# ML0101EN-Clas-SVM-cancer-py-v1

February 28, 2019

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://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 |

| Field name | Description |
|---|---|
| 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-geo.objectstorage.softlayer.net/cf-courses-d

--2019-02-28 23:11:03--  https://s3-api.us-geo.objectstorage.softlayer.net/cf-courses-data/Cogni
Resolving s3-api.us-geo.objectstorage.softlayer.net (s3-api.us-geo.objectstorage.softlayer.net).
Connecting to s3-api.us-geo.objectstorage.softlayer.net (s3-api.us-geo.objectstorage.softlayer.n
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

2019-02-28 23:11:03 (976 KB/s) - cell_samples.csv saved [20675/20675]
```

### 0.0.1 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 | 2 |
| 1 | 1002945 | 5 | 4 | 4 | 5 | 7 | 10 | 3 | 2 | 1 | 2 |
| 2 | 1015425 | 3 | 1 | 1 | 1 | 2 | 2 | 3 | 1 | 1 | 2 |
| 3 | 1016277 | 6 | 8 | 8 | 1 | 3 | 4 | 3 | 7 | 1 | 2 |
| 4 | 1017023 | 4 | 1 | 1 | 3 | 2 | 1 | 3 | 1 | 1 | 2 |

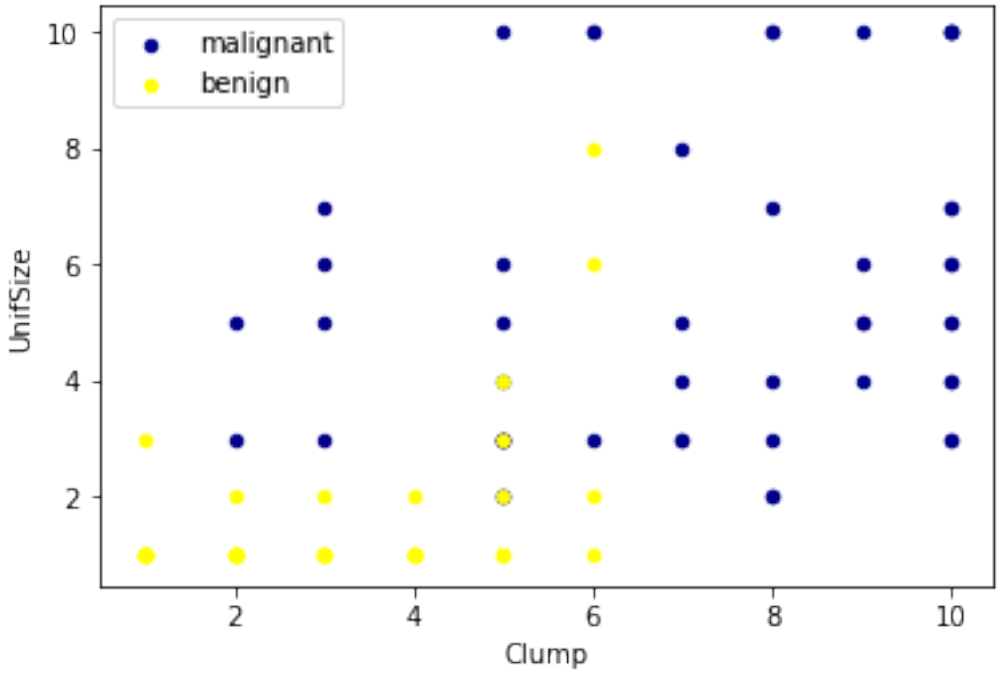
```
3           3          7     1       2
4           3          1     1       2
```

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 [4]: ax = cell_df[cell_df['Class'] == 4][0:50].plot(kind='scatter', x='Clump', y='UnifSize',
        cell_df[cell_df['Class'] == 2][0:50].plot(kind='scatter', x='Clump', y='UnifSize', color
        plt.show()
```




## 0.1 Data pre-processing and selection

Lets first look at columns data types:

```
In [5]: cell_df.dtypes
```

```
Out[5]: 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 [6]: 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[6]: 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 [7]: feature_df = cell_df[['Clump', 'UnifSize', 'UnifShape', 'MargAdh', 'SingEpiSize', 'BareN
        X = np.asarray(feature_df)
        X[0:5]

Out[7]: 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 [8]: cell_df['Class'] = cell_df['Class'].astype('int')
        y = np.asarray(cell_df['Class'])
        y [0:5]

Out[8]: array([2, 2, 2, 2, 2])
```

### 0.2 Train/Test dataset

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

```
In [9]: 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 [10]: from sklearn import svm
         clf = svm.SVC(kernel='rbf')
         clf.fit(X_train, y_train)
```

```
/home/jupyterlab/conda/lib/python3.6/site-packages/sklearn/svm/base.py:196: FutureWarning: The d
  "avoid this warning.", FutureWarning)
```

```
Out[10]: 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 [11]: yhat = clf.predict(X_test)
         yhat [0:5]
```

```
Out[11]: array([2, 4, 2, 4, 2])
```

Evaluation

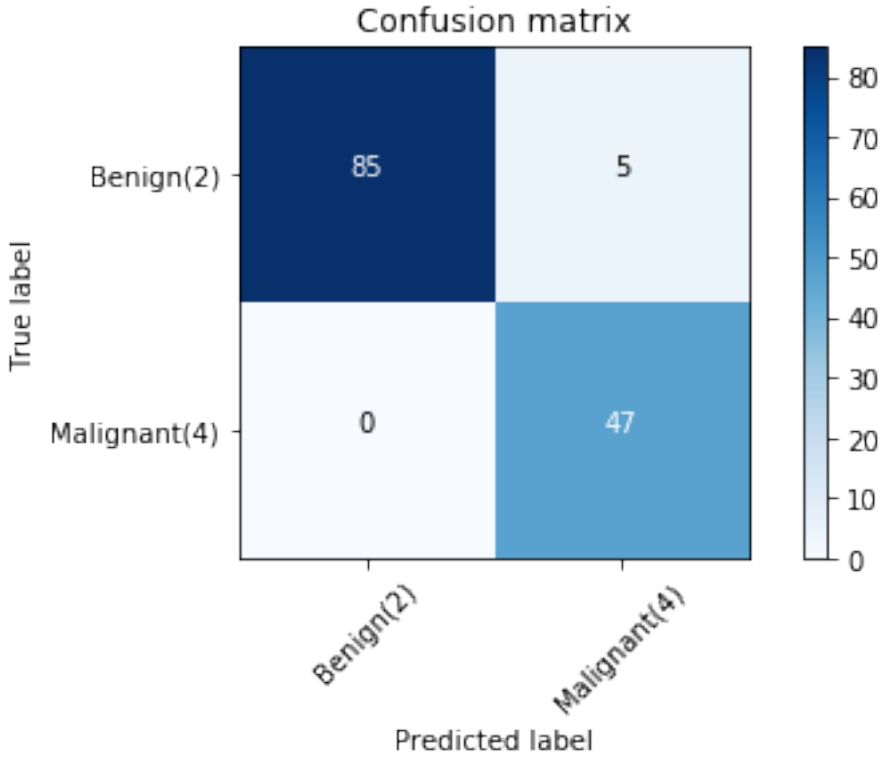
```
In [16]: from sklearn.metrics import classification_report, confusion_matrix
         import itertools
```

In [17]:
```
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 [18]:
```
# 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
```

| | 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 [19]: from sklearn.metrics import f1_score
         f1_score(y_test, yhat, average='weighted')
```

```
Out[19]: 0.9639038982104676
```

Lets try jaccard index for accuracy:

```
In [20]: from sklearn.metrics import jaccard_similarity_score
         jaccard_similarity_score(y_test, yhat)
```

```
Out[20]: 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 [26]: # write your code here
         from sklearn import svm
         clf2 = svm.SVC(kernel='linear')
         clf2.fit(X_train, y_train)
         yhat2 = clf2.predict(X_test)
         yhat2 [0:5]

         f1_score(y_test, yhat2, average='weighted')
         jaccard_similarity_score(y_test, yhat2)

         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
```

Double-click **here** for the solution.

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

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Thanks for completing this lesson!

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Saeed Aghabozorgi, PhD is a Data Scientist in IBM with a track record of developing enterprise level applications that substantially increases clients' ability to turn data into actionable knowledge. He is a researcher in data mining field and expert in developing advanced analytic methods like machine learning and statistical modelling on large datasets.