SVM_ML_08

March 15, 2022

```
[ ]: from sklearn import datasets
     cancer = datasets.load_breast_cancer()
```

```
[ ]: print("Features: ", cancer.feature_names)
     print("Labels: ", cancer.target_names)
```

```
Features:  ['mean radius' 'mean texture' 'mean perimeter' 'mean area'
 'mean smoothness' 'mean compactness' 'mean concavity'
 'mean concave points' 'mean symmetry' 'mean fractal dimension'
 'radius error' 'texture error' 'perimeter error' 'area error'
 'smoothness error' 'compactness error' 'concavity error'
 'concave points error' 'symmetry error' 'fractal dimension error'
 'worst radius' 'worst texture' 'worst perimeter' 'worst area'
 'worst smoothness' 'worst compactness' 'worst concavity'
 'worst concave points' 'worst symmetry' 'worst fractal dimension']
Labels:  ['malignant' 'benign']
```

```
[ ]: cancer.data.shape
```

```
[ ]: (569, 30)
```

```
[ ]: print(cancer.data[0:5])
```

```
[[1.799e+01 1.038e+01 1.228e+02 1.001e+03 1.184e-01 2.776e-01 3.001e-01
  1.471e-01 2.419e-01 7.871e-02 1.095e+00 9.053e-01 8.589e+00 1.534e+02
  6.399e-03 4.904e-02 5.373e-02 1.587e-02 3.003e-02 6.193e-03 2.538e+01
  1.733e+01 1.846e+02 2.019e+03 1.622e-01 6.656e-01 7.119e-01 2.654e-01
  4.601e-01 1.189e-01]
 [2.057e+01 1.777e+01 1.329e+02 1.326e+03 8.474e-02 7.864e-02 8.690e-02
  7.017e-02 1.812e-01 5.667e-02 5.435e-01 7.339e-01 3.398e+00 7.408e+01
  5.225e-03 1.308e-02 1.860e-02 1.340e-02 1.389e-02 3.532e-03 2.499e+01
  2.341e+01 1.588e+02 1.956e+03 1.238e-01 1.866e-01 2.416e-01 1.860e-01
  2.750e-01 8.902e-02]
 [1.969e+01 2.125e+01 1.300e+02 1.203e+03 1.096e-01 1.599e-01 1.974e-01
  1.279e-01 2.069e-01 5.999e-02 7.456e-01 7.869e-01 4.585e+00 9.403e+01
  6.150e-03 4.006e-02 3.832e-02 2.058e-02 2.250e-02 4.571e-03 2.357e+01
  2.553e+01 1.525e+02 1.709e+03 1.444e-01 4.245e-01 4.504e-01 2.430e-01
  3.613e-01 8.758e-02]
 [1.142e+01 2.038e+01 7.758e+01 3.861e+02 1.425e-01 2.839e-01 2.414e-01
```

```
 1.052e-01 2.597e-01 9.744e-02 4.956e-01 1.156e+00 3.445e+00 2.723e+01
 9.110e-03 7.458e-02 5.661e-02 1.867e-02 5.963e-02 9.208e-03 1.491e+01
 2.650e+01 9.887e+01 5.677e+02 2.098e-01 8.663e-01 6.869e-01 2.575e-01
 6.638e-01 1.730e-01]
[2.029e+01 1.434e+01 1.351e+02 1.297e+03 1.003e-01 1.328e-01 1.980e-01
 1.043e-01 1.809e-01 5.883e-02 7.572e-01 7.813e-01 5.438e+00 9.444e+01
 1.149e-02 2.461e-02 5.688e-02 1.885e-02 1.756e-02 5.115e-03 2.254e+01
 1.667e+01 1.522e+02 1.575e+03 1.374e-01 2.050e-01 4.000e-01 1.625e-01
 2.364e-01 7.678e-02]]
```

```python
print(cancer.target)
```

```
[0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 1 0 0 0 0 0 0 0 0 1 0 1 1 1 1 1 0 0 1 0 0 1 1 1 1 0 1 0 0 1 1 1 1 0 1 0 0
 1 0 1 0 0 1 1 1 0 0 1 0 0 0 1 1 1 0 1 1 0 0 1 1 1 0 0 1 1 1 1 0 1 1 0 1 1
 1 1 1 1 1 0 0 0 1 0 0 1 1 1 0 0 1 0 1 0 0 1 0 0 1 1 0 1 1 0 1 1 1 1 0 1
 1 1 1 1 1 1 1 0 1 1 1 1 0 0 1 0 1 1 0 0 1 1 0 0 1 1 1 1 0 1 1 0 0 0 1 0
 1 0 1 1 1 0 1 1 0 0 1 0 0 0 0 1 0 0 0 1 0 1 0 1 1 0 1 0 0 0 0 1 1 0 0 1 1
 1 0 1 1 1 1 1 1 0 0 1 1 0 1 1 0 0 1 0 1 1 1 1 1 0 1 1 1 1 1 0 1 0 0 0 0 0
 0 0 0 0 0 0 0 1 1 1 1 1 1 0 1 0 1 1 0 1 1 0 1 0 0 1 1 1 1 1 1 1 1 1 1 1
 1 0 1 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 0 1 1 1 0 1 0 1 1 1 0 0 0 1 1
 1 1 0 1 0 1 0 1 1 1 0 1 1 1 1 1 1 1 0 0 0 1 1 1 1 1 1 1 1 0 0 1 0 0
 0 1 0 0 1 1 1 1 0 1 1 1 1 1 1 0 1 1 1 1 0 1 1 0 1 1 0 0 1 1 1 1 1 0 1 1 1 1 1
 1 0 1 1 1 1 0 1 1 0 1 1 0 1 1 1 1 1 1 1 1 1 0 1 0 0 1 0 1 1 1 1 1 0 1 1
 0 1 0 1 1 0 1 0 1 1 1 1 1 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 0 1
 1 1 1 1 1 0 1 0 1 1 0 1 1 1 1 1 0 0 1 0 1 0 1 1 1 1 0 1 1 0 1 0 1 0 0
 1 1 1 0 1 1 1 1 1 1 1 1 1 0 1 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 0 0 0 0 0 0 1]
```

```python
from sklearn.model_selection import train_test_split
X_train,X_test,y_train,y_test = train_test_split(cancer.data,cancer.target,␣
 ↪test_size=0.2, random_state=0)
```

```python
from sklearn import svm
clf = svm.SVC(kernel='linear')
clf.fit(X_train,y_train)
y_pred =clf.predict(X_test)
```

```python
y_pred
```

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

```python
from sklearn.metrics import accuracy_score
score = accuracy_score(y_test,y_pred)
score
```

0.956140350877193

```python
from sklearn import metrics
cm = metrics.confusion_matrix(y_test,y_pred)
cm
```

```
array([[46,  1],
       [ 4, 63]], dtype=int64)
```

```python
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
plt.figure(figsize=(10,6))
sns.heatmap(cm,annot=True, fmt=".3f", linewidths=.5, square=True,
 ↪cmap='Spectral')
plt.xlabel("Actual Labels")
plt.ylabel("Predicted labels")
all_sample = "SVM model accuracy:{0}".format(score, ".2f")
plt.title(all_sample, size=15)
```

Text(0.5, 1.0, 'SVM model accuracy:0.956140350877193')

SVM model accuracy:0.956140350877193