Support Vector Machines

Introduction

In machine learning, support vector machines (SVMs, also support vector networks) are supervised learning models with associated learning algorithms that analyze data used for classification and regression analysis. A Support Vector Machine (SVM) is a discriminative classifier formally defined by a separating hyperplane. In other words, given labeled training data (supervised learning), the algorithm outputs an optimal hyperplane which categorizes new examples.

What is Support Vector Machine

An SVM model is a representation of the examples as points in space, mapped so that the examples of the separate categories are divided by a clear gap that is as wide as possible. In addition to performing linear classification, SVMs can efficiently perform a non-linear classification, implicitly mapping their inputs into high-dimensional feature spaces.

What does SVM do?

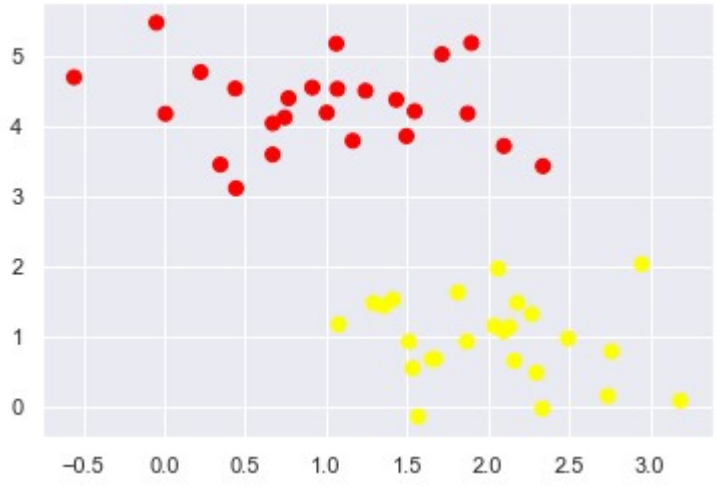
Given a set of training examples, each marked as belonging to one or the other of two categories, an SVM training algorithm builds a model that assigns new examples to one category or the other, making it a non-probabilistic binary linear classifier. SVM is an example of discriminative classification: rather than modeling each class, we simply find a line or curve (in two dimensions) or manifold (in multiple dimensions) that divides the classes from each other.

Here we'll discuss an example about SVM classification using machine learning tools i.e. scikit-learn compatible with Python.

We begin with the standard imports:

In [3]:
```
%matplotlib inline
import numpy as np
import matplotlib.pyplot as plt
from scipy import stats

# use seaborn plotting defaults
import seaborn as sns; sns.set()
```

In [4]:
```
from sklearn.datasets.samples_generator import make_blobs
X, y = make_blobs(n_samples=50, centers=2,
                  random_state=0, cluster_std=0.60)
plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn');
```

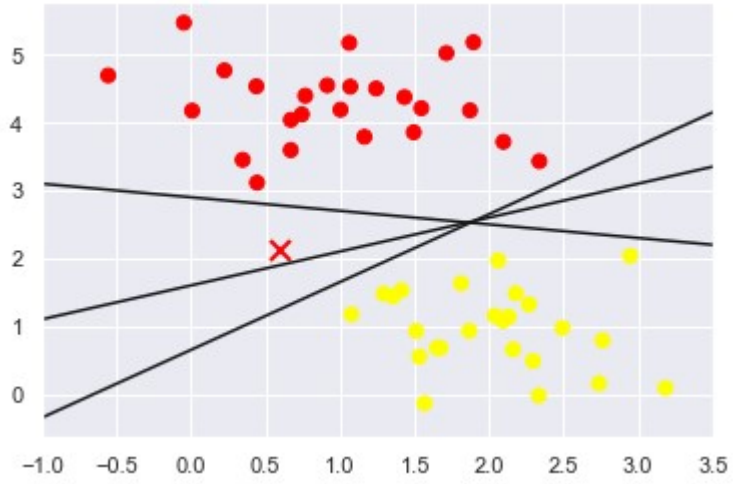


A linear discriminative classifier would attempt to draw a straight line separating the two sets of data, and thereby create a model for classification. For two dimensional data like that shown here, this is a task we could do by hand. But immediately we see a problem: there is more than one possible dividing line that can perfectly discriminate between the two classes!

We can draw them as follows:

In [5]:

```
xfit = np.linspace(-1, 3.5)
plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
plt.plot([0.6], [2.1], 'x', color='red', markeredgewidth=2, markersize=10

for m, b in [(1, 0.65), (0.5, 1.6), (-0.2, 2.9)]:
    plt.plot(xfit, m * xfit + b, '-k')

plt.xlim(-1, 3.5);
```

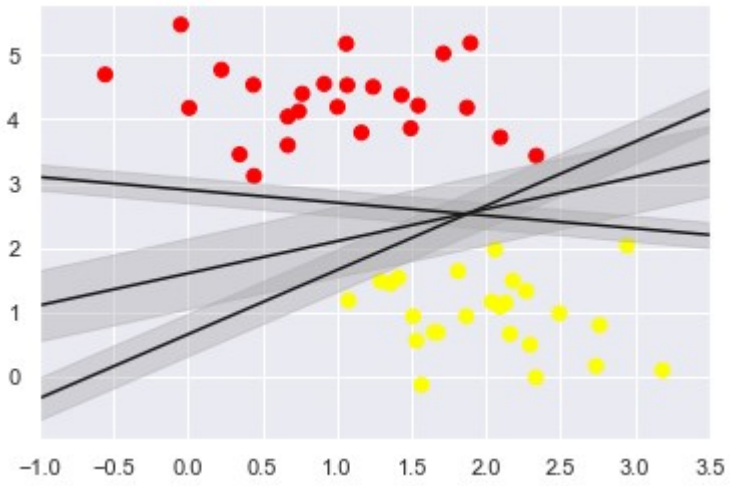


These are three very different separators which, nevertheless, perfectly discriminate between these samples. Depending on which you choose, a new data point (e.g., the one marked by the "X" in this plot) will be assigned a different label! Evidently our simple intuition of "drawing a line between classes" is not enough, and we need to think a bit deeper.

Maximising the margin

Support vector machines offer one way to improve on this. The intuition is this: rather than simply drawing a zero-width line between the classes, we can draw around each line a margin of some width, up to the nearest point. Here is an example of how this might look:

In [7]:
```
xfit = np.linspace(-1, 3.5)
plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')

for m, b, d in [(1, 0.65, 0.33), (0.5, 1.6, 0.55), (-0.2, 2.9, 0.2)]:
    yfit = m * xfit + b
    plt.plot(xfit, yfit, '-k')
    plt.fill_between(xfit, yfit - d, yfit + d, edgecolor='none',
                     color='#AAAAAA', alpha=0.4)

plt.xlim(-1, 3.5);
```



In support vector machines, the line that maximizes this margin is the one we will choose as the optimal model. Support vector machines are an example of such a maximum margin estimator.

Fitting a SVM

Let's see the result of an actual fit to this data: we will use Scikit-Learn's support vector classifier to train an SVM model on this data. For the time being, we will use a linear kernel and set the C parameter to a very large number (we'll discuss the meaning of these in more depth momentarily).

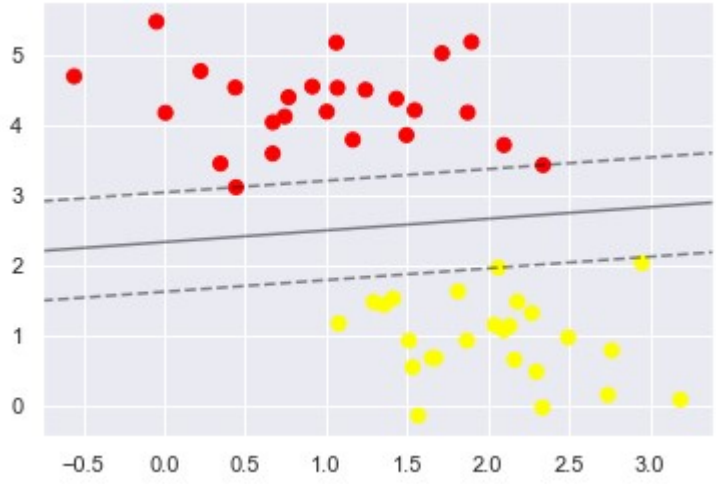
In [8]:
```
from sklearn.svm import SVC # "Support vector classifier"
model = SVC(kernel='linear', C=1E10)
model.fit(X, y)
```

Out[8]:
```
SVC(C=10000000000.0, cache_size=200, class_weight=None, coef0=0.0,
    decision_function_shape='ovr', degree=3, gamma='auto_deprecated',
    kernel='linear', max_iter=-1, probability=False, random_state=None,
    shrinking=True, tol=0.001, verbose=False)
```

To better visualize what's happening here, let's create a quick convenience function that will plot SVM decision boundaries for us:

In [9]:
```
def plot_svc_decision_function(model, ax=None, plot_support=True):
    """Plot the decision function for a 2D SVC"""
    if ax is None:
        ax = plt.gca()
    xlim = ax.get_xlim()
    ylim = ax.get_ylim()

    # create grid to evaluate model
    x = np.linspace(xlim[0], xlim[1], 30)
    y = np.linspace(ylim[0], ylim[1], 30)
    Y, X = np.meshgrid(y, x)
    xy = np.vstack([X.ravel(), Y.ravel()]).T
    P = model.decision_function(xy).reshape(X.shape)

    # plot decision boundary and margins
    ax.contour(X, Y, P, colors='k',
               levels=[-1, 0, 1], alpha=0.5,
               linestyles=['--', '-', '--'])

    # plot support vectors
    if plot_support:
        ax.scatter(model.support_vectors_[:, 0],
                   model.support_vectors_[:, 1],
                   s=300, linewidth=1, facecolors='none');
    ax.set_xlim(xlim)
    ax.set_ylim(ylim)
```

In [10]:
```
plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
plot_svc_decision_function(model);
```



This is the dividing line that maximizes the margin between the two sets of points. Notice that a few of the training points just touch the margin. These points are the pivotal elements of this fit, and are known as the support *vectors* attribute of the classifier:

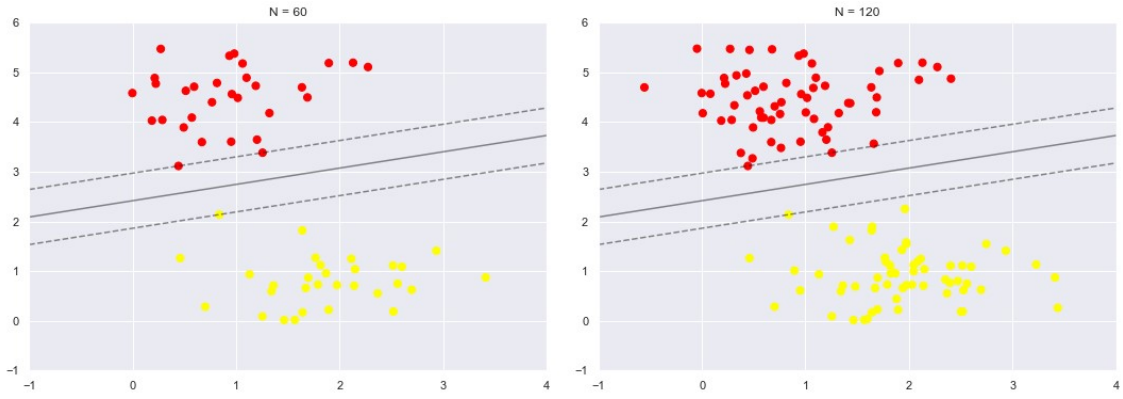
In [12]:
```
model.support_vectors_
```

Out[12]:
```
array([[0.44359863, 3.11530945],
       [2.33812285, 3.43116792],
       [2.06156753, 1.96918596]])
```

A key to this classifier's success is that for the fit, only the position of the support vectors matter; any points further from the margin which are on the correct side do not modify the fit! Technically, this is because these points do not contribute to the loss function used to fit the model, so their position and number do not matter so long as they do not cross the margin.

We can see this, for example, if we plot the model learned from the first 60 points and first 120 points of this dataset:

In [13]:
```
def plot_svm(N=10, ax=None):
    X, y = make_blobs(n_samples=200, centers=2,
                      random_state=0, cluster_std=0.60)
    X = X[:N]
    y = y[:N]
    model = SVC(kernel='linear', C=1E10)
    model.fit(X, y)

    ax = ax or plt.gca()
    ax.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
    ax.set_xlim(-1, 4)
    ax.set_ylim(-1, 6)
    plot_svc_decision_function(model, ax)

fig, ax = plt.subplots(1, 2, figsize=(16, 6))
fig.subplots_adjust(left=0.0625, right=0.95, wspace=0.1)
for axi, N in zip(ax, [60, 120]):
    plot_svm(N, axi)
    axi.set_title('N = {0}'.format(N))
```

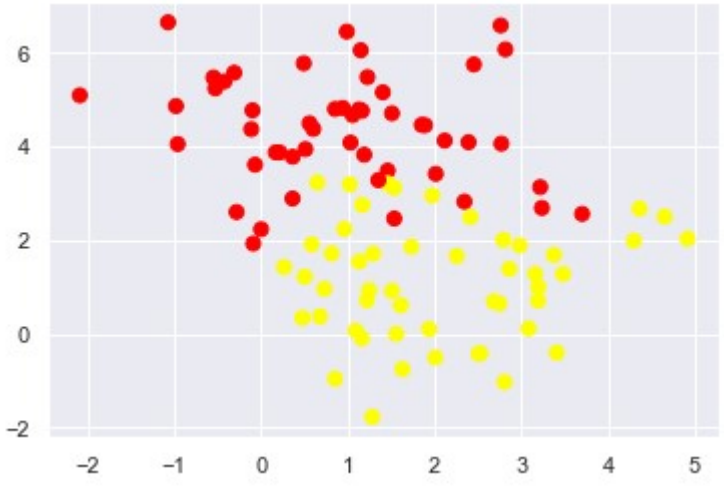


In [17]:
```
from ipywidgets import interact, fixed
interact(plot_svm, N=[50, 100, 200], ax=fixed(None));
```

Tuning SVM: Softening The Margins

Our discussion thus far has centered around very clean datasets, in which a perfect decision boundary exists. But what if your data has some amount of overlap? For example, you may have data like this:

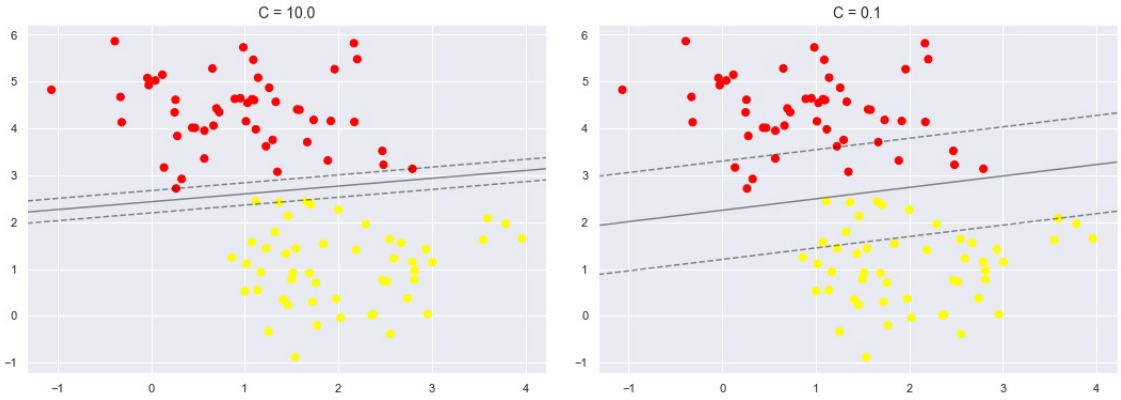
In [25]:
```
X, y = make_blobs(n_samples=100, centers=2,
                  random_state=0, cluster_std=1.2)
plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn');
```



To handle this case, the SVM implementation has a bit of a fudge-factor which "softens" the margin: that is, it allows some of the points to creep into the margin if that allows a better fit. The hardness of the margin is controlled by a tuning parameter, most often known as C . For very large C , the margin is hard, and points cannot lie in it. For smaller C , the margin is softer, and can grow to encompass some points.

The plot shown below gives a visual picture of how a changing C parameter affects the final fit, via the softening of the margin:

In [32]:
```
X, y = make_blobs(n_samples=100, centers=2,
                  random_state=0, cluster_std=0.8)

fig, ax = plt.subplots(1, 2, figsize=(16, 6))
fig.subplots_adjust(left=0.0625, right=0.95, wspace=0.1)

for axi, C in zip(ax, [10.0, 0.1]):
    model = SVC(kernel='linear', C=C).fit(X, y)
    axi.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
    plot_svc_decision_function(model, axi)
    axi.scatter(model.support_vectors_[:, 0],
                model.support_vectors_[:, 1],
                s=300, lw=1, facecolors='none');
    axi.set_title('C = {0:.1f}'.format(C), size=14)
```



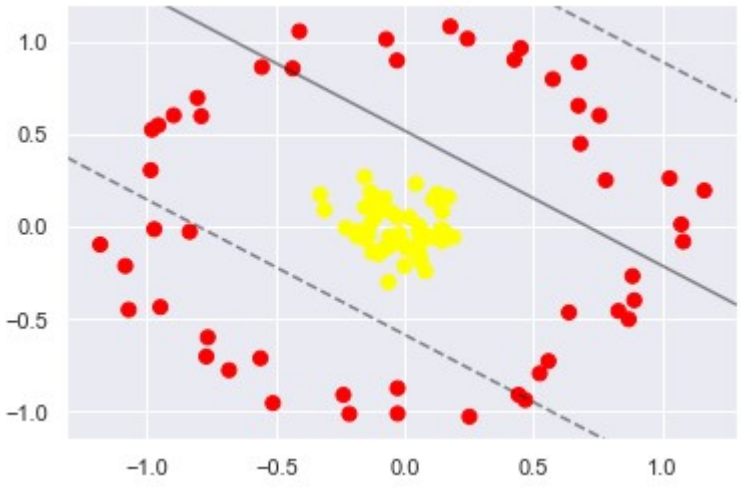
The optimal value of the C parameter will depend on your dataset, and should be tuned using cross-validation

Kernel SVM

SVM algorithms use a set of mathematical functions that are defined as the kernel. The function of kernel is to take data as input and transform it into the required form. Different SVM algorithms use different types of kernel functions. These functions can be different types. For example linear, nonlinear, polynomial, radial basis function (RBF), and sigmoid. Kernel functions can be used for sequence data, graphs, text, images, as well as vectors. The most used type of kernel function is RBF. Because it has localized and finite response along the entire x-axis.

To motivate the need for kernels, let's look at some data that is not linearly separable:

In [18]:
```
from sklearn.datasets.samples_generator import make_circles
X, y = make_circles(100, factor=.1, noise=.1)

clf = SVC(kernel='linear').fit(X, y)

plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
plot_svc_decision_function(clf, plot_support=False);
```



It is clear that no linear discrimination will ever be able to separate this data. But we can think about how we might project the data into a higher dimension such that a linear separator would be sufficient. For example, one simple projection we could use would be to compute a radial basis function centered on the middle clump:

In [19]:
```
r = np.exp(-(X ** 2).sum(1))
```

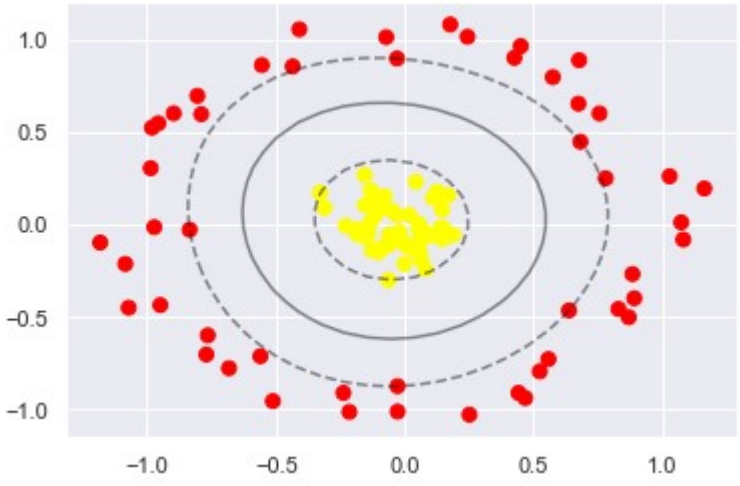
We can visualize this extra data dimension using a three-dimensional plot

In [21]:
```
from mpl_toolkits import mplot3d

def plot_3D(elev=30, azim=30, X=X, y=y):
    ax = plt.subplot(projection='3d')
    ax.scatter3D(X[:, 0], X[:, 1], r, c=y, s=50, cmap='autumn')
    ax.view_init(elev=elev, azim=azim)
    ax.set_xlabel('x')
    ax.set_ylabel('y')
    ax.set_zlabel('r')

interact(plot_3D, elev=[-90, 0, 90], azip=(-180, 180),
         X=fixed(X), y=fixed(y));
```

We can see that with this additional dimension, the data becomes trivially linearly separable, by drawing a separating plane at, say, r=0.7.

In [22]:
```
clf = SVC(kernel='rbf', C=1E6)
clf.fit(X, y)

plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
plot_svc_decision_function(clf)
plt.scatter(clf.support_vectors_[:, 0], clf.support_vectors_[:, 1],
            s=300, lw=1, facecolors='none');
```

```
C:\ProgramData\Anaconda3\lib\site-packages\sklearn\svm\base.py:193: Futur
  "avoid this warning.", FutureWarning)
```



Using this kernelized support vector machine, we learn a suitable nonlinear decision boundary. This kernel transformation strategy is used often in machine learning to turn fast linear methods into fast nonlinear methods, especially for models in which the kernel trick can be used.

Other Popular Kernels

Polynomial Kernel: In machine learning, the polynomial kernel is a kernel function commonly used with support vector machines (SVMs) and other kernelized models, that represents the similarity of vectors (training samples) in a feature space over polynomials of the original variables, allowing learning of non-linear models.

Intuitively, the polynomial kernel looks not only at the given features of input samples to determine their similarity, but also combinations of these. In the context of regression analysis, such combinations are known as interaction features. The (implicit) feature space of a polynomial kernel is equivalent to that of polynomial regression, but without the combinatorial blowup in the number of parameters to be learned.

Pros and Cons

We have seen here a brief intuitive introduction to the principals behind support vector machines. These methods are a powerful classification method for a number of reasons:
Their dependence on relatively few support vectors means that they are very compact models, and take up very little memory. Once the model is trained, the prediction phase is very fast.
Because they are affected only by points near the margin, they work well with high-dimensional data—even data with more dimensions than samples, which is a challenging regime for other algorithms.
Their integration with kernel methods makes them very versatile, able to adapt to many types of data.

However, SVMs have several disadvantages as well:

The scaling with the number of samples N is $\mathcal{O}[N^3]$ at worst, or $\mathcal{O}[N^2]$ for efficient implementations. For large numbers of training samples, this computational cost can be prohibitive.
The results are strongly dependent on a suitable choice for the softening parameter C . This must be carefully chosen via cross-validation, which can be expensive as datasets grow in size.
The results do not have a direct probabilistic interpretation. This can be estimated via an internal cross-validation (see the probability parameter of SVC), but this extra estimation is costly.

With those traits in mind, generally one can turn to SVMs once other simpler, faster, and less tuning-intensive methods have been shown to be insufficient for my needs. Nevertheless, if you have the CPU cycles to commit to training and cross-validating an SVM on your data, the method can lead to excellent results.

Questionnaire

Perform a SVM Classification on the pima indians diabetes dataset and modify the kernel types and C parameter to check for varying model performances

In [78]:
```
# load the diabetes dataset
import numpy as np
import pandas as pd
data = pd.read_csv("diabetes.csv")

data.head()
X = data.iloc[:,0:8]
y = data.iloc[:,8]
```

In [85]:
```
# splitting X and y into training and testing sets
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.4,

# training the model on training set
from sklearn.svm import SVC # "Support Vector Classifier"
clb = SVC(C=1, kernel='linear')
clb.fit(X_train, y_train)

# making predictions on the testing set
y_pred = clb.predict(X_test)

# comparing actual response values (y_test) with predicted response value
from sklearn import metrics
print("SVM accuracy(in %):", metrics.accuracy_score(y_test, y_pred)*100)
```

```
Linear SVM accuracy(in %): 77.27272727272727
```

2. When should we use SVM

SVM can be used for best results in the following cases:

1) When number of features (variables) and number of training data is very large (say millions of features and millions of instances (data)).
2) When sparsity in the problem is very high, i.e., most of the features have zero value.
3) It is the best for document classification problems where sparsity is high and features/instances are also very high.
4) It also performs very well for problems like image classification, genes classsification, drug disambiguation etc. where number of features are high.