Support Vector Machine

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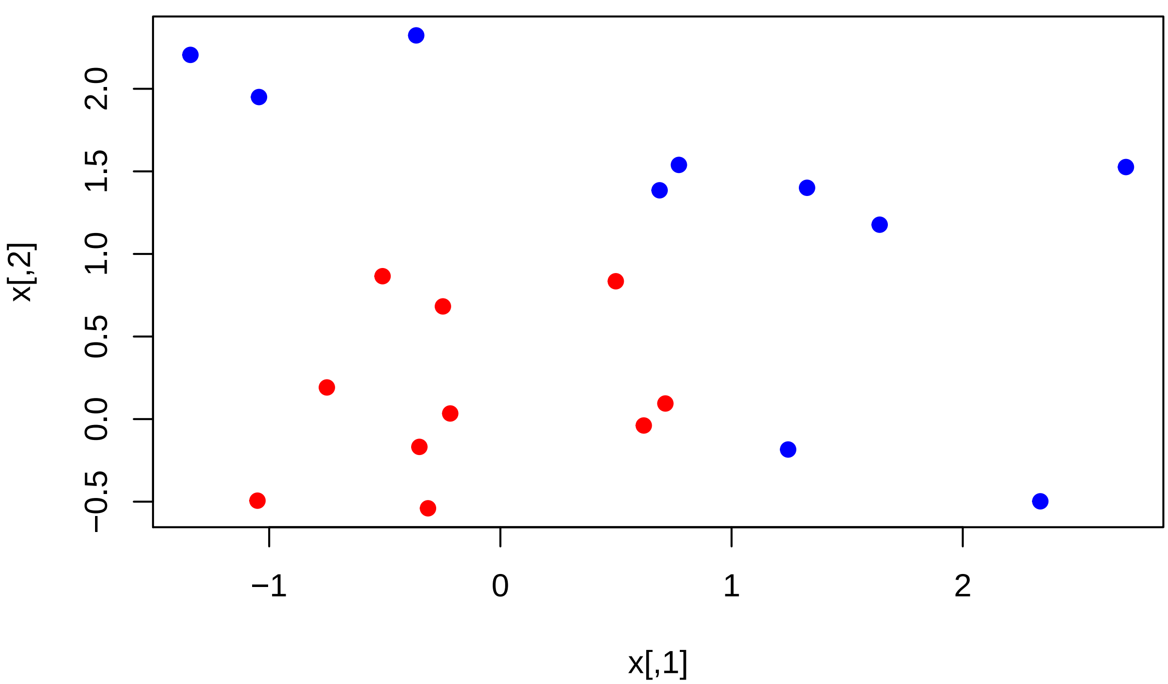
4 januari 2016

To demonstrate the SVM, it is easiest to work in low dimensions, so we can see the data.

Linear SVM classifer

Lets generate some data in two dimensions, and make them a little seperated.

```
set.seed(10111)

x=matrix(rnorm(40), 20, 2)
y=rep(c(-1,1), c(10,10))
x[y==1,]=x[y==1,]+1


plot(x,col=y+3, pch=19)
```

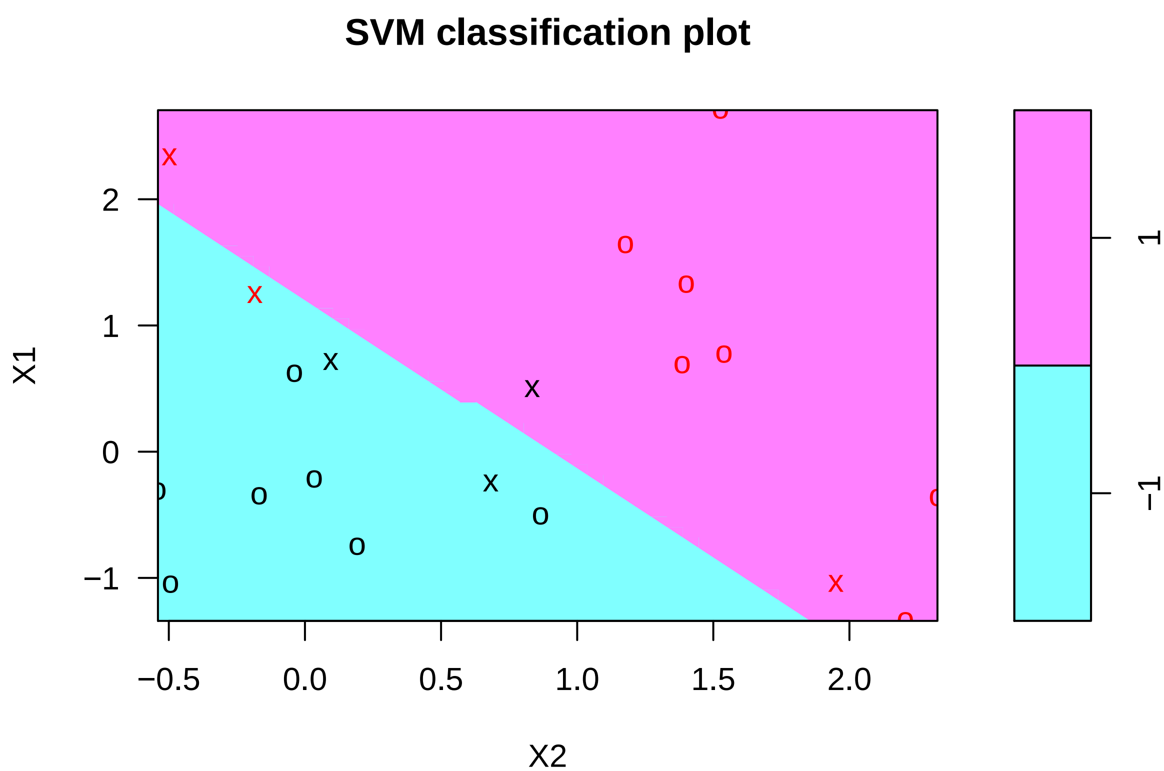


Now we load the packages `e1071` which contains the `svm` function we will use. We then compute the fit. Notice that we have to specify a `cost` parameters, which is a tuning parameters.

```r
library(e1071)
dat=data.frame(x,y=as.factor(y))
svmfit=svm(y~., data=dat, kernel="linear", cost=10, scale=FALSE)

print(svmfit)
```

```
##
## Call:
## svm(formula = y ~ ., data = dat, kernel = "linear", cost = 10,
##     scale = FALSE)
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  linear
##        cost:  10
##       gamma:  0.5
##
## Number of Support Vectors:  6
```

```r
plot(svmfit, dat)
```

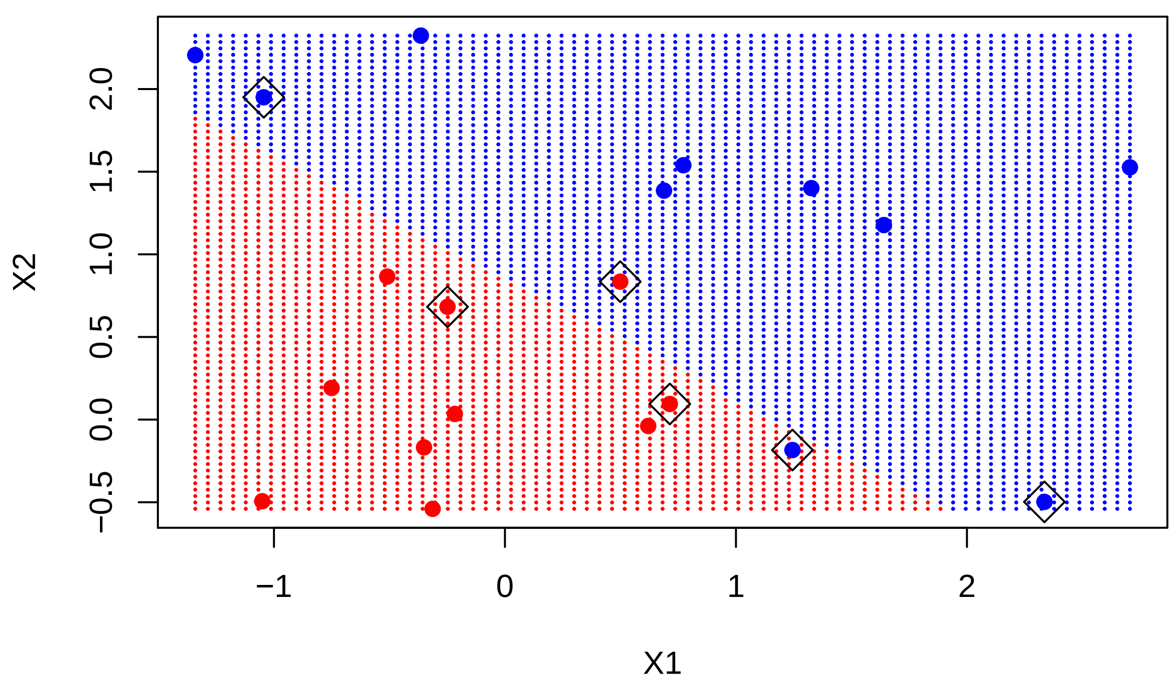


As Mentioned in the chapther, the plot function is somewhat crude, and plots X2 on the horizontial axis (unlike what R would do automatically for a matrix). Lets see how we might make Own plot.

The first thing we will do is make a grid of values for X1 and X2. We will write a function to do that, in case we want to reuse it. It uses the handy function `expand grid`, and produces the cordinates of n*n points on a lattice covering the domain of `x`.Having made the lattice, we make a prediction at each point on the lattice. We then plot the lattice, color-coded according to the classification. Now we can see the decision boundary.

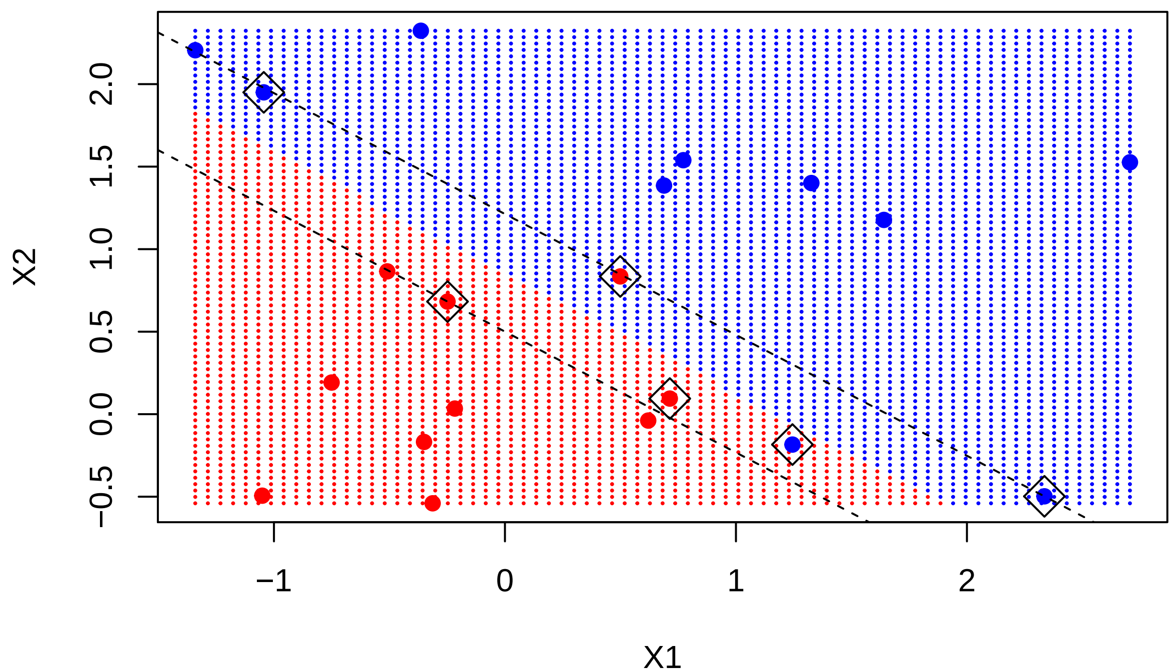
The support points (points on the margin, or on the wrong side of the margin) are the indexed in the `$index` component of the fit.

```
make.grid=function(x, n=75){
  grange=apply(x, 2, range)
  x1=seq(from=grange[1,1], to=grange[2,1], length=n)
  x2=seq(from=grange[1,2], to=grange[2,2], length=n)
  expand.grid(X1=x1, X2=x2)
}
xgrid=make.grid(x)
ygrid=predict(svmfit, xgrid)

### Plot the xgrid ###
plot(xgrid, col=c("red","blue")[as.numeric(ygrid)], pch=20, cex=.2)
points(x, col=y+3, pch=19)

points(x[svmfit$index,], pch=5, cex=2)
```



The `svm` function is not too friendly, in that we have to do some work to get back the linear coefficients, as decribed in the text. Probably the reason is that this only make sense for a linear kernels, and the function is more general. Here we will use a formula to extract the coefficients, for those interested in where this comes from, have a look in chapther 12 of ELS ("Element of statistical learning").

```
beta=drop(t(svmfit$coefs)%*%x[svmfit$index,])
beta0=svmfit$rho

plot(xgrid, col=c("red", "blue")[as.numeric(ygrid)], pch=20, cex=.2)
points(x, col=y+3, pch=19)
points(x[svmfit$index,], pch=5, cex=2)
abline((beta0-1)/beta[2], -beta[1]/beta[2], lty=2)
abline((beta0+1)/beta[2], -beta[1]/beta[2], lty=2)
```



Nonlinear SVM

```
### Load data ###
library(e1071)
load(url("http://www-stat.stanford.edu/~tibs/ElemStatLearn
/datasets/ESL.mixture.rda"))

### names for the variable ###
names(ESL.mixture)
```

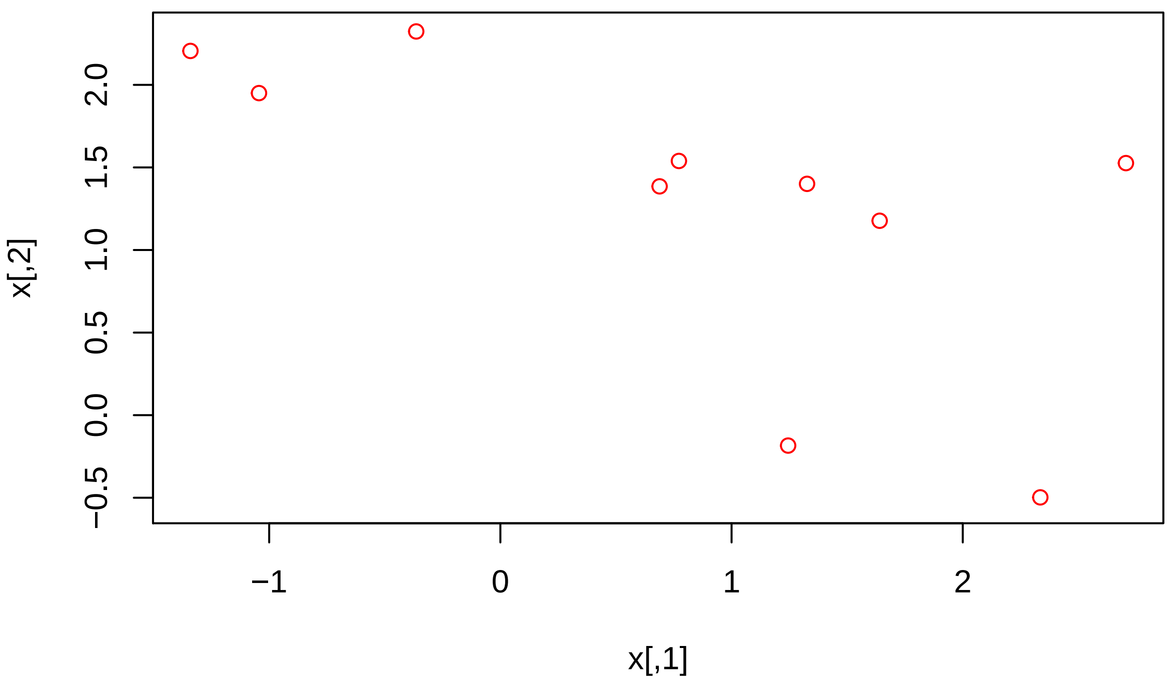
```
## [1] "x"        "y"        "xnew"     "prob"     "marginal" "px1"
## [7] "px2"      "means"
```

```r
attach(ESL.mixture)
```

```
## The following objects are masked _by_ .GlobalEnv:
##
##     x, y
```

These data are also two dimensional. Lets plot them and fit a nonlinear SVM, using a radial Learning.

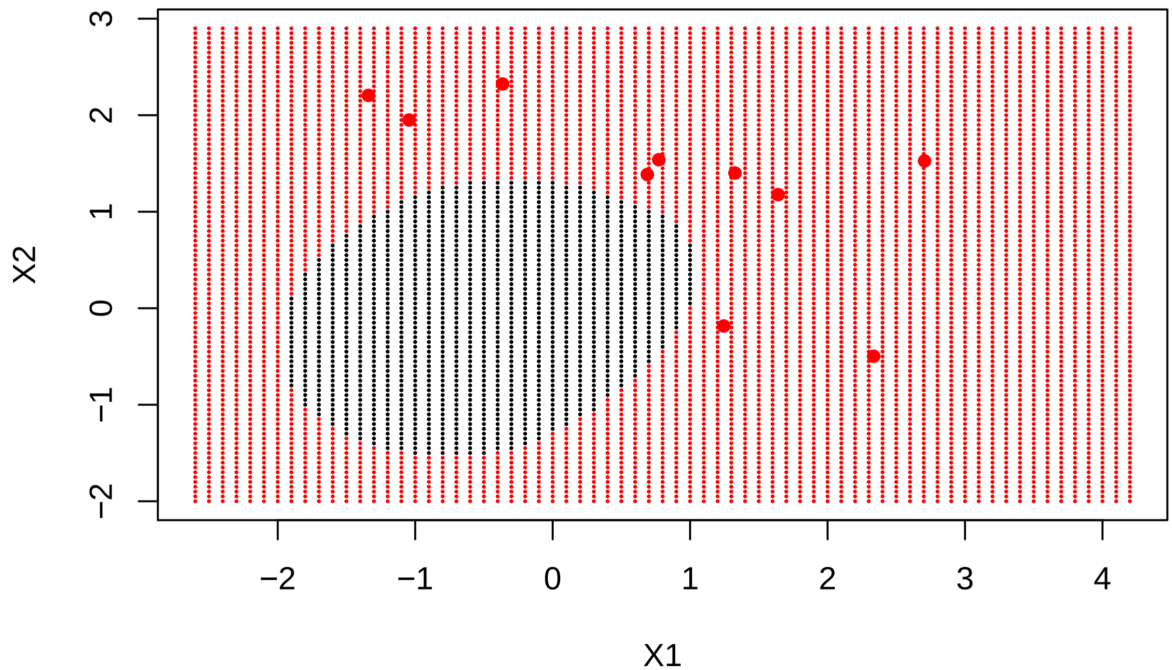
```r
plot(x, col=y+1)
```




```r
dat=data.frame(y=factor(y), x)

### SVM model ###
fit=svm(factor(y)~., data=dat, scale=FALSE, kernel="radial", cost=5)
```

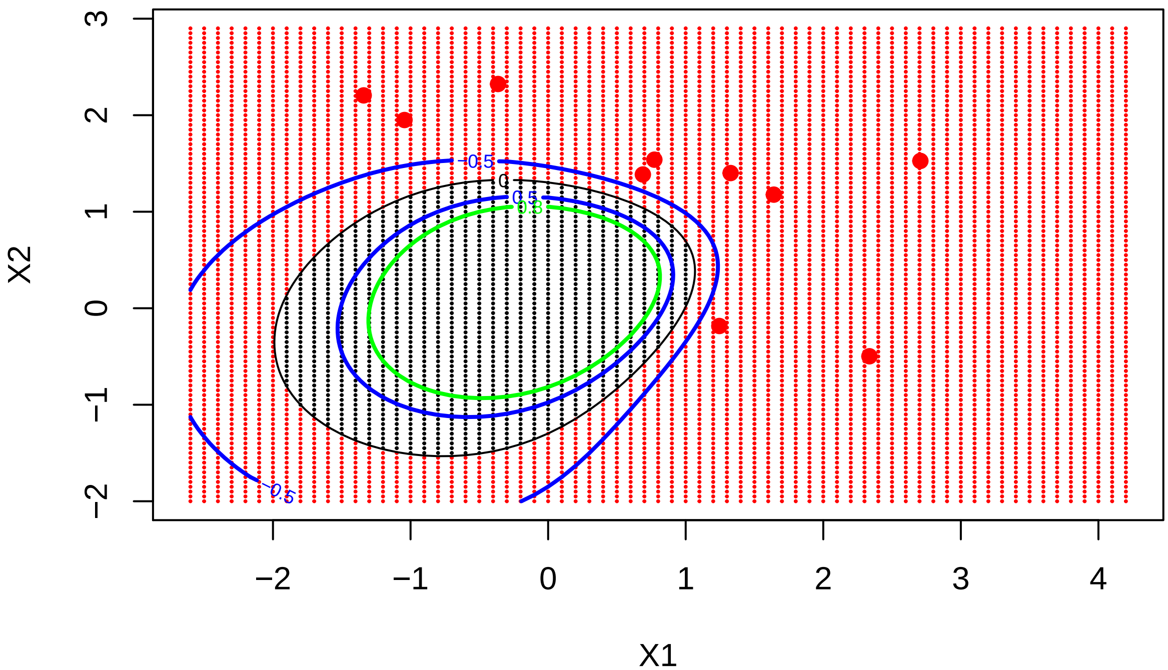
Now we are going to create a grid, as before, and make predictions on the grid. These data have the grid points for each variable include on the data frame.

```r
xgrid=expand.grid(X1=px1, X2=px2)
ygrid=predict(fit, xgrid)

plot(xgrid, col=as.numeric(ygrid), pch=20, cex=0.2)
points(x, col=y+1, pch=19, cex=0.8)
```



We can furher, and have the predict function produce the actual function function estimates at each of our grid points. We can include the actual decisions boundary on the plot by making use of the contour function. On the data frame is also `prob`, which is the ture probability of class 1 for these data, at the gridpoints. If we plot its 0.5 contour, that will give us the *Bayes Decisions Boundary*, which is the best one could ever do.

```
func=predict(fit, xgrid, decision.values = TRUE)
func=(attributes(func)$decision)


xgrid=expand.grid(X1=px1,X2=px2)
ygird=predict(fit, xgrid)

plot(xgrid, col=as.factor(ygrid), pch=20, cex=0.2)
points(x, col=y+1, pch=19)

contour(px1, px2, matrix(func,69 ,99), level=0, add=TRUE)
contour(px1, px2, matrix(func,69 ,99), level=0.5, add=TRUE, col="blue", lwd=2)
contour(px1, px2, matrix(func,69 ,99), level=0.8, add=TRUE, col="green", lwd=2)

contour(px1, px2, matrix(func,69 ,99), level=-0.5, add=TRUE, col="blue", lwd=2)
```



3
2
1
0
−1
−2
X2
−2
−1
0
1
2
3
4
X1
-0.5
0
0.5
0.8
-0.5