

```
In [21]: # Applying 10-Fold Cross Validation
    kfold = KFold(n_splits=10, random_state=100, shuffle= True)

# instantiate a GassianNB object
    gnb_modell = GaussianNB()

# create kfold gnb model
    gnb_results_kfold = model_selection.cross_val_score(gnb_modell, X = X, y = y,

# compute and display scores from kfold gnb model
    print('Cross-validation scores:{}'.format(gnb_results_kfold))

# compute Average cross-validation score and display
    print('\nAverage cross-validation score: {:.4f}'.format(gnb_results_kfold.mea)

Cross-validation scores:[0.7012987  0.66233766  0.77922078  0.75324675  0.75324675
    0.80519481  0.81818182  0.71052632  0.78947368]

Average cross-validation score: 0.7526
```

# Observation:

#### Compare Results of Q1 and Q2:

The results of evaluation metrics for question One (In[13]) and question 2 (In[16]) shows that the gaussian NB model has a higher accuracy than the logistic regression model. Other evaluation metrics for classification models include precision and recall. Accuracy can be deceiving depending on the context of the model. There in recall and precision is more dependable. From the evaluation metrics of both models (In[13] and In[16]). Ideally precision is something we want to maximise. Gassian NB model also has better recall and precision than the Logistic Regression model. We might say that both model's performance is good based on the accuracy. But, if we see from the sensitivity of both models (In[13] and In[16]), indicates that there are still many False Negatives (FN) from the prediction result, so we can say that the model still needs some improvements to increase the sensitivity score, therefore decrease the False Negative occurrences.

#### Compare Results of Q1 and Q3:

Performing a cross validation on the logistic regression as opposed to the regular train-test split log regression(In[13]) produced a model with higher accuracy(In[19]) than the latter.

#### Results Q4:

Results from q4 (In[21]) shows that the model is less accuracte than the model derived in q2 (In[19]) meaning that the kfold doesn't improve the model.