SVM (Support Vector Machines)

In this notebook, you will use SVM (Support Vector Machines) to build and train a model using human cell records, and classify cells to whether the samples are benign or malignant.

SVM works by mapping data to a high-dimensional feature space so that data points can be categorized, even when the data are not otherwise linearly separable. A separator between the categories is found, then the data is transformed in such a way that the separator could be drawn as a hyperplane. Following this, characteristics of new data can be used to predict the group to which a new record should belong.

In [4]:
```
#!pip install scikit-learn==0.23.1
```

In [5]:
```
import piplite
await piplite.install(['pandas'])
await piplite.install(['matplotlib'])
await piplite.install(['numpy'])
await piplite.install(['scikit-learn'])
await piplite.install(['scipy'])
```

In [6]:
```
import pandas as pd
import pylab as pl
import numpy as np
import scipy.optimize as opt
from sklearn import preprocessing
from sklearn.model_selection import train_test_split
%matplotlib inline
import matplotlib.pyplot as plt
```

In [7]:
```
from pyodide.http import pyfetch

async def download(url, filename):
    response = await pyfetch(url)
    if response.status == 200:
        with open(filename, "wb") as f:
            f.write(await response.bytes())
```

Load the Cancer data

The example is based on a dataset that is publicly available from the UCI Machine Learning Repository (Asuncion and Newman, 2007)[http://mlearn.ics.uci.edu/MLRepository.html (http://mlearn.ics.uci.edu/MLRepository.html)]. The dataset consists of several hundred human cell sample records, each of which contains the values of a set of cell characteristics. The fields in each record are:

Field name	Description
ID	Clump thickness
Clump	Clump thickness
UnifSize	Uniformity of cell size
UnifShape	Uniformity of cell shape
MargAdh	Marginal adhesion
SingEpiSize	Single epithelial cell size
BareNuc	Bare nuclei
BlandChrom	Bland chromatin
NormNucl	Normal nucleoli
Mit	Mitoses
Class	Benign or malignant

In [8]:
```
path="https://cf-courses-data.s3.us.cloud-object-storage.appdomain.cloud/IBMDeveloperSkillsNetwork-ML0101EN-SkillsNetwork/labs/Module%203/data/cell_samples.csv"
```

Load Data From CSV File

In [9]:
```
await download(path, "cell_samples.csv")
```

In [10]:
```
cell_df = pd.read_csv("cell_samples.csv")
cell_df.head()
```

Out[10]:

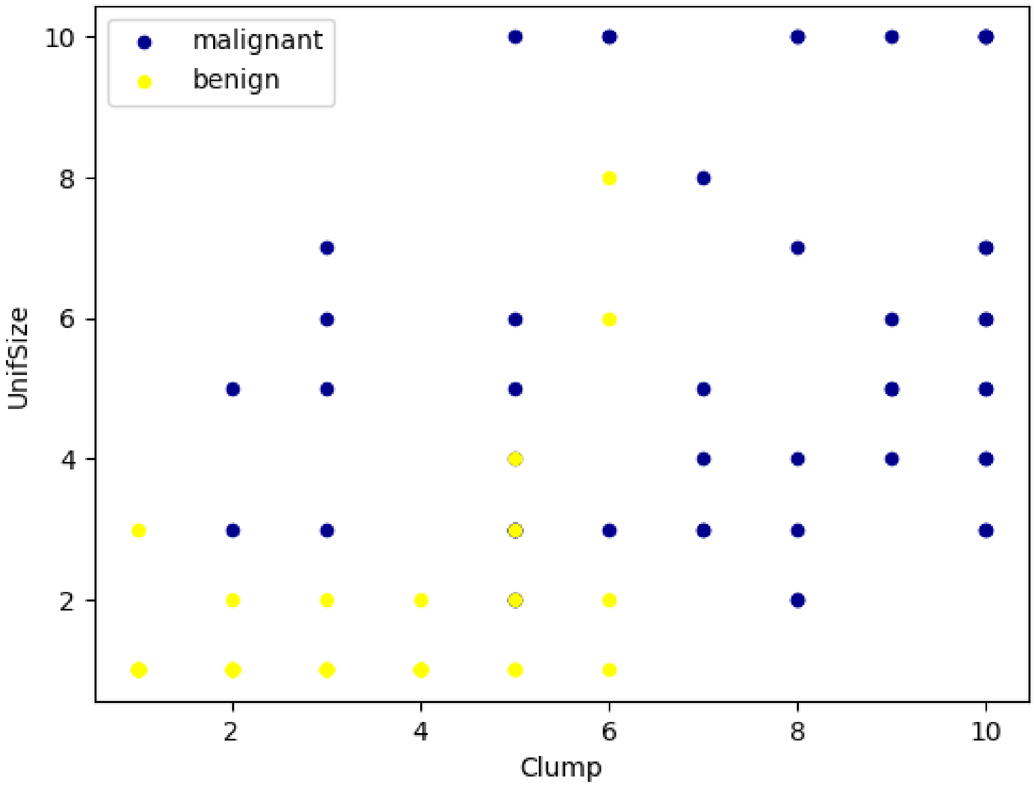
	ID	Clump	UnifSize	UnifShape	MargAdh	SingEpiSize	BareNuc	BlandChrom	NormNucl
0	1000025	5	1	1	1	2	1	3	1
1	1002945	5	4	4	5	7	10	3	2
2	1015425	3	1	1	1	2	2	3	1
3	1016277	6	8	8	1	3	4	3	7
4	1017023	4	1	1	3	2	1	3	1

The ID field contains the patient identifiers. The characteristics of the cell samples from each patient are contained in fields Clump to Mit. The values are graded from 1 to 10, with 1 being the closest to benign.

The Class field contains the diagnosis, as confirmed by separate medical procedures, as to whether the samples are benign (value = 2) or malignant (value = 4).

Let's look at the distribution of the classes based on Clump thickness and Uniformity of cell size:

In [11]:
```
ax = cell_df[cell_df['Class'] == 4][0:50].plot(kind='scatter', x='Clump', y
='UnifSize', color='DarkBlue', label='malignant');
cell_df[cell_df['Class'] == 2][0:50].plot(kind='scatter', x='Clump', y='Uni
fSize', color='Yellow', label='benign', ax=ax);
plt.show()
```




```
<Figure size 640x480 with 0 Axes>
```

Data pre-processing and selection

Let's first look at columns data types:

In [12]:
```
cell_df.dtypes
```

Out[12]:
```
ID              int64
Clump           int64
UnifSize        int64
UnifShape       int64
MargAdh         int64
SingEpiSize     int64
BareNuc        object
BlandChrom      int64
NormNucl        int64
Mit             int64
Class           int64
dtype: object
```

It looks like the **BareNuc** column includes some values that are not numerical. We can drop those rows:

In [13]:
```
cell_df = cell_df[pd.to_numeric(cell_df['BareNuc'], errors='coerce').notnul
l()]
cell_df['BareNuc'] = cell_df['BareNuc'].astype('int')
cell_df.dtypes
```

Out[13]:
```
ID             int64
Clump          int64
UnifSize       int64
UnifShape      int64
MargAdh        int64
SingEpiSize    int64
BareNuc        int32
BlandChrom     int64
NormNucl       int64
Mit            int64
Class          int64
dtype: object
```

In [14]:
```
feature_df = cell_df[['Clump', 'UnifSize', 'UnifShape', 'MargAdh', 'SingEpi
Size', 'BareNuc', 'BlandChrom', 'NormNucl', 'Mit']]
X = np.asarray(feature_df)
X[0:5]
```

Out[14]:
```
array([[ 5,  1,  1,  1,  2,  1,  3,  1,  1],
       [ 5,  4,  4,  5,  7, 10,  3,  2,  1],
       [ 3,  1,  1,  1,  2,  2,  3,  1,  1],
       [ 6,  8,  8,  1,  3,  4,  3,  7,  1],
       [ 4,  1,  1,  3,  2,  1,  3,  1,  1]], dtype=int64)
```

We want the model to predict the value of Class (that is, benign (=2) or malignant (=4)). As this field can have one of only two possible values, we need to change its measurement level to reflect this.

In [15]:
```
cell_df['Class'] = cell_df['Class'].astype('int')
y = np.asarray(cell_df['Class'])
y [0:5]
```

Out[15]:
```
array([2, 2, 2, 2, 2])
```

Train/Test dataset

We split our dataset into train and test set:

In [16]:
```
X_train, X_test, y_train, y_test = train_test_split( X, y, test_size=0.2, random_state=4)
print ('Train set:', X_train.shape,  y_train.shape)
print ('Test set:', X_test.shape,  y_test.shape)
```

```
Train set: (546, 9) (546,)
Test set: (137, 9) (137,)
```

Modeling (SVM with Scikit-learn)

The SVM algorithm offers a choice of kernel functions for performing its processing. Basically, mapping data into a higher dimensional space is called kernelling. The mathematical function used for the transformation is known as the kernel function, and can be of different types, such as:

1.Linear
2.Polynomial
3.Radial basis function (RBF)
4.Sigmoid

Each of these functions has its characteristics, its pros and cons, and its equation, but as there's no easy way of knowing which function performs best with any given dataset. We usually choose different functions in turn and compare the results. Let's just use the default, RBF (Radial Basis Function).

In [17]:
```
from sklearn import svm
clf = svm.SVC(kernel='rbf')
clf.fit(X_train, y_train)
```

Out[17]:
```
SVC()
```

After being fitted, the model can then be used to predict new values:

In [18]:
```
yhat = clf.predict(X_test)
yhat [0:5]
```

Out[18]:
```
array([2, 4, 2, 4, 2])
```

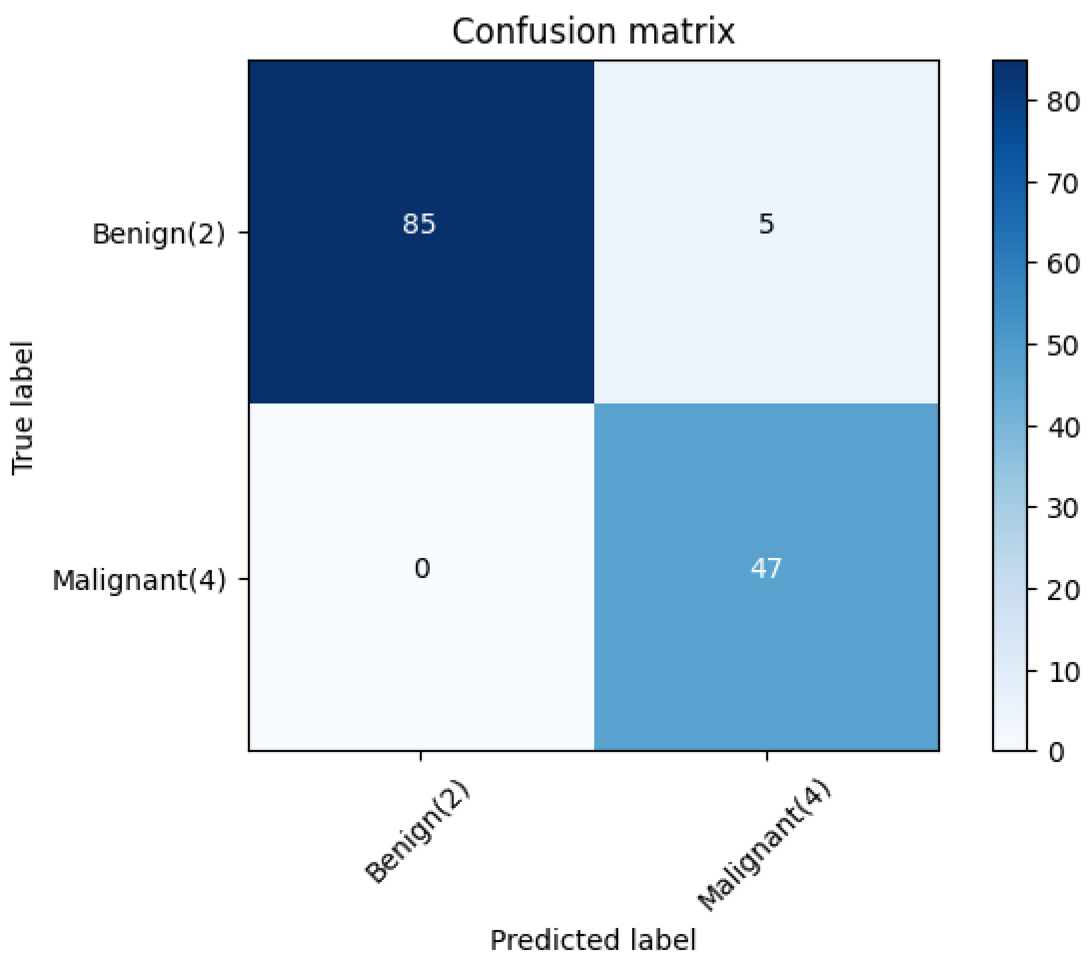
Evaluation

In [19]:
```
from sklearn.metrics import classification_report, confusion_matrix
import itertools
```

In [20]:
```
def plot_confusion_matrix(cm, classes,
                          normalize=False,
                          title='Confusion matrix',
                          cmap=plt.cm.Blues):
    """
    This function prints and plots the confusion matrix.
    Normalization can be applied by setting `normalize=True`.
    """
    if normalize:
        cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
        print("Normalized confusion matrix")
    else:
        print('Confusion matrix, without normalization')

    print(cm)

    plt.imshow(cm, interpolation='nearest', cmap=cmap)
    plt.title(title)
    plt.colorbar()
    tick_marks = np.arange(len(classes))
    plt.xticks(tick_marks, classes, rotation=45)
    plt.yticks(tick_marks, classes)

    fmt = '.2f' if normalize else 'd'
    thresh = cm.max() / 2.
    for i, j in itertools.product(range(cm.shape[0]), range(cm.shape[1])):
        plt.text(j, i, format(cm[i, j], fmt),
                 horizontalalignment="center",
                 color="white" if cm[i, j] > thresh else "black")

    plt.tight_layout()
    plt.ylabel('True label')
    plt.xlabel('Predicted label')
```

In [21]:
```
# Compute confusion matrix
cnf_matrix = confusion_matrix(y_test, yhat, labels=[2,4])
np.set_printoptions(precision=2)

print (classification_report(y_test, yhat))

# Plot non-normalized confusion matrix
plt.figure()
plot_confusion_matrix(cnf_matrix, classes=['Benign(2)','Malignant(4)'],norm
alize= False,  title='Confusion matrix')
```

```
              precision    recall  f1-score   support

           2       1.00      0.94      0.97        90
           4       0.90      1.00      0.95        47

    accuracy                           0.96       137
   macro avg       0.95      0.97      0.96       137
weighted avg       0.97      0.96      0.96       137

Confusion matrix, without normalization
[[85  5]
 [ 0 47]]
```



You can also easily use the **f1_score** from sklearn library:

In [22]:
```
from sklearn.metrics import f1_score
f1_score(y_test, yhat, average='weighted')
```

Out[22]: 0.9639038982104676

Let's try the jaccard index for accuracy:

In [23]:
```
from sklearn.metrics import jaccard_score
jaccard_score(y_test, yhat,pos_label=2)
```

Out[23]: 0.9444444444444444

Appendix

Using linear function

In [24]:
```
clf2 = svm.SVC(kernel='linear')
clf2.fit(X_train, y_train)
yhat2 = clf2.predict(X_test)
print("Avg F1-score: %.4f" % f1_score(y_test, yhat2, average='weighted'))
print("Jaccard score: %.4f" % jaccard_score(y_test, yhat2,pos_label=2))
```

```
Avg F1-score: 0.9639
Jaccard score: 0.9444
```