```
In [1]:
         import pandas as pd
         import numpy as np
         from scipy import stats
         import math
         # matplotlit and seaborn for visualizations
         import seaborn as sns
         import matplotlib.pyplot as plt
         plt.rcParams['font.size'] = 12
         # Suppress warnings from pandas
         import warnings
         warnings.filterwarnings('ignore')
         # modeling
         import lightgbm as lgb
         # utilities
         from sklearn.model selection import train test split
         from sklearn.metrics import roc_auc_score
         sns.set style("darkgrid")
         # memory management
         import gc
         import os
         # 운영체제별 한글 폰트 설정
         if os.name == 'posix': # Mac 환경 폰트 설정
             plt.rc('font', family='AppleGothic')
         elif os.name == 'nt': # Windows 환경 폰트 설정
             plt.rc('font', family='Malgun Gothic')
         plt.rc('axes', unicode_minus=False) # 마이너스 폰트 설정
         # 글씨 선명하게 출력하는 설정
         %config InlineBackend.figure format = 'retina'
         df = pd.read_csv("dataset2.csv")
         # import mglearn
         # from sklearn.model selection import KFold
         # from sklearn.preprocessing import LabelEncoder
In [2]:
         len(df[df['당뇨여부']==1])
Out[2]: 46579
In [3]:
        nodang = df[df['당뇨여부']==0].copy()
         dang = df[df['당뇨여부']==1].copy()
         print(len(nodang))
         print(len(dang))
        1133541
        46579
In [4]:
        X = df[['허리둘레','연령대코드(5세단위)', '감마지티피']].copy()
         y = df[['당뇨여부']].copy()
```

원본

```
In [5]: # from imblearn.under_sampling import RandomUnderSampler
          # rus = RandomUnderSampler(random state=42, sampling strategy=0.1)
          # X rus, y rus = rus.fit resample(X, y)
 In [6]:
          # print(len(X rus))
          # print(len(y rus))
          # print(np.sum(y_rus))
 In [7]:
         # y_rus
 In [8]:
         X train, X test, y train, y test = train test split(X,y.values, stratify = y,
          from lightgbm import LGBMClassifier, plot importance
          from sklearn.preprocessing import StandardScaler, RobustScaler
          sc = RobustScaler()
          x_train = sc.fit_transform(X_train)
          x test = sc.transform(X test)
          lgb = LGBMClassifier(n_estimators=400)
          evals = [(x test, y test)]
 In [9]:
          # lgb.fit(x train, y train, early stopping rounds=100, eval metric="logloss",
          lgb.fit(x train, y train, eval metric="logloss", eval set=evals, verbose=False
 Out[9]: LGBMClassifier(n_estimators=400)
In [10]:
          y pred = lgb.predict(x test)
        정확도
In [11]:
          lgb.score(x test, y test)
Out[11]: 0.9605082533979595
        예측 결과
In [12]:
          print("당뇨로 예측한 데이터 수 :", np.sum(y pred))
          print("실제 당뇨 데이터 수 :", np.sum(y_test))
          print("전체 데이터 수 :", len(y test))
         당뇨로 예측한 데이터 수 : 9.0
         실제 당뇨 데이터 수 : 9316.0
         전체 데이터 수 : 236024
        TN, FP, FN, TP
In [13]:
          from sklearn import metrics
          metrics.confusion matrix(y test, y pred)
          # [[TN, FP],
```

[FN, TP]]

```
Out[13]: array([[226701,
                            7],
               9314,
                             2]])
```

```
TN, FP, FN, TP 검토
In [14]:
         y test = y test.reshape(-1)
In [15]:
         P = sum(y test)
          TP = sum((y_test==1) & (y_pred==1))
          TPR = TP/P
          FN = sum((y test==1) & (y pred==0))
          FNR = FN/P
          N = sum(y test==0)
          TN = sum((y test==0) & (y pred==0))
          TNR = TN/N
          FP = sum((y_test==0) & (y_pred==1))
          FPR = FP/N
          print(TN, FP, FN, TP)
          print(TPR, FPR)
         226701 7 9314 2
         0.00021468441391155003 3.087672248001835e-05
        데이터 별 당뇨 분류 확률
In [16]:
          y pred proba = lgb.predict proba(x test)
          y pred proba
Out[16]: array([[0.94253565, 0.05746435],
                [0.98651095, 0.01348905],
                [0.89112273, 0.10887727],
                [0.89079286, 0.10920714],
                [0.94649197, 0.05350803],
                [0.85027254, 0.14972746]])
```

[당뇨X 확률, 당뇨 확률]

```
In [17]:
          y pred probashape
Out[17]: (236024, 2)
```

데이터 별 당뇨로 예측할 확률

```
In [18]:
         pos_proba = y_pred_proba[:,1]
         # np.unique(pos proba)
         print(len(pos_proba[pos_proba > 0.8]))
         0
In [19]:
         print("pos proba 최솟값 :", min(pos proba))
         print("pos_proba 최댓값:", max(pos_proba))
         pos proba 최솟값 : 4.730731419585e-06
         pos proba 최댓값: 0.6290574690060121
In [20]:
```

```
plt.hist(pos proba, range=(min(pos proba), max(pos proba)), bins=20)
Out[20]: (array([1.23419e+05, 5.57010e+04, 3.47960e+04, 1.60380e+04, 4.56300e+03,
                 1.07200e+03, 2.62000e+02, 7.70000e+01, 3.60000e+01, 1.70000e+01,
                 1.00000e+01, 1.00000e+01, 7.00000e+00, 3.00000e+00, 3.00000e+00,
                 1.00000e+00, 1.00000e+00, 4.00000e+00, 2.00000e+00, 2.00000e+00]),
          array([4.73073142e-06, 3.14573676e-02, 6.29100046e-02, 9.43626415e-02,
                 1.25815278e-01, 1.57267915e-01, 1.88720552e-01, 2.20173189e-01,
                 2.51625826e-01, 2.83078463e-01, 3.14531100e-01, 3.45983737e-01,
                 3.77436374e-01, 4.08889011e-01, 4.40341648e-01, 4.71794284e-01,
                 5.03246921e-01, 5.34699558e-01, 5.66152195e-01, 5.97604832e-01,
                 6.29057469e-01]),
          <BarContainer object of 20 artists>)
          120000
          100000
          80000
          60000
          40000
          20000
```

당뇨 예측 확률과 실제 데이터

0.1

0.2

0.3

0.4

0.5

0.6

0.6

0

0.0

```
In [21]:
          pos_sample_pos_proba = pos_proba[y_test==1]
          neg_sample_pos_proba = pos_proba[y_test==0]
In [22]:
          plt.hist([pos_sample_pos_proba, neg_sample_pos_proba], histtype="barstacked")
          plt.legend(["Positive samples", "Negative samples"])
          plt.xlabel("Predicted probability of positive class")
          plt.ylabel("Number of samples")
Out[22]: Text(0, 0.5, 'Number of samples')
            175000
                                                   Positive samples
                                                   Negative samples
            150000
          Number of samples
            125000
            100000
             75000
             50000
             25000
                  0
```

ROC Curve

0.0

0.1

0.2

0.3

Predicted probability of positive class

0.4

```
In [23]: fpr, tpr, thresholds = metrics.roc_curve(y_test, pos_proba)

In [24]: plt.plot(fpr, tpr, '*-')
    plt.plot([0,1], [0,1], 'r--')
    plt.legend(['Logistic regression', 'Random Classifier'])
    plt.xlabel('FPR')
    plt.ylabel('TPR')
    plt.title('ROC curve')
Out[24]: Text(0.5, 1.0, 'ROC curve')
```

ROC curve

1.0

Logistic regression
--- Random Classifier

0.8

0.6

0.4

0.2

0.0

0.0

0.0

0.2

0.4

0.6

0.8

1.0

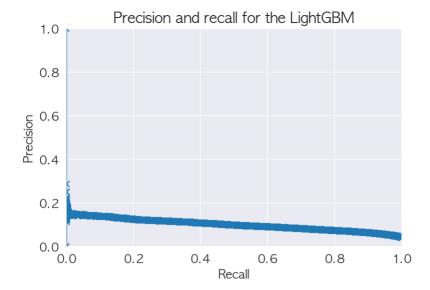
AUC Score

```
In [25]: metrics.roc_auc_score(y_test, pos_proba)
Out[25]: 0.7540966086434535
```

Precision, Recall, Accuracy

```
In [26]:
          precision = TP/(TP+FP)
          recall = TP/(TP+FN)
          accuracy = (TP+TN)/(TP+FP+TN+FN)
          print("precision :",precision)
          print("recall :", recall)
          print("accuracy :", accuracy)
         precision : 0.22222222222222
         recall : 0.00021468441391155003
         accuracy: 0.9605082533979595
In [27]:
          precision2, recall2, thresholds2 = metrics.precision recall curve(y test, pos
In [28]:
          plt.plot(recall2, precision2, '-x')
          plt.xlabel('Recall')
          plt.ylabel('Precision')
          plt.title('Precision and recall for the LightGBM')
          plt.xlim([0,1])
          plt.ylim([0,1])
```

```
Out[28]: (0.0, 1.0)
```



In [29]: metrics.auc(recall2, precision2)

Out[29]: 0.09879438452487636

In []: