In [99]:
```
import numpy as np
import pandas as pd
import matplotlib as mpl
import matplotlib.pyplot as plt
import mglearn
%matplotlib inline
import seaborn as sns
import platform
from matplotlib import font_manager , rc

if platform.system() == 'Darwin':
  rc('font' , family = 'AppleGothic')
elif platform.system() == 'Windows':
  path = 'C:/Windows/Fonts/malgun.ttf'
  font_name = font_manager.FontProperties(fname = path).get_name()
  rc('font' , family = font_name)
else:
  print('모름')
plt.rcParams['axes.unicode_minus'] = False
import warnings
warnings.filterwarnings('ignore')
```
executed in 23ms, finished 17:18:24 2023-11-02

In [100]:
```
from sklearn.metrics import accuracy_score, precision_score, recall_score, roc_auc_score
from sklearn.metrics import f1_score, confusion_matrix, roc_curve, precision_recall_curve
def get(y_test, pred=None, pred_proba=None):
    confusion = confusion_matrix(y_test, pred)
    accuracy = accuracy_score(y_test, pred)
    precision = precision_score(y_test, pred)
    recall = recall_score(y_test, pred)
    f1 = f1_score(y_test, pred)
    #roc_auc = roc_auc_score(y_test, pred_proba)

    print('오차 행렬(혼동 행렬)')
    print(confusion)

    print(f'정확도:{accuracy:.4f}, 정밀도:{precision:.4f}, 재현율:{recall:.4f}, F1:{f1:.4f}')

def model_fit(model , train_input , train_target):
    model.fit(train_input , train_target)
    pred = model.predict(test_input)
    return get(test_target , pred)
```
executed in 13ms, finished 17:18:24 2023-11-02

1 피마 인디언 당뇨병 예측

1.1 데이터셋 로딩

In [101]:
```
df = pd.read_csv('diabetes.csv')
```
executed in 14ms, finished 17:18:24 2023-11-02

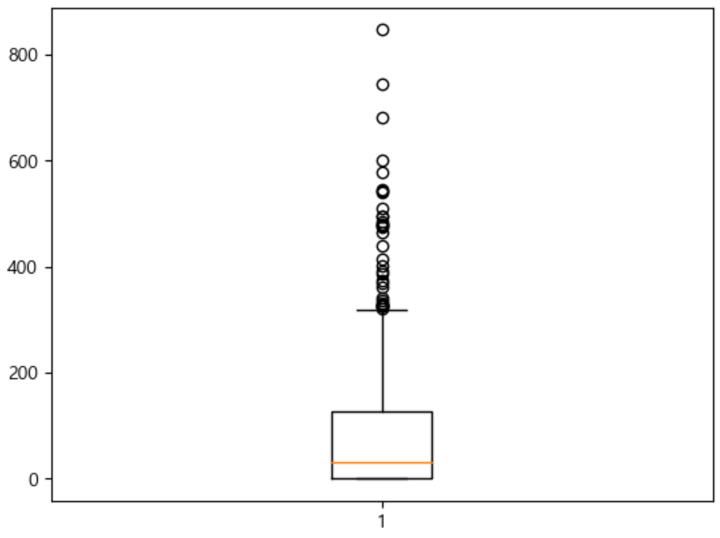
1.2 전처리

In [102]:
```
df.describe().T
```
executed in 28ms, finished 17:18:24 2023-11-02

Out[102]:

	count	mean	std	min	25%	50%	75%	max
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000	199.00
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000	122.00
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.00000	99.00
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.25000	846.00
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.60000	67.10
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	2.42
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	81.00
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000	1.00

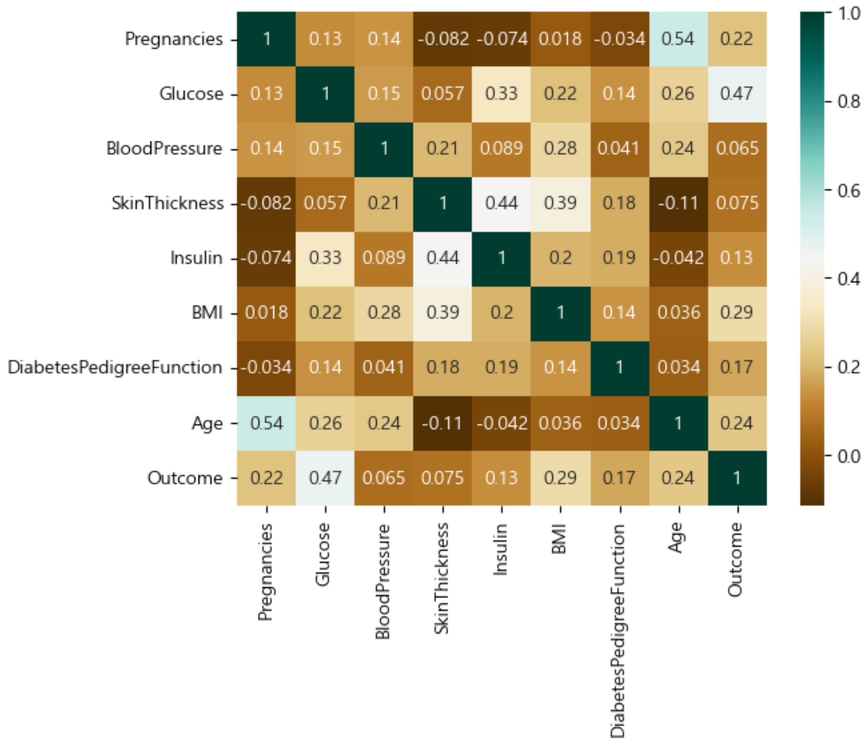
In [103]:
```
plt.boxplot(df.Insulin)
plt.show()
```
executed in 77ms, finished 17:18:24 2023-11-02



- 인슐린 수치를 boxplot으로 보면 , 이상치가 많은데 , 이 이상치는 당뇨에 밀접한 관련이 있어보인다. 상관관계를 보자.

In [104]:
```
sns.heatmap(df.corr() , annot = True , cmap = 'BrBG')
```
executed in 345ms, finished 17:18:25 2023-11-02

Out[104]:
```
<Axes: >
```



	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1	0.13	0.14	-0.082	-0.074	0.018	-0.034	0.54	0.22
Glucose	0.13	1	0.15	0.057	0.33	0.22	0.14	0.26	0.47
BloodPressure	0.14	0.15	1	0.21	0.089	0.28	0.041	0.24	0.065
SkinThickness	-0.082	0.057	0.21	1	0.44	0.39	0.18	-0.11	0.075
Insulin	-0.074	0.33	0.089	0.44	1	0.2	0.19	-0.042	0.13
BMI	0.018	0.22	0.28	0.39	0.2	1	0.14	0.036	0.29
DiabetesPedigreeFunction	-0.034	0.14	0.041	0.18	0.19	0.14	1	0.034	0.17
Age	0.54	0.26	0.24	-0.11	-0.042	0.036	0.034	1	0.24
Outcome	0.22	0.47	0.065	0.075	0.13	0.29	0.17	0.24	1

- Outcome과 인슐린의 상관계수는 0.13으로 , 그닥 높지 않다. 그러면 이상치를 지우자

In [105]:
```
#이상치 인덱스를 확인하는 함수
def get_outlier(df = None , column = None , weight = 1.5):
    fraud = df[df['Outcome'] == 1][column]
    quantile_25 = np.percentile(fraud.values , 25)
    quantile_75 = np.percentile(fraud.values , 75)
    iqr = quantile_75 - quantile_25
    iqr_weight = iqr * weight
    lowest_val = quantile_25 - iqr_weight
    highest_val = quantile_75 + iqr_weight
    outlier_index = fraud[(fraud<lowest_val)|(fraud>highest_val)].index
    return outlier_index
```
executed in 14ms, finished 17:18:25 2023-11-02

In [106]:
```
index_ = get_outlier(df = df , column = 'Insulin' , weight = 1.5)
```
executed in 14ms, finished 17:18:25 2023-11-02

In [107]:
```
df.drop(index_ , axis = 0 , inplace = True)
```
executed in 15ms, finished 17:18:25 2023-11-02

In [108]:
```
df.info()
```
executed in 12ms, finished 17:18:25 2023-11-02

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 756 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               756 non-null    int64  
 1   Glucose                   756 non-null    int64  
 2   BloodPressure             756 non-null    int64  
 3   SkinThickness             756 non-null    int64  
 4   Insulin                   756 non-null    int64  
 5   BMI                       756 non-null    float64
 6   DiabetesPedigreeFunction  756 non-null    float64
 7   Age                       756 non-null    int64  
 8   Outcome                   756 non-null    int64  
dtypes: float64(2), int64(7)
memory usage: 59.1 KB
```

- 이상치 12개가 제거되었다

In [109]:
```
df.describe().T
```
executed in 29ms, finished 17:18:25 2023-11-02

Out[109]:

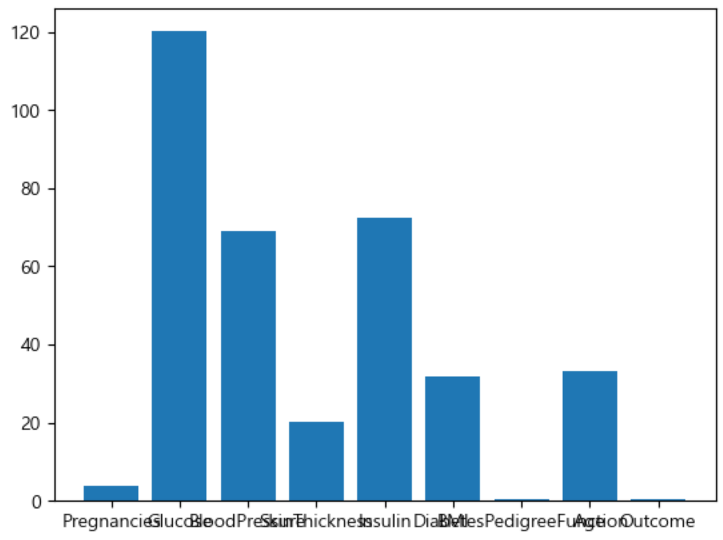
	count	mean	std	min	25%	50%	75%	max
Pregnancies	756.0	3.849206	3.373604	0.000	1.000	3.0000	6.0000	17.00
Glucose	756.0	120.142857	31.560109	0.000	99.000	116.0000	139.0000	199.00
BloodPressure	756.0	69.064815	19.449777	0.000	63.500	72.0000	80.0000	122.00
SkinThickness	756.0	20.322751	15.941335	0.000	0.000	23.0000	32.0000	99.00
Insulin	756.0	72.461640	99.404811	0.000	0.000	18.0000	122.0000	744.00
BMI	756.0	31.948942	7.915590	0.000	27.200	32.0000	36.5250	67.10
DiabetesPedigreeFunction	756.0	0.469896	0.326644	0.078	0.244	0.3705	0.6245	2.42
Age	756.0	33.160053	11.691489	21.000	24.000	29.0000	40.0000	81.00
Outcome	756.0	0.338624	0.473555	0.000	0.000	0.0000	1.0000	1.00

In [110]:
```
df.mean(axis = 0)
```
executed in 14ms, finished 17:18:25 2023-11-02

Out[110]:
```
Pregnancies                   3.849206
Glucose                     120.142857
BloodPressure                69.064815
SkinThickness                20.322751
Insulin                      72.461640
BMI                          31.948942
DiabetesPedigreeFunction      0.469896
Age                          33.160053
Outcome                       0.338624
dtype: float64
```

In [111]:
```
plt.bar(x = df.mean(axis = 0).index , height = df.mean(axis = 0))
```
executed in 138ms, finished 17:18:25 2023-11-02

Out[111]:
```
<BarContainer object of 9 artists>
```



- 수치들의 평균을 시각화했는데 , 제각각이다. 정규화하는 것이 좋겠다.

In [112]:
```
from sklearn.preprocessing import StandardScaler
ss = StandardScaler()
```
executed in 14ms, finished 17:18:25 2023-11-02

In [113]:
```
data = df.iloc[:,:-1]
target = df.iloc[:,-1]
```
executed in 15ms, finished 17:18:25 2023-11-02

In [114]:
```
data_scaled = ss.fit_transform(data)
```
executed in 14ms, finished 17:18:25 2023-11-02

In [115]:
```
target.value_counts()
```
executed in 15ms, finished 17:18:25 2023-11-02

Out[115]:
```
0    500
1    256
Name: Outcome, dtype: int64
```

- 두배 차이 나니까 조절하자

In [116]:
```
from sklearn.model_selection import train_test_split
```
executed in 13ms, finished 17:18:25 2023-11-02

In [117]:
```
train_input , test_input , train_target , test_target = train_test_split(data_scaled , target , test_size = 0.2 , random_state = 0 , s
```
executed in 13ms, finished 17:18:25 2023-11-02

- knn , LogisticRegression , RandomForestClassifier , LGBMClassifier 4개 사용하자

실제 당뇨병 환자중에 당뇨병이 아니라고 진단하면 심각하기 때문에 , 재현율(recall)에 초점을 두기

In [118]:
```
from lightgbm import LGBMClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression
lgb = LGBMClassifier(random_state = 0)
kn = KNeighborsClassifier()
rf = RandomForestClassifier(random_state = 0)
lr = LogisticRegression(random_state = 0)
```
executed in 13ms, finished 17:18:25 2023-11-02

In [119]:
```
model = [lgb,kn,rf,lr]
recall_ = []
precision_ = []
for i in model:
    print(i.__class__.__name__)
    print(model_fit(i , train_input , train_target))
    print()
    print()
    print()
    recall = recall_score(test_target , i.predict(test_input))
    precision = precision_score(test_target , i.predict(test_input))
    recall_.append(recall)
    precision_.append(precision)
```
executed in 342ms, finished 17:18:25 2023-11-02

```
LGBMClassifier
오차 행렬(혼동 행렬)
[[89 12]
 [19 32]]
정확도:0.7961, 정밀도:0.7273, 재현율:0.6275, F1:0.6737
None



KNeighborsClassifier
오차 행렬(혼동 행렬)
[[90 11]
 [21 30]]
정확도:0.7895, 정밀도:0.7317, 재현율:0.5882, F1:0.6522
None



RandomForestClassifier
오차 행렬(혼동 행렬)
[[91 10]
 [19 32]]
정확도:0.8092, 정밀도:0.7619, 재현율:0.6275, F1:0.6882
None



LogisticRegression
오차 행렬(혼동 행렬)
[[91 10]
 [20 31]]
정확도:0.8026, 정밀도:0.7561, 재현율:0.6078, F1:0.6739
None
```

In [120]:
```
np.mean(recall_)
```
executed in 14ms, finished 17:18:25 2023-11-02

Out[120]:
```
0.6127450980392157
```

- 4개의 모델 재현율 평균은 0.61

1.3 오버샘플링

In [121]:
```
from imblearn.over_sampling import SMOTE
smote = SMOTE(random_state = 0)
train_input_over , train_target_over = smote.fit_resample(train_input , train_target)
```
executed in 14ms, finished 17:18:25 2023-11-02

In [122]:
```
recall__ = []
precision__ = []
for i in model:
    print(i.__class__.__name__)
    print(model_fit(i , train_input_over , train_target_over))
    print()
    print()
    print()
    recall = recall_score(test_target , i.predict(test_input))
    precision = precision_score(test_target , i.predict(test_input))
    recall__.append(recall)
    precision__.append(precision)
```
executed in 422ms, finished 17:18:26 2023-11-02

```
LGBMClassifier
오차 행렬(혼동 행렬)
[[87 14]
 [20 31]]
정확도:0.7763, 정밀도:0.6889, 재현율:0.6078, F1:0.6458
None



KNeighborsClassifier
오차 행렬(혼동 행렬)
[[80 21]
 [13 38]]
정확도:0.7763, 정밀도:0.6441, 재현율:0.7451, F1:0.6909
None



RandomForestClassifier
오차 행렬(혼동 행렬)
[[90 11]
 [20 31]]
정확도:0.7961, 정밀도:0.7381, 재현율:0.6078, F1:0.6667
None



LogisticRegression
오차 행렬(혼동 행렬)
[[82 19]
 [13 38]]
정확도:0.7895, 정밀도:0.6667, 재현율:0.7451, F1:0.7037
None
```

In [123]:
```
np.mean(recall__)
```
executed in 15ms, finished 17:18:26 2023-11-02

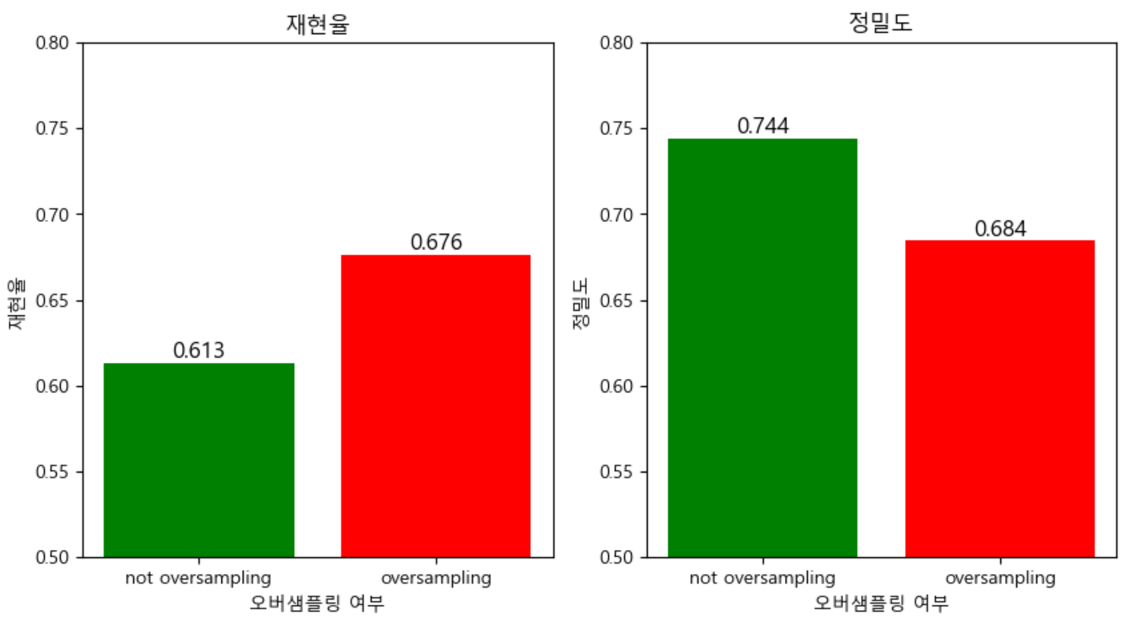
Out[123]:
```
0.6764705882352942
```

- 재현율이 0.61에서 0.67로 올랐다

In [124]:
```
plt.figure(figsize = (10,5))
plt.subplot(1,2,1)
x = plt.bar(x = [1,2] , height = [np.mean(recall_) , np.mean(recall__)] , color = ['green','red'])
plt.xticks([1,2] , ['not oversampling' , 'oversampling'])

for i in x:
    height = round(i.get_height() , 3)
    plt.text(i.get_x()+i.get_width()/2.0,height,  height, ha = 'center',va='bottom',size=12)

plt.ylim(0.5,0.8)

plt.title('재현율')
plt.xlabel('오버샘플링 여부')
plt.ylabel('재현율')

plt.subplot(1,2,2)

y = plt.bar(x = [1,2] , height = [np.mean(precision_) , np.mean(precision__)] , color = ['green','red'])
plt.xticks([1,2] , ['not oversampling' , 'oversampling'])

for i in y:
    height = round(i.get_height() , 3)
    plt.text(i.get_x()+i.get_width()/2.0,height,  height, ha = 'center',va='bottom',size=12)

plt.ylim(0.5,0.8)

plt.title('정밀도')
plt.xlabel('오버샘플링 여부')
plt.ylabel('정밀도')
```

```
executed in 278ms, finished 17:18:26 2023-11-02
```

Out[124]:
```
Text(0, 0.5, '정밀도')
```



- 재현율은 올라갔지만 , 정밀도는 내려갔다.

정밀도는 당뇨라 예측했을 때 당뇨가 아닌 것(FP)에 영향을 받고 재현율은 당뇨가 아니라 예측했는데 알고보니 당뇨인 것(FN)에 영향을 받으니 , 이 데이터에선 재현율이 낮으면 심각도가 더 높아진다고 할 수 있다

In [ ]:

In [ ]:

In [ ]: