```
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', '트리글리세라이드', 'LDL콜레스테롤']].
        y = df[['당뇨여부']].copy()
```

비당뇨: 당뇨 = 10:1

```
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))
         512369
         512369
         당뇨여부
                   46579.0
         dtype: float64
 In [7]:
          y_rus
                 당뇨여부
 Out[7]:
               0
                    0.0
                    0.0
               2
                    0.0
               3
                    0.0
               4
                    0.0
          512364
                     1.0
          512365
                     1.0
          512366
                     1.0
          512367
                     1.0
          512368
                     1.0
         512369 rows × 1 columns
 In [8]:
          X_train, X_test, y_train, y_test = train_test_split(X_rus,y_rus.values,strati
          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)
In [11]:
          is_correct = y_pred == y_test
```

정확도

```
In [12]: lgb.score(x_test, y_test)
Out[12]: 0.9088646876280813
```

.. _ . .

예측 결과

```
In [13]:

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 : 83.0
실제 당뇨 데이터 수 : 9316.0
전체 데이터 수 : 102474
```

TN, FP, FN, TP

TN, FP, FN, TP 검토

```
In [15]:
    y_test = y_test.reshape(-1)

In [16]:
    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)
```

93105 53 9286 30 0.0032202662086732504 0.0005689259108181798

데이터 별 당뇨 분류 확률

```
[0.94328932, 0.05671068],
...,
[0.91316966, 0.08683034],
[0.97393098, 0.02606902],
[0.81341741, 0.18658259]])
```

[당뇨X 확률, 당뇨 확률]

```
In [18]: y_pred_proba.shape
Out[18]: (102474, 2)
```

데이터 별 당뇨로 예측할 확률

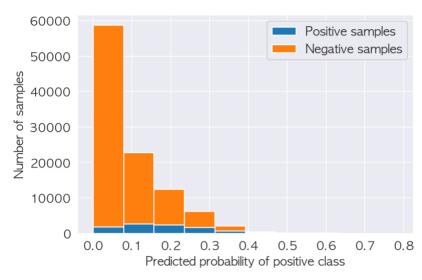
```
In [19]:
          pos proba = y pred proba[:,1]
          # np.unique(pos proba)
          print(len(pos proba[pos proba > 0.8]))
In [20]:
          print("pos proba 최솟값 :", min(pos proba))
          print("pos proba 최댓값 :", max(pos proba))
         pos proba 최솟값 : 2.289555246743766e-05
         pos proba 최댓값 : 0.785069221268276
In [21]:
          plt.hist(pos proba, range=(min(pos proba), max(pos proba)), bins=20)
Out[21]: (array([3.9555e+04, 1.9100e+04, 1.3219e+04, 9.4970e+03, 7.0110e+03,
                  5.4040e+03, 3.7080e+03, 2.4780e+03, 1.3370e+03, 6.7100e+02,
                  2.6600e+02, 9.8000e+01, 6.0000e+01, 2.8000e+01, 1.9000e+01,
                 1.3000e+01, 5.0000e+00, 3.0000e+00, 0.0000e+00, 2.0000e+00]),
          array([2.28955525e-05, 3.92752118e-02, 7.85275281e-02, 1.17779844e-01,
                  1.57032161e-01, 1.96284477e-01, 2.35536793e-01, 2.74789110e-01,
                  3.14041426e-01, 3.53293742e-01, 3.92546058e-01, 4.31798375e-01,
                  4.71050691e-01, 5.10303007e-01, 5.49555324e-01, 5.88807640e-01,
                  6.28059956e-01, 6.67312272e-01, 7.06564589e-01, 7.45816905e-01,
                 7.85069221e-01]),
          <BarContainer object of 20 artists>)
          40000
          35000
          30000
          25000
          20000
          15000
          10000
           5000
              0
                 0.0
                     0.1
                           0.2
                                0.3
                                     0.4
                                          0.5
                                               0.6
                                                    0.7
```

당뇨 예측 확률과 실제 데이터

```
pos_sample_pos_proba = pos_proba[y_test==1]
neg_sample_pos_proba = pos_proba[y_test==0]
```

```
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[23]: Text(0, 0.5, 'Number of samples')

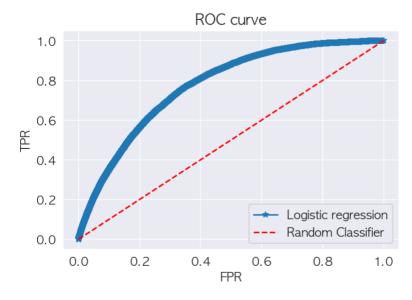


ROC Curve

```
In [24]: fpr, tpr, thresholds = metrics.roc_curve(y_test, pos_proba)

In [25]: 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[25]: Text(0.5, 1.0, 'ROC curve')



AUC Score

```
In [26]: metrics.roc_auc_score(y_test, pos_proba)
Out[26]: 0.7740775824828727
```

```
Precision, Recall, Accuracy
In [27]:
          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: 0.3614457831325301
         recall: 0.0032202662086732504
         accuracy: 0.9088646876280813
In [28]:
          precision2, recall2, thresholds2 = metrics.precision_recall_curve(y_test, pos
In [29]:
          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[29]: (0.0, 1.0)
                      Precision and recall for the LightGBM
            1.0
            0.8
         Precision
0.4
            0.6
            0.2
           0.0
                       0.2
                                0.4
                                         0.6
                                                  0.8
                                                           1.0
                                    Recall
```

```
In [30]: metrics.auc(recall2, precision2)

Out[30]: 0.23254835035776453

In []:
```