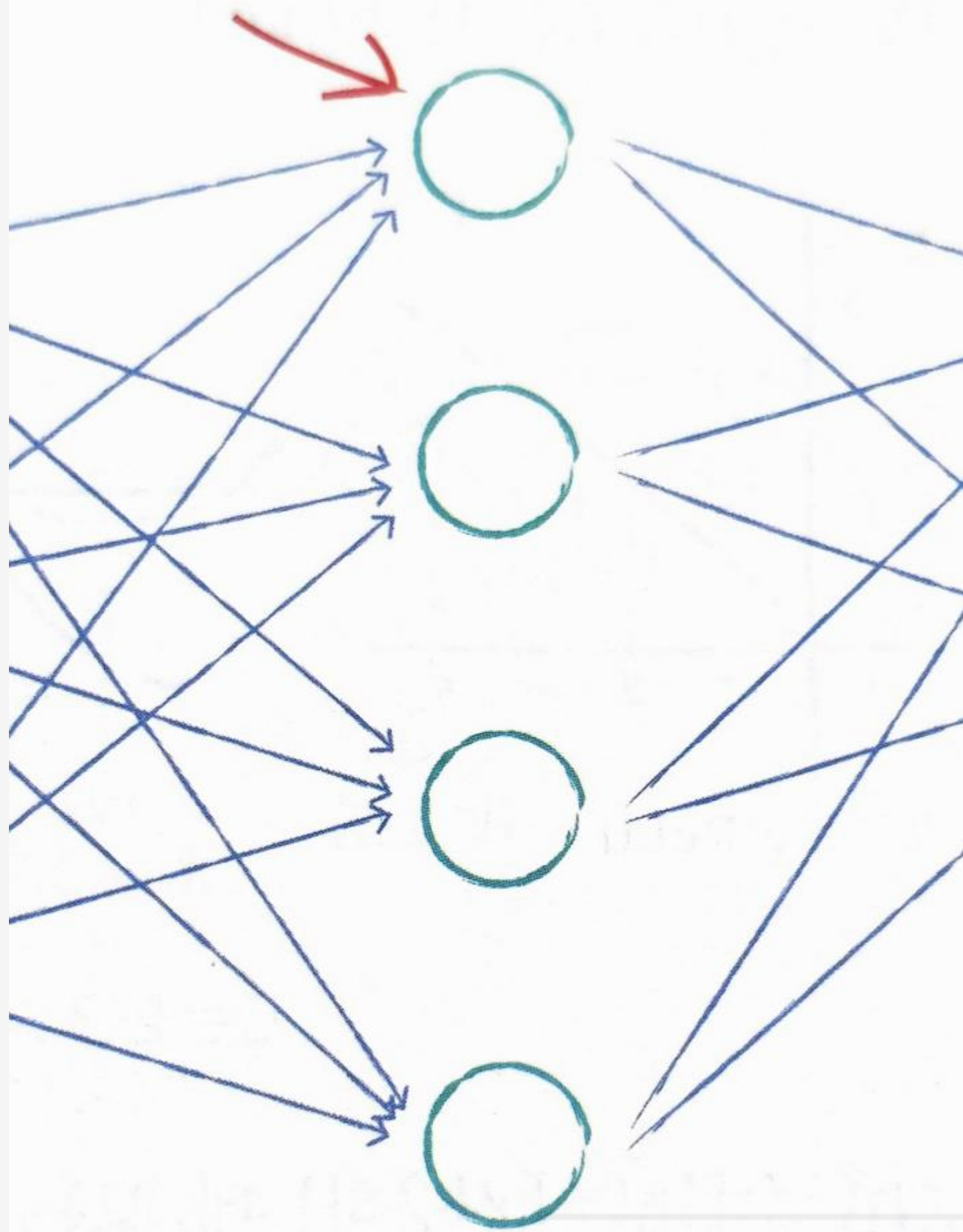


모델 설계하기

+

$\text{sigmoid}(X \times W + b)$
인공 뉴런



은닉층 (hidden layer)

목차

01

생존율 예측

- 폐암 수술 환자의 생존율을
예측하는 모델 구현

02

당뇨병 예측

- 피마 인디언 당뇨병을
예측하는 모델 구현

01

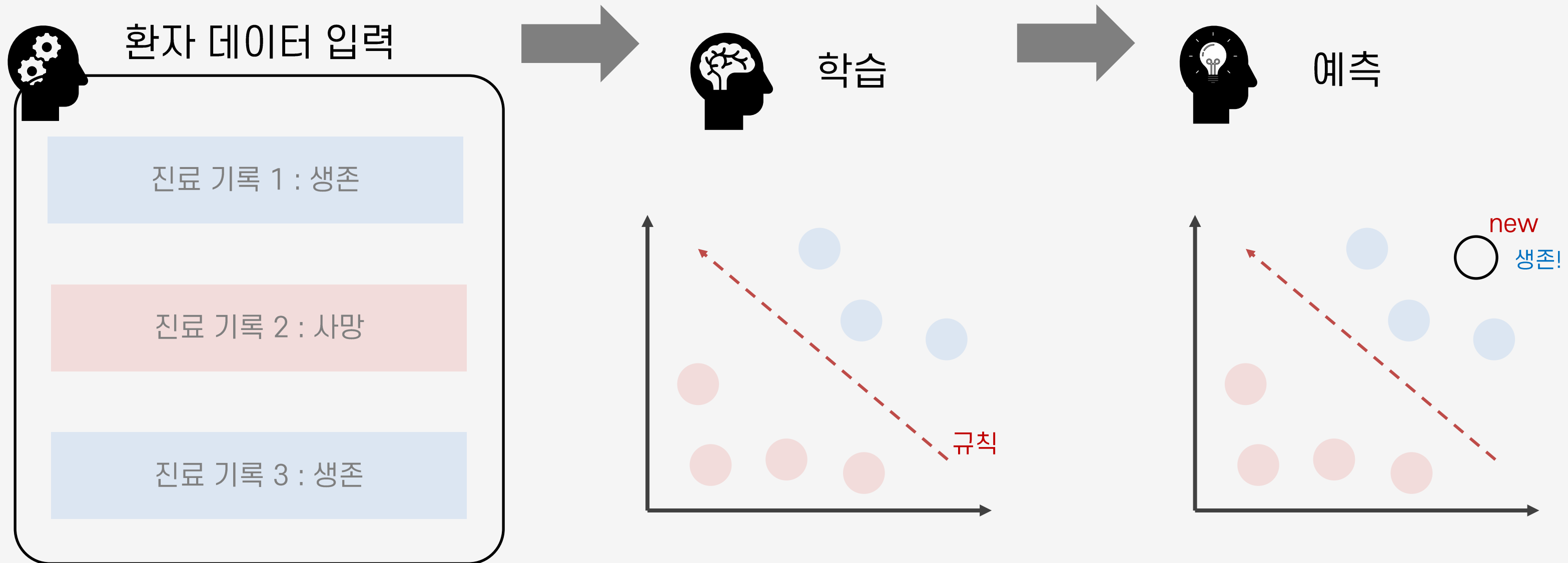
생존율 예측

폐암 수술 환자의 생존율을 예측하는 모델 구현

“

수술하기 전
수술 후의 생존율을
예측할 방법이 없을까?

“예측?”



+

기존 환자 데이터

- 수술 전 진단 데이터와 수술 후 생존 결과를 기록한 실제 의료 기록 데이터
- 18개 항목으로 구분
- 1~17까지 속성, 18번째 항목은 클래스

1 293,1,3.8,2.8,0,0,0,0,0,0,12,0,0,0,1,0,62,0
 2 1,2,2.88,2.16,1,0,0,0,1,1,14,0,0,0,1,0,60,0
 3 8,2,3.19,2.5,1,0,0,0,1,0,11,0,0,1,1,0,66,1
 4 14,2,3.98,3.06,2,0,0,0,1,1,14,0,0,0,1,0,80,1
 5 17,2,2.21,1.88,0,0,1,0,0,0,12,0,0,0,1,0,56,0
 6 18,2,2.96,1.67,0,0,0,0,0,0,12,0,0,0,1,0,61,0
 7 35,2,2.76,2.2,1,0,0,0,1,0,11,0,0,0,0,0,76,0
 8 42,2,3.24,2.52,1,0,0,0,1,0,12,0,0,0,1,0,63,1
 9 65,2,3.15,2.76,1,0,1,0,1,0,12,0,0,0,1,0,59,0
 10 111,2,4.48,4.2,0,0,0,0,0,0,12,0,0,0,1,0,55,0
 11 121,2,3.84,2.56,1,0,0,0,1,0,11,0,0,0,0,0,59,0
 12 123,2,2.8,2.12,1,0,0,1,1,0,13,0,0,0,1,0,80,0
 13 130,2,5.6,4.64,1,0,0,0,1,0,11,0,0,0,1,0,45,0
 14 132,2,2.12,1.72,1,0,0,0,0,0,12,0,0,0,1,0,74,0
 15 133,2,2.5,71.1,0,0,0,1,0,0,13,0,0,0,1,0,64,1
 16 137,2,3.76,3.08,1,0,0,0,1,0,13,0,0,0,1,0,54,0
 17 141,2,2.16,1.56,1,0,0,0,1,0,11,0,0,0,1,0,63,0
 18 145,2,3.64,2.48,2,0,0,0,1,1,11,0,0,0,1,0,70,0
 19 164,2,2.4,1.96,1,0,0,0,1,0,12,0,0,0,0,0,73,0
 20 165,2,3.2,4,1,0,0,0,1,0,14,0,0,0,1,0,58,0
 21 167,2,3.4,2.12,1,0,0,0,1,1,11,0,0,0,1,0,62,0
 22 172,2,2.88,2.2,0,0,0,0,0,0,12,1,0,0,1,0,62,0
 23 173,2,3.16,2.56,1,0,1,1,1,0,12,0,0,1,1,0,62,0
 24 193,2,3.08,2.48,1,0,0,0,1,0,11,0,0,0,0,0,49,0
 25 203,2,4.08,2.56,1,1,1,0,0,0,13,0,0,0,1,0,54,0
 26 204,2,3.6,3.92,0,0,0,0,0,0,12,0,0,0,1,0,56,0
 27 210,2,2.8,1.6,1,0,1,0,1,1,12,0,0,0,1,0,53,1
 28 216,2,2.66,8.56,1,0,1,0,1,0,12,0,0,0,1,0,61,0
 29 217,2,3.24,1.88,1,0,0,0,1,0,12,0,0,0,1,0,61,0
 30 243,2,4.88,3.44,0,0,1,0,1,0,14,0,0,0,1,0,75,1
 31 275,2,4.04,2.76,1,0,0,0,1,0,12,0,0,0,1,0,55,1
 32 284,2,2.32,1.68,1,0,1,0,1,0,12,0,0,0,1,0,64,0
 33 295,2,2.64,1.92,1,0,0,0,1,0,11,1,0,0,1,0,63,0
 34 316,2,3.4,2.76,1,0,1,0,1,0,12,0,0,0,1,0,56,0
 35 324,2,2.58,1.64,2,0,1,0,1,1,12,0,0,0,1,0,63,0
 36 331,2,2.94,76,1,0,1,1,1,0,12,0,0,0,0,0,61,0
 37 335,2,4,3.12,1,0,0,0,1,0,12,0,0,0,1,0,67,1
 38 346,2,3.12,2.72,2,0,0,0,1,1,14,0,0,0,1,0,70,0
 39 347,2,3.48,2.84,1,0,0,0,0,1,11,0,0,0,1,0,58,0
 40 349,2,4.2,3.6,1,0,0,0,0,1,11,0,0,0,1,0,39,1

“ 구현

✓ 데이터

✓ 모델 설정

✓ 실행

✓ 출력

```
Data_set = numpy.loadtxt("dataset/ThoracicSurgery.csv", delimiter=",")

X = Data_set[:,0:17] #속성
Y = Data_set[:,17]   #클래스

model = Sequential()
model.add(Dense(30, input_dim=17, activation='relu')) #은닉층
model.add(Dense(1, activation='sigmoid')) #출력층

model.compile(loss='mean_squared_error', optimizer='adam', metrics=['accuracy'])
model.fit(X, Y, epochs=30, batch_size=10)

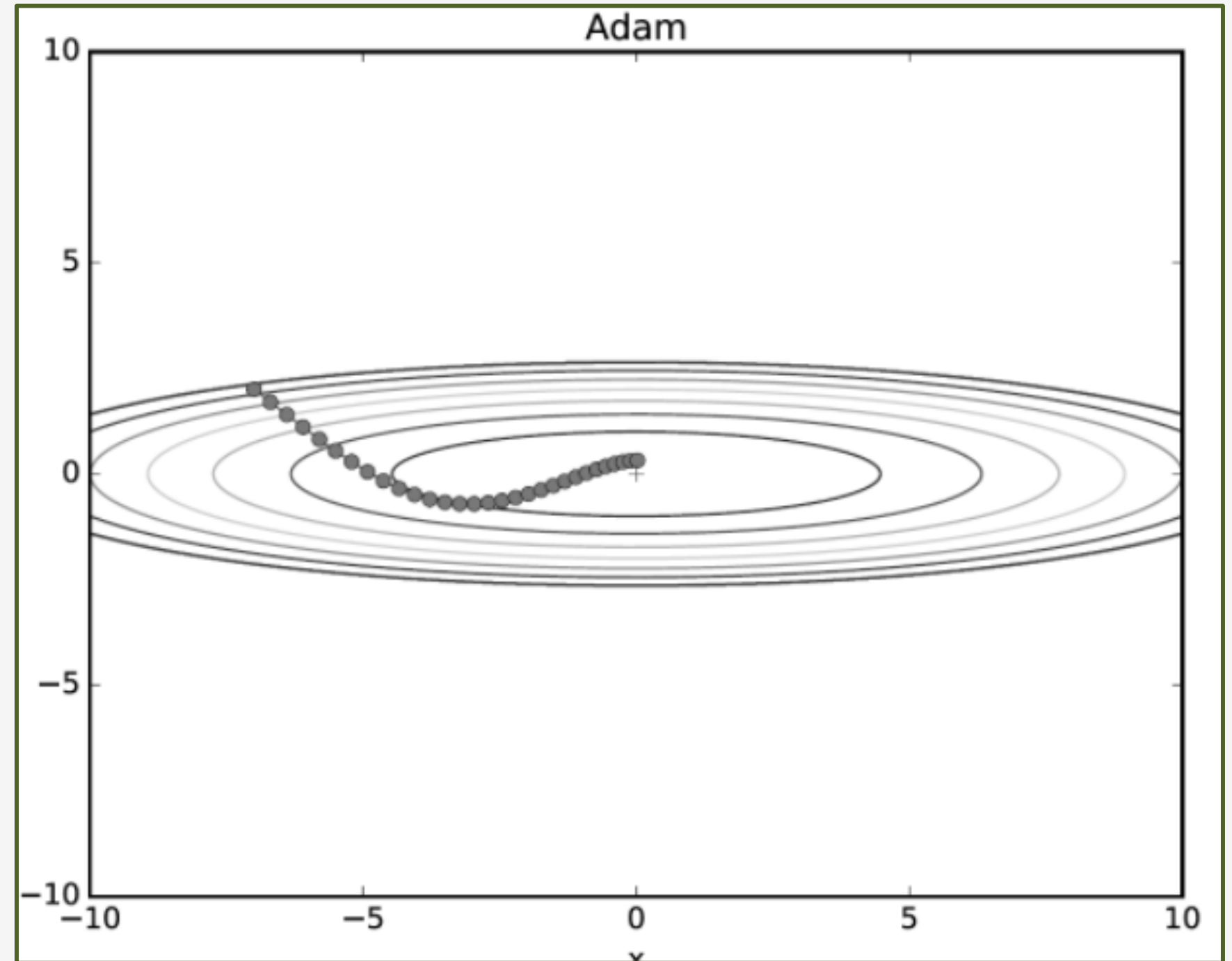
print("\n Accuracy: %.4f" % (model.evaluate(X, Y)[1]))
```

Accuracy: 0.8553

+

“아담?”

- 잘 모르면 Adam
- 진동과 폭을 줄이는 모멘텀
+
- 학습률을 조정해나가는 알엠에스프롭
- Adam = 방향 + 스텝사이즈



“정확도 높이기

01. 학습 횟수

epochs=1500, batch_size=20

Accuracy: 0.9106

02. 층

Layer (type)	Output Shape	Param #
dense_142 (Dense)	(None, 30)	540
dense_143 (Dense)	(None, 1)	31



Layer (type)	Output Shape	Param #
dense_137 (Dense)	(None, 60)	1080
dense_138 (Dense)	(None, 30)	1830
dense_139 (Dense)	(None, 1)	31

Accuracy: 0.8511

03. 둘 다

epochs=2000, batch_size=20

Layer (type)	Output Shape	Param #
dense_154 (Dense)	(None, 90)	1620
dense_155 (Dense)	(None, 60)	5460
dense_156 (Dense)	(None, 30)	1830
dense_157 (Dense)	(None, 1)	31

Accuracy: 0.9745

02

당뇨병 예측

피마 인디언 당뇨병을 예측하는 모델 구현

피마 인디언 데이터

- 768명/8개의 속성/1개의 클래스

1	2	3	4	5	6	7	8
임신 횟수	공복 혈당 농도	혈압	삼두근 피부 주름 두께	혈청 인슐린	체질량 지수	당뇨병 가족력	나이

1 6,148,72,35,0,33.6,0.627,50,1
 2 1,85,66,29,0,26.6,0.351,31,0
 3 8,183,64,0,0,23.3,0.672,32,1
 4 1,89,66,23,94,28.1,0.167,21,0
 5 0,137,40,35,168,43.1,2.288,33,1
 6 5,116,74,0,0,25.6,0.201,30,0
 7 3,78,50,32,88,31.0,0.248,26,1
 8 10,115,0,0,0,35.3,0.134,29,0
 9 2,197,70,45,543,30.5,0.158,53,1
 10 8,125,96,0,0,0.0,0.232,54,1
 11 4,110,92,0,0,37.6,0.191,30,0
 12 10,168,74,0,0,38.0,0.537,34,1
 13 10,139,80,0,0,27.1,1.441,57,0
 14 1,189,60,23,846,30.1,0.398,59,1
 15 5,166,72,19,175,25.8,0.587,51,1
 16 7,100,0,0,0,30.0,0.484,32,1
 17 0,118,84,47,230,45.8,0.551,31,1
 18 7,107,74,0,0,29.6,0.254,31,1
 19 1,103,30,38,83,43.3,0.183,33,0
 20 1,115,70,30,96,34.6,0.529,32,1
 21 3,126,88,41,235,39.3,0.704,27,0
 22 8,99,84,0,0,35.4,0.388,50,0
 23 7,196,90,0,0,39.8,0.451,41,1
 24 9,119,80,35,0,29.0,0.263,29,1
 25 11,143,94,33,146,36.6,0.254,51,1
 26 10,125,70,26,115,31.1,0.205,41,1
 27 7,147,76,0,0,39.4,0.257,43,1
 28 1,97,66,15,140,23.2,0.487,22,0
 29 13,145,82,19,110,22.2,0.245,57,0
 30 5,117,92,0,0,34.1,0.337,38,0

구현

✓ 데이터

✓ 모델 설정

✓ 실행

✓ 출력

Accuracy: 0.9805

```
from keras.models import Sequential
from keras.layers import Dense
import numpy
import tensorflow as tf

seed = 0
numpy.random.seed(seed)
tf.random.set_seed(seed)

dataset = numpy.loadtxt("dataset/pima-indians-diabetes.csv", delimiter=",")
X = dataset[:,0:8]
Y = dataset[:,8]

model = Sequential()
model.add(Dense(36, input_dim=8, activation='relu'))
model.add(Dense(24, activation='relu'))
model.add(Dense(12, activation='relu'))
model.add(Dense(1, activation='sigmoid'))

model.compile(loss='binary_crossentropy',
              optimizer='adam',
              metrics=['accuracy'])

model.fit(X, Y, epochs=3000, batch_size=20)

print("\n Accuracy: %.4f" % (model.evaluate(X, Y)[1]))
```

“

정보마다
발병률에
얼마큼 영향을 미칠까?

“ 임신횟수와 당뇨병 발병률

```
import pandas as pd

df=pd.read_csv('dataset/pima-indians-diabetes.csv', names=["pregnant", "plasma", "pressure", "thickness",
                                                         "insulin", "BMI", "pedigree","age", "class"])

print(df[['pregnant', 'class']].groupby(['pregnant'], as_index=False).mean().sort_values(by='pregnant', ascending=True))
```

	pregnant	class
0	0	0.342342
1	1	0.214815
2	2	0.184466
3	3	0.360000
4	4	0.338235
5	5	0.368421
6	6	0.320000
7	7	0.555556
8	8	0.578947
9	9	0.642857
10	10	0.416667
11	11	0.636364
12	12	0.444444
13	13	0.500000
14	14	1.000000
15	15	1.000000
16	17	1.000000

“ 상관계수 확인하기



```
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
```



```
df=pd.read_csv('dataset/pima-indians-diabetes.csv', names=["pregnant", "plasma", "pressure", "thickness",
                                                         "insulin", "BMI", "pedigree", "age", "class"])
```

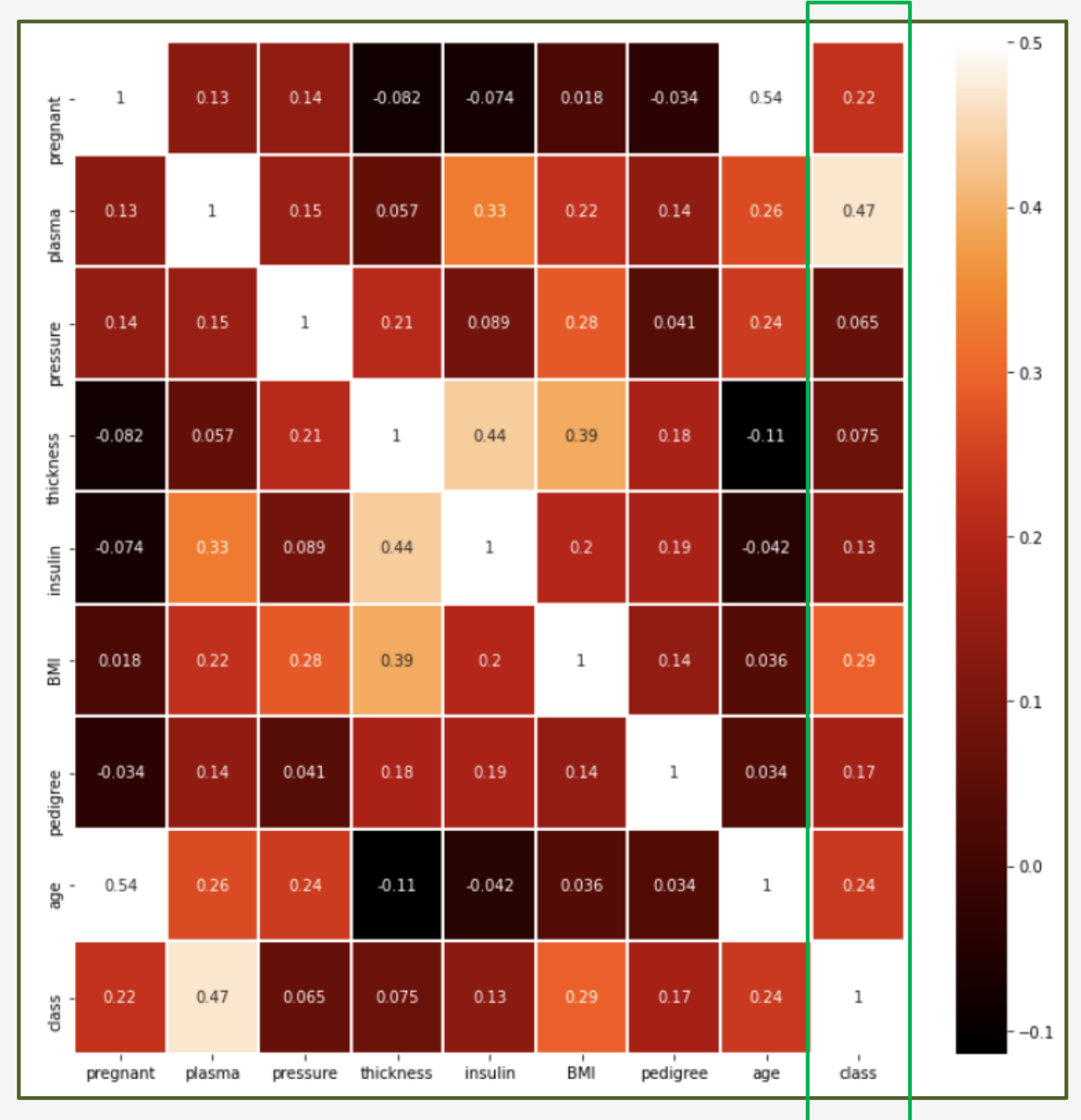


```
plt.figure(figsize = (12, 12))
sns.heatmap(df.corr(), linewidths=0.1, vmax=0.5, cmap=plt.cm.gist_heat, linecolor='white', annot=True)

plt.show()
```

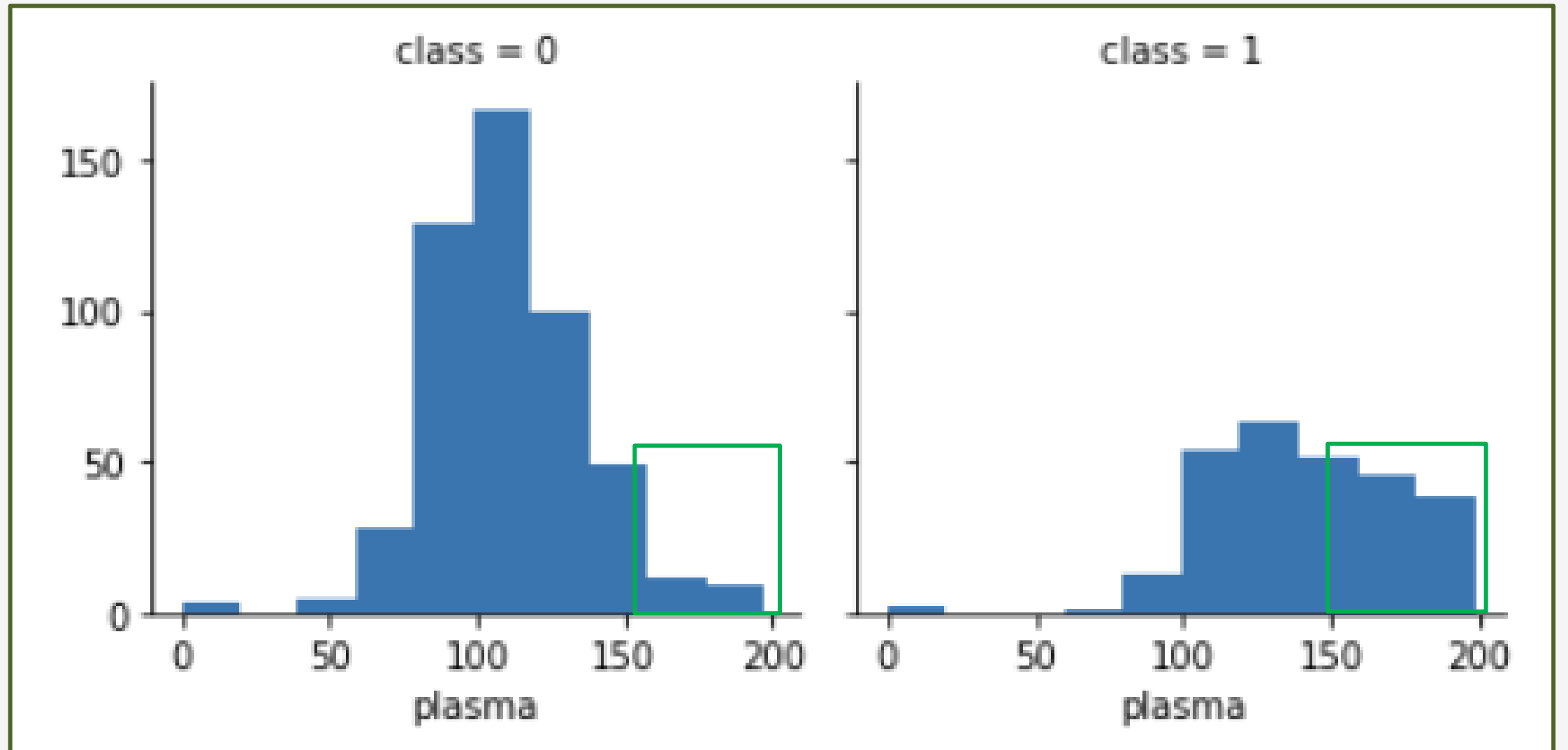
+

상관관계 확인하기



+

상관관계 확인하기



Accuracy: 0.7461

발표를 들어주셔서
감사합니다 :))