```
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()
```

### 비당뇨: 당뇨 = 10:4

```
In [5]: from imblearn.under_sampling import RandomUnderSampler
          rus = RandomUnderSampler(random state=42, sampling strategy=0.4)
          X rus, y rus = rus.fit resample(X, y)
 In [6]:
          print(len(X_rus))
          print(len(y rus))
          print(np.sum(y_rus))
         163026
         163026
         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
          163021
                     1.0
         163022
                     1.0
         163023
                     1.0
         163024
                     1.0
         163025
                     1.0
        163026 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)
```

### 정확도

```
In [11]: lgb.score(x_test, y_test)

Out[11]: 0.7279335091700914
```

## 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 : 4751.0
실제 당뇨 데이터 수 : 9316.0
전체 데이터 수 : 32606
```

### TN, FP, FN, TP

# TN, FP, FN, TP 검토

[ 6718, 2598]])

```
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)
         21137 2153 6718 2598
```

# 데이터 별 당뇨 분류 확률

0.2788750536711035 0.09244310863031344

```
[0.46410203, 0.53589797],
[0.8565563, 0.1434437]])
```

#### [당뇨X 확률, 당뇨 확률]

```
In [17]: y_pred_proba.shape
Out[17]: (32606, 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]))
         45
In [19]:
          print("pos proba 최솟값 :", min(pos proba))
          print("pos proba 최댓값 :", max(pos proba))
         pos proba 최솟값 : 6.387191488081119e-06
         pos proba 최댓값 : 0.9409455513526367
In [20]:
          plt.hist(pos proba, range=(min(pos proba), max(pos proba)), bins=20)
         (array([3944., 3018., 2337., 2316., 2229., 2237., 2383., 2522., 2530.,
                 2695., 2388., 1881., 1133., 547., 260., 102., 39.,
                   15.,
                           6.]),
          array([6.38719149e-06, 4.70533454e-02, 9.41003036e-02, 1.41147262e-01,
                 1.88194220e-01, 2.35241178e-01, 2.82288136e-01, 3.29335095e-01,
                 3.76382053e-01, 4.23429011e-01, 4.70475969e-01, 5.17522927e-01,
                 5.64569886e-01, 6.11616844e-01, 6.58663802e-01, 7.05710760e-01,
                 7.52757719e-01, 7.99804677e-01, 8.46851635e-01, 8.93898593e-01,
                 9.40945551e-01]),
          <BarContainer object of 20 artists>)
         4000
         3500
         3000
         2500
         2000
          1500
         1000
          500
             0
               0.0
                        0.2
                                0.4
                                         0.6
                                                 0.8
```

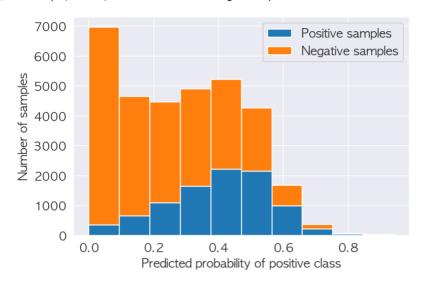
### 당뇨 예측 확률과 실제 데이터

```
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")
```

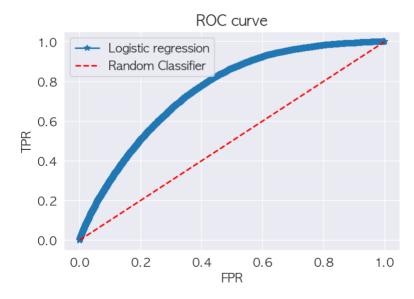
```
plt.legend(["Positive samples", "Negative samples"])
plt.xlabel("Predicted probability of positive class")
plt.ylabel("Number of samples")
```

Out[22]: Text(0, 0.5, 'Number of samples')



### **ROC Curve**

Out[24]: Text(0.5, 1.0, 'ROC curve')



### **AUC Score**

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

# 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 : 0.5468322458429804
          recall : 0.2788750536711035
          accuracy: 0.7279335091700914
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)
                      Precision and recall for the LightGBM
            1.0
            0.8
          Precision 0.9
            0.6
            0.2
            0.0
                                 0.4
               0.0
                        0.2
                                          0.6
                                                   0.8
                                                            1.0
                                    Recall
```

```
In [29]: metrics.auc(recall2, precision2)
Out[29]: 0.4959928902983133
In []:
```