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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.

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```
In [1]: 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
```

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://mllearn.ics.uci.edu/MLRepository.html> (<http://mllearn.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

For the purposes of this example, we're using a dataset that has a relatively small number of predictors in each record. To download the data, we will use `!wget` to download it from IBM Object Storage.

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```
In [2]: #Click here and press Shift+Enter
!wget -O cell_samples.csv https://s3-api.us-gio.objectstorage.softlayer.net/cf-courses-data/CognitiveClass/ML0101ENV3/labs/cell_samples.csv

--2020-02-03 17:02:49-- https://s3-api.us-gio.objectstorage.softlayer.net/cf-courses-data/CognitiveClass/ML0101ENV3/labs/cell_samples.csv
Resolving s3-api.us-gio.objectstorage.softlayer.net (s3-api.us-gio.objectstorage.softlayer.net)... 67.228.254.196
Connecting to s3-api.us-gio.objectstorage.softlayer.net (s3-api.us-gio.objectstorage.softlayer.net)|67.228.254.196|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 20675 (20K) [text/csv]
Saving to: 'cell_samples.csv'

cell_samples.csv  100%[=====>]  20.19K  --.-KB/s    in 0.02s

2020-02-03 17:02:49 (1010 KB/s) - 'cell_samples.csv' saved [20675/20675]
```

Load Data From CSV File

```
In [3]: cell_df = pd.read_csv("cell_samples.csv")
        cell_df.head()
```

Out[3]:

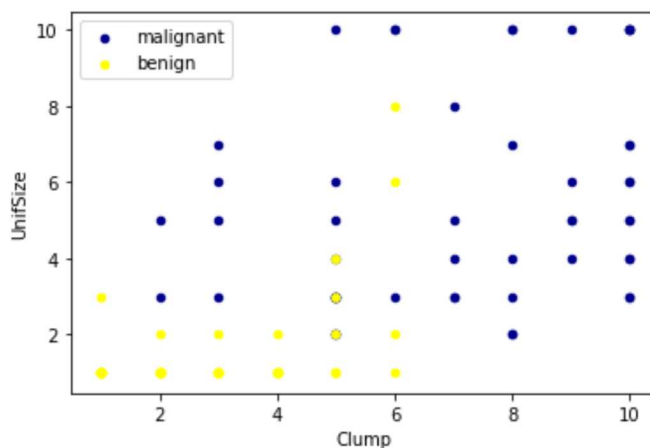
	ID	Clump	UnifSize	UnifShape	MargAdh	SingEpiSize	BareNuc	BlandChrom	NormNucl	Mit	Class
0	1000025	5	1	1	1	2	1	3	1	1	
1	1002945	5	4	4	5	7	10	3	2	1	
2	1015425	3	1	1	1	2	2	3	1	1	
3	1016277	6	8	8	1	3	4	3	7	1	
4	1017023	4	1	1	3	2	1	3	1	1	

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).

Lets look at the distribution of the classes based on Clump thickness and Uniformity of cell size:

```
In [6]: 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='UnifSize', color='Yellow', label='benign', ax=ax);
        plt.show()
```



Data pre-processing and selection

Lets first look at columns data types:

```
In [7]: cell_df.dtypes
```

```
Out[7]: 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 [8]: cell_df = cell_df[pd.to_numeric(cell_df['BareNuc'], errors='coerce').notnull()]
cell_df['BareNuc'] = cell_df['BareNuc'].astype('int')
cell_df.dtypes
```

```
Out[8]: ID                int64
Clump                int64
UnifSize            int64
UnifShape            int64
MargAdh             int64
SingEpiSize         int64
BareNuc              int64
BlandChrom           int64
NormNucl             int64
Mit                  int64
Class                int64
dtype: object
```

```
In [9]: feature_df = cell_df[['Clump', 'UnifSize', 'UnifShape', 'MargAdh', 'SingEpiSize',
    'BareNuc', 'BlandChrom', 'NormNucl', 'Mit']]
X = np.asarray(feature_df)
X[0:5]
```

```
Out[9]: 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]])
```

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

```
Out[10]: array([2, 2, 2, 2, 2])
```

Train/Test dataset

Okay, we split our dataset into train and test set:

```
In [11]: 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) for this lab.

```
In [12]: from sklearn import svm
         clf = svm.SVC(kernel='rbf')
         clf.fit(X_train, y_train)
```

```
/home/jupyterlab/conda/envs/python/lib/python3.6/site-packages/sklearn/svm/base
e.py:196: FutureWarning: The default value of gamma will change from 'auto' to
'scale' in version 0.22 to account better for unscaled features. Set gamma exp
licitly to 'auto' or 'scale' to avoid this warning.
      "avoid this warning.", FutureWarning)
```

```
Out[12]: SVC(C=1.0, cache_size=200, class_weight=None, coef0=0.0,
          decision_function_shape='ovr', degree=3, gamma='auto_deprecated',
          kernel='rbf', max_iter=-1, probability=False, random_state=None,
          shrinking=True, tol=0.001, verbose=False)
```

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

```
In [13]: yhat = clf.predict(X_test)
         yhat [0:5]
```

```
Out[13]: array([2, 4, 2, 4, 2])
```

Evaluation

```
In [14]: from sklearn.metrics import classification_report, confusion_matrix
         import itertools
```

```
In [15]: 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 [16]: # Compute confusion matrix
cnf_matrix = confusion_matrix(y_test, yhat, labels=[2,4])
np.set_printoptions(precision=2)

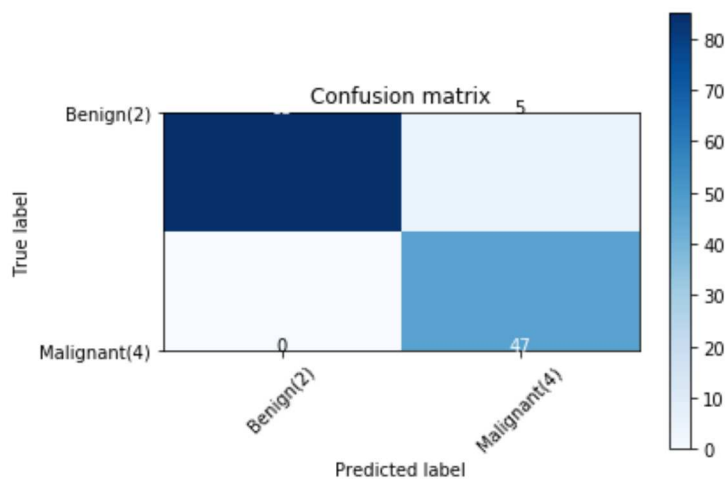
print (classification_report(y_test, yhat))

# Plot non-normalized confusion matrix
plt.figure()
plot_confusion_matrix(cnf_matrix, classes=['Benign(2)', 'Malignant(4)'],normalize
= 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
micro avg	0.96	0.96	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 [17]: from sklearn.metrics import f1_score
f1_score(y_test, yhat, average='weighted')
```

```
Out[17]: 0.9639038982104676
```

Lets try jaccard index for accuracy:

```
In [18]: from sklearn.metrics import jaccard_similarity_score
jaccard_similarity_score(y_test, yhat)
```

```
Out[18]: 0.9635036496350365
```

Practice

Can you rebuild the model, but this time with a **linear** kernel? You can use **kernel='linear'** option, when you define the svm. How the accuracy changes with the new kernel function?

```

In [33]: # write your code here
# 1) set up the model
modelApp2 = svm.SVC(kernel="linear")

# 2) train (fit) the model
modelApp2.fit(X_train, y_train)

# 3) predict via model
y_hat2 = modelApp2.predict(X_test)
y_hat2

# 4) test (evaluate the prediction accuracy of) the model

# 4.1 confusion matrix
confusion = confusion_matrix(y_test, y_hat2)
#print (confusion)
plot_confusion_matrix(confusion, classes=['Benign(2)', 'Malignant(4)'])

# 4.2 all classification statistics
print(classification_report(y_test, y_hat2))

# 4.3 f1 score via sklearn
print(f1_score(y_test, y_hat2, average="weighted"))

# 4.4 jaccard score
print(jaccard_similarity_score(y_test, y_hat2))

```

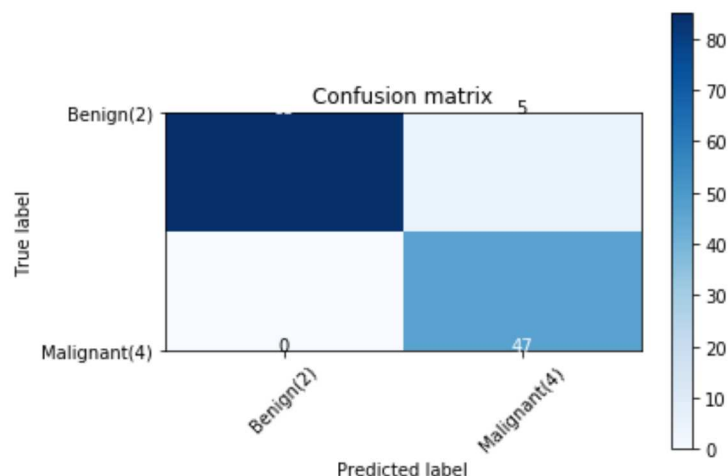
Confusion matrix, without normalization

```
[[85  5]
 [ 0 47]]
```

	precision	recall	f1-score	support
2	1.00	0.94	0.97	90
4	0.90	1.00	0.95	47
micro avg	0.96	0.96	0.96	137
macro avg	0.95	0.97	0.96	137
weighted avg	0.97	0.96	0.96	137

```
0.9639038982104676
```

```
0.9635036496350365
```



Double-click [here](#) for the solution.


```
In [34]: 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_similarity_score(y_test, yhat2))

Avg F1-score: 0.9639
Jaccard score: 0.9635
```

Want to learn more?

IBM SPSS Modeler is a comprehensive analytics platform that has many machine learning algorithms. It has been designed to bring predictive intelligence to decisions made by individuals, by groups, by systems – by your enterprise as a whole. A free trial is available through this course, available here: [SPSS Modeler \(http://cocl.us/ML0101EN-SPSSModeler\)](http://cocl.us/ML0101EN-SPSSModeler).

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Thanks for completing this lesson!

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