In [31]:

```
from sklearn.datasets import load_wine
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt

import torch
import torch.nn as nn
import torch.nn.functional as F
import torch.optim as optim
from sklearn.model_selection import train_test_split

from sklearn.svm import SVC

%matplotlib inline
```

Data Load, 전처리, 시각화

In [32]:

```
wine = load_wine()
```

In [33]:

```
print(wine.DESCR)
```

```
.. _wine_dataset:

Wine recognition dataset
------------------------

**Data Set Characteristics:**

    :Number of Instances: 178 (50 in each of three classes)
    :Number of Attributes: 13 numeric, predictive attributes and th
e class
    :Attribute Information:
   - Alcohol
   - Malic acid
   - Ash
  - Alcalinity of ash
   - Magnesium
  - Total phenols
   - Flavanoids
   - Nonflavanoid phenols
   - Proanthocyanins
  - Color intensity
   - Hue
   - OD280/OD315 of diluted wines
   - Proline

    - class:
            - class_0
            - class_1
            - class_2

    :Summary Statistics:

    ============================== ==== ===== ======= =====
                                    Min   Max   Mean     SD
    ============================== ==== ===== ======= =====
    Alcohol:                       11.0  14.8    13.0   0.8
    Malic Acid:                    0.74  5.80    2.34  1.12
    Ash:                           1.36  3.23    2.36  0.27
```

```
    Alcalinity of Ash:            10.6  30.0    19.5   3.3
    Magnesium:                    70.0 162.0    99.7  14.3
    Total Phenols:                0.98  3.88    2.29  0.63
    Flavanoids:                   0.34  5.08    2.03  1.00
    Nonflavanoid Phenols:         0.13  0.66    0.36  0.12
    Proanthocyanins:              0.41  3.58    1.59  0.57
    Colour Intensity:              1.3  13.0     5.1   2.3
    Hue:                          0.48  1.71    0.96  0.23
    OD280/OD315 of diluted wines: 1.27  4.00    2.61  0.71
    Proline:                       278  1680     746   315
    ============================= ==== ===== ======= =====

    :Missing Attribute Values: None
    :Class Distribution: class_0 (59), class_1 (71), class_2 (48)
    :Creator: R.A. Fisher
    :Donor: Michael Marshall (MARSHALL%PLU@io.arc.nasa.gov)
    :Date: July, 1988

This is a copy of UCI ML Wine recognition datasets.
https://archive.ics.uci.edu/ml/machine-learning-databases/wine/wine
.data

The data is the results of a chemical analysis of wines grown in th
e same
region in Italy by three different cultivators. There are thirteen
different
measurements taken for different constituents found in the three ty
pes of
wine.

Original Owners:

Forina, M. et al, PARVUS -
An Extendible Package for Data Exploration, Classification and Corr
elation.
Institute of Pharmaceutical and Food Analysis and Technologies,
Via Brigata Salerno, 16147 Genoa, Italy.

Citation:

Lichman, M. (2013). UCI Machine Learning Repository
[https://archive.ics.uci.edu/ml]. Irvine, CA: University of Califor
nia,
School of Information and Computer Science.

.. topic:: References

  (1) S. Aeberhard, D. Coomans and O. de Vel,
  Comparison of Classifiers in High Dimensional Settings,
  Tech. Rep. no. 92-02, (1992), Dept. of Computer Science and Dept.
of
  Mathematics and Statistics, James Cook University of North Queens
land.
  (Also submitted to Technometrics).

  The data was used with many others for comparing various
  classifiers. The classes are separable, though only RDA
  has achieved 100% correct classification.
  (RDA : 100%, QDA 99.4%, LDA 98.9%, 1NN 96.1% (z-transformed data)
)
  (All results using the leave-one-out technique)

  (2) S. Aeberhard, D. Coomans and O. de Vel,
  "THE CLASSIFICATION PERFORMANCE OF RDA"
  Tech. Rep. no. 92-01, (1992), Dept. of Computer Science and Dept.
of
  Mathematics and Statistics, James Cook University of North Queens
land.
  (Also submitted to Journal of Chemometrics).
```

In [34]:

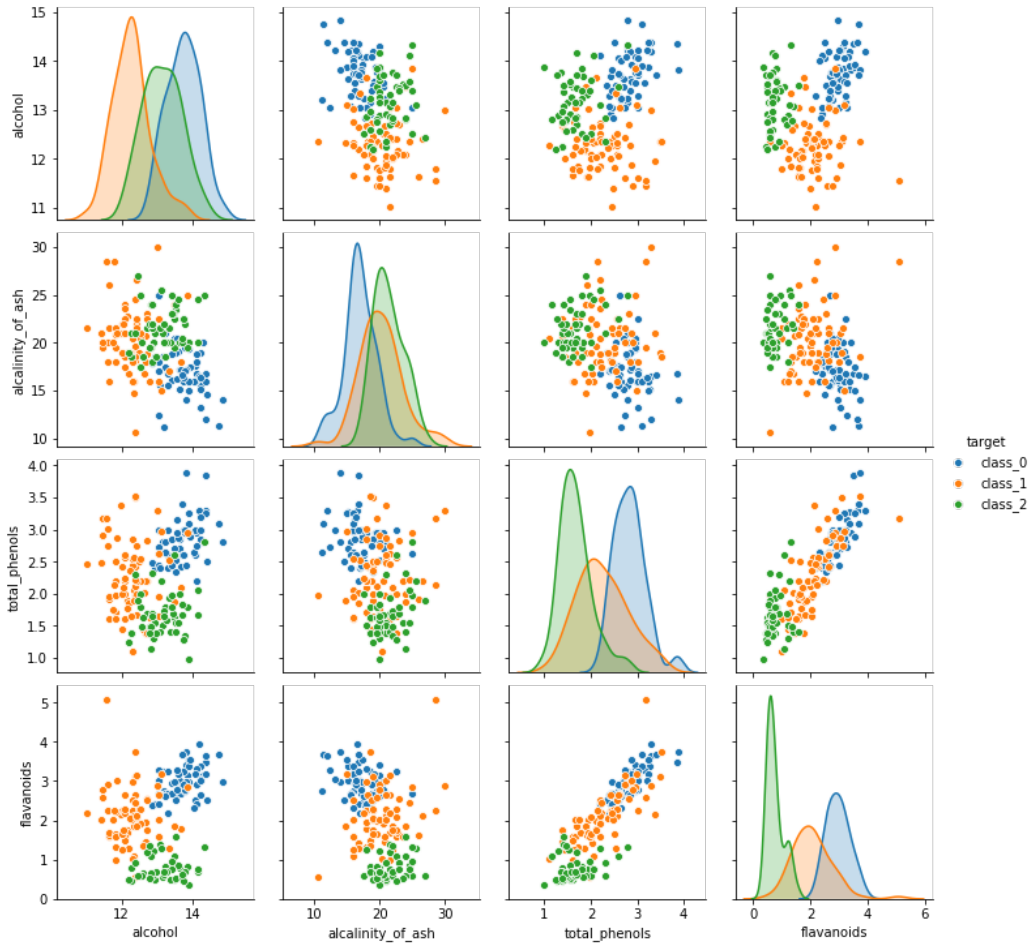
```
df = pd.DataFrame(wine.data, columns = wine.feature_names)
sy = pd.Series(wine.target, dtype="category")
sy = sy.cat.rename_categories(wine.target_names)
df['target'] = sy
df.head()
```

Out[34]:

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phenols	flavanoids	nonflavanoid_phenols	proanth
0	14.23	1.71	2.43	15.6	127.0	2.80	3.06	0.28	
1	13.20	1.78	2.14	11.2	100.0	2.65	2.76	0.26	
2	13.16	2.36	2.67	18.6	101.0	2.80	3.24	0.30	
3	14.37	1.95	2.50	16.8	113.0	3.85	3.49	0.24	
4	13.24	2.59	2.87	21.0	118.0	2.80	2.69	0.39	

In [38]:

```
sns.pairplot(vars=["alcohol", "alcalinity_of_ash", "total_phenols",
"flavanoids"],
             hue="target", data=df)
plt.show()
```



In [39]:

```
print(wine)
```

```
{'data': array([[1.423e+01, 1.710e+00, 2.430e+00, ..., 1.040e+00, 3
.920e+00,
```

```
        1.065e+03],
       [1.320e+01, 1.780e+00, 2.140e+00, ..., 1.050e+00, 3.400e+00,
        1.050e+03],
       [1.316e+01, 2.360e+00, 2.670e+00, ..., 1.030e+00, 3.170e+00,
        1.185e+03],
       ...,
       [1.327e+01, 4.280e+00, 2.260e+00, ..., 5.900e-01, 1.560e+00,
        8.350e+02],
       [1.317e+01, 2.590e+00, 2.370e+00, ..., 6.000e-01, 1.620e+00,
        8.400e+02],
       [1.413e+01, 4.100e+00, 2.740e+00, ..., 6.100e-01, 1.600e+00,
        5.600e+02]]), 'target': array([0, 0, 0, 0, 0, 0, 0, 0, 0
, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1,
1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
2, 2,
       2, 2]), 'target_names': array(['class_0', 'class_1', 'class_
2'], dtype='<U7'), 'DESCR': '.. _wine_dataset:\n\nWine recognition
dataset\n------------------------\n\n**Data Set Characteristics:**
\n\n    :Number of Instances: 178 (50 in each of three classes)\n
:Number of Attributes: 13 numeric, predictive attributes and the cl
ass\n    :Attribute Information:\n \t\t- Alcohol\n \t\t- Malic acid
\n \t\t- Ash\n\t\t- Alcalinity of ash  \n \t\t- Magnesium\n\t\t- To
tal phenols\n \t\t- Flavanoids\n \t\t- Nonflavanoid phenols\n \t\t-
Proanthocyanins\n\t\t- Color intensity\n \t\t- Hue\n \t\t- OD280/OD
315 of diluted wines\n \t\t- Proline\n\n    - class:\n            -
class_0\n            - class_1\n            - class_2\n\t\t\n    :
Summary Statistics:\n    \n    ============================== ==== =
==== ======= =====\n                                      Min   Max
Mean     SD\n    ============================== ==== ===== ======= =
====\n    Alcohol:                        11.0  14.8    13.0   0.8\n
Malic Acid:                    0.74  5.80    2.34  1.12\n    Ash:
1.36  3.23    2.36  0.27\n    Alcalinity of Ash:              10.6
30.0    19.5   3.3\n    Magnesium:                     70.0 162.0
99.7  14.3\n    Total Phenols:                 0.98  3.88    2.29
0.63\n    Flavanoids:                    0.34  5.08    2.03  1.00\n
Nonflavanoid Phenols:          0.13  0.66    0.36  0.12\n    Proanth
ocyanins:               0.41  3.58    1.59  0.57\n    Colour Intens
ity:              1.3  13.0     5.1   2.3\n    Hue:
0.48  1.71    0.96  0.23\n    OD280/OD315 of diluted wines: 1.27  4
.00    2.61  0.71\n    Proline:                        278  1680
746   315\n    ============================== ==== ===== ======= ===
==\n\n    :Missing Attribute Values: None\n    :Class Distribution:
class_0 (59), class_1 (71), class_2 (48)\n    :Creator: R.A. Fisher
\n    :Donor: Michael Marshall (MARSHALL%PLU@io.arc.nasa.gov)\n
:Date: July, 1988\n\nThis is a copy of UCI ML Wine recognition data
sets.\nhttps://archive.ics.uci.edu/ml/machine-learning-databases/wi
ne/wine.data\n\nThe data is the results of a chemical analysis of w
ines grown in the same\nregion in Italy by three different cultivat
ors. There are thirteen different\nmeasurements taken for different
constituents found in the three types of\nwine.\n\nOriginal Owners:
\n\nForina, M. et al, PARVUS - \nAn Extendible Package for Data Exp
loration, Classification and Correlation. \nInstitute of Pharmaceut
ical and Food Analysis and Technologies,\nVia Brigata Salerno, 1614
7 Genoa, Italy.\n\nCitation:\n\nLichman, M. (2013). UCI Machine Lea
rning Repository\n[https://archive.ics.uci.edu/ml]. Irvine, CA: Uni
versity of California,\nSchool of Information and Computer Science.
\n\n.. topic:: References\n\n  (1) S. Aeberhard, D. Coomans and O.
```

de Vel, \n Comparison of Classifiers in High Dimensional Settings, \n Tech. Rep. no. 92-02, (1992), Dept. of Computer Science and Dep t. of \n Mathematics and Statistics, James Cook University of Nor th Queensland. \n (Also submitted to Technometrics). \n\n The dat a was used with many others for comparing various \n classifiers. The classes are separable, though only RDA \n has achieved 100% co rrect classification. \n (RDA : 100%, QDA 99.4%, LDA 98.9%, 1NN 96 .1% (z-transformed data)) \n (All results using the leave-one-out technique) \n\n (2) S. Aeberhard, D. Coomans and O. de Vel, \n "T HE CLASSIFICATION PERFORMANCE OF RDA" \n Tech. Rep. no. 92-01, (19 92), Dept. of Computer Science and Dept. of \n Mathematics and Sta tistics, James Cook University of North Queensland. \n (Also submi tted to Journal of Chemometrics).\n', 'feature_names': ['alcohol', 'malic_acid', 'ash', 'alcalinity_of_ash', 'magnesium', 'total_pheno ls', 'flavanoids', 'nonflavanoid_phenols', 'proanthocyanins', 'colo r_intensity', 'hue', 'od280/od315_of_diluted_wines', 'proline']}

In [40]:

```
wine.data
```

Out[40]:

```
array([[1.423e+01, 1.710e+00, 2.430e+00, ..., 1.040e+00, 3.920e+00,
        1.065e+03],
       [1.320e+01, 1.780e+00, 2.140e+00, ..., 1.050e+00, 3.400e+00,
        1.050e+03],
       [1.316e+01, 2.360e+00, 2.670e+00, ..., 1.030e+00, 3.170e+00,
        1.185e+03],
       ...,
       [1.327e+01, 4.280e+00, 2.260e+00, ..., 5.900e-01, 1.560e+00,
        8.350e+02],
       [1.317e+01, 2.590e+00, 2.370e+00, ..., 6.000e-01, 1.620e+00,
        8.400e+02],
       [1.413e+01, 4.100e+00, 2.740e+00, ..., 6.100e-01, 1.600e+00,
        5.600e+02]])
```

In [41]:

```
wine.target
```

Out[41]:

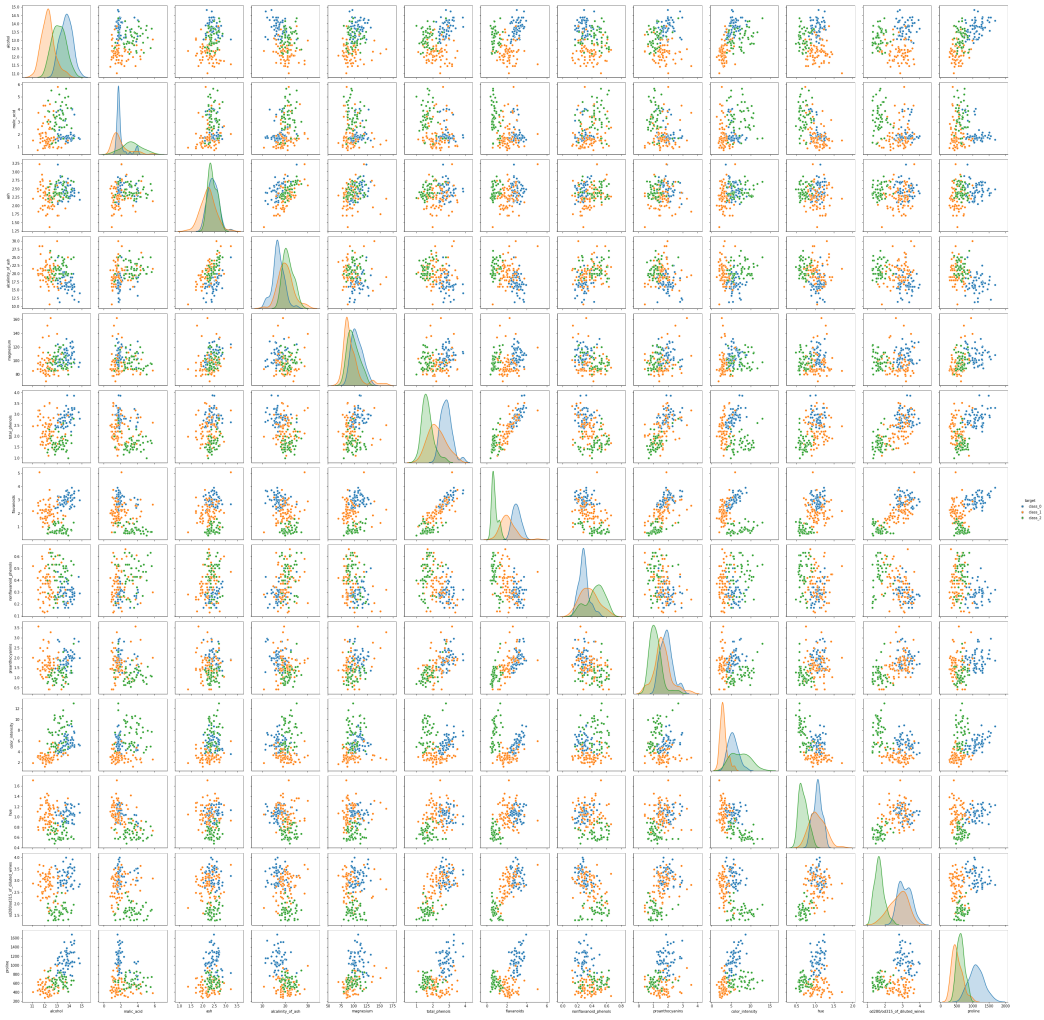
```
array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1,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

In [42]:

```
x_data = df.iloc[:, :-1]
y_data = df.iloc[:, [-1]]

sns.pairplot(df, hue="target", height=3)
```

```
plt.show()
```



In [43]:

```
df
```

Out[43]:

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phenols	flavanoids	nonflavanoid_phenols	proan
0	14.23	1.71	2.43	15.6	127.0	2.80	3.06	0.28	
1	13.20	1.78	2.14	11.2	100.0	2.65	2.76	0.26	
2	13.16	2.36	2.67	18.6	101.0	2.80	3.24	0.30	
3	14.37	1.95	2.50	16.8	113.0	3.85	3.49	0.24	
4	13.24	2.59	2.87	21.0	118.0	2.80	2.69	0.39	
...	...	...	...	...	...	...	...	...	
173	13.71	5.65	2.45	20.5	95.0	1.68	0.61	0.52	
174	13.40	3.91	2.48	23.0	102.0	1.80	0.75	0.43	
175	13.27	4.28	2.26	20.0	120.0	1.59	0.69	0.43	
176	13.17	2.59	2.37	20.0	120.0	1.65	0.68	0.53	
177	14.13	4.10	2.74	24.5	96.0	2.05	0.76	0.56	

178 rows × 14 columns

In [44]:

```
df = df.drop('od280/od315_of_diluted_wines', axis = 1)
```

In [45]:

```
df.corr()
```

Out[45]:

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phenols	flavanoids	nonfl
alcohol	1.000000	0.094397	0.211545	-0.310235	0.270798	0.289101	0.236815	
malic_acid	0.094397	1.000000	0.164045	0.288500	-0.054575	-0.335167	-0.411007	
ash	0.211545	0.164045	1.000000	0.443367	0.286587	0.128980	0.115077	
alcalinity_of_ash	-0.310235	0.288500	0.443367	1.000000	-0.083333	-0.321113	-0.351370	
magnesium	0.270798	-0.054575	0.286587	-0.083333	1.000000	0.214401	0.195784	
total_phenols	0.289101	-0.335167	0.128980	-0.321113	0.214401	1.000000	0.864564	
flavanoids	0.236815	-0.411007	0.115077	-0.351370	0.195784	0.864564	1.000000	
nonflavanoid_phenols	-0.155929	0.292977	0.186230	0.361922	-0.256294	-0.449935	-0.537900	
proanthocyanins	0.136698	-0.220746	0.009652	-0.197327	0.236441	0.612413	0.652692	
color_intensity	0.546364	0.248985	0.258887	0.018732	0.199950	-0.055136	-0.172379	
hue	-0.071747	-0.561296	-0.074667	-0.273955	0.055398	0.433681	0.543479	
proline	0.643720	-0.192011	0.223626	-0.440597	0.393351	0.498115	0.494193	

In [46]:

```
from sklearn.svm import SVC
from sklearn import metrics
```

In [47]:

```
x_data = df.iloc[:,:-1]
x_data
```

Out[47]:

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phenols	flavanoids	nonflavanoid_phenols	proan
0	14.23	1.71	2.43	15.6	127.0	2.80	3.06	0.28	
1	13.20	1.78	2.14	11.2	100.0	2.65	2.76	0.26	
2	13.16	2.36	2.67	18.6	101.0	2.80	3.24	0.30	
3	14.37	1.95	2.50	16.8	113.0	3.85	3.49	0.24	
4	13.24	2.59	2.87	21.0	118.0	2.80	2.69	0.39	
...	...	...	...	...	...	...	...	...	
173	13.71	5.65	2.45	20.5	95.0	1.68	0.61	0.52	
174	13.40	3.91	2.48	23.0	102.0	1.80	0.75	0.43	
175	13.27	4.28	2.26	20.0	120.0	1.59	0.69	0.43	
176	13.17	2.59	2.37	20.0	120.0	1.65	0.68	0.53	
177	14.13	4.10	2.74	24.5	96.0	2.05	0.76	0.56	

178 rows × 12 columns

In [29]:

```
y_data = df.iloc[:, -1]
y_data
```

Out[29]:

```
0       class_0
1       class_0
2       class_0
3       class_0
4       class_0
         ...
173     class_2
174     class_2
175     class_2
176     class_2
177     class_2
Name: target, Length: 178, dtype: category
Categories (3, object): [class_0, class_1, class_2]
```

Train Data, Test Data split

In [48]:

```
x_data = x_data.values
y_data = y_data.values
x_train, x_test, y_train, y_test = train_test_split(x_data, y_data, test_size
= 0.3)
```

PipeLining & Fit

다항식 특성이 많아지면 모델의 속도가 느려진다. 따라서 커널 트릭을 사용하여 SVM모델을 만들어 속도를 조금 향상시킨다. 이때 Kernel에 따른 속도 및 정확도를 비교하기 위해 sklearn에서 제공하는 여러가지 kernel들을 사용하여 모델을 만든다.

Grid Search를 통해 최적의 하이퍼파라미터 찾기

In [72]:

```
from sklearn.model_selection import GridSearchCV
```

Poly Kernel

In [83]:

```
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler
poly_kernel_svm_clf = Pipeline([
    ('scaler', StandardScaler()),
    ('svm_clf', SVC(kernel='poly', degree=3, coef0=0.001, C=5))
])
param_grid = {'svm_clf__C': [0.001, 0.01, 0.1, 1, 10, 100], 'svm_clf__gamma':
[0.001, 0.01, 0.1, 1, 10, 100]}
grid_poly = GridSearchCV(poly_kernel_svm_clf, param_grid = param_grid, cv = 5)
grid_poly.fit(x_train, y_train)
```

```
C:\Users\pc\Anaconda3\lib\site-packages\sklearn\utils\validation.py
:760: DataConversionWarning: A column-vector y was passed when a 1d
array was expected. Please change the shape of y to (n_samples, ),
for example using ravel().
  y = column_or_1d(y, warn=True)
C:\Users\pc\Anaconda3\lib\site-packages\sklearn\utils\validation.py
:760: DataConversionWarning: A column-vector y was passed when a 1d
array was expected. Please change the shape of y to (n_samples, ),
for example using ravel().
  y = column_or_1d(y, warn=True)
```

```
  y = column_or_1d(y, warn=True)
C:\Users\pc\Anaconda3\lib\site-packages\sklearn\utils\validation.py
:760: DataConversionWarning: A column-vector y was passed when a 1d
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C:\Users\pc\Anaconda3\lib\site-packages\sklearn\utils\validation.py
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C:\Users\pc\Anaconda3\lib\site-packages\sklearn\utils\validation.py
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C:\Users\pc\Anaconda3\lib\site-packages\sklearn\utils\validation.py
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array was expected. Please change the shape of y to (n_samples, ),
for example using ravel().
  y = column_or_1d(y, warn=True)
C:\Users\pc\Anaconda3\lib\site-packages\sklearn\utils\validation.py
:760: DataConversionWarning: A column-vector y was passed when a 1d
array was expected. Please change the shape of y to (n_samples, ),
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```

Out[83]:

```
GridSearchCV(cv=5, error_score=nan,
             estimator=Pipeline(memory=None,
                                steps=[('scaler',
                                        StandardScaler(copy=True,
                                                       with_mean=
True,
                                                       with_std=T
rue)),
                                       ('svm_clf',
                                        SVC(C=5, break_ties=False,
                                            cache_size=200, class
_weight=None,
                                            coef0=0.001,
                                            decision_function_sha
pe='ovr',
                                            degree=3, gamma='scal
e',
                                            kernel='poly', max_it
er=-1,
                                            probability=False,
                                            random_state=None, shr
inking=True,
                                            tol=0.001, verbose=Fa
lse))],
                                verbose=False),
             iid='deprecated', n_jobs=None,
             param_grid={'svm_clf__C': [0.001, 0.01, 0.1, 1, 10, 10
0],
                         'svm_clf__gamma': [0.001, 0.01, 0.1, 1, 1
0, 100]},
             pre_dispatch='2*n_jobs', refit=True, return_train_scor
e=False,
             scoring=None, verbose=0)
```

rbf Kernel

In [80]:

```
rbf_kernel_svm_clf = Pipeline([
        ("scaler", StandardScaler()),
        ("svm_clf", SVC(kernel="rbf", gamma=5, C=0.001))
    ])

rbf_kernel_svm_clf.fit(x_train, y_train)
param_grid = {'svm_clf__C': [0.001, 0.01, 0.1, 1, 10, 100], 'svm_clf__gamma':
[0.001, 0.01, 0.1, 1, 10, 100]}
grid_rbf = GridSearchCV(rbf_kernel_svm_clf, param_grid = param_grid, cv = 5)
grid_rbf.fit(x_train, y_train)
```

```
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```

Out[80]:

```
GridSearchCV(cv=5, error_score=nan,
             estimator=Pipeline(memory=None,
                                steps=[('scaler',
                                        StandardScaler(copy=True,
                                                       with_mean=
True,
                                                       with_std=T
rue)),
                                       ('svm_clf',
                                        SVC(C=0.001, break_ties=Fa
lse,
                                            cache_size=200, class
_weight=None,
                                            coef0=0.0,
                                            decision_function_sha
pe='ovr',
                                            degree=3, gamma=5, ker
nel='rbf',
                                            max_iter=-1, probabil
ity=False,
                                            random_state=None, shr
inking=True,
                                            tol=0.001, verbose=Fa
lse))],
                                verbose=False),
             iid='deprecated', n_jobs=None,
             param_grid={'svm_clf__C': [0.001, 0.01, 0.1, 1, 10, 10
0],
                         'svm_clf__gamma': [0.001, 0.01, 0.1, 1, 1
0, 100]},
             pre_dispatch='2*n_jobs', refit=True, return_train_scor
e=False,
             scoring=None, verbose=0)
```

In [81]:

```
sigmoid_kernel_svm_clf = Pipeline([
        ("scaler", StandardScaler()),
        ("svm_clf", SVC(kernel="sigmoid", gamma=5, C=0.1))
    ])
sigmoid_kernel_svm_clf.fit(x_train, y_train)
param_grid = {'svm_clf__C': [0.001, 0.01, 0.1, 1, 10, 100], 'svm_clf__gamma':
[0.001, 0.01, 0.1, 1, 10, 100]}
grid_sigmoid = GridSearchCV(sigmoid_kernel_svm_clf, param_grid = param_grid,
cv = 5)
grid_sigmoid.fit(x_train, y_train)
```

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```

Out[81]:

```
GridSearchCV(cv=5, error_score=nan,
             estimator=Pipeline(memory=None,
                                steps=[('scaler',
                                        StandardScaler(copy=True,
                                                       with_mean=
True,
                                                       with_std=T
rue)),
                                       ('svm_clf',
                                        SVC(C=0.1, break_ties=Fals
e,
                                            cache_size=200, class
_weight=None,
                                            coef0=0.0,
                                            decision_function_sha
pe='ovr',
                                            degree=3, gamma=5, ker
nel='sigmoid',
                                            max_iter=-1, probabil
ity=False,
                                            random_state=None, shr
inking=True,
                                            tol=0.001, verbose=Fa
lse))],
                                verbose=False),
             iid='deprecated', n_jobs=None,
             param_grid={'svm_clf__C': [0.001, 0.01, 0.1, 1, 10, 10
0],
                         'svm_clf__gamma': [0.001, 0.01, 0.1, 1, 1
0, 100]},
             pre_dispatch='2*n_jobs', refit=True, return_train_scor
e=False,
             scoring=None, verbose=0)
```

In [82]:

```
linear_kernel_svm_clf = Pipeline([
        ("scaler", StandardScaler()),
        ("svm_clf", SVC(kernel="linear", gamma=5, C=0.01))
    ])
linear_kernel_svm_clf.fit(x_train, y_train)
param_grid = {'svm_clf__C': [0.001, 0.01, 0.1, 1, 10, 100], 'svm_clf__gamma':
[0.001, 0.01, 0.1, 1, 10, 100]}
grid_linear = GridSearchCV(linear_kernel_svm_clf, param_grid = param_grid, cv
= 5)
grid_linear.fit(x_train, y_train)
```

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```

Out[82]:

```
GridSearchCV(cv=5, error_score=nan,
             estimator=Pipeline(memory=None,
                                steps=[('scaler',
                                        StandardScaler(copy=True,
```

```
                                                                   with_mean=
True,
                                                                   with_std=T
rue)),
                                                ('svm_clf',
                                                 SVC(C=0.01, break_ties=Fal
se,
                                                     cache_size=200, class
_weight=None,
                                                     coef0=0.0,
                                                     decision_function_sha
pe='ovr',
                                                     degree=3, gamma=5, ker
nel='linear',
                                                     max_iter=-1, probabil
ity=False,
                                                     random_state=None, shr
inking=True,
                                                     tol=0.001, verbose=Fa
lse))],
                                       verbose=False),
             iid='deprecated', n_jobs=None,
             param_grid={'svm_clf__C': [0.001, 0.01, 0.1, 1, 10, 10
0],
                         'svm_clf__gamma': [0.001, 0.01, 0.1, 1, 1
0, 100]},
             pre_dispatch='2*n_jobs', refit=True, return_train_scor
e=False,
             scoring=None, verbose=0)
```

In [84]:

```python
kernel_grid = [grid_poly, grid_rbf, grid_sigmoid, grid_linear]
kernel_names = ["poly_kernel_svm_clf", "rbf_kernel_svm_clf",
"sigmoid_kernel_svm_clf", "linear_kernel_svm_clf"]
for i in range(len(kernel_svms)):
    print(kernel_names[i])
    print('optimal train score: {:.3f}'.format(kernel_grid[i].best_score_))
    print('test score: {:.3f}'.format(kernel_grid[i].score(x_test, y_test)))
    print('optimal parameter: {}'.format(kernel_grid[i].best_params_))
    print()
```

```
poly_kernel_svm_clf
optimal train score: 0.992
test score: 0.926
optimal parameter: {'svm_clf__C': 0.001, 'svm_clf__gamma': 1}

rbf_kernel_svm_clf
optimal train score: 0.992
test score: 0.926
optimal parameter: {'svm_clf__C': 10, 'svm_clf__gamma': 0.01}

sigmoid_kernel_svm_clf
optimal train score: 1.000
test score: 0.926
optimal parameter: {'svm_clf__C': 10, 'svm_clf__gamma': 0.01}

linear_kernel_svm_clf
optimal train score: 1.000
test score: 0.926
optimal parameter: {'svm_clf__C': 0.1, 'svm_clf__gamma': 0.001}
```

정리: Test Score는 모두 92.6%로 거의 같았지만, 최적의 parameter들은 kernel마다 다 다르다! 따라서 반드시 svm을 사용할 때는 parameter들의 튜닝이 필수적으로

SVM을 사용할 때는 **parameter**들의 튜닝이 필수적으로 요구된다.

Q. 어떤상황에 어떤 **kernel**을 사용할 것인가**?**

Q. 커널을 쓸 수 있는 상황은 언제인가**?**