Introduction to SVMs:

SVMs are used in applications like handwriting recognition, intrusion detection, face detection, email classification, gene classification, and in web pages. This is one of the reasons we use SVMs in machine learning. It can handle both classification and regression on linear and non-linear data.

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. Let you have basic understandings from this article before you proceed further. Here I'll discuss an example about SVM classification of cancer UCI datasets using machine learning tools i.e. scikit-learn compatible with Python. **Pre-requisites:** Numpy, Pandas, matplotlib, scikit-learn Let's have a quick example of support vector classification. First we need to create a dataset:

python3

importing scikit learn with make_blobs

from sklearn.datasets.samples_generator import make_blobs

creating datasets X containing n_samples

Y containing two classes

X, Y = make_blobs(n_samples=500, centers=2,

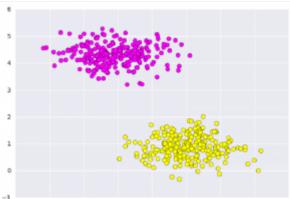
random_state=0, cluster_std=0.40)

import matplotlib.pyplot as plt

plotting scatters

plt.scatter(X[:, 0], X[:, 1], c=Y, s=50, cmap='spring');

plt.show()



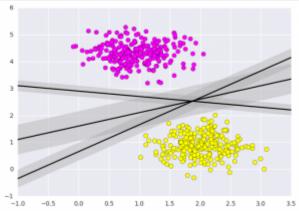
Output: -1.05 100 105 100 125 200 2.5 300 35 What Support vector machines do, is to not only draw a line between two classes here, but consider a region about the line of some given width. Here's an example of what it can look like:

python3

creating linspace between -1 to 3.5

xfit = np.linspace(-1, 3.5)

```
# plotting scatter
plt.scatter(X[:, 0], X[:, 1], c=Y, s=50, cmap='spring')
# plot a line between the different sets of data
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);
plt.show()
```



Importing datasets

This is the intuition of support vector machines, which optimize a linear discriminant model representing the perpendicular distance between the datasets. Now let's train the

classifier using our training data. Before training, we need to import cancer datasets as csv file where we will train two features out of all features.

python3 # importing required libraries import numpy as np import pandas as pd import matplotlib.pyplot as plt # reading csv file and extracting class column to y. $x = pd.read csv("C:\...\cancer.csv")$ a = np.array(x)y = a[:,30] # classes having 0 and 1# extracting two features x = np.column_stack((x.malignant,x.benign)) # 569 samples and 2 features x.shape print (x),(y)

Fitting a Support Vector Machine

Now we'll fit a Support Vector Machine Classifier to these points. While the mathematical details of the likelihood model are interesting, we'll let read about those elsewhere. Instead, we'll just treat the scikit-learn algorithm as a black box which accomplishes the above task.

```
# import support vector classifier

# "Support Vector Classifier"

from sklearn.svm import SVC

clf = SVC(kernel='linear')
```

```
# fitting x samples and y classes

clf.fit(x, y)
```

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

```
• python3

clf.predict([[120, 990]])

clf.predict([[85, 550]])

array([ 0.])
```

array([1.])

Let's have a look on the graph how does this show.

This is obtained by analyzing the data taken and pre-processing methods to make optimal hyperplanes using matplotlib function.

