COVID-19 Detection on Chest X-Ray Images: A comparison of CNN architectures and ensembles

논문요약

흉부 X-ray 영상으로 코로나바이러스 질병 진단을 제안함

비임상적 접근과 인공 지능 기술의 사용에 중점을 두고 COVID-19를 가진 사람들을 탐지하고 식별하는 것을 목표

DenseNet169를 사용하여 이미지 특징을 추출하고 XGBoost 알고리즘을 분류에 사용

검출 정확도는 98.24% 3등급 문제에선 89.70%의 정확도에 도달

DNN 훈련이 필요하지 않아서 다른 제안된 방법보다 빠르고 계산 복잡도가 낮다는 장점을 가짐

Flow

- 데이터 처리 - 모델 생성 - 학습 - 검증 - 검증 평가

라이브러리 준비

In [17]:
```
from glob import glob
import cv2
from matplotlib import pyplot as plt
import numpy as np
from sklearn.model_selection import train_test_split
from keras.applications.densenet import DenseNet169
from sklearn.model_selection import cross_validate, KFold
from keras.losses import SparseCategoricalCrossentropy, CategoricalCrossentropy
from xgboost import XGBClassifier
from sklearn.metrics import mean_squared_error, r2_score, accuracy_score, confusion_matrix, f1_score, precision_s
# from google.colab import drive
```

데이터 저장

In [13]:
```
images_path = {}
images_path["Covid"] = glob("./train/Covid-19/*.png")
images_path["Covid"] += glob("./train/Covid-19/*.jpeg")
images_path["Covid"] += glob("./train/Covid-19/*.jpg")
images_path['Covid']
```

Out[13]:
```
['./train/Covid-19\\1-s2.0-S1684118220300682-main.pdf-002-a1.png',
 './train/Covid-19\\1-s2.0-S1684118220300682-main.pdf-002-a2.png',
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 './train/Covid-19\\1.CXRCTThoraximagesofCOVID-19fromSingapore.pdf-000-fig1a.png',
 './train/Covid-19\\1.CXRCTThoraximagesofCOVID-19fromSingapore.pdf-000-fig1b.png',
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 './train/Covid-19\\ciaa199.pdf-001-c.png',
 './train/Covid-19\\covid-19-infection-exclusive-gastrointestinal-symptoms-pa.png',
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 './train/Covid-19\\covid-19-pneumonia-28.png',
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```
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'./train/Covid-19\\1-s2.0-S0929664620300449-gr2_lrg-c.jpg',
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'./train/Covid-19\\all14238-fig-0001-m-c.jpg',
'./train/Covid-19\\all14238-fig-0002-m-d.jpg',
'./train/Covid-19\\all14238-fig-0002-m-e.jpg',
'./train/Covid-19\\all14238-fig-0002-m-f.jpg',
'./train/Covid-19\\covid-19-pneumonia-12.jpg',
'./train/Covid-19\\covid-19-pneumonia-15-PA.jpg',
'./train/Covid-19\\covid-19-pneumonia-19.jpg',
'./train/Covid-19\\covid-19-pneumonia-2.jpg',
'./train/Covid-19\\covid-19-pneumonia-24-day12.jpg',
'./train/Covid-19\\covid-19-pneumonia-24-day6.jpg',
'./train/Covid-19\\covid-19-pneumonia-24-day7.jpg',
'./train/Covid-19\\covid-19-pneumonia-30-PA.jpg',
'./train/Covid-19\\covid-19-pneumonia-7-PA.jpg',
'./train/Covid-19\\covid-19-pneumonia-evolution-over-a-week-1-day0-PA.jpg',
'./train/Covid-19\\covid-19-pneumonia-evolution-over-a-week-1-day3.jpg',
'./train/Covid-19\\covid-19-pneumonia-evolution-over-a-week-1-day4.jpg',
'./train/Covid-19\\covid-19-pneumonia-rapidly-progressive-12-hours.jpg',
'./train/Covid-19\\covid-19-pneumonia-rapidly-progressive-3-days.jpg',
'./train/Covid-19\\covid-19-pneumonia-rapidly-progressive-admission.jpg',
```

```
'./train/Covid-19\\covid-19-rapidly-progressive-acute-respiratory-distress-syndrome-ards-admission.jpg',
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'./train/Covid-19\\covid-19-rapidly-progressive-acute-respiratory-distress-syndrome-ards-day-2.jpg',
'./train/Covid-19\\jkms-35-e79-g001-l-a.jpg',
'./train/Covid-19\\jkms-35-e79-g001-l-b.jpg',
'./train/Covid-19\\jkms-35-e79-g001-l-c.jpg',
'./train/Covid-19\\kjr-21-e24-g001-l-a.jpg',
'./train/Covid-19\\kjr-21-e24-g002-l-a.jpg',
'./train/Covid-19\\kjr-21-e24-g003-l-a.jpg',
'./train/Covid-19\\kjr-21-e25-g001-l-a.jpg',
'./train/Covid-19\\lancet-case2a.jpg',
'./train/Covid-19\\lancet-case2b.jpg']
```

In [15]:

```
images_path = {}

images_path["Covid"] = glob("./train/Covid-19/*.png")
images_path["Covid"] += glob("./train/Covid-19/*.jpeg")
images_path["Covid"] += glob("./train/Covid-19/*.jpg")

images_path["NoFindings"] = glob("./train/No_findings/*.png")
images_path["NoFindings"] += glob("./train/No_findings/*.jpeg")
images_path["NoFindings"] += glob("./train/No_findings/*.jpg")

images_path["Pneumonia"] = glob("./train/Pneumonia/*.png")
images_path["Pneumonia"] += glob("./train/Pneumonia/*.jpeg")
images_path["Pneumonia"] += glob("./train/Pneumonia/*.jpg")

print(images_path["Covid"])
print()
print(images_path["NoFindings"])
print()
print(images_path["Pneumonia"])

images_class = {
    "Covid": 0,
    "Pneumonia": 1,
    "NoFindings": 2
}
```

```
['./train/Covid-19\\1-s2.0-S1684118220300682-main.pdf-002-a1.png', './train/Covid-19\\1-s2.0-S1684118220300682-ma
in.pdf-002-a2.png', './train/Covid-19\\1-s2.0-S1684118220300682-main.pdf-003-b1.png', './train/Covid-19\\1-s2.0-S
1684118220300682-main.pdf-003-b2.png', './train/Covid-19\\1.CXRCTThoraximagesofCOVID-19fromSingapore.pdf-000-fig1
a.png', './train/Covid-19\\1.CXRCTThoraximagesofCOVID-19fromSingapore.pdf-000-fig1b.png', './train/Covid-19\\1.CX
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ngapore.pdf-001-fig2b.png', './train/Covid-19\\1.CXRCTThoraximagesofCOVID-19fromSingapore.pdf-002-fig3a.png', './
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-003-fig4b.png', './train/Covid-19\\23E99E2E-447C-46E5-8EB2-D35D12473C39.png', './train/Covid-19\\41591_2020_819_
Fig1_HTML.webp-day10.png', './train/Covid-19\\41591_2020_819_Fig1_HTML.webp-day5.png', './train/Covid-19\\7EF28E1
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-b.png', './train/Covid-19\\ciaa199.pdf-001-c.png', './train/Covid-19\\covid-19-infection-exclusive-gastrointesti
nal-symptoms-pa.png', './train/Covid-19\\covid-19-pneumonia-14-PA.png', './train/Covid-19\\covid-19-pneumonia-28.
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.jpeg', './train/Covid-19\\2C26F453-AF3B-4517-BB9E-802CF2179543.jpeg', './train/Covid-19\\31BA3780-2323-493F-8AED
-62081B9C383B.jpeg', './train/Covid-19\\353889E0-A1E8-4F9E-A0B8-F24F36BCFBFB.jpeg', './train/Covid-19\\39EE8E69-5
801-48DE-B6E3-BE7D1BCF3092.jpeg', './train/Covid-19\\446B2CB6-B572-40AB-B01F-1910CA07086A.jpeg', './train/Covid-1
9\\53EC07C9-5CC6-4BE4-9B6F-D7B0D72AAA7E.jpeg', './train/Covid-19\\58cb9263f16e94305c730685358e4e_jumbo.jpeg', './
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irus.jpeg', './train/Covid-19\\auntminnie-c-2020_01_28_23_51_6665_2020_01_28_Vietnam_coronavirus.jpeg', './train/
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\\C6EA0BE5-B01E-4113-B194-18D956675E25.jpeg', './train/Covid-19\\CD50BA96-6982-4C80-AE7B-5F67ACDBFA56.jpeg', './t
rain/Covid-19\\D7AF463C-2369-492D-908D-BE1911CCD74C.jpeg', './train/Covid-19\\E1724330-1866-4581-8CD8-CEC9B8AFEDD
E.jpeg', './train/Covid-19\\E63574A7-4188-4C8D-8D17-9D67A18A1AFA.jpeg', './train/Covid-19\\F2DE909F-E19C-4900-92F
5-8F435B031AC6.jpeg', './train/Covid-19\\F4341CE7-73C9-45C6-99C8-8567A5484B63.jpeg', './train/Covid-19\\F63AB6CE-
1968-4154-A70F-913AF154F53D.jpeg', './train/Covid-19\\FE9F9A5D-2830-46F9-851B-1FF4534959BE.jpeg', './train/Covid-
19\\figure1-5e71be566aa8714a04de3386-98-left.jpeg', './train/Covid-19\\figure1-5e73d7ae897e27ff066a30cb-98.jpeg',
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0.png', './train/Pneumonia\\00009987_004.png', './train/Pneumonia\\00010012_015.png', './train/Pneumonia\\0001001
2_016.png', './train/Pneumonia\\00010012_024.png', './train/Pneumonia\\00010066_007.png', './train/Pneumonia\\000
10092_003.png', './train/Pneumonia\\00010092_035.png', './train/Pneumonia\\00010092_037.png', './train/Pneumonia\
\00010120_008.png', './train/Pneumonia\\00010120_010.png', './train/Pneumonia\\00010120_029.png', './train/Pneumo
nia\\00010165_007.png', './train/Pneumonia\\00010190_007.png', './train/Pneumonia\\00010222_019.png', './train/Pn
eumonia\\00010248_000.png', './train/Pneumonia\\00010277_000.png', './train/Pneumonia\\00010308_011.png', './trai
n/Pneumonia\\00010311_002.png', './train/Pneumonia\\00010334_010.png', './train/Pneumonia\\00010347_001.png', './
train/Pneumonia\\00010352_022.png', './train/Pneumonia\\00010375_000.png', './train/Pneumonia\\00010375_001.png',
'./train/Pneumonia\\00010384_033.png', './train/Pneumonia\\00010384_034.png', './train/Pneumonia\\00010384_035.pn
g', './train/Pneumonia\\00010384_036.png', './train/Pneumonia\\00010399_001.png', './train/Pneumonia\\00010427_01
4.png', './train/Pneumonia\\00010447_018.png', './train/Pneumonia\\00010471_001.png', './train/Pneumonia\\0001047
8_006.png', './train/Pneumonia\\00010505_018.png', './train/Pneumonia\\00010509_003.png', './train/Pneumonia\\000
10524_001.png', './train/Pneumonia\\00010530_028.png', './train/Pneumonia\\00010531_012.png', './train/Pneumonia\
\00010531_058.png', './train/Pneumonia\\00010531_073.png', './train/Pneumonia\\00010531_074.png', './train/Pneumo
nia\\00010531_075.png', './train/Pneumonia\\00010531_076.png', './train/Pneumonia\\00010544_000.png', './train/Pn
eumonia\\00010544_007.png', './train/Pneumonia\\00010544_022.png', './train/Pneumonia\\00010544_023.png', './trai
n/Pneumonia\\00010544_029.png', './train/Pneumonia\\00010544_031.png', './train/Pneumonia\\00010552_005.png', './
train/Pneumonia\\00010586_000.png', './train/Pneumonia\\00010604_005.png', './train/Pneumonia\\00010610_003.png',
'./train/Pneumonia\\00010652_000.png', './train/Pneumonia\\00010693_012.png', './train/Pneumonia\\00010695_012.pn
g', './train/Pneumonia\\00010706_000.png', './train/Pneumonia\\00010773_017.png', './train/Pneumonia\\00010773_01
9.png', './train/Pneumonia\\00010773_020.png', './train/Pneumonia\\00010780_007.png', './train/Pneumonia\\0001079
0_005.png', './train/Pneumonia\\00010828_023.png', './train/Pneumonia\\00010924_003.png', './train/Pneumonia\\000
10943_000.png', './train/Pneumonia\\00011020_000.png', './train/Pneumonia\\00011097_002.png', './train/Pneumonia\
\00011104_004.png', './train/Pneumonia\\00011136_002.png', './train/Pneumonia\\00011147_000.png', './train/Pneumo
nia\\00011188_002.png', './train/Pneumonia\\00011237_006.png', './train/Pneumonia\\00011237_066.png', './train/Pn
eumonia\\00011237_067.png', './train/Pneumonia\\00011237_112.png', './train/Pneumonia\\00011251_010.png', './trai
n/Pneumonia\\00011328_007.png', './train/Pneumonia\\00011460_043.png', './train/Pneumonia\\00011472_001.png', './
train/Pneumonia\\00011514_015.png', './train/Pneumonia\\00011544_010.png', './train/Pneumonia\\00011545_000.png',
'./train/Pneumonia\\00011564_008.png', './train/Pneumonia\\00011583_000.png', './train/Pneumonia\\00011583_007.pn
g', './train/Pneumonia\\00011585_000.png', './train/Pneumonia\\00011592_001.png', './train/Pneumonia\\00011598_04
3.png', './train/Pneumonia\\00011632_012.png', './train/Pneumonia\\00011632_013.png', './train/Pneumonia\\0001163
8_000.png', './train/Pneumonia\\00011702_010.png', './train/Pneumonia\\00011702_058.png', './train/Pneumonia\\000
11702_059.png', './train/Pneumonia\\00011704_000.png', './train/Pneumonia\\00011709_000.png', './train/Pneumonia\
\00011723_021.png', './train/Pneumonia\\00011827_010.png', './train/Pneumonia\\00011831_008.png', './train/Pneumo
nia\\00011831_015.png', './train/Pneumonia\\00011842_002.png', './train/Pneumonia\\00011882_000.png', './train/Pn
eumonia\\00011925_032.png', './train/Pneumonia\\00011945_011.png', './train/Pneumonia\\00011956_003.png', './trai
n/Pneumonia\\00011960_006.png', './train/Pneumonia\\00011966_006.png', './train/Pneumonia\\00011966_007.png', './
train/Pneumonia\\00011966_016.png', './train/Pneumonia\\00011973_015.png', './train/Pneumonia\\00012012_007.png',
'./train/Pneumonia\\00012045_005.png', './train/Pneumonia\\00012094_009.png', './train/Pneumonia\\00012094_011.pn
g', './train/Pneumonia\\00012097_005.png', './train/Pneumonia\\00012141_013.png', './train/Pneumonia\\00012141_02
2.png', './train/Pneumonia\\00012158_021.png', './train/Pneumonia\\00012158_025.png', './train/Pneumonia\\0001221
1_000.png', './train/Pneumonia\\00012229_003.png']
```

데이터의 개수

In [16]:

```
print(len(images_path['Covid']))
print(len(images_path['NoFindings']))
print(len(images_path['Pneumonia']))
```

```
125
500
500
```

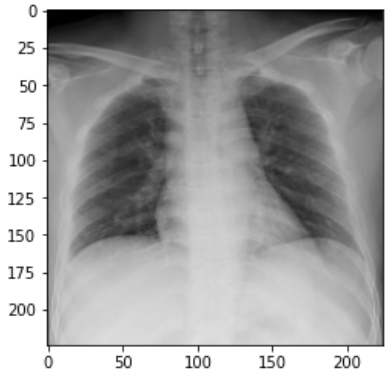
데이터 출력

In [ ]:

```
""
X = []
Y = []

for label in images_path:
    for image_path in images_path[label]:
        image = cv2.imread(image_path)
        image = cv2.resize(image,(224, 224))
        X.append(image)
        Y.append(images_class[label])
```

In [ ]:
```
plt.imshow(X[0])
plt.show()
```

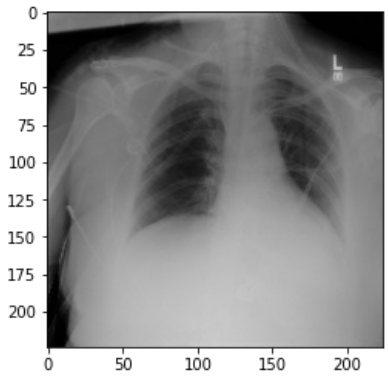


In [ ]:
```
print(np.array(X).shape)
print(np.array(Y).shape)

plt.imshow(X[1124])
```

```
(1125, 224, 224, 3)
(1125,)
```

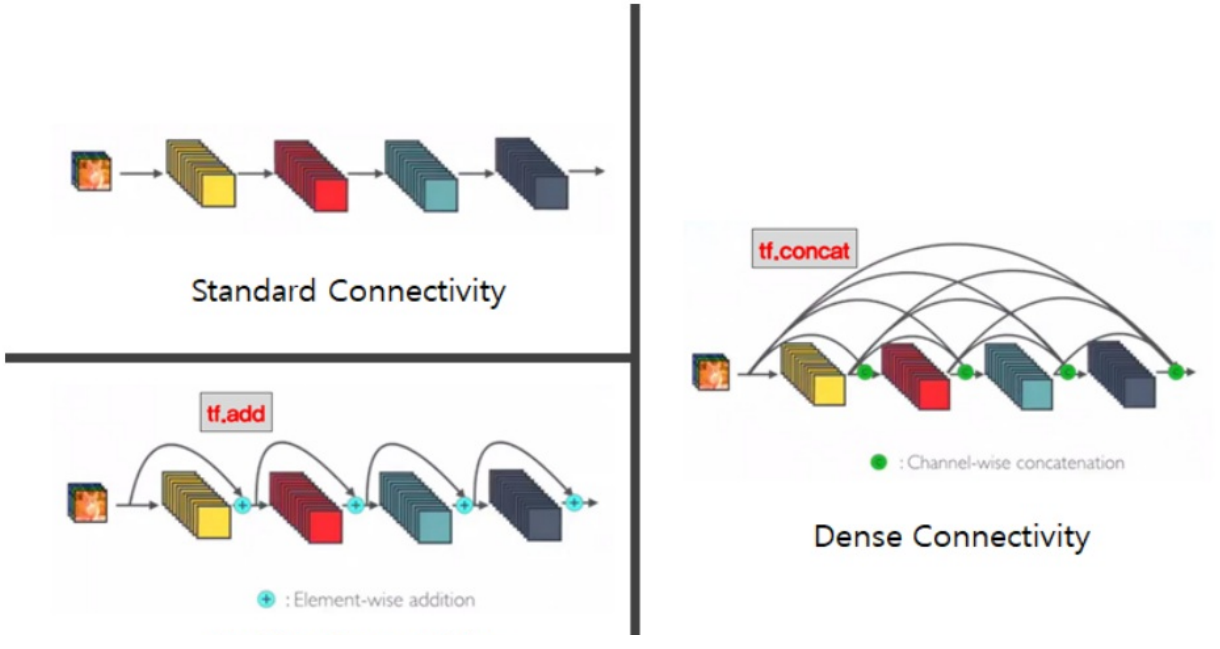
Out[ ]:
```
<matplotlib.image.AxesImage at 0x7fb4972ef690>
```



모델 생성

DenseNet이란 ResNet의 ShortCut 개념을 확장해 CNN 구조를 바꾸는 시도를 한 알고리즘

> ResNet이란 Microsoft에서 개발한 알고리즘(layer의 구조가 깊어질수록 정확도가 감소하는 문제를 해결하기 위해 제안됨)



ResNet Connectivity

Densely connected convolution networks CVPR 2017 oral presentation slide

In [ ]:
```
x = np.array(X)
y = np.array(Y)

# initial pre trained model
pre_trained_models = {}
pre_trained_models["DenseNet169"] = DenseNet169(include_top=False, input_shape=(224, 224, 3), pooling="avg")
```

```
Downloading data from https://storage.googleapis.com/tensorflow/keras-applications/densenet/densenet169_weights_tf_dim_ordering_tf_kernels_notop.h5
51879936/51877672 [==============================] - 1s 0us/step
51888128/51877672 [==============================] - 1s 0us/step
```

In [ ]:
```
features = pre_trained_models["DenseNet169"].predict(x)
```

train, test데이터 나누기

In [ ]:
```
X_train, X_test, Y_train, Y_test = train_test_split(x, y, test_size=0.2, random_state=80)

X_train = pre_trained_models["DenseNet169"].predict(X_train)
X_test = pre_trained_models["DenseNet169"].predict(X_test)
```

분류

XGBoost는 과적합 방지가 가능한 규제가 포함되어 있고 CART를 기반으로 한다 (즉, 분류와 회귀 둘 다 가능)

결국 Gradient Boost을 기반으로 함 (GBM이란 예측모형의 앙상블 방법론 중 부스팅계열에 속하는 알고리즘)

(부스팅이란 약한 분류기를 결합해 강한 분류기를 만드는 과정)

In [ ]:
```
XGB_Classifier = XGBClassifier(learning_rate=0.44, n_estimators=100, random_state=0, seed=0, gamma=0)


#XGBClassifier(값이 높을수록 과적합 하기 쉽다,트리의 수, random값을 고정하는 역할,seed,loss function 정의에 따라 튜닝)
```

In [ ]:
```
#모델을 학습시킴
XGB_Classifier.fit(X_train, Y_train)


#test데이터 예측하기
Y_pred = XGB_Classifier.predict(X_test)
Y_pred
```

Out[ ]:
```
array([1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 1, 0, 0, 0, 2, 1, 2, 2, 1, 1, 1, 1,
       1, 2, 2, 2, 1, 1, 2, 1, 2, 2, 2, 2, 2, 1, 2, 0, 2, 2, 2, 1, 2, 2,
       1, 0, 2, 1, 2, 2, 2, 2, 2, 1, 2, 2, 2, 1, 1, 1, 2, 2, 2, 1, 2, 2,
       1, 0, 1, 2, 1, 1, 1, 2, 1, 0, 1, 2, 1, 1, 2, 2, 2, 1, 1, 2, 1, 1,
       2, 2, 1, 2, 2, 1, 0, 1, 2, 1, 1, 2, 1, 1, 1, 2, 1, 1, 2, 2, 2, 1,
       2, 2, 1, 2, 1, 1, 1, 1, 0, 1, 0, 2, 2, 2, 0, 2, 1, 1, 2, 1, 2, 2,
       1, 2, 1, 2, 2, 2, 2, 2, 0, 1, 0, 0, 1, 2, 0, 1, 1, 1, 1, 1, 2, 1,
       0, 2, 2, 2, 1, 1, 1, 1, 1, 2, 1, 2, 1, 2, 0, 0, 2, 0, 1, 1, 1, 1,
       2, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 0, 2, 1, 2, 1, 2, 1, 2, 2, 2,
       2, 1, 1, 2, 2, 1, 2, 1, 1, 1, 2, 1, 2, 2, 2, 2, 2, 2, 1, 2, 2, 1,
       2, 2, 2, 2, 1])
```

모델 검증

In [ ]:
```
result = {}


result["Accuracy score"] = accuracy_score(Y_test, Y_pred)
result["confusion matrix"] = confusion_matrix(Y_test, Y_pred)
```

```
result["f1 score"] = f1_score(Y_test, Y_pred, average="macro")
result["precision score"] = precision_score(Y_test, Y_pred, average="macro")
result["Sensitivity"] = result["confusion matrix"][0,0] / (result["confusion matrix"][0,0] + result["confusion ma
result["Specifity"] = result["confusion matrix"][1,1] / (result["confusion matrix"][1,0] + result["confusion matr

print(f"\nAccuracy score : ", result["Accuracy score"])
print(f"\nconfusion matrix : \n", result["confusion matrix"])
print(f"\nf1 score : ", result["f1 score"])
print(f"\nprecision score : ", result["precision score"])
print(f"\nSpecifity : ", result["Specifity"])
print(f"\nSensitivity : ", result["Sensitivity"])
```

```
Accuracy score :  0.8666666666666667

confusion matrix :
 [[19  1  2]
 [ 1 88 14]
 [ 0 12 88]]

f1 score :  0.876750700280112

precision score :  0.8891469916222392

Specifity :  0.9887640449438202

Sensitivity :  0.95
```

1. Accuracy score : 정확도 수치
2. confusion matrix : prediction 성능을 측정하기 위해 예측값과 실제값을 시각화한 표
3. f1 score : 불균형 분류문제에서 주로 사용 precision과 recall의 조화평균
4. precision score : 정밀도 수치로 긍정으로 예측한 것 중 실제로 맞춘 비율
5. Specifity : 특이도 수치로 부정을 얼마나 잘 예측했는지 나타내는 지표
6. Sensitivity : True Positive Rate로 실제 Positive를 얼마나 잘 예측했는지 (민감도로써 AUC를 구할때 중요한 척도로 사용됨)

검사 평가

ROC curve는 의학, 보건학, 간호학 쪽에서 많이 쓰이는 분석기법

Confusion Matrix만으로는 모델의 평가 척도로써 부족할 수 있어서 모델의 효율성을 평가하는 척도로 ROC Curve라는 것이 존재

ROC curve와 x축을 이루고 있는 면적의 넓이를 AUC, AUC의 값이 1에 가까울수록 효율적인 모델

In [ ]:

```
from sklearn.metrics import roc_curve, auc

from sklearn import preprocessing
y_test = preprocessing.label_binarize(Y_test, classes=[0, 1])
y_pred = preprocessing.label_binarize(Y_pred, classes=[0, 1])
print(y_test.shape)
print(y_pred.shape)

n_classes = list(Y_test.shape)

# Compute ROC curve and ROC area for each class
fpr = dict()
tpr = dict()
roc_auc = dict()
for i in range(2):
    fpr[i], tpr[i], _ = roc_curve(y_test[:, i], y_pred[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i])

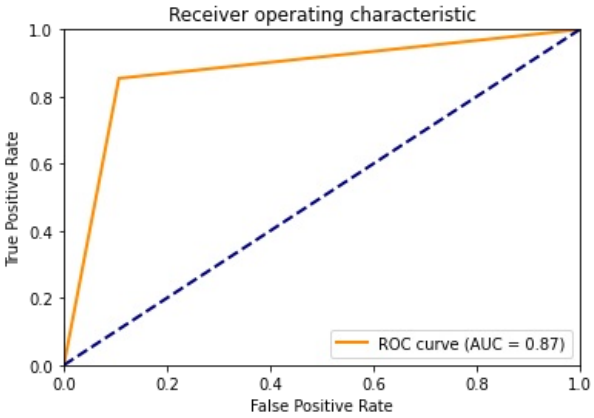
# Compute micro-average ROC curve and ROC area

fpr["micro"], tpr["micro"], _ = roc_curve(y_test.ravel(), y_pred.ravel())
roc_auc["micro"] = auc(fpr["micro"], tpr["micro"])

plt.figure()
lw = 2
plt.plot(fpr[1], tpr[1], color='darkorange',
         lw=lw, label='ROC curve (AUC = %0.2f)' % roc_auc[1])
plt.plot([0, 1], [0, 1], color='navy', lw=lw, linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.0])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
```

```
plt.title('Receiver operating characteristic')
plt.legend(loc="lower right")
plt.savefig("roc.svg", format="svg")
plt.show()
```

```
(225, 2)
(225, 2)
```



x축(False Positive Rate)과 y축(True Positive Rate), 휨 정도를 봐야함

예를 들어 병원에 코로나 검사를 받기 위해 내원했을때 의사(판단자)가 암에 걸렸다고 판단했을때

1. FPR : 실제 걸리지 않았는데 암에 걸렸다고 판단한 것
2. TPR : 실제 걸려있고 암에 걸렸다고 판단한 것
3. 휨 정도 : 두 그룹을 잘 구별한다면 ROC 커버는 좌상단에 붙게됨 (가까워질수록 좋음)

In [ ]:

```
import sklearn
import pandas as pd

scoring = ['precision_macro', 'f1_macro', "accuracy"]

rs = 229
cv = KFold(n_splits=5, random_state=rs, shuffle=True)
scores = cross_validate(XGB_Classifier,features, y, cv=cv, scoring=scoring)
scr = pd.DataFrame(scores)
print(f"======== KFold random state {rs} ==========")
print(scr)
print("accuracy avg : ", scr["test_accuracy"].mean())
```

```
======== KFold random state 229 ==========
    fit_time  score_time  test_precision_macro  test_f1_macro  test_accuracy
0  18.184703    0.008893              0.879793       0.822236       0.826667
1  18.221328    0.009802              0.882701       0.871037       0.871111
2  17.754335    0.009262              0.854204       0.849678       0.826667
3  18.037497    0.008770              0.875222       0.866672       0.848889
4  17.408080    0.009241              0.828070       0.810838       0.795556
accuracy avg :  0.8337777777777777
```

분류 모델 성능 평가 지표

In [ ]:

```
f = 0
for train_ix, test_ix in cv.split(features):
    # get data
    train_X, test_X = features[train_ix], features[test_ix]
    train_y, test_y = y[train_ix], y[test_ix]
    # fit model
    model = XGB_Classifier
    model.fit(train_X, train_y)
    # evaluate model
    yhat = model.predict(test_X)
    acc = accuracy_score(test_y, yhat)
    # store score
    print(f"\n confusion matrix fold {f}")
    f = f+1
    print(confusion_matrix(test_y, yhat))
```

```
 confusion matrix fold 0
[[13  4  2]
 [ 0 94 12]
```

```
 [ 0 21 79]]

 confusion matrix fold 1
[[24  3  2]
 [ 1 94 14]
 [ 1  8 78]]

 confusion matrix fold 2
[[30  0  2]
 [ 2 67 22]
 [ 0 13 89]]

 confusion matrix fold 3
[[16  0  2]
 [ 1 81 17]
 [ 0 14 94]]

 confusion matrix fold 4
[[22  3  2]
 [ 1 69 25]
 [ 1 14 88]]
```