차원 축소

1.환경준비

(1) 라이브러리 로딩

In [1]:
```
!pip install plotly
import plotly.graph_objects as go
```

```
Requirement already satisfied: plotly in c:\users\user\anaconda3\lib\site-packages (5.9.0)
Requirement already satisfied: tenacity>=6.2.0 in c:\users\user\anaconda3\lib\site-packages (f
rom plotly) (8.2.2)
```

In [2]:
```
# 기본 라이브러리 가져오기
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import *

from sklearn.datasets import load_breast_cancer, load_digits, load_iris, make_swiss_roll
from sklearn.preprocessing import MinMaxScaler

from sklearn.decomposition import PCA
```

(2) 샘플 데이터 생성하기

In [3]:
```
# 럭비공 형태의 샘플 데이터 생성 함수
def generate_rugby_data(n_points=1000, a=1, b=1.5, c=2):
    phi = np.random.uniform(0, np.pi, n_points)
    theta = np.random.uniform(0, 2*np.pi, n_points)
    x = a * np.sin(phi) * np.cos(theta)
    y = b * np.sin(phi) * np.sin(theta)
    z = c * np.cos(phi)
    X = np.column_stack((x, y, z))
    return X

rugby = generate_rugby_data()

# 스위스롤 데이터
swiss_roll, _ = make_swiss_roll(n_samples=1000, noise=0.2)
```

In [4]:
```
# 3차원 스캐터 함수 생성
def my_3d_Scatter(X) :
    fig = go.Figure()
    fig.add_trace(go.Scatter3d(x=X[:, 0], y=X[:, 1], z=X[:, 2],
                               mode='markers', marker=dict(size=2, color='blue'),
                               name='Original Data'))
```

```
    fig.update_layout(margin=dict(l=0, r=0, b=0, t=0),
                      scene=dict(xaxis_title='X Axis', yaxis_title='Y Axis', zaxis_title='Z Ax

    fig.show()
```

2.PCA 개념이해

(1) 럭비공 형태의 데이터 차원 축소

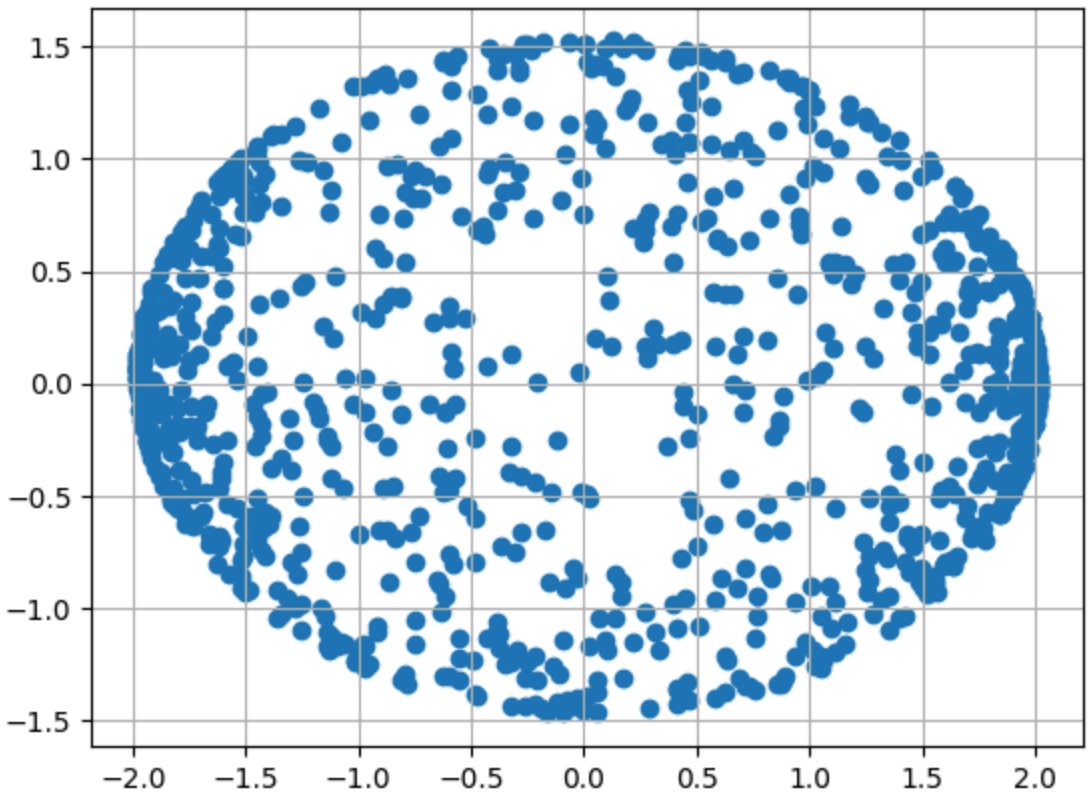
- 원본 데이터 둘러보기

In [5]:
```
my_3d_Scatter(rugby)
```

- 차원 축소

In [6]:
```
# PCA를 이용하여 2개의 주성분으로 차원 축소
pca = PCA(n_components=2)
X_pca = pca.fit_transform(rugby)

# PCA 축소 데이터 조회
```

```
plt.scatter(X_pca[:, 0], X_pca[:, 1])
plt.grid()
plt.show()
```



In [ ]:

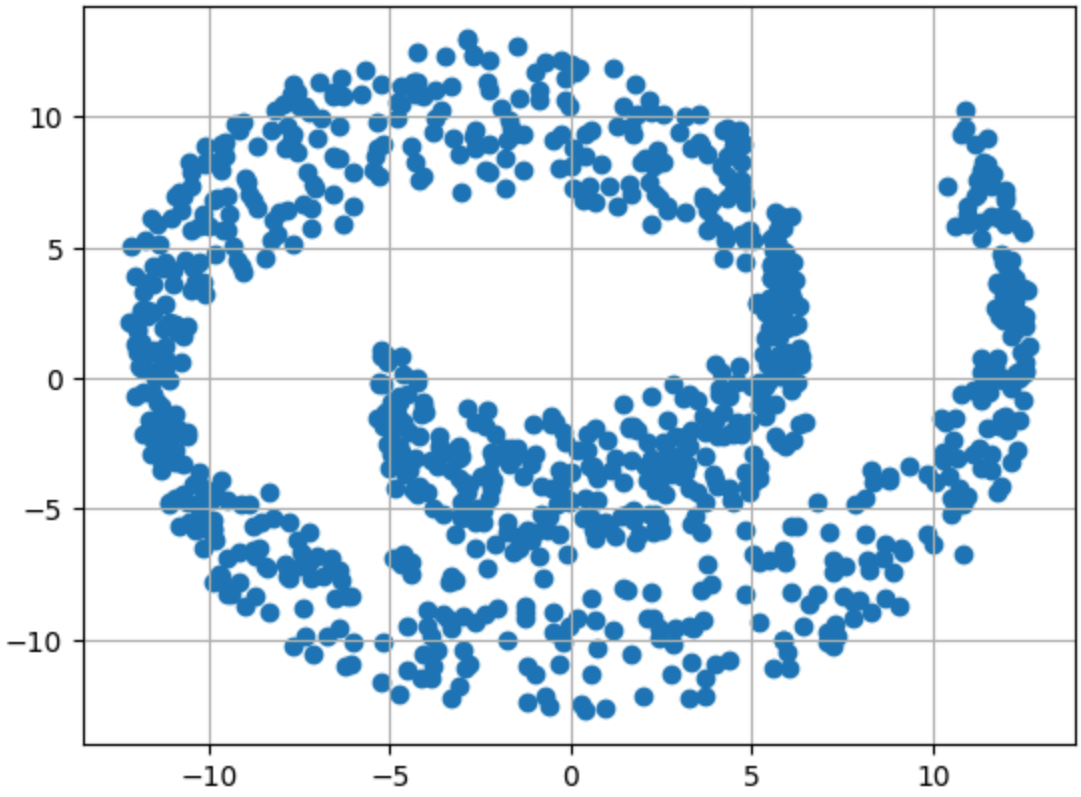
(2) 스위스롤 형태의 데이터 차원 축소

- 원본 데이터 둘러보기

In [7]:
```
my_3d_Scatter(swiss_roll)
```

- 차원 축소

In [8]:
```
# PCA를 이용하여 2개의 주성분으로 차원 축소
pca = PCA(n_components=2)
X_pca = pca.fit_transform(swiss_roll)

# PCA 축소 데이터 조회
plt.scatter(X_pca[:, 0], X_pca[:, 1])
plt.grid()
plt.show()
```



3.PCA 사용해보기

(1) 데이터 준비

- 데이터 로딩

In [53]:
```
iris = pd.read_csv("https://raw.githubusercontent.com/DA4BAM/dataset/master/iris.csv")
target = 'Species'
x = iris.drop(target, axis = 1)
y = iris.loc[:, target]
```

In [54]:
```
x.head()
```

Out[54]:

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
0	5.1	3.5	1.4	0.2
1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2
3	4.6	3.1	1.5	0.2
4	5.0	3.6	1.4	0.2

- 스케일링

In [55]:
```
scaler = MinMaxScaler()
x2 = scaler.fit_transform(x)

# (옵션)데이터프레임 변환
x2 = pd.DataFrame(x2, columns= x.columns)
```

(2) 주성분 분석

In [56]:
```
from sklearn.decomposition import PCA
```

In [57]:
```
# feature 수
x2.shape[1]
```

Out[57]:
```
4
```

- 주 성분 분석 수행

In [58]:
```
# 주성분 수 2개
n = 2
pca = PCA(n_components = n) # 2차원으로 축소

# 만들고, 적용하기(결과는 넘파이 어레이)
x2_pc = pca.fit_transform(x2)
```

In [59]:
```
# 2개의 주성분
x2_pc[:5]
```

Out[59]:
```
array([[-0.63070293,  0.10757791],
       [-0.62290494, -0.10425983],
       [-0.6695204 , -0.05141706],
       [-0.65415276, -0.10288487],
       [-0.64878806,  0.13348758]])
```

In [60]:
```
# (옵션) 데이터프레임으로 변환
x2_pc = pd.DataFrame(x2_pc, columns = ['PC1', 'PC2'])
x2_pc.head()
```

Out[60]:

	PC1	PC2
0	-0.630703	0.107578
1	-0.622905	-0.104260
2	-0.669520	-0.051417
3	-0.654153	-0.102885
4	-0.648788	0.133488

- 기존 데이터에 차원 축소된 데이터를 붙여 봅시다.

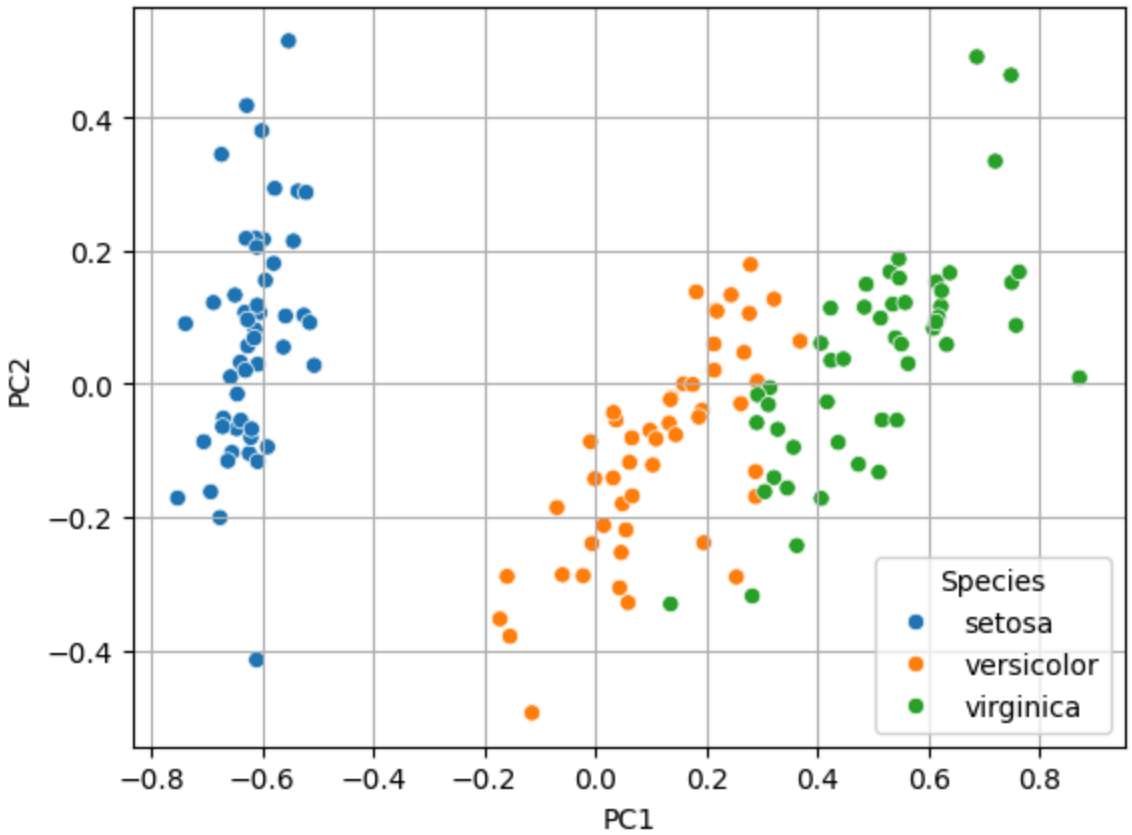
In [61]:
```
pd.concat([iris, x2_pc], axis = 1).head()
```

Out[61]:

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	PC1	PC2
0	5.1	3.5	1.4	0.2	setosa	-0.630703	0.107578
1	4.9	3.0	1.4	0.2	setosa	-0.622905	-0.104260
2	4.7	3.2	1.3	0.2	setosa	-0.669520	-0.051417
3	4.6	3.1	1.5	0.2	setosa	-0.654153	-0.102885
4	5.0	3.6	1.4	0.2	setosa	-0.648788	0.133488

- 두개의 주성분 시각화

In [62]:
```
sns.scatterplot(x = 'PC1', y = 'PC2', data = x2_pc, hue = y)
plt.grid()
plt.show()
```



4.고차원 데이터 차원축소

(1) 데이터 준비

1) 데이터 로딩

In [63]:
```
# breast_cancer 데이터 로딩
cancer=load_breast_cancer()
x = cancer.data
y = cancer.target
```

```
x = pd.DataFrame(x, columns=cancer.feature_names)

x.shape
```

Out[63]: (569, 30)

In [20]:
```
x.head()
```

Out[20]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	dime
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0

5 rows × 30 columns

In [21]:
```
x.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 30 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   mean radius              569 non-null    float64
 1   mean texture             569 non-null    float64
 2   mean perimeter           569 non-null    float64
 3   mean area                569 non-null    float64
 4   mean smoothness          569 non-null    float64
 5   mean compactness         569 non-null    float64
 6   mean concavity           569 non-null    float64
 7   mean concave points      569 non-null    float64
 8   mean symmetry            569 non-null    float64
 9   mean fractal dimension   569 non-null    float64
 10  radius error             569 non-null    float64
 11  texture error            569 non-null    float64
 12  perimeter error          569 non-null    float64
 13  area error               569 non-null    float64
 14  smoothness error         569 non-null    float64
 15  compactness error        569 non-null    float64
 16  concavity error          569 non-null    float64
 17  concave points error     569 non-null    float64
 18  symmetry error           569 non-null    float64
 19  fractal dimension error  569 non-null    float64
 20  worst radius             569 non-null    float64
 21  worst texture            569 non-null    float64
 22  worst perimeter          569 non-null    float64
 23  worst area               569 non-null    float64
 24  worst smoothness         569 non-null    float64
 25  worst compactness        569 non-null    float64
 26  worst concavity          569 non-null    float64
 27  worst concave points     569 non-null    float64
 28  worst symmetry           569 non-null    float64
 29  worst fractal dimension  569 non-null    float64
dtypes: float64(30)
memory usage: 133.5 KB
```

In [22]:
```
x.describe().T
```

Out[22]:

	count	mean	std	min	25%	50%	75%	r
mean radius	569.0	14.127292	3.524049	6.981000	11.700000	13.370000	15.780000	28.11
mean texture	569.0	19.289649	4.301036	9.710000	16.170000	18.840000	21.800000	39.28
mean perimeter	569.0	91.969033	24.298981	43.790000	75.170000	86.240000	104.100000	188.50
mean area	569.0	654.889104	351.914129	143.500000	420.300000	551.100000	782.700000	2501.00
mean smoothness	569.0	0.096360	0.014064	0.052630	0.086370	0.095870	0.105300	0.16
mean compactness	569.0	0.104341	0.052813	0.019380	0.064920	0.092630	0.130400	0.34
mean concavity	569.0	0.088799	0.079720	0.000000	0.029560	0.061540	0.130700	0.42
mean concave points	569.0	0.048919	0.038803	0.000000	0.020310	0.033500	0.074000	0.20
mean symmetry	569.0	0.181162	0.027414	0.106000	0.161900	0.179200	0.195700	0.30
mean fractal dimension	569.0	0.062798	0.007060	0.049960	0.057700	0.061540	0.066120	0.09
radius error	569.0	0.405172	0.277313	0.111500	0.232400	0.324200	0.478900	2.87
texture error	569.0	1.216853	0.551648	0.360200	0.833900	1.108000	1.474000	4.88
perimeter error	569.0	2.866059	2.021855	0.757000	1.606000	2.287000	3.357000	21.98
area error	569.0	40.337079	45.491006	6.802000	17.850000	24.530000	45.190000	542.20
smoothness error	569.0	0.007041	0.003003	0.001713	0.005169	0.006380	0.008146	0.03
compactness error	569.0	0.025478	0.017908	0.002252	0.013080	0.020450	0.032450	0.13
concavity error	569.0	0.031894	0.030186	0.000000	0.015090	0.025890	0.042050	0.39
concave points error	569.0	0.011796	0.006170	0.000000	0.007638	0.010930	0.014710	0.05
symmetry error	569.0	0.020542	0.008266	0.007882	0.015160	0.018730	0.023480	0.07
fractal dimension error	569.0	0.003795	0.002646	0.000895	0.002248	0.003187	0.004558	0.02
worst radius	569.0	16.269190	4.833242	7.930000	13.010000	14.970000	18.790000	36.04
worst texture	569.0	25.677223	6.146258	12.020000	21.080000	25.410000	29.720000	49.54
worst perimeter	569.0	107.261213	33.602542	50.410000	84.110000	97.660000	125.400000	251.20

	count	mean	std	min	25%	50%	75%	r
worst area	569.0	880.583128	569.356993	185.200000	515.300000	686.500000	1084.000000	4254.00
worst smoothness	569.0	0.132369	0.022832	0.071170	0.116600	0.131300	0.146000	0.22
worst compactness	569.0	0.254265	0.157336	0.027290	0.147200	0.211900	0.339100	1.05
worst concavity	569.0	0.272188	0.208624	0.000000	0.114500	0.226700	0.382900	1.25
worst concave points	569.0	0.114606	0.065732	0.000000	0.064930	0.099930	0.161400	0.29
worst symmetry	569.0	0.290076	0.061867	0.156500	0.250400	0.282200	0.317900	0.66
worst fractal dimension	569.0	0.083946	0.018061	0.055040	0.071460	0.080040	0.092080	0.20

2) 스케일링

- 거리계산 기반 차원축소이므로 스케일링 필요

In [64]:
```
scaler = MinMaxScaler()
x = scaler.fit_transform(x)

# (옵션)데이터프레임 변환
x = pd.DataFrame(x, columns=cancer.feature_names)
```

3) 데이터 분할

- train, validation 분할

In [65]:
```
x_train, x_val, y_train, y_val = train_test_split(x, y, test_size = .3, random_state = 20)
```

(2) 주성분 만들기

In [66]:
```
from sklearn.decomposition import PCA
```

In [67]:
```
# feature 수
x_train.shape[1]
```

Out[67]:
```
30
```

- 주 성분 분석 수행

In [68]:
```
# 주성분을 몇개로 할지 결정(최대값 : 전체 feature 수)
n = x_train.shape[1] # feautre 수

# 주성분 분석 선언
```

```
pca = PCA(n_components=n)

# 만들고, 적용하기
x_train_pc = pca.fit_transform(x_train)
x_val_pc = pca.transform(x_val)
```

- 편리하게 사용하기 위해 데이터프레임으로 변환

In [69]:
```
# 칼럼이름 생성
column_names = [ 'PC'+str(i+1) for i in range(n) ]
column_names
```

Out[69]:
```
['PC1',
 'PC2',
 'PC3',
 'PC4',
 'PC5',
 'PC6',
 'PC7',
 'PC8',
 'PC9',
 'PC10',
 'PC11',
 'PC12',
 'PC13',
 'PC14',
 'PC15',
 'PC16',
 'PC17',
 'PC18',
 'PC19',
 'PC20',
 'PC21',
 'PC22',
 'PC23',
 'PC24',
 'PC25',
 'PC26',
 'PC27',
 'PC28',
 'PC29',
 'PC30']
```

In [70]:
```
# 데이터프레임으로 변환하기
x_train_pc = pd.DataFrame(x_train_pc, columns = column_names)
x_val_pc = pd.DataFrame(x_val_pc, columns = column_names)
x_train_pc
```

Out[70]:

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
0	0.215422	0.112002	-0.208768	-0.293000	-0.032626	-0.135166	-0.022526	-0.032558	0.047827
1	0.869455	0.174561	-0.277555	-0.177606	0.142633	-0.032379	0.224845	0.131471	0.013562
2	-0.298314	0.259637	0.090626	0.118568	-0.017034	0.139689	-0.001580	0.037095	-0.016287
3	0.862285	0.165837	0.061614	0.199085	0.347577	-0.180729	0.228333	-0.067238	-0.069730
4	-0.229030	0.149323	-0.483832	0.331190	-0.096083	-0.016467	-0.082057	0.026775	0.036597
...	...	...	...	...	...	...	...	...	...
393	0.741352	-0.388231	0.040183	0.074092	-0.068445	0.075507	0.024218	0.060493	-0.133940
394	0.336910	0.050769	-0.187677	-0.248374	-0.064661	0.098182	0.056833	0.054760	0.031554
395	-0.467700	0.063227	0.217000	-0.247931	-0.060940	-0.031664	-0.024826	-0.024798	-0.032136
396	-0.320752	0.297598	0.063923	-0.290258	0.132390	-0.028911	0.168774	-0.034643	-0.047127
397	-0.186368	0.088527	0.156500	0.234542	0.190558	-0.095791	-0.097599	0.019651	0.044739

398 rows × 30 columns

- 문1) 다음의 조건으로 주성분을 추출해 봅시다.
  - 주성분 1개로 선언하고, x_train을 이용해서 주성분 추출
  - 주성분 2개로 선언하고, x_train을 이용해서 주성분 추출
  - 주성분 3개로 선언하고, x_train을 이용해서 주성분 추출

In [47]:
```
# 주성분 1개짜리
n = 1
pca = PCA(n_components = n)

# 만들고, 적용하기(결과는 넘파이 어레이)
x_train_pc_1 = pca.fit_transform(x_train)
```

In [48]:
```
# 주성분 2개짜리
n = 2
pca = PCA(n_components = n)

# 만들고, 적용하기(결과는 넘파이 어레이)
x_train_pc_2 = pca.fit_transform(x_train)
```

In [49]:
```
# 주성분 3개짜리
n = 3
pca = PCA(n_components = n)

# 만들고, 적용하기(결과는 넘파이 어레이)
x_train_pc_3 = pca.fit_transform(x_train)
```

- 문2) 각 주성분 결과에서 상위 3개 행씩 조회하여 비교해 봅시다.

In [33]:
```
x_train_pc_1[:3]
```

Out[33]:
```
array([[ 0.21542202],
       [ 0.86945519],
       [-0.29831397]])
```

In [34]:
```
x_train_pc_2[:3]
```

Out[34]:
```
array([[ 0.21542202,  0.11200241],
       [ 0.86945519,  0.1745606 ],
       [-0.29831397,  0.25963695]])
```

In [35]:
```
x_train_pc_3[:2]
```

Out[35]:
```
array([[ 0.21542202,  0.11200241, -0.20876766],
       [ 0.86945519,  0.1745606 , -0.27755476]])
```

In [36]:
```
print(x_train_pc_1[:3])
print()
print(x_train_pc_2[:3])
print()
print(x_train_pc_3[:3])
```

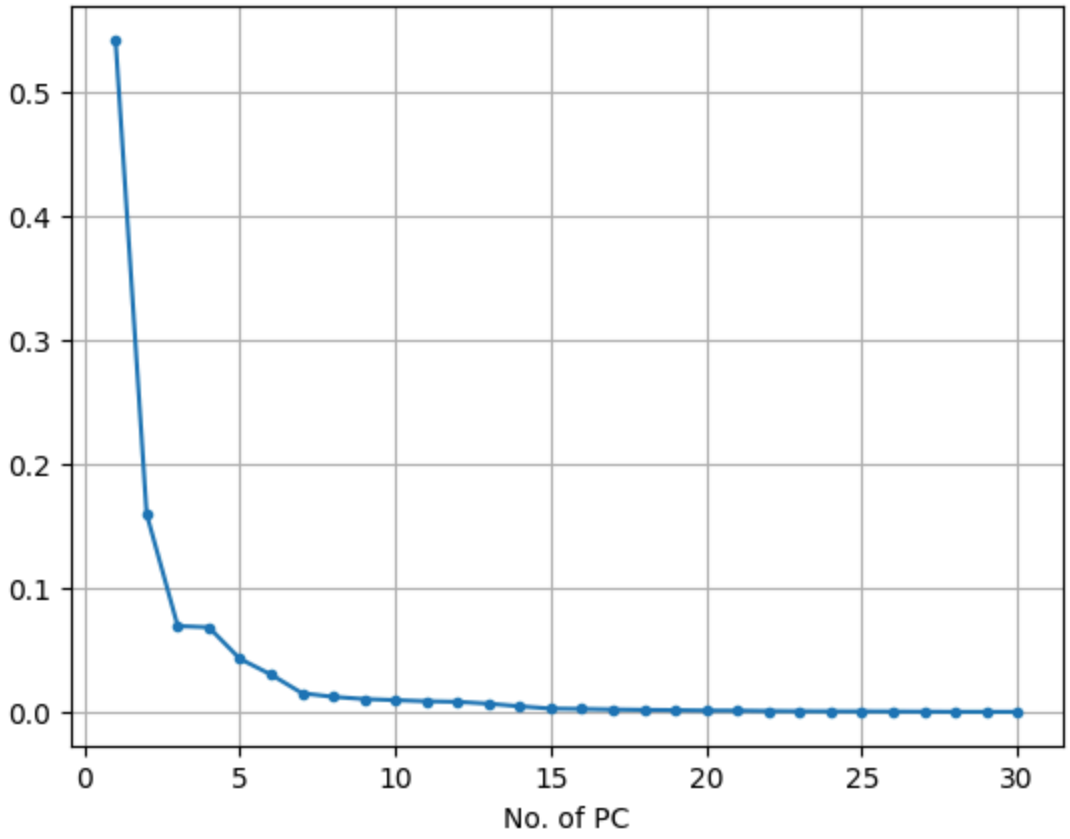
```
[[ 0.21542202]
 [ 0.86945519]
 [-0.29831397]]

[[ 0.21542202  0.11200241]
 [ 0.86945519  0.1745606 ]
 [-0.29831397  0.25963695]]

[[ 0.21542202  0.11200241 -0.20876766]
 [ 0.86945519  0.1745606  -0.27755476]
 [-0.29831397  0.25963695  0.09062589]]
```

(3) 주성분 누적 분산 그래프

- 그래프를 보고 적절한 주성분의 개수를 지정(elbow method!)
- x축 : PC 수
- y축 : 전체 분산크기 - 누적 분산크기

In [41]:
```
# 주성분을 몇개로 할지 결정(최대값 : 전체 feature 수)
n = x_train.shape[1]
# 주성분 분석 선언
pca = PCA(n_components=n)
# 만들고, 적용하기
x_train_pc = pca.fit_transform(x_train)
x_val_pc = pca.transform(x_val)
```

In [38]:
```
plt.plot(range(1,n+1), pca.explained_variance_ratio_, marker = '.')
plt.xlabel('No. of PC')
plt.grid()
plt.show()
```



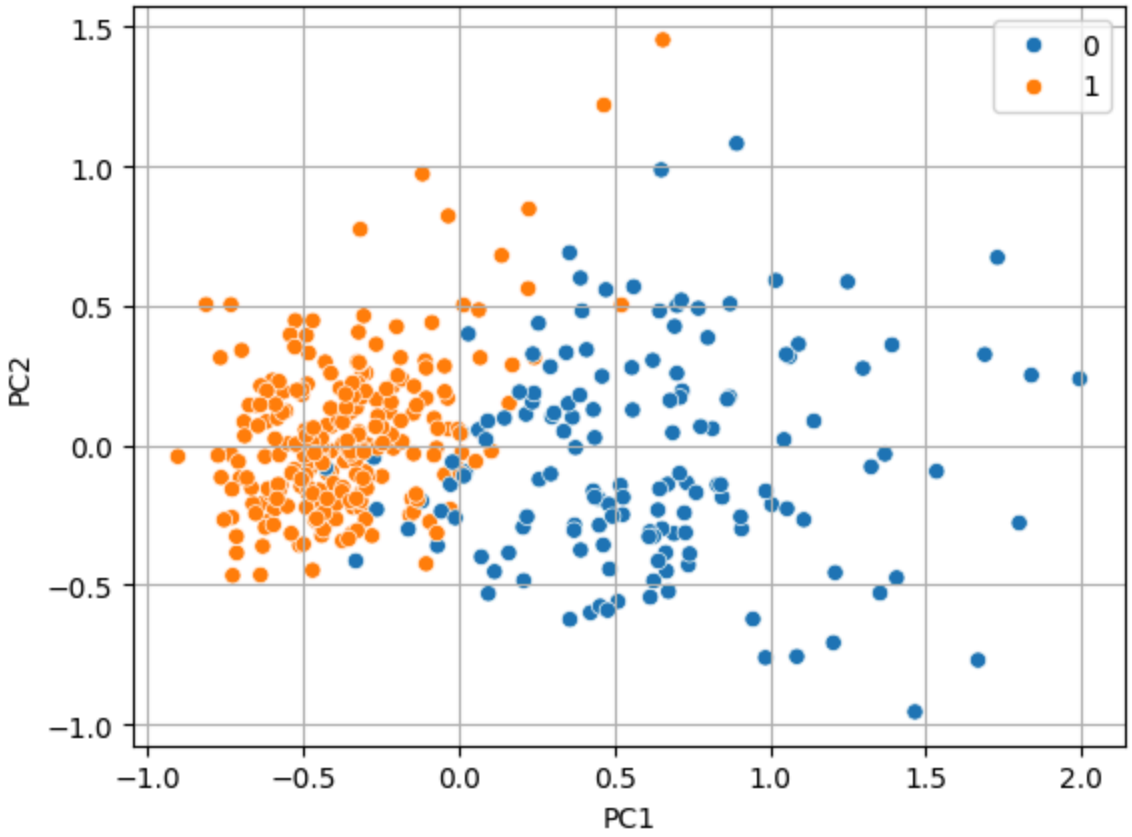
주성분 개수 몇개면 충분할까요?

In [ ]:

(4) 시각화

- 주 성분 중 상위 2개를 뽑아 시각화 해 봅시다.

In [71]:
```
sns.scatterplot(x = 'PC1', y = 'PC2', data = x_train_pc, hue = y_train)
plt.grid()
plt.show()
```



5.지도학습으로 연계하기

(1) 원본데이터로 모델 생성하기

- knn 알고리즘으로 분류 모델링을 수행합니다.
- k : 기본값으로 지정

- 학습

In [72]:
```
model0 = KNeighborsClassifier()
model0.fit(x_train, y_train)
```

Out[72]:
```
▾ KNeighborsClassifier
KNeighborsClassifier()
```

- 예측 및 평가

In [73]:
```
x_val = np.array(x_val)
```

In [74]:
```
# 원본데이터 모델의 성능
pred0 = model0.predict(x_val)

print(confusion_matrix(y_val, pred0))
```

```
print(accuracy_score(y_val, pred0))
print(classification_report(y_val, pred0))
```

```
C:\Users\User\anaconda3\Lib\site-packages\sklearn\base.py:464: UserWarning:

X does not have valid feature names, but KNeighborsClassifier was fitted with feature names
```

```
[[ 62   2]
 [  3 104]]
0.9707602339181286
              precision    recall  f1-score   support

           0       0.95      0.97      0.96        64
           1       0.98      0.97      0.98       107

    accuracy                           0.97       171
   macro avg       0.97      0.97      0.97       171
weighted avg       0.97      0.97      0.97       171
```

(2) 실습

- 다음의 조건으로 모델을 만들고 성능을 확인해 봅시다.
  - 알고리즘 : KNN

1) 주성분 상위 1개로 모델 만들기

In [75]:
```
column_names[:2]
```

Out[75]:
```
['PC1', 'PC2']
```

In [76]:
```
cols = column_names[:1]
x_train_pc1 = x_train_pc.loc[:, cols]
x_val_pc1 = x_val_pc.loc[:, cols]
```

In [77]:
```
x_train_pc1.shape
```

Out[77]:
```
(398, 1)
```

- 주성분 1개로 만든 모델 Vs. 전체 변수로 만든 모델

In [78]:
```
x_train_pc1.shape[1]
```

Out[78]:
```
1
```

In [79]:
```
# KNN 모델링, 주성분 1개로 모델링
model1 = KNeighborsClassifier()
model1.fit(x_train, y_train)
```

Out[79]:
```
KNeighborsClassifier()
```

In [80]:
```
# 원본데이터 모델의 성능
pred1 = model1.predict(x_val)

print(confusion_matrix(y_val, pred1))
print(accuracy_score(y_val, pred1))
print(classification_report(y_val, pred1))
```

```
[[ 62   2]
 [  3 104]]
0.9707602339181286
              precision    recall  f1-score   support

           0       0.95      0.97      0.96        64
           1       0.98      0.97      0.98       107

    accuracy                           0.97       171
   macro avg       0.97      0.97      0.97       171
weighted avg       0.97      0.97      0.97       171
```

```
C:\Users\User\anaconda3\Lib\site-packages\sklearn\base.py:464: UserWarning:

X does not have valid feature names, but KNeighborsClassifier was fitted with feature names
```

2) 주성분 2개로 모델링

In [81]:
```
n = 2
# 데이터 준비
cols = column_names[:n]
x_train_pc_n = x_train_pc.loc[:, cols]
x_val_pc_n = x_val_pc.loc[:, cols]

# 모델링
model_n = KNeighborsClassifier()
model_n.fit(x_train_pc_n, y_train)
```

Out[81]:
```
KNeighborsClassifier()
```

In [84]:
```
# 예측
pred_n = model_n.predict(x_val_pc_n)

# 평가
print(confusion_matrix(y_val, pred_n))
print(accuracy_score(y_val, pred_n))
print(classification_report(y_val, pred_n))
```

```
[[ 63   1]
 [  5 102]]
0.9649122807017544
              precision    recall  f1-score   support

           0       0.93      0.98      0.95        64
           1       0.99      0.95      0.97       107

    accuracy                           0.96       171
   macro avg       0.96      0.97      0.96       171
weighted avg       0.97      0.96      0.97       171
```

6.[추가]t-SNE

(1) 학습(차원축소)

In [ ]:
```
from sklearn.manifold import TSNE
```

In [ ]:
```
# 2차원으로 축소하기
tsne = TSNE(n_components = 2, random_state=20)
x_tsne = tsne.fit_transform(x)

# 사용의 편리함을 위해 DataFrame으로 변환
x_tsne = pd.DataFrame(x_tsne, columns = ['T1','T2'])
```

In [ ]:
```
x_tsne.shape
```

(2) 시각화

In [ ]:
```
plt.figure(figsize=(6,6))
sns.scatterplot(x = 'T1', y = 'T2', data = x_tsne, hue = y)
plt.grid()
```

(3) 실습

1) 데이터 준비

- 샘플데이터 로딩

In [ ]:
```
digits = load_digits()
x = digits.data
y = digits.target

y = pd.Categorical(y)
```

In [ ]:
```
x.shape
```

- 둘러보기

In [ ]:
```
print(x[0].reshape(8,8))
```

In [ ]:
```
# f, axes = plt.subplots(5, 2, sharey=True, figsize=(16,6))
plt.figure(figsize=(10, 4))
for i in range(10):
    plt.subplot(2, 5, i + 1)
    plt.imshow(x[i,:].reshape([8,8]), cmap='gray');
```

- 스케일링

In [ ]:
```
# 최대, 최소값
np.min(x), np.max(x)
```

In [ ]:
```
# 최대값으로 나누면 Min Max 스케일링이 됩니다.
x = x / 16
```

2) PCA

- 주성분 2개로 차원을 축소하고
- 시각화 합니다.

In [ ]:
```
# 차원 축소
pca = PCA(n_components=2)
x_pca = pca.fit_transform(x)

# 데이터프레임으로 변환(옵션)
x_pca = pd.DataFrame(x_pca, columns = ['PC1', 'PC2'])
```

In [ ]:
```
# 시각화
plt.figure(figsize=(8, 8))
sns.scatterplot(x = 'PC1', y = 'PC2', data = x_pca, hue = y)
plt.grid()
plt.show()
```

3) tSNE

- 2차원으로 축소하고
- 시각화 합니다.

In [ ]:
```
tsne = TSNE(n_components = 2, random_state=20)
x_tsne = tsne.fit_transform(x)

# 데이터프레임으로 변환(옵션)
x_tsne = pd.DataFrame(x_tsne, columns = ['T1', 'T2'])
```

In [ ]:
```
# 시각화
plt.figure(figsize=(8, 8))
sns.scatterplot(x = 'T1', y = 'T2', data = x_tsne, hue = y)
plt.grid()
plt.show()
```

In [ ]: