# **HW 7**

This assignment covers several aspects of Regularizations & Tree type Classifier. **DO NOT ERASE MARKDOWN CELLS AND INSTRUCTIONS IN YOUR HW submission** 

- Q QUESTION
- A Where to input your answer

# Instructions

Keep the following in mind for all notebooks you develop:

- Structure your notebook.
- Use headings with meaningful levels in Markdown cells, and explain the questions each piece of code is to answer or the reason it is there.
- Make sure your notebook can always be rerun from top to bottom.
- Please start working on this assignment as soon as possible. If you are a beginner in
  Python this might take a long time. One of the objectives of this assignment is to help you
  learn python and scikit-learn package.
- See README.md (README.md) for homework submission instructions

# **Related Tutorials**

- <u>Lasso Regression L1 Regularization (https://scikit-learn.org/stable/modules/generated</u>/sklearn.linear model.LassoCV.html)
- <u>Ridge Regression L2 Regularization (https://scikit-learn.org/stable/modules/generated/sklearn.discriminant\_analysis.LinearDiscriminantAnalysis.html)</u>
- <u>Metrics: Precision-Recall curve (https://scikit-learn.org/stable/auto\_examples /model\_selection/plot\_precision\_recall.html)</u>

# **Data Processing**

#### Data

- Get the exploratory data and the following files from <u>link (https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+%28Diagnostic%29)</u>
- Save metadata and the original data from download <u>Link (https://archive.ics.uci.edu</u> /ml/datasets/Breast+Cancer+Wisconsin+%28Diagnostic%29) to your local HW folder.

or

You can use from the data folder in the 20222Spring repository.

Q1 Get training data from the dataframe

- 1. Load breast-cancer-wisconsin.data into data frame
- 2. Note: the data file does not contains column names, so include appropriate column names by exploring the metadata file
- 3. Replace Non-Numeric values with 0
- 4. Replace Class label 2 with 0 and 4 with 1
- 5. Print head of the dataframe

#### A1 Replace ??? with code in the code cell below

## In [25]:

import numpy as np import pandas as pd from sklearn.model\_selection import train\_test\_split

### Out[25]:

		Sample code number	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	No Nuc
_	0	1000025	5	1	1	1	2	1	3	
	1	1002945	5	4	4	5	7	10	3	
	2	1015425	3	1	1	1	2	2	3	
	3	1016277	6	8	8	1	3	4	3	
	4	1017023	4	1	1	3	2	1	3	
	5	1017122	8	10	10	8	7	10	9	
	6	1018099	1	1	1	1	2	10	3	
	7	1018561	2	1	2	1	2	1	3	
	8	1033078	2	1	1	1	2	1	1	
	9	1033078	4	2	1	1	2	1	2	

#### In [26]:

61: N 16: 11/

Out[26]: Sample code number 0 Clump Thickness 0 Uniformity of Cell Size 0 Uniformity of Cell Shape 0 Marginal Adhesion 0 Single Epithelial Cell Size 0 Bare Nuclei 0 Bland Chromatin 0 Normal Nucleoli 0 0 Mitoses Class 0

dtype: int64

```
In [29]: # Replace Non numeric values with 0
df['Bare Nuclei'] = pd.to_numeric(df['Bare Nuclei'], errors = 'coerce').fi

#Replace the Class label values following above given instructions
df['Class'].replace(2,0, inplace=True)
df['Class'].replace(4,1, inplace=True)
```

#### Q2

- 1. Assign values of Class column to y, note you have to use .values method
- 2. Drop Class column from data frame,
- 3. Assign df values to x
- 4. Normalize the x dataset using sklearn StandardScaler
- 5. Split dataset into train and test data use train\_test\_split with test\_size = 0.2, stratify y and random\_state = 1238

A2 Replace ??? with code in the code cell below

```
In [32]:
          ▶ # Assign values of ```Class``` column to y, note you have to use .values me
             y = df.Class.values
             # Drop 'Class' column from data frame,
             df.drop(columns = ['Class'], inplace = True)
             \# Assign df values to x
             x = df.values
             # View shape of x and y
             print(x.shape)
             print(y.shape)
             (699, 10)
             (699,)
          ▶ from sklearn.preprocessing import StandardScaler
In [34]:
             sc= StandardScaler()
             sc.fit(x)
          ★ xtrain, xtest, ytrain, ytest = train_test_split(X_scaled,y, test_size = 0.
In [38]:
```

# Model Regularization

# Ridge Regularization/ Ridge Regression

Q3 Train Ridge Regularization Model

- Create a Ridge Regularization Model using sklearn library, (See the documenttaion for details)
- 2. Fit the model with the train data

- 3. Predict the values with the test data
- 4. Print the coefficients of the model
- 5. Calculate the test MSE
- 6. Get the score from the model using test data
- 7. Plot Precision-Recall Curve from the true & predicted test data

#### Note

- Here we generate an array of cost values ranging from very big to very small
  - cost here is variable alpha: alpha is equivalent to lambda in the lesson 13.
     RidgeRegression
- Associated with each alpha value is a vector of ridge regression coefficients that we store
  in a matrix, with 100 rows (one for each value of alpha) and 10 columns (one for each
  predictor).

A3 Replace ??? with code in the code cell below

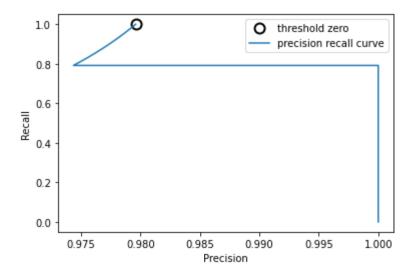
```
In [46]:
            from sklearn.model_selection import train_test_split
            from sklearn.linear_model import Ridge, Lasso
            from sklearn.metrics import mean_squared_error
            alphas = 0.5*(10**np.linspace(10,-2,100))
            ridge = Ridge()
            coefs = []
            for a in alphas:
               ridge.set_params(alpha = a)
               ridge.fit(X_scaled, y)
               coefs.append(ridge.coef_)
            pred1 = ridge.predict(xtest) # Use this model to predict the test data
            print(pd.Series(ridge.coef_, index = df.columns)) # Print coefficients
            mse = mean_squared_error(ytest, pred1) # Calculate the test MSE
            print("Test mean squared error (MSE): {:.2f}".format(mse))
```

```
Clump Thickness
Uniformity of Cell Size
                           0.067962
Uniformity of Cell Shape
                           0.051032
Marginal Adhesion
                            0.015905
Single Epithelial Cell Size 0.015844
Bare Nuclei
                            0.166585
Bland Chromatin
                            0.050569
Normal Nucleoli
                            0.053877
Mitoses
                            0.004013
dtype: float64
Test mean squared error (MSE): 0.03
0.8512905227365962
```

# Precision-Recall Curve for Ridge1

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Out[68]: <matplotlib.legend.Legend at 0x1dee8bc1a60>



#### Q4 Train Ridge Regression Model on the training set, and evaluate

- 1. Now, Create a Ridge Regression passing alpha = 4
- 2. Fit the model with the train data
- 3. Predict the values with the test data
- 4. Print the coefficients of the model
- Calculate the test MSE
- Get the score from the model using test data
- 7. Plot Precision-Recall Curve from the true & predicted test data

#### A4 Replace ??? with code in the code cell below

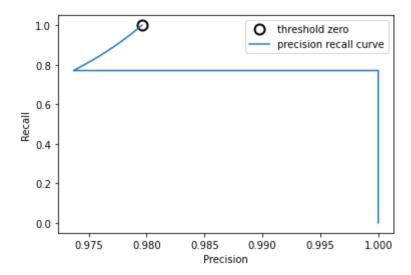
```
In [52]: In ridge2 = Ridge(alpha = 4)
    ridge2.fit(xtrain, ytrain)
    pred2 = ridge2.predict(xtest)

#print model coefficients
    print(pd.Series(ridge2.coef_, index = df.columns))
    mse = mean_squared_error(ytest, pred2)
```

```
print("Test mean squared error (MSE): {:.2f}".format(mse))
#print score
Samplé code number '
                              -0:004275
Clump Thickness
                               0.088294
Uniformity of Cell Size
                               0.063768
Uniformity of Cell Shape
                               0.049717
Marginal Adhesion
                               0.027027
Single Epithelial Cell Size
                               0.014242
Bare Nuclei
                               0.171456
Bland Chromatin
                               0.049034
Normal Nucleoli
                               0.047177
Mitoses
                               0.003699
dtype: float64
Test mean squared error (MSE): 0.03
0.846931627351646
```

# 

Out[53]: <matplotlib.legend.Legend at 0x1dee8a1aa30>



Q5 Train Ridge Regression Model on the training set, and evaluate

- 1. Now, Create a Ridge Regression passing alpha = 100
- 2. Fit the model with the train data
- 3. Predict the values with the test data
- 4. Print the coefficients of the model
- 5. Calculate the test MSE

- 6. Get the score from the model using test data
- 7. Plot Precision-Recall Curve from the true & predicted test data

Δ5 Replace ??? with code in the code cell below

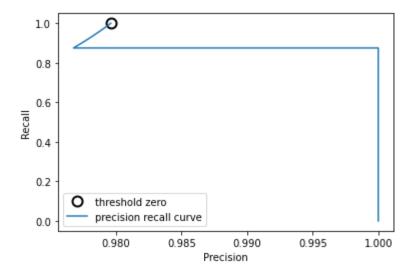
Sample code number -0.005360 Clump Thickness 0.082332 Uniformity of Cell Size 0.055674 Uniformity of Cell Shape 0.057688 Marginal Adhesion 0.037537 Single Epithelial Cell Size 0.023271 Bare Nuclei 0.135765 Bland Chromatin 0.054714 Normal Nucleoli 0.045838 Mitoses 0.006558

dtype: float64

Test mean squared error (MSE): 0.03

0.846805444478338

### Out[55]: <matplotlib.legend.Legend at 0x1dee8a89e80>



#### Q6 Train Ridge Regression Model on the training set, and evaluate

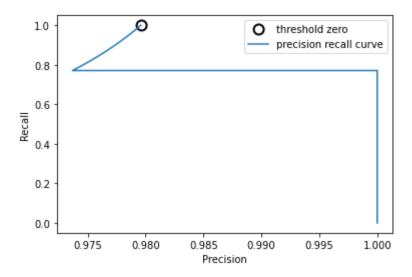
- Now, Create a Ridge Regression passing alpha = 0
- 2. Fit the model with the train data
- 3. Predict the values with the test data
- 4. Print the coefficients of the model
- 5. Calculate the test MSE
- 6. Get the score from the model using test data
- 7. Plot Precision-Recall Curve from the true & predicted test data

#### A6 Replace ??? with code in the code cell below

```
In [58]: In [58]
```

```
Samplé code number
                              -0:004197
Clump Thickness
                               0.088481
Uniformity of Cell Size
                               0.065116
Uniformity of Cell Shape
                               0.048488
Marginal Adhesion
                               0.026220
Single Epithelial Cell Size
                               0.013646
Bare Nuclei
                               0.173741
Bland Chromatin
                               0.048471
Normal Nucleoli
                               0.047323
Mitoses
                               0.003577
dtype: float64
Test mean squared error (MSE): 0.03
Test mean squared error (MSE): 0.03
0.8467604517795323
```

### Out[59]: <matplotlib.legend.Legend at 0x1dee8af6e50>



#### Q7 Study the codes above and answer the following questions:\*

- 1. Why when passing alpha = 100, the coefficients become very small?
- 2. Does alpha = 4 improve the MSE comparing to regular least squares?
- 3. How the size of alphas affects MSE and the Score of the models?

#### A7 Your answers:

1. The larger is the alpha, the higher is the smoothness constraints. Higher alpha makes coefficients much smaller with less flexibility of the fit.

- 2. No, the performence degrades comparing with the Regular Least Squares(RLS) (Which basically is the fit with alpha=0). alpha=0 or RLS achieves MSE=0.04
- 3. The higher value of alpha makes the model less flexible with the test data and the model becomes overfitted. The smaller value of alpha helps to generalized the model. So, the Score and MSE also increases with the test data.

# Lasso Regularization

#### Q8 Create a Lasso Regression passing max iter = 10000

- 1. set the alphas from the 3rd question for setting parameters in Lasso
- 2. Fit the model with the train data
- 3. Predict the values with the test data
- 4. Print the coefficients of the model
- 5. Calculate the test MSE
- 6. Get the score from the model using test data
- 7. Plot Precision-Recall Curve from the true & predicted test data

#### **A8**

Replace ??? with code in the code cell below

Sample code number

-0.000071

## **ElasticNet**

### Q9 Create a ElasticNet passing max\_iter = 10000

- 1. Use Cross Validation 15 times for searching best value of alpha for ElasticNet.
- 2. Fit the model with the train data
- 3. Print the best\_alpha value
- 4. Create a new ElasticNet using best value of alpha
- 5. Fit the model with the train data
- 6. Print the coefficients of the model
- 7. Calculate the test MSE
- 8. Get the score from the model using test data
- 9. Plot Precision-Recall Curve from the true & predicted test data

#### **A9**

Replace ??? with code in the code cell below

```
Best alpha: 0.01
Test mean squared error (MSE): 0.03
Sample code number -0.000000
Clump Thickness 0.085611
Uniformity of Cell Size 0.065678
Uniformity of Cell Shape 0.050153
Marginal Adhesion 0.025481
```

## Q10 Observe the lasso.coef and ridge.coef, and discuss the findings below

#### A10

Your answer goes here:

Answer: In the Lasso regression, the model works better when coefficients of the model is smaller. But on the otherhand, in Ridge regression, the model performs better with higher values of coefficients.

#### Q11

1. Is it a good choice to use Lasso regression when most of the columns are significantly useful for the target value? Give explanation supporting your answer.

#### **A11**

Your answer goes here.

Answer: Lasso regression is a good fit for dataset where many columns are not useful for our goal task. Lasso regression helps us to remove most of the not useful columns. But if all the columns are mostly related to the target then dropping many columns may hurt the