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Life Changing Education

Chapter 15. Logistic Regression

Logistic Regression

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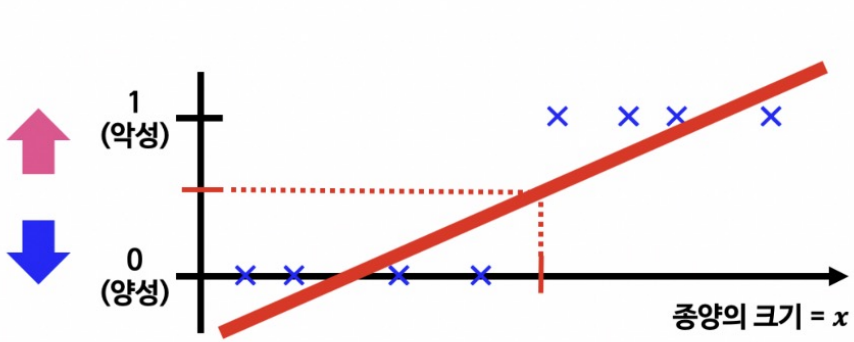
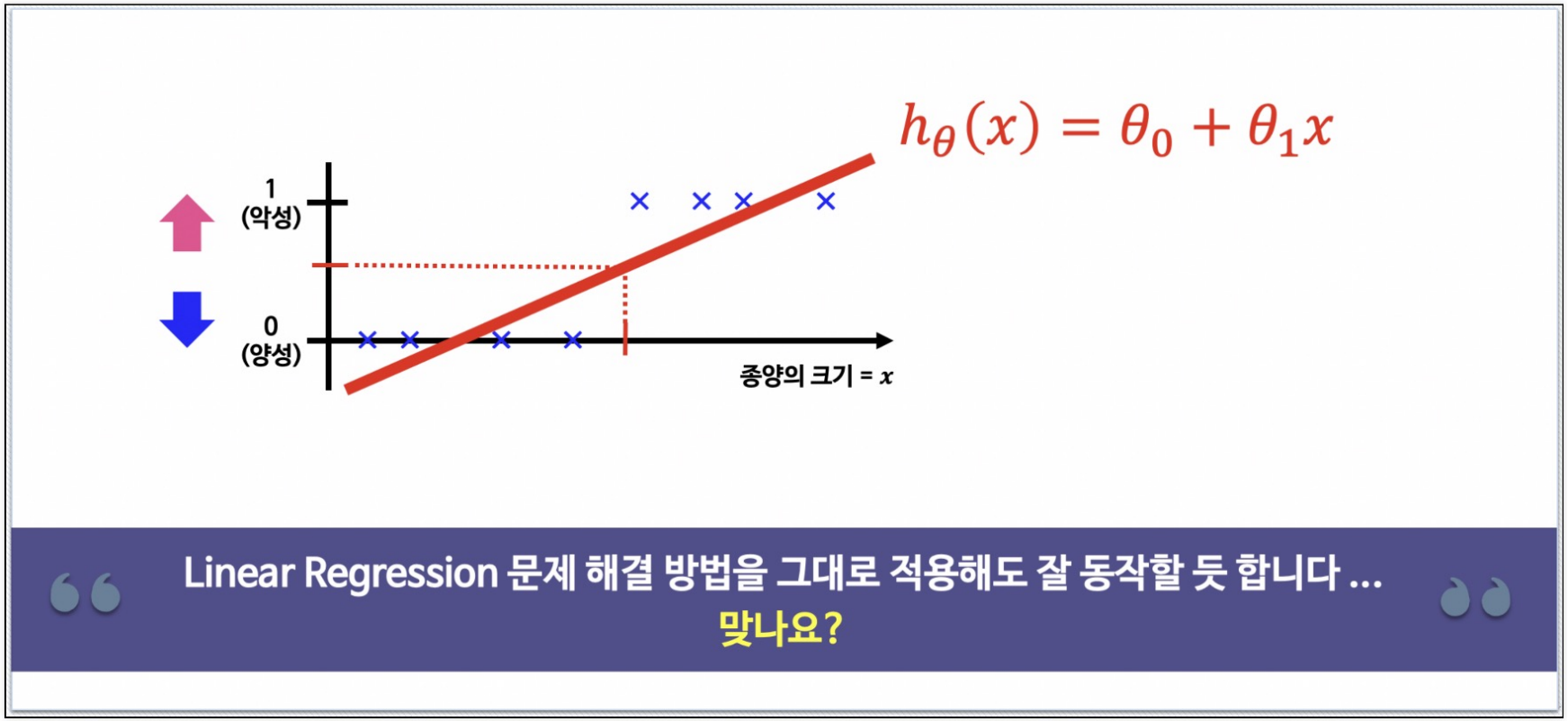
분류?? 회귀?? 악성 종양을 찾는 문제

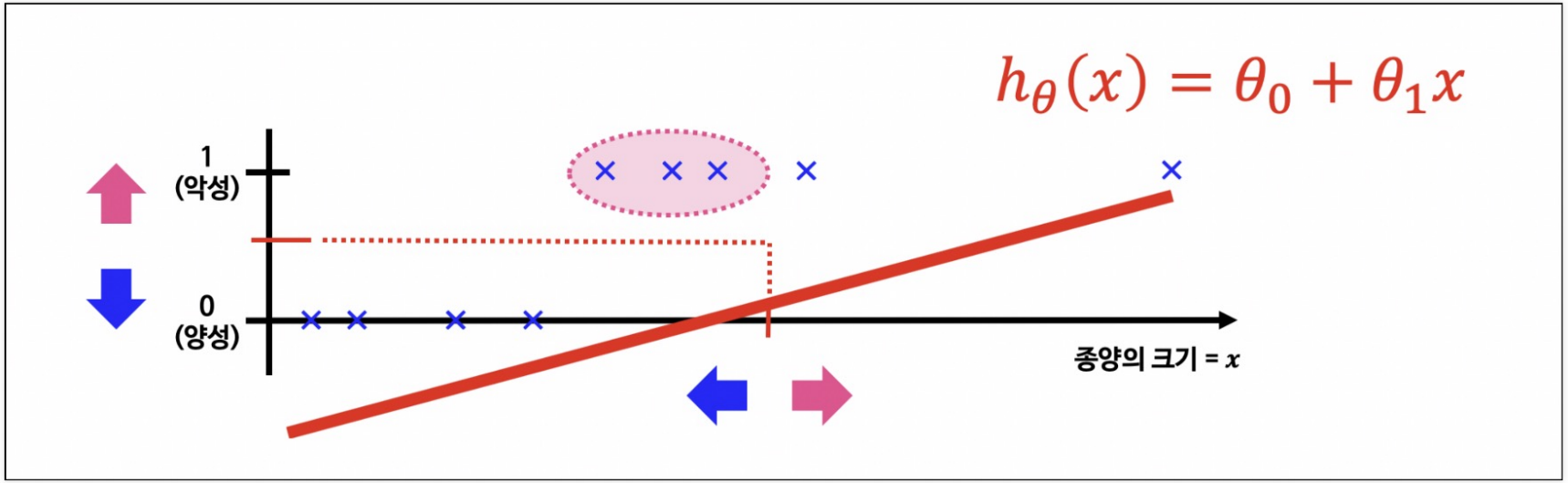


- $h_\theta(x)$가 0.5보다 크거나 같으면 1(악성)으로 예측
- $h_\theta(x)$가 0.5보다 작으면 0(양성)으로 예측

Linear Regression을 분류 문제에 적용할 수 있을까?



Linear Regression으로는 분류하는 게 적용하기 힘들듯 하다



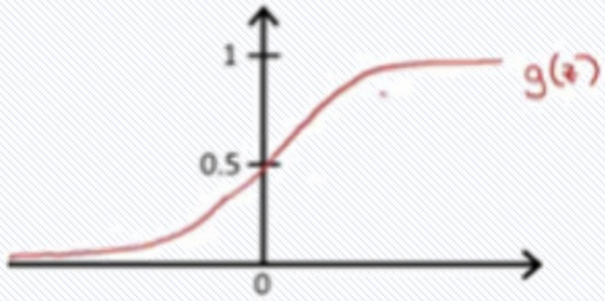
모델 재설정

분류 문제는 0 또는 1로 예측해야 하나 Linear Regression을 그대로 적용하면
예측값 $h_\theta(x)$는 **0보다 작거나 1보다 큰 값을 가질 수 있음**

$h_\theta(x)$가 항상 **0에서 1 사이의 값을 갖도록** Hypothesis 함수를 수정!!

$$h_\theta(x) = g(\theta_0 + \theta_1 x)$$

$$g(z) = \frac{1}{1+e^{-z}}$$



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어떻게 생긴 걸까? Logistic Function - 간단히 확인하러 가기

```
import numpy as np

z = np.arange(-10, 10, 0.01)
g = 1 / (1+np.exp(-z))
```

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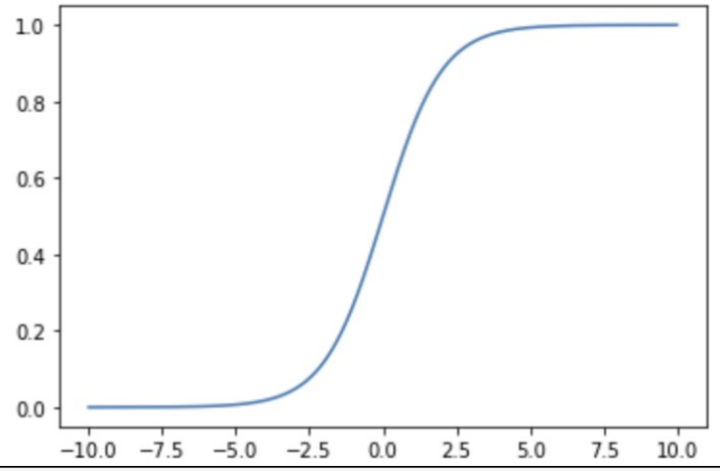
Python 유저 답게 확인

```
import matplotlib.pyplot as plt
%matplotlib inline

plt.plot(z, g);
```



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앙마는 디테일에~~~

```
plt.figure(figsize=(12,8))
ax = plt.gca()

ax.plot(z, g)
ax.spines['left'].set_position('zero')
ax.spines['right'].set_color('none')
ax.spines['bottom'].set_position('center')
ax.spines['top'].set_color('none')

plt.show()
```

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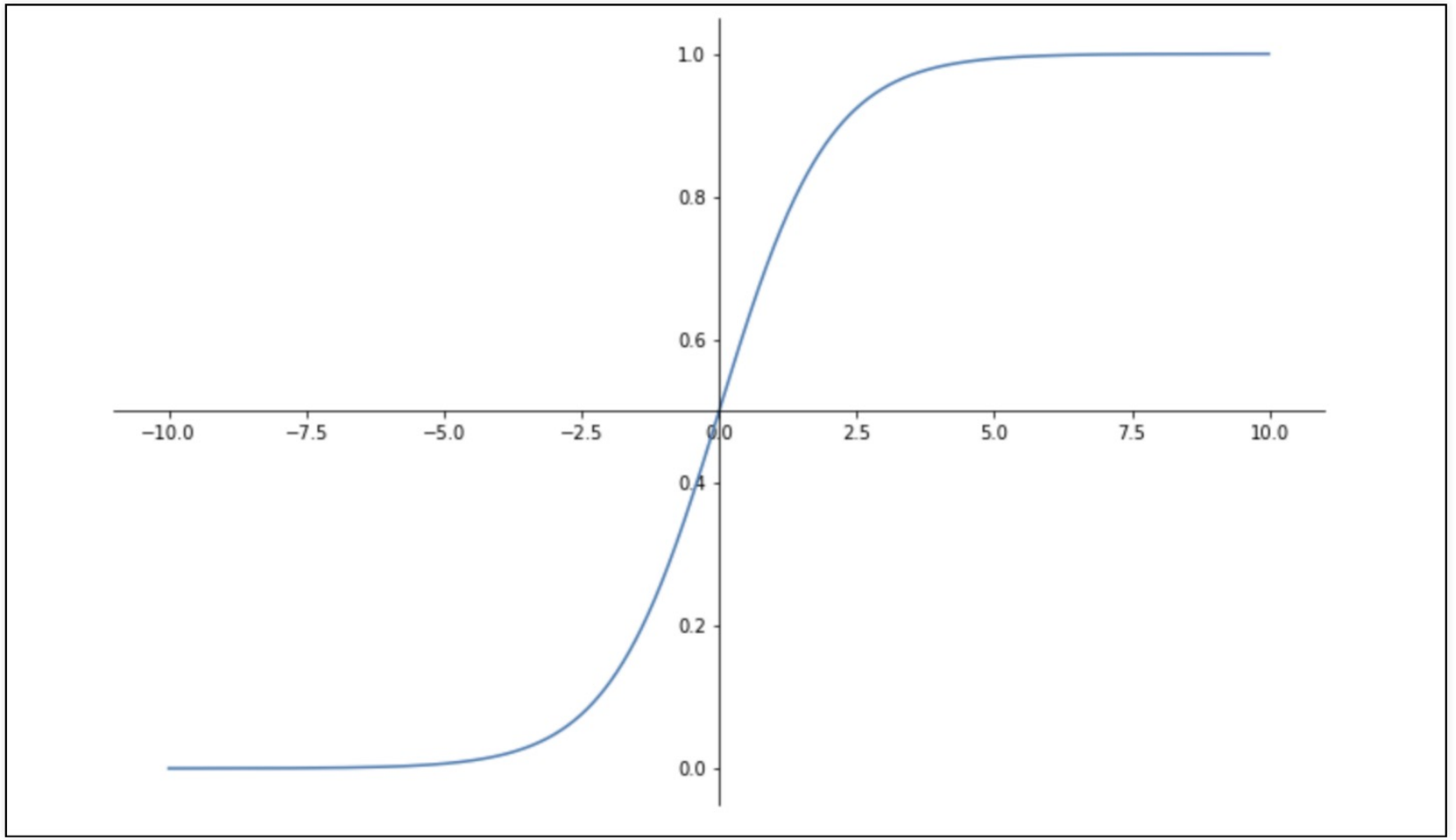
이런 결과도 눈에 익혀두자~



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Hypothesis 함수의 결과에 따른 분류

$h_\theta(x)$는 주어진 입력 x(종양의 크기)에서의 **예측 결과가 1(악성)이 될 확률**을 의미함

→ $h_\theta(x)$가 0.7이라면... 환자의 종양이 악성일 확률이 70%임

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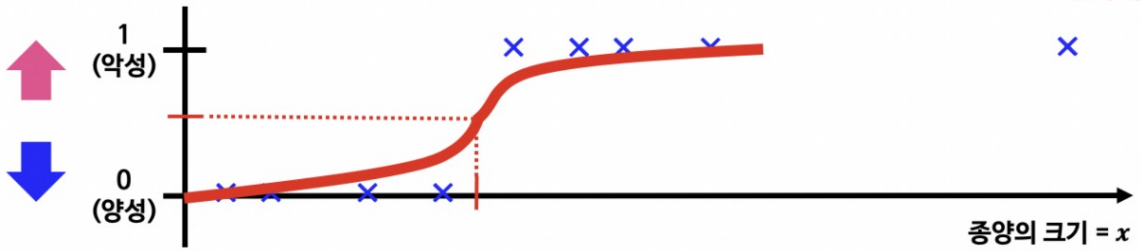
분류 문제용 hypothesis

$$h_\theta(x) = g(\theta_0 + \theta_1 x) = \frac{1}{1+e^{-(\theta_0+\theta_1 x)}}$$



- $h_\theta(x)$가 0.5보다 크거나 같으면 1(악성)으로 예측
- $h_\theta(x)$가 0.5보다 작으면 0(양성)으로 예측

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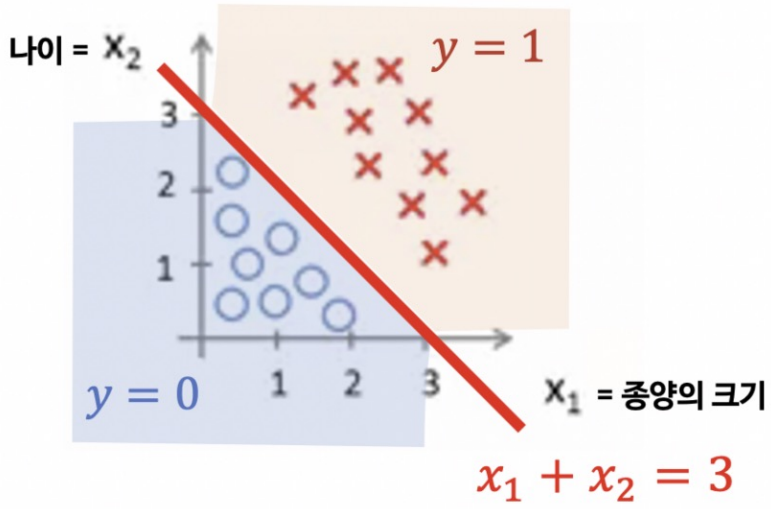
Decision Boundary

$$h_\theta(x) = g(\theta_0 + \theta_1 x_1 + \theta_2 x_2)$$



$-3 + x_1 + x_2 \geq 0$ 이면
$y = 1$로 예측 (악성)

$-3 + x_1 + x_2 < 0$ 이면
$y = 0$으로 예측 (양성)

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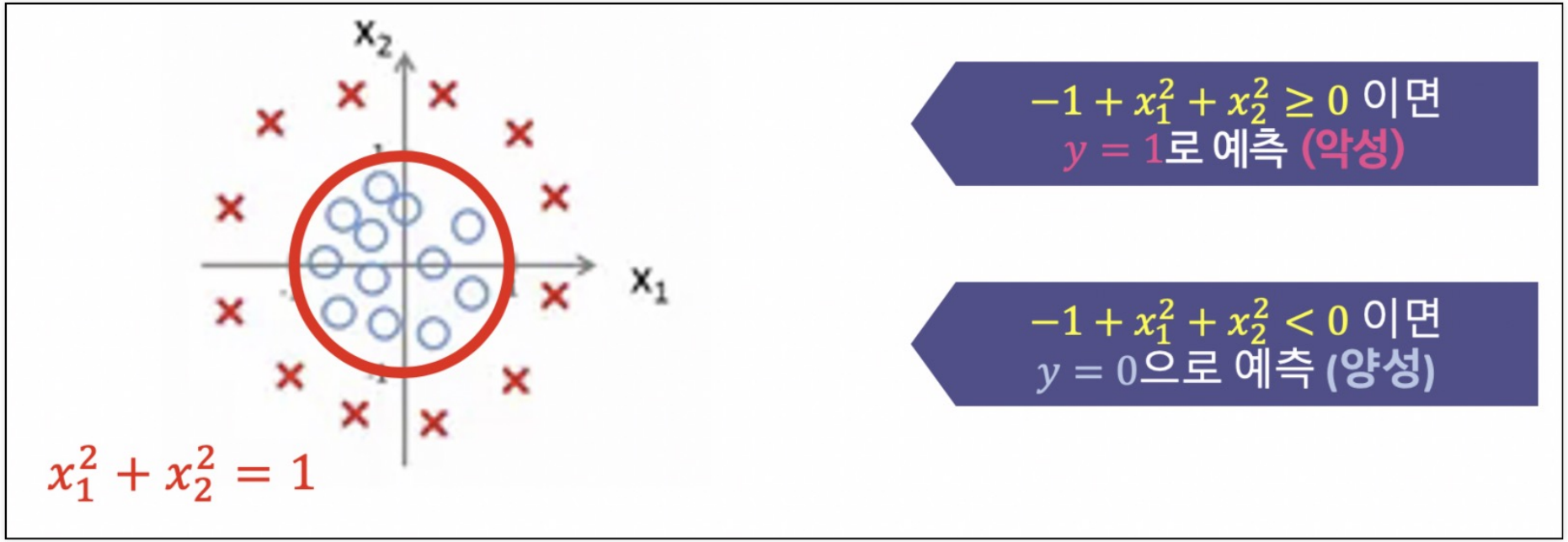
또다른 Decision Boundary



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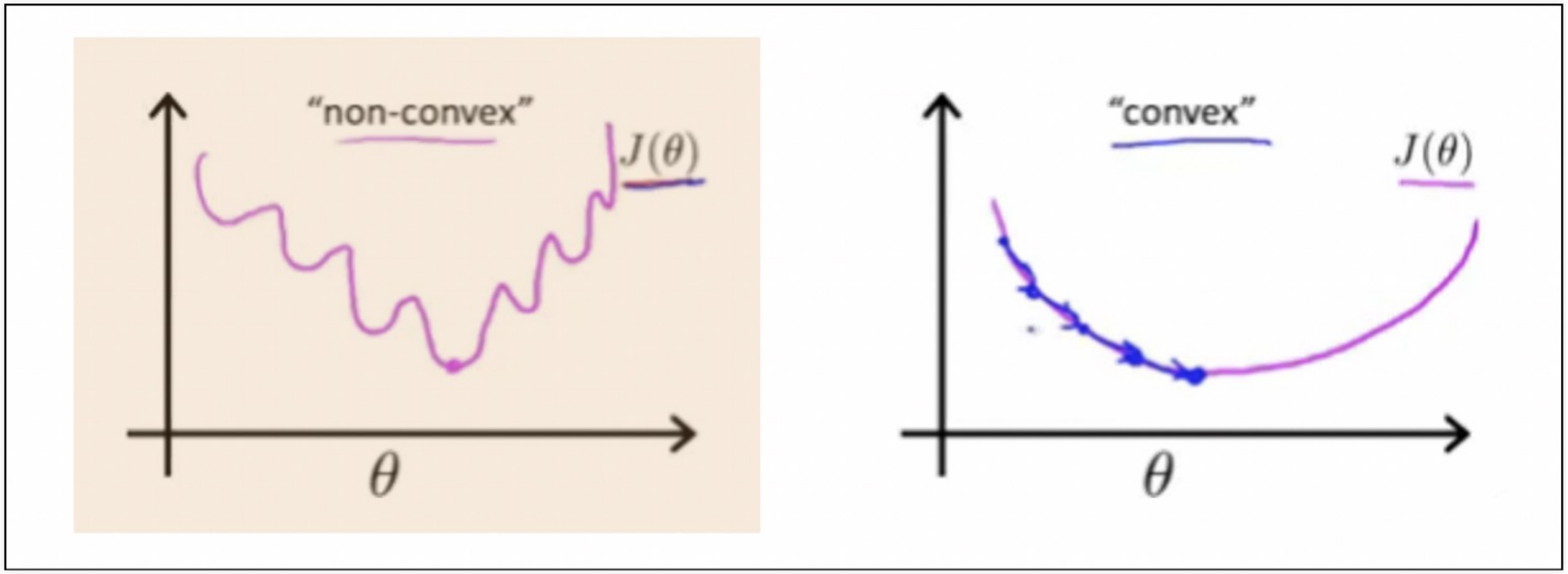
Cost Function은 어떻게?



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Logistic Regression에서 Cost Function을 재정의

$$J(\boldsymbol{\theta}) = \frac{1}{m}\sum_{i=1}^{m} Cost\left(h_{\boldsymbol{\theta}}\left(\boldsymbol{x}^{(i)}\right), y^{(i)}\right)$$

$$Cost(h_{\boldsymbol{\theta}}(\boldsymbol{x}), y) = \begin{cases} -\log(h_{\boldsymbol{\theta}}(\boldsymbol{x})) & y = 1 \\ -\log(1 - h_{\boldsymbol{\theta}}(\boldsymbol{x})) & y = 0 \end{cases}$$

Learning 알고리즘은 동일

수렴할 때까지 반복 {

$$\theta := \theta - \alpha \frac{d}{d\theta} J(\theta)$$

}

학습률
(Learning Rate)

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Logistic Reg. Cost Function의 그래프

```
h = np.arange(0.01, 1, 0.01)

C0 = -np.log(1-h)
C1 = -np.log(h)

plt.figure(figsize=(12,8))
plt.plot(h, C0, label='y=0')
plt.plot(h, C1, label='y=1')
plt.legend()

plt.show()
```

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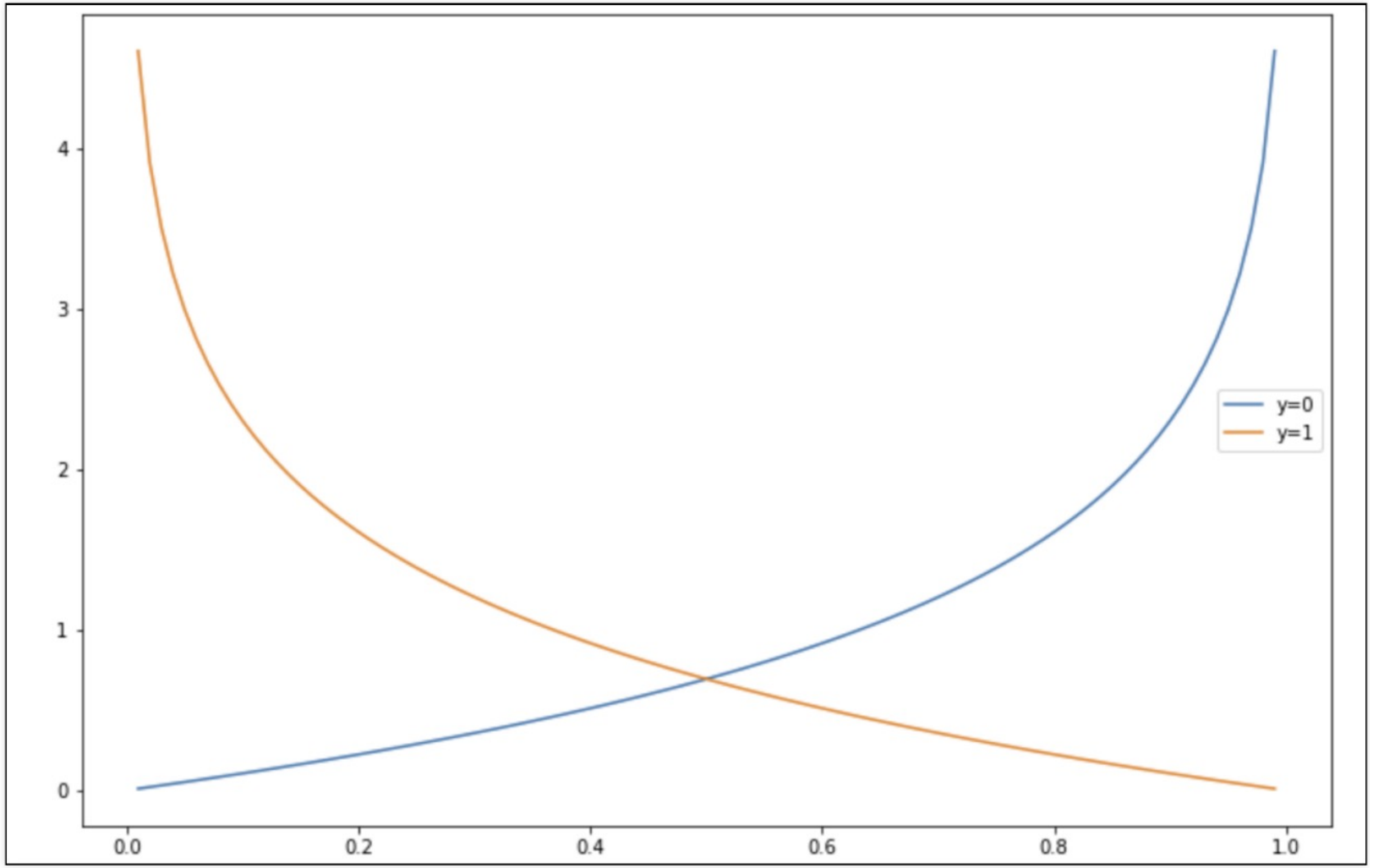
어떻게 생겼나



직접 실습하기

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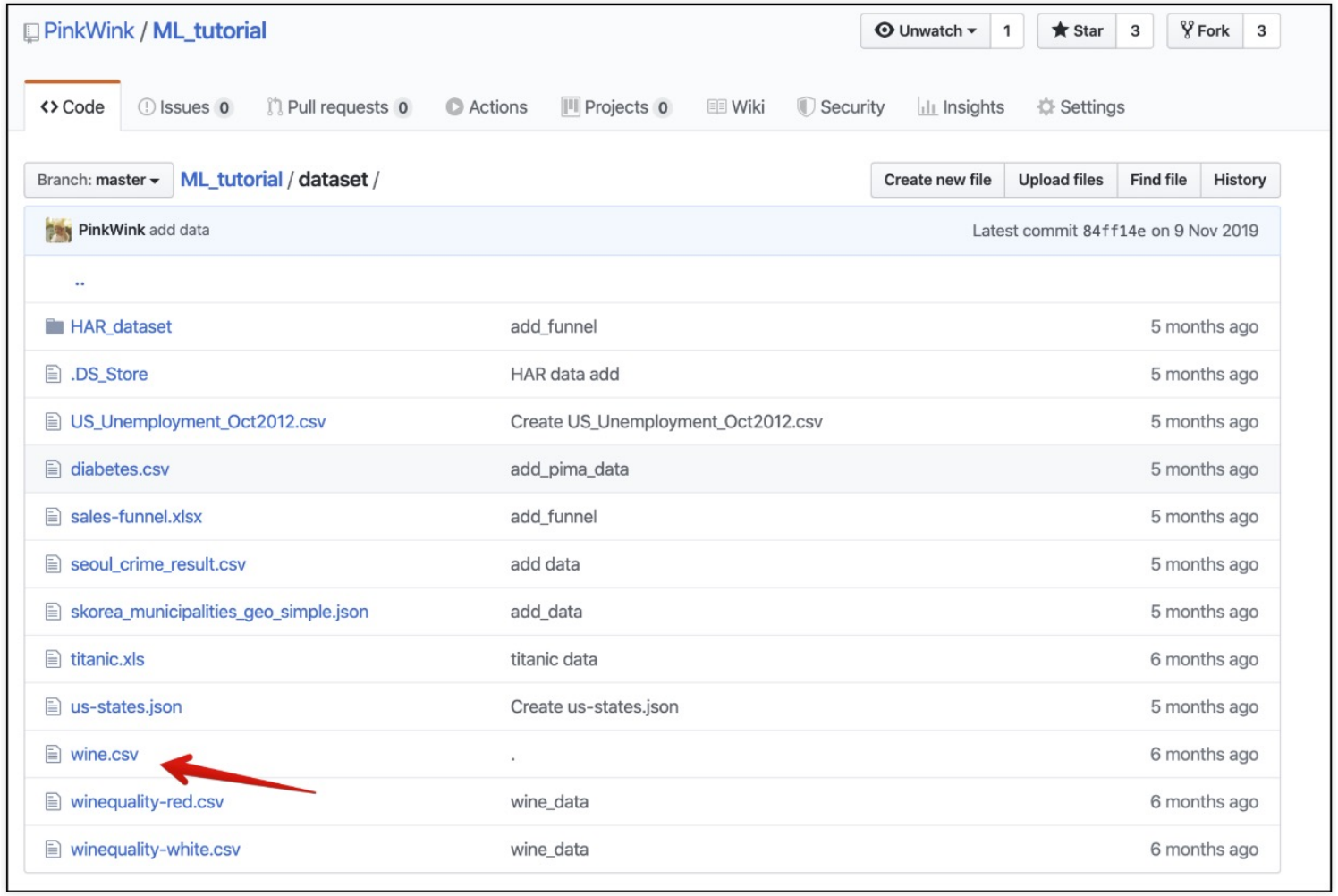
일단 통합 와인데이터 찾기



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데이터 받기

```
import pandas as pd

wine_url = 'https://raw.githubusercontent.com/PinkWink/ML_tutorial/'+\
                                                    'master/dataset/wine.csv'
wine = pd.read_csv(wine_url, index_col=0)
wine.head()
```

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality	color
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5	1
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	5	1
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	5	1
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	6	1
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5	1

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맛 등급 만들어 넣기

```
wine['taste'] = [1. if grade>5 else 0. for grade in wine['quality']]

X = wine.drop(['taste', 'quality'], axis=1)
y = wine['taste']
```

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데이터 분리

```
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
                                                    random_state = 13)
```

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초 간단 로지스틱 회귀 테스트

```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score

lr = LogisticRegression(solver='liblinear', random_state=13)
lr.fit(X_train, y_train)

y_pred_tr = lr.predict(X_train)
y_pred_test = lr.predict(X_test)

print('Train Acc : ', accuracy_score(y_train, y_pred_tr))
print('Test Acc : ', accuracy_score(y_test, y_pred_test))
```

```
Train Acc :  0.7425437752549547
Test Acc :  0.7438461538461538
```

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스케일러까지 적용해서 파이프라인 구축

```
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler

estimators = [('scaler', StandardScaler()),
              ('clf', LogisticRegression(solver='liblinear', random_state=13))]

pipe = Pipeline(estimators)
```

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fit~~~

```
pipe.fit(X_train, y_train)
```

```
Pipeline(memory=None,
         steps=[('scaler',
                 StandardScaler(copy=True, with_mean=True, with_std=True)),
                ('clf',
                 LogisticRegression(C=1.0, class_weight=None, dual=False,
                                    fit_intercept=True, intercept_scaling=1,
                                    l1_ratio=None, max_iter=100,
                                    multi_class='auto', n_jobs=None,
                                    penalty='l2', random_state=13,
                                    solver='liblinear', tol=0.0001, verbose=0,
                                    warm_start=False))],
         verbose=False)
```

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상승효과가 있긴 하다

```
y_pred_tr = pipe.predict(X_train)
y_pred_test = pipe.predict(X_test)

print('Train Acc : ', accuracy_score(y_train, y_pred_tr))
print('Test Acc : ', accuracy_score(y_test, y_pred_test))
```

```
Train Acc :  0.7444679622859341
Test Acc :  0.7469230769230769
```

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Decision Tree와의 비교를 위한 작업

```
from sklearn.tree import DecisionTreeClassifier

wine_tree = DecisionTreeClassifier(max_depth=2, random_state=13)
wine_tree.fit(X_train, y_train)

models = {'logistic regression':pipe_lr, 'decision tree':wine_tree}
```

뒤의 실습에서도 해당 단어는 **pipe** 로 작성합니다.

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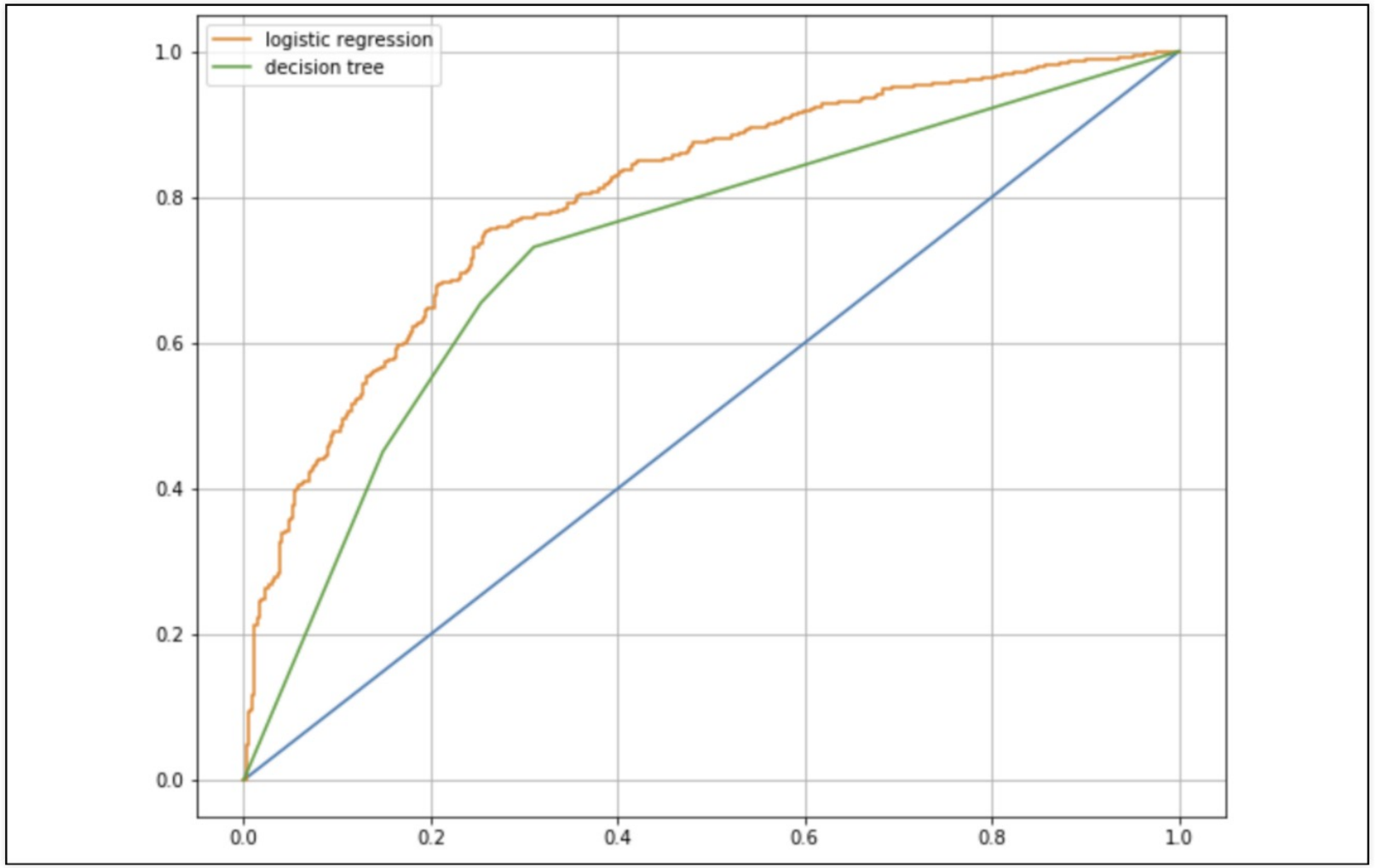
AUC 그래프를 이용한 모델간 비교

```
from sklearn.metrics import roc_curve

plt.figure(figsize=(10,8))
plt.plot([0,1], [0,1])
for model_name, model in models.items():
    pred = model.predict_proba(X_test)[:, 1]
    fpr, tpr, thresholds = roc_curve(y_test, pred)
    plt.plot(fpr, tpr, label=model_name)

plt.grid()
plt.legend()
plt.show()
```



PIMA 인디언 당뇨병 예측

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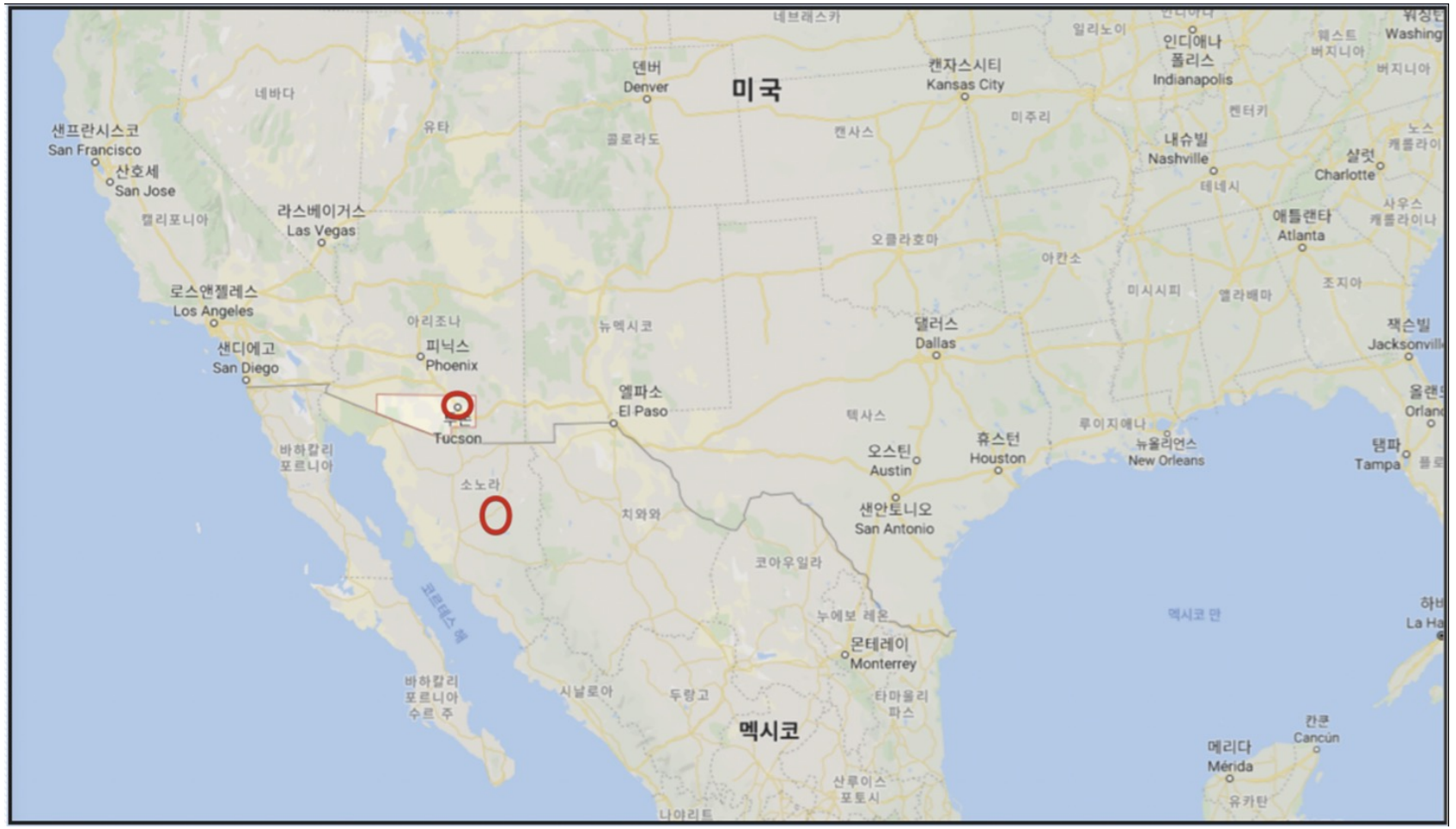
PIMA 인디언 문제?



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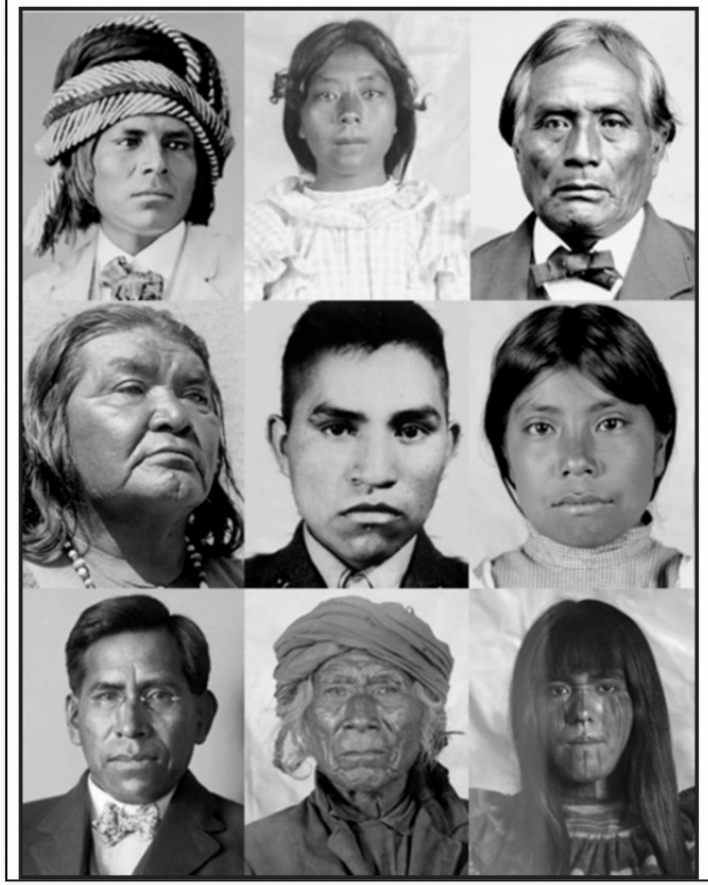
PIMA 인디언 당뇨병 문제



- 50년대까지 PIMA 인디언은 당뇨가 없었음
- 20세기 말, 50%가 당뇨에 걸림
- 50년만에 50%의 인구가 당뇨에 걸림

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본래 강가에서 수렵하던 가난한 소수 인디언

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이 중, 미국 쪽 PIMA 인디언은 미국 정부에 의해 강제 이주 후 식량을 배급 받음

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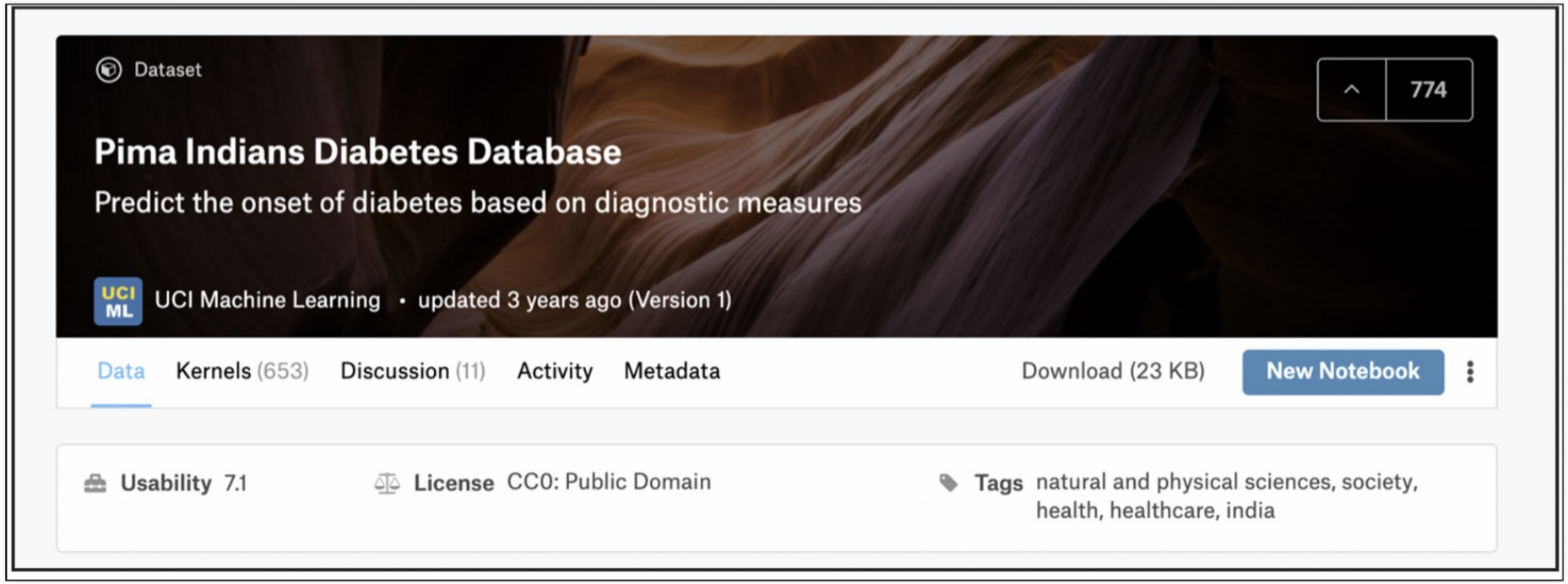
원래 데이터는 Kaggle



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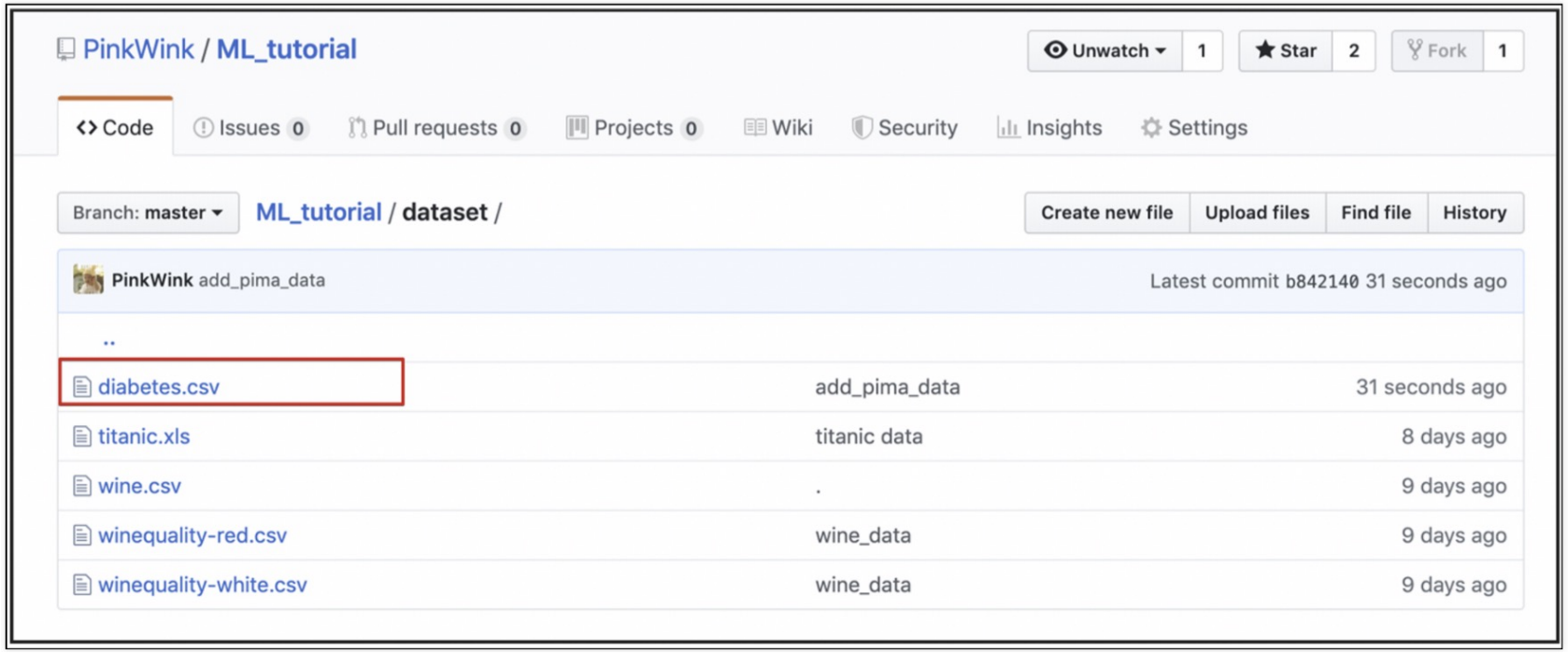
이 데이터를 PinkWink's GitHub에 보관 중



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Data의 컬럼의 의미

Pregnancies	임신 횟수
Glucose	포도당 부하 검사 수치
BloodPressure	혈압
Skin Thickness	팔 삼두근 뒤쪽의 피하지방 측정값
Insulin	혈청 인슐린
BMI	체질량지수
Diabetes Pedigree Funtion	당뇨 내력 가중치 값
Age	나이
Outcome	클래스 결정. 당뇨 유무

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데이터 읽기

```
import pandas as pd

PIMA_url = 'https://raw.githubusercontent.com/PinkWink/ML_tutorial/master/'+\
                                                'dataset/diabetes.csv'

PIMA = pd.read_csv(PIMA_url)
PIMA.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

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데이터 확인

```
PIMA.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   Pregnancies               768 non-null    int64
 1   Glucose                   768 non-null    int64
 2   BloodPressure             768 non-null    int64
 3   SkinThickness             768 non-null    int64
 4   Insulin                   768 non-null    int64
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64
 8   Outcome                   768 non-null    int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

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float으로 데이터 변환

```
PIMA = PIMA.astype('float')
PIMA.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   Pregnancies               768 non-null    float64
 1   Glucose                   768 non-null    float64
 2   BloodPressure             768 non-null    float64
 3   SkinThickness             768 non-null    float64
 4   Insulin                   768 non-null    float64
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    float64
 8   Outcome                   768 non-null    float64
dtypes: float64(9)
memory usage: 54.1 KB
```

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일단 상관관계 확인

```
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline

plt.figure(figsize=(12,10))
sns.heatmap(PIMA.corr(), cmap="YlGnBu")
plt.show()
```

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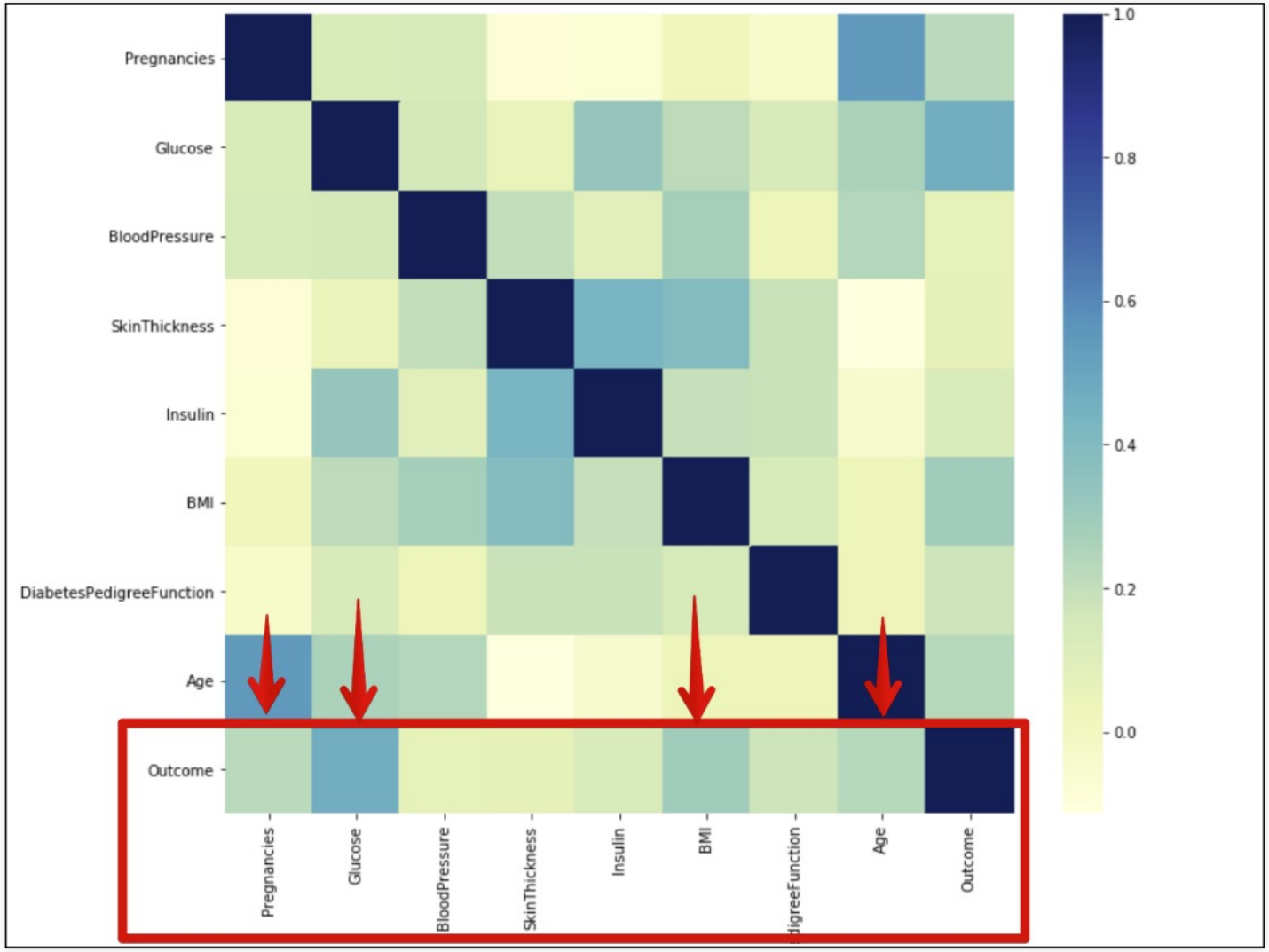
Outcome과 다른 특성과의 관계



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그런데 0 이 있다

```
(PIMA==0).astype(int).sum()
```

```
Pregnancies                 111
Glucose                       5
BloodPressure                35
SkinThickness               227
Insulin                     374
BMI                          11
DiabetesPedigreeFunction      0
Age                           0
Outcome                     500
dtype: int64
```

- 결측치는 데이터에 따라 그 정의가 다르다. 지금은 0이라는 숫자가 혈압에 있다는 것은 확실히 문제겠지

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의학적 지식과 PIMA 인디언에 대한 정보가 없으므로 일단 평균값으로 대체

```
zero_features = ['Glucose', 'BloodPressure', 'SkinThickness', 'BMI']
PIMA[zero_features] = PIMA[zero_features].replace(0, PIMA[zero_features].mean())
(PIMA==0).astype(int).sum()
```

```
Pregnancies                 111
Glucose                       0
BloodPressure                 0
SkinThickness                 0
Insulin                     374
BMI                           0
DiabetesPedigreeFunction      0
Age                           0
Outcome                     500
dtype: int64
```

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데이터를 나누고

```
from sklearn.model_selection import train_test_split

X = PIMA.drop(['Outcome'], axis=1)
y = PIMA['Outcome']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
                                                    random_state = 13,
                                                    stratify = y)
```

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Pipeline을 만들고

```
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression

estimators = [('scaler', StandardScaler()),
              ('clf', LogisticRegression(solver='liblinear', random_state=13))]

pipe_lr = Pipeline(estimators)
pipe_lr.fit(X_train, y_train)
pred = pipe_lr.predict(X_test)
```

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몇몇 수치를 확인

```
from sklearn.metrics import (accuracy_score, recall_score, precision_score,
                             roc_auc_score, f1_score)

print('Accuracy : ', accuracy_score(y_test, pred))
print('Recall : ', recall_score(y_test, pred))
print('Precision : ', precision_score(y_test, pred))
print('AUC score : ', roc_auc_score(y_test, pred))
print('f1 score : ', f1_score(y_test, pred))
```

```
Accuracy :  0.7727272727272727
Recall :  0.6111111111111112
Precision :  0.7021276595744681
AUC score :  0.7355555555555556
f1 score :  0.6534653465346535
```

- 그러나 상대적 의미를 가질 수 없어서 이 수치 자체를 평가할 수는 없다.

zero-base /

다변수 방정식의 각 계수 값을 확인할 수 있다

```
coeff = list(pipe_lr['clf'].coef_[0])
labels = list(X_train.columns)
```

```
coeff
```

```
[0.354265888441265,
 1.2014244425037581,
 -0.15840135536286712,
 0.03394657712929959,
 -0.16286471953988135,
 0.6204045219895111,
 0.36669355795578745,
 0.17195965447035086]
```

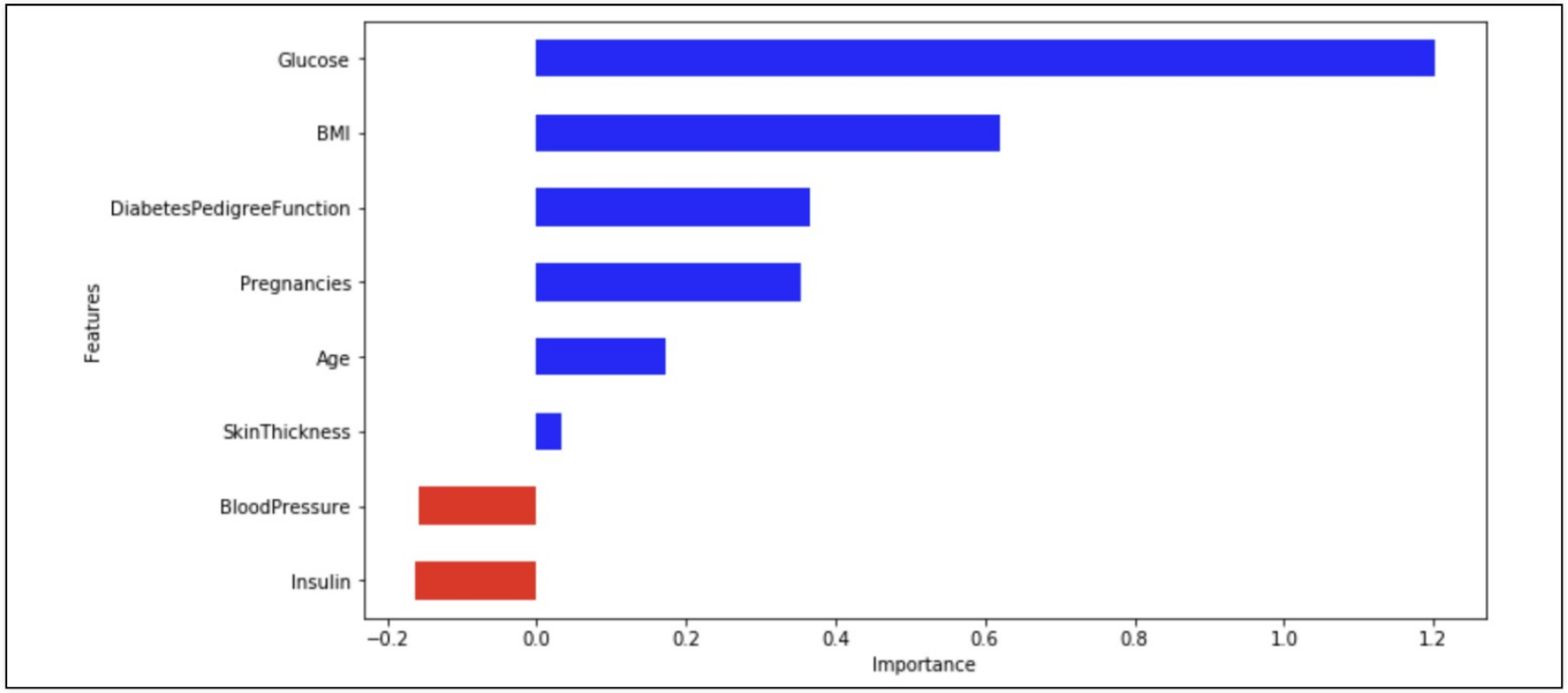
zero-base /

중요한 feature에 대해 그려볼까

```
features = pd.DataFrame({'Features':labels, 'importance':coeff})
features.sort_values(by=['importance'], ascending=True, inplace=True)
features['positive'] = features['importance'] > 0
features.set_index('Features', inplace=True)
features['importance'].plot(kind='barh',
                            figsize=(11, 6),
                            color=features['positive'].map({True:'blue',
                                                            False:'red'}))
plt.xlabel('Importance')
plt.show()
```

zero-base /

해석을 해볼 수 있을까



- 포도당, BMI 등은 당뇨에 영향을 미치는 정도가 높다.
- 혈압은 예측에 부정적 영향을 준다.
- 연령이 BMI보다 출력 변수와 더 관련되어 있었지만, 모델은 BMI와 Glucose에 더 의존함.