INF552 Homework 7

Group members and contribution :
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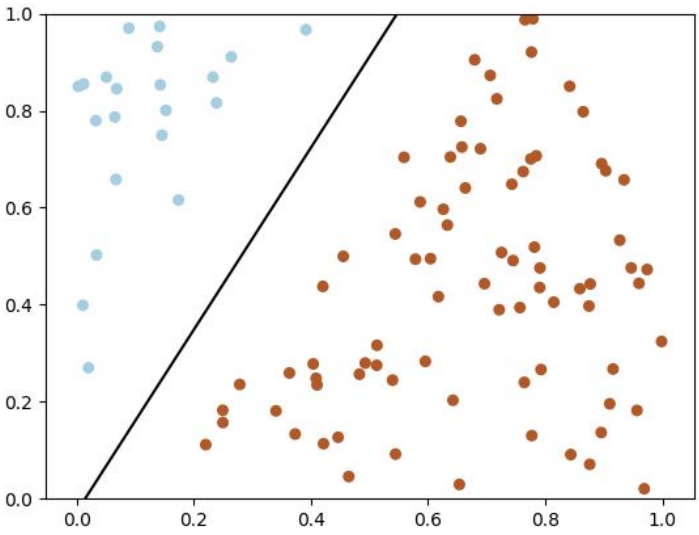
Part 1: Implementation

- Output after running the program

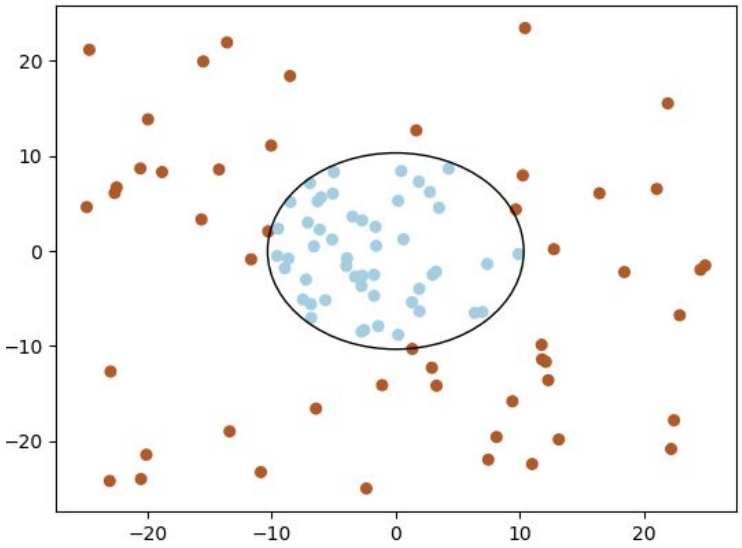
1. Linear separable (svm_linear.py)

Equation : $w^T x+b$
Weight = [7.2500563 -3.86188924]
B = [-0.10698734]

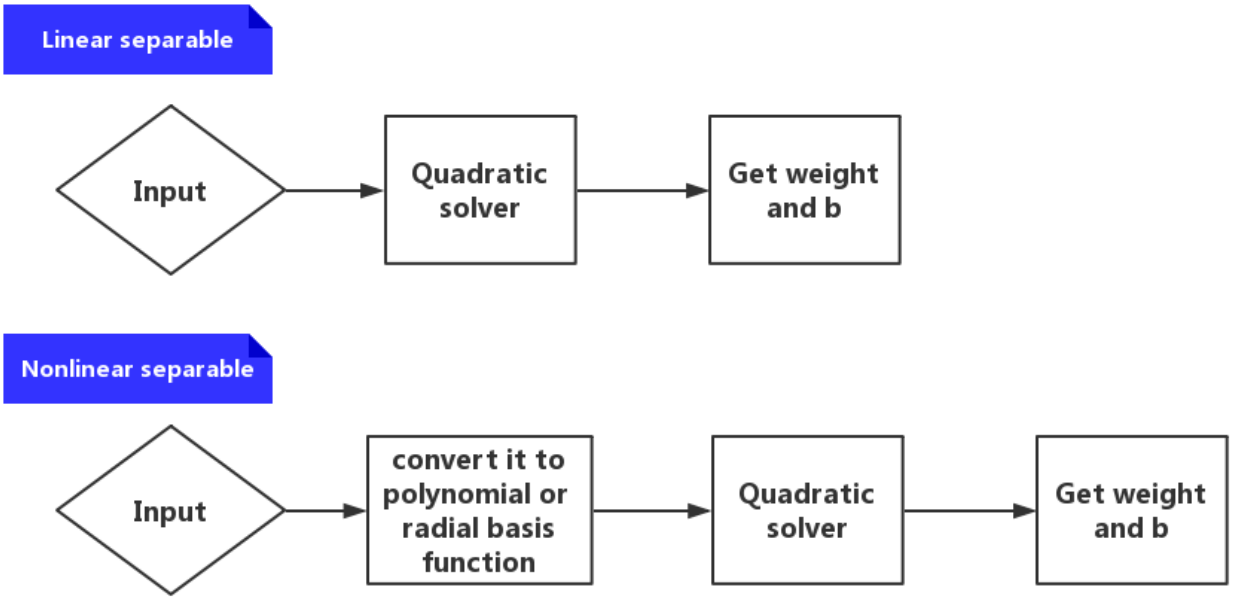


2. Nonlinear separable (svm_nonlinear.py)

Kernel function : polynomial function
$K(x, x') = z^T z = (1+x^T x')^2$
Equation : $w^T z+b$ (linear line in z space)
Weight = [2.77180846e-18 5.47976504e-02 1.63711136e-01 -7.64687397e-03
-2.89071336e-02 7.74955804e-02]
B = [-17.03884588]



- Data structures

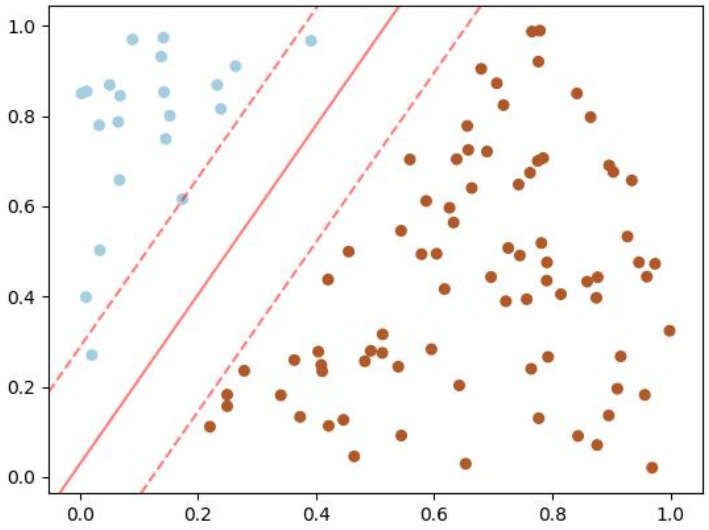


- Code-level optimization
  - Quadratic solver : We have store each variables on array and matrix to use quadratic solver in python.
  - Vectorization : We have used arrays for vectorization to calculate fast.
  - Weight, b are also stored in array once we get the solution through quadratic solver.

- ## Challenges
  - Nonlinear : There are several choices of nonlinear curve such as polynomial, radial basis function (gaussian basis function) etc. We had a hard time to figure out what nonlinear function would properly separate the data points into two parts. What we have done is that we have chosen the function separates the data points the most properly among polynomial, radial basis function.

Part 2: Software Familiarization

1. Linear separable

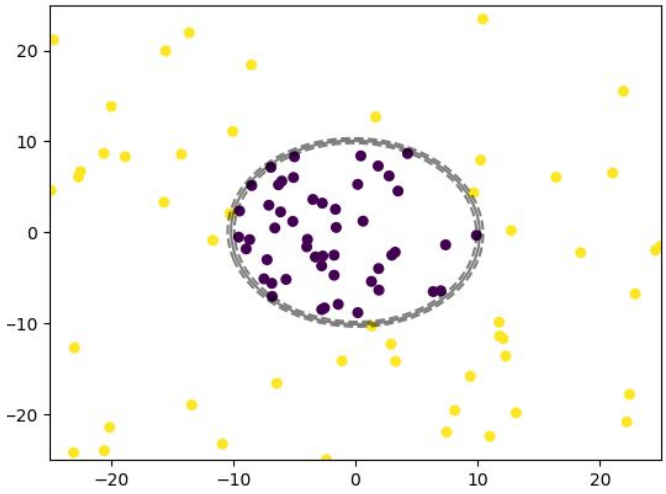


Weight = [[7.25046744 -3.8608154]]
Support vector = [[0.3917889 0.96675591]
[0.02066458 0.27003158]
[0.24979414 0.18230306]]
B = [-0.10758606]
Accuracy = 100.0 %

2. nonlinear separable

Support vector = [[-6.90647562 7.14833849]
[9.90143538 -0.31483149]
[-10.260969 2.07391791]
[1.3393313 -10.29098822]]

b= [-18.92792843]



How to improve our code

- The hyperspace equation can be tuned using hyper-parameters such as Gamma.

Part 3: Applications

- SVMs are helpful in text and hypertext categorization as their application can significantly reduce the need for labeled training instances in both the standard inductive and transductive settings.
- The SVM algorithm has been widely applied in the biological and other sciences. They have been used to classify proteins with up to 90% of the compounds classified correctly. Permutation tests based on SVM weights have been suggested as a mechanism for interpretation of SVM models. Support vector machine weights have also been used to interpret SVM models in the past. Posthoc interpretation of support vector machine models in order to identify features used by the model to make predictions is a relatively new area of research with special significance in the biological sciences.