

ML practice

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Files

- sample_data
- HR_comma_sep.csv
- heart_disease.csv

```
from sklearn.datasets import load_wine
wine=load_wine()
wine
```

```
      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, 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, 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, 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]),
'frame': None,
'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\nNumber
of Instances: 178\n\nNumber of Attributes: 13 numeric, predictive attributes and the class\n\nAttribute Information:\n
- Alcohol\n
- Malic acid\n
- Ash\n
- Alcalinity of ash\n
- Magnesium\n
- Total phenols\n
- Flavanoids\n
- Nonflavanoid phenols\n
- Proanthocyanins\n
- Color intensity\n
- Hue\n
- OD280/OD315 of diluted wines\n
- Proline\n
- class_0\n
- class_1\n
- class_2\n\nSummary
```

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sample_dataHR_comma_sep.csvheart_disease.csv

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```
'proline']}]
```

```
[62] wine.feature_names
```

```
['alcohol',
 'malic_acid',
 'ash',
 'alcalinity_of_ash',
 'magnesium',
 'total_phenols',
 'flavanoids',
 'nonflavanoid_phenols',
 'proanthocyanins',
 'color_intensity',
 'hue',
 'od280/od315_of_diluted_wines',
 'proline']
```

```
[63] wine.target_names
```

```
array(['class_0', 'class_1', 'class_2'], dtype='<U7')'
```

```
a=wine.data
b=wine.target
```

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```
b=wine.target

[67] from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(a,b,test_size=0.3)

from sklearn.naive_bayes import GaussianNB
z=GaussianNB()
y=z.fit(x_train,y_train)
y

GaussianNB
GaussianNB()

[73] y.score(x_test,y_test)

0.9814814814814815

[74] y.predict(x_test)

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

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

```
from sklearn.model_selection import cross_val_score
g=cross_val_score(GaussianNB(),x_train,y_train,cv=4)
g
```

```
array([1.          , 1.          , 0.96774194, 0.96774194])
```

```
[78] from sklearn.naive_bayes import MultinomialNB
g=MultinomialNB()
h=g.fit(x_train,y_train)
h
```

```
MultinomialNB
MultinomialNB()
```

```
[79] h.score(x_test,y_test)
```

```
0.8333333333333334
```

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```
g=MultinomialNB()
h=g.fit(x_train,y_train)
h

[79] h.score(x_test,y_test)

0.8333333333333334

h.predict(x_test)

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

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