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Support Vector Machine

Practice and task given in the video.

In [8]:

```
## import sckit learn data set library

from sklearn import datasets

#Load Data set

cancer = datasets.load_breast_cancer()
```

In [9]:

```
## Print the name of the features

print("Features: ",cancer.feature_names)

#print the label type of cancer (malignant, benign)
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']
```

In [10]:

```
#print data feature shape
cancer.data.shape
```

Out[10]:

```
(569, 30)
```

In [11]:

```
# print the cancer data features (top 5 records)

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]]
```

In [12]:

```
# print the cancer labels (0 : malignant , 1 : benign)
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 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 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 0 0 1 1 0 1 1 0 0 1 0 1 1 1 1 0 1 1 1 1 1 0 1 0 0 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
 1 0 1 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 1 1 1 0 1 0 1 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 1 1 1 0 0 1 0 0
 0 1 0 0 1 1 1 1 1 0 1 1 1 1 1 0 1 1 1 0 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1
 1 0 1 1 1 1 1 0 1 1 0 1 1 1 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 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 1 0 1
 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 1 0 1 1 0 1 0 1 0 0
 1 1 1 0 1 1 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 1 0 0 0 0 0 0 1]
```

In [13]:

```
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_
```

In [17]:

```
# import svm library

from sklearn import svm

#Create a SVM classifier
clf = svm.SVC(kernel="linear").fit(X_train,y_train)

# making prediction on data set

y_pred = clf.predict(X_test)
y_pred
```

Out[17]:

```
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])
```

In [19]:

```
from sklearn import metrics

score = metrics.accuracy_score(y_test,y_pred)
```

```
# Model Accuracy: how often is the classifier correct?

print("Accuracy: ",metrics.accuracy_score(y_test,y_pred))
```

```
Accuracy:  0.956140350877193
```

In [21]:

```
#Model Precision: What percentage of positive tuoles are labeled as such?

print("Precision: ",metrics.precision_score(y_test,y_pred))

#Model Recall: What percentage of positive tuoles are labeled as such?

print("Recall: ",metrics.recall_score(y_test,y_pred))
```

```
Precision:  0.984375
Recall:  0.9402985074626866
```

In [22]:

```
from sklearn import metrics

cm = metrics.confusion_matrix(y_test,y_pred)
cm
```

Out[22]:

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

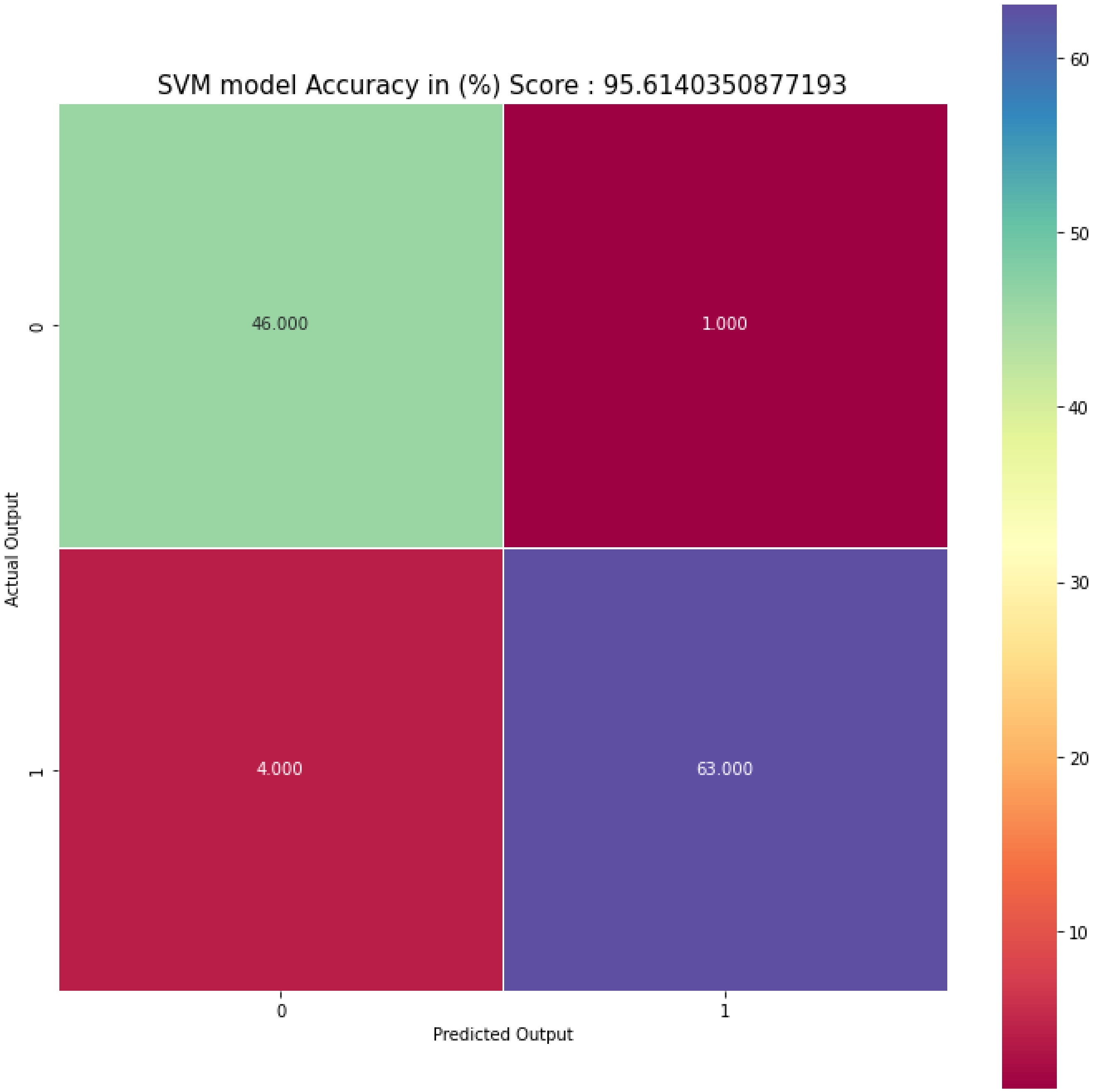
In [23]:

```
import seaborn as sns
import matplotlib.pyplot as plt
plt.figure(figsize=(12,12))
sns.heatmap(cm, annot = True, fmt=".3f",linewidths=".5",square=True,cmap = "Spectral")
plt.xlabel("Predicted Output")
plt.ylabel("Actual Output")

all_sample_title = "SVM model Accuracy in (%) Score : {0}".format(score*100)
plt.title(all_sample_title,size=15)
```

Out[23]:

```
Text(0.5, 1.0, 'SVM model Accuracy in (%) Score : 95.6140350877193')
```



SVM model Accuracy in (%) Score : 95.6140350877193

In [ ]: