```
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 = 10:6

```
In [5]: from imblearn.under_sampling import RandomUnderSampler
          rus = RandomUnderSampler(random state=42, sampling strategy=0.6)
          X rus, y rus = rus.fit resample(X, y)
 In [6]:
          print(len(X_rus))
          print(len(y rus))
          print(np.sum(y_rus))
         124210
         124210
         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
                     ...
          124205
                     1.0
          124206
                     1.0
          124207
                     1.0
          124208
                     1.0
          124209
                     1.0
         124210 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]: 0.7095241928991225
```

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 : 8624.0
실제 당뇨 데이터 수 : 9316.0
전체 데이터 수 : 24842
```

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)
         12264 3262 3954 5362
```

데이터 별 당뇨 분류 확률

0.5755689136968656 0.21009918845807032

```
[0.84751974, 0.15248026], ..., [0.93294934, 0.06705066], [0.57965178, 0.42034822], [0.35799092, 0.64200908]])
```

[당뇨X 확률, 당뇨 확률]

```
In [18]: y_pred_proba.shape
Out[18]: (24842, 2)
```

데이터 별 당뇨로 예측할 확률

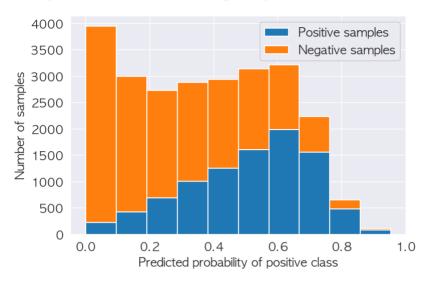
```
In [19]:
          pos proba = y pred proba[:,1]
          # np.unique(pos proba)
          print(len(pos proba[pos proba > 0.8]))
         369
In [20]:
          print("pos_proba 최솟값 :", min(pos_proba))
          print("pos proba 최댓값 :", max(pos proba))
         pos proba 최솟값: 0.0005754555701419514
         pos proba 최댓값 : 0.9533263517418327
In [21]:
          plt.hist(pos proba, range=(min(pos proba), max(pos proba)), bins=20)
Out[21]: (array([2067., 1877., 1511., 1487., 1375., 1356., 1442., 1440., 1483.,
                  1453., 1534., 1604., 1693., 1521., 1309., 921., 465., 192.,
                           24.]),
          array([5.75455570e-04, 4.82130004e-02, 9.58505452e-02, 1.43488090e-01,
                  1.91125635e-01, 2.38763180e-01, 2.86400724e-01, 3.34038269e-01,
                 3.81675814e-01, 4.29313359e-01, 4.76950904e-01, 5.24588448e-01,
                 5.72225993e-01, 6.19863538e-01, 6.67501083e-01, 7.15138628e-01,
                 7.62776173e-01, 8.10413717e-01, 8.58051262e-01, 9.05688807e-01,
                 9.53326352e-01]),
          <BarContainer object of 20 artists>)
          2000
          1750
          1500
          1250
          1000
           750
           500
           250
             0
                        0.2
                                0.4
                                         0.6
                                                 0.8
                                                         1.0
```

당뇨 예측 확률과 실제 데이터

```
In [22]:
    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')

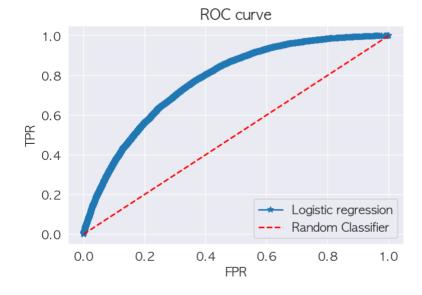


ROC Curve

```
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)
```

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: 0.6217532467532467
          recall: 0.5755689136968656
          accuracy: 0.7095241928991225
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
            0.2
            0.0
              0.0
                        0.2
                                                   0.8
                                 0.4
                                          0.6
                                                            1.0
                                    Recall
```

```
In [30]: metrics.auc(recall2, precision2)
Out[30]: 0.6322996950532986
In []:
```