# IPA 주관 인공지능센터 기본(fundamental) 과정

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## In [1]:

```
import numpy as np
import pandas as pd
import matplotlib as mpl
import matplotlib.pyplot as plt
import seaborn as sns
import missingno as mino
%matplotlib inline
```

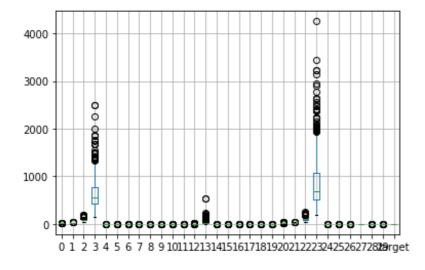
#### In [2]:

```
from sklearn.datasets import load_breast_cancer

data = load_breast_cancer()
X, y = pd.DataFrame(data.data), pd.DataFrame(data.target, columns=['target'])
cancer = pd.concat([X, y], axis=1)
cancer.boxplot()
```

#### Out[2]:

<matplotlib.axes.\_subplots.AxesSubplot at 0x7f2c4423ab38>



### In [3]:

n 9298429262812202 n n28921n399754n8n73

JU 12 J2 02 012 202 0 . 02 0 J2 1 0 0 J J 1 0 1 0 0 1 0 In [4]: from sklearn.model selection import train test split X train, X test, y train, y test = train test split(cancer.iloc[:, :-1], cancer.iloc[:, -1]) In [5]: from sklearn.preprocessing import MinMaxScaler from sklearn.pipeline import Pipeline pipe = Pipeline([('scaler', MinMaxScaler()), ('knn', KNeighborsClassifier() ) ] ) pipe.fit(X train, y train) Out[5]: Pipeline (memory=None, steps=[('scaler', MinMaxScaler(copy=True, feature range=(0, 1))), ('knn', KNeighborsClassifier(algorithm='auto', leaf size=30, metric='minkowski', metric\_params=None n jobs=None, n neighbors=5, p=2, weights='uniform'))], verbose=False) In [6]: pipe.steps Out[6]: [('scaler', MinMaxScaler(copy=True, feature range=(0, 1))), ('knn', KNeighborsClassifier(algorithm='auto', leaf size=30, metric='minkowski', metric params=None, n jobs=None, n neighbors=5, p=2, weights='uniform'))] In [7]: from sklearn.preprocessing import RobustScaler from sklearn.decomposition import PCA from sklearn.pipeline import make pipeline make pipeline(RobustScaler(), PCA()) Out[7]: Pipeline (memory=None, steps=[('robustscaler', RobustScaler(copy=True, quantile range=(25.0, 75.0), with centering=True, with scaling=True)), ('pca', PCA(copy=True, iterated power='auto', n components=None, random state=None, svd solver='auto', tol=0.0, whiten=False))], verbose=False)

In [8]:

```
from sklearn.preprocessing import StandardScaler
make pipeline(StandardScaler(), PCA(n components=2), StandardScaler())
Out[8]:
Pipeline (memory=None,
         steps=[('standardscaler-1',
                 StandardScaler(copy=True, with mean=True, with std=True)),
                ('pca',
                 PCA(copy=True, iterated power='auto', n components=2,
                     random state=None, svd solver='auto', tol=0.0,
                     whiten=False)),
                ('standardscaler-2',
                 StandardScaler(copy=True, with mean=True, with std=True))],
         verbose=False)
                                                                          ≫ ▶
In [9]:
temp = []
for i in range(cancer.shape[1] - 1, 1, -1):
    pca = PCA(i)
    x = pca.fit transform(cancer.iloc[:, :-1])
    knn = KNeighborsClassifier()
    t = cross val score(knn, x, cancer.iloc[:, -1], cv=10)
    temp.append(np.mean(t))
np.max(temp)
Out[9]:
0.9316286405669347
In [10]:
from sklearn.model selection import GridSearchCV
for i in range(cancer.shape[1] - 1, 1, -1):
    pipe = make pipeline(PCA(i), KNeighborsClassifier())
    grid = GridSearchCV(
        pipe, {'kneighborsclassifier n neighbors': [n for n in range(1, 11)
] } ,
        cv=10,
        iid=True)
    grid.fit(cancer.iloc[:, :-1], cancer.iloc[:, -1])
    print(grid.best params )
4
{'kneighborsclassifier n neighbors': 10}
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```

```
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{'kneighborsclassifier __n_neighbors': 10}
{'kneighborsclassifier __n_neighbors': 10}
{'kneighborsclassifier __n_neighbors': 8}
```