**Code**

%Read the file

[X] = xlsread('CellDNA.xls');

Y = X(:,14);

X(:,14) = [];

%Standardize variables

ZX = [zscore(X)];

%Convert the response variables into non-interesting = 0 and interesting=1 value

for i = 1:length(Y)

if Y(i,1) > 0

Y(i,1) = 1;

else

Y(i,1) = 0;

end

end;

%Create SVM model

SVMModel = fitcsvm(ZX, Y);

%SVMModel = fitcsvm(X, Y, 'Standardize', true);

%Find Support vectors

sv = SVMModel.SupportVectors;

size(sv)

%Find top 3 support vectors

theta = SVMModel.Beta;

theta0 = SVMModel.Bias;

result=X\*theta + theta0 ;

top=sort(abs(result));

top(1)

top(2)

top(3)

%Find values

result(131)

result(165)

result(892)

result(1057)

**Answer the following questions:**

1.How many support vectors did you find?

**Solution:**

There are 228 support vectors

SVMModel = fitcsvm(ZX, Y);

%SVMModel = fitcsvm(X, Y, 'Standardize', true);

sv = SVMModel.SupportVectors;

size(sv)

2.List top 3 records that have the smallest \*\*absolute\*\* values from wT•X + b

calculation.

**Solution:**

0.0643

0.0715

0.0859

theta = SVMModel.Beta;

theta0 = SVMModel.Bias;

result=X\*theta + theta0;

top=sort(abs(result));

top(1)

top(2)

top(3)

3.What are the “wT•X + b” values for the following records: 131, 165, 892, 001057?

Anything special about those values of these few records?

result(131)

result(165)

result(892)

result(1057)

131 = -300.9989

165 = -11.4094

892 = 10.7256

1057 = -374.4515

Look at the Theta values for 131,1057, they are extremely large, they could be the potential outliers