Support Vector Machines (SVMs)

for classification

Freddy Hernández

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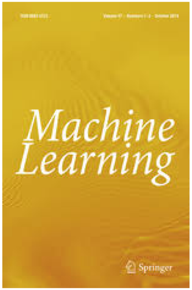
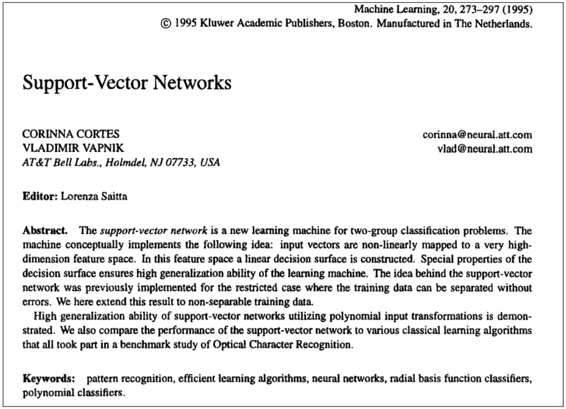
Support Vector Machines (SVMs)

SVMs were developed by Cortes & Vapnik (1995) for binary classification.

Url: https://link.springer.com/article/10.1023/A:1022627411411





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Support-Vector Networks

CORINNA CORTES corinna@neural.att.com
VLADIMIR VAPNIK vlad@neural.att.com
AT&T Bell Labs., Holmdel, NJ 07733, USA

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Abstract. The *support-vector network* is a new learning machine for two-group classification problems. The machine conceptually implements the following idea: input vectors are non-linearly mapped to a very high-dimension feature space. In this feature space a linear decision surface is constructed. Special properties of the decision surface ensures high generalization ability of the learning machine. The idea behind the support-vector network was previously implemented for the restricted case where the training data can be separated without errors. We here extend this result to non-separable training data.

High generalization ability of support-vector networks utilizing polynomial input transformations is demonstrated. We also compare the performance of the support-vector network to various classical learning algorithms that all took part in a benchmark study of Optical Character Recognition.

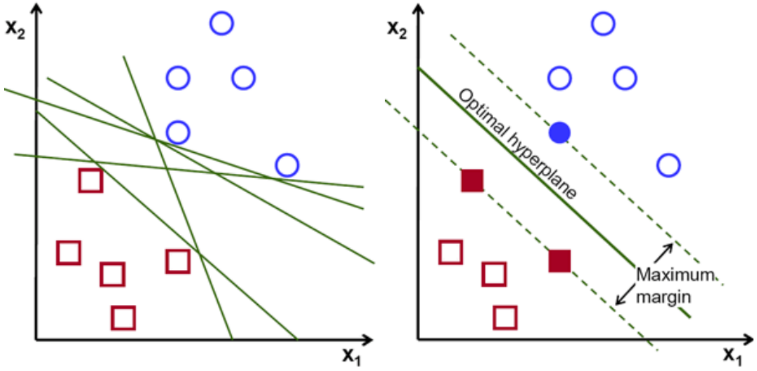
Keywords: pattern recognition, efficient learning algorithms, neural networks, radial basis function classifiers, polynomial classifiers.

An overview of Support Vector Machines

https://www.svm-tutorial.com/2017/02/svms-overview-support-vector-machines/

Idea

The objective of the Support Vector Machine algorithm is to find the hyperplane that has the maximum margin in an *N*-dimensional space that distinctly classifies the data points.



R packages

1. The first implementation of SVM in R (R Development Core Team 2005) was introduced in the **e1071** (Dimitriadou, Hornik, Leisch, Meyer, and Weingessel 2005) package.
2. Package **kernlab** features a variety of kernel-based methods and includes a SVM method based on the optimizers used in libsvm and bsvm (Hsu and Lin 2002c).
3. Package **klaR** (Roever, Raabe, Luebke, and Ligges 2005) includes an interface to SVMlight, a popular SVM implementation that additionally offers classification tools such as Regularized Discriminant Analysis.
4. package **svmpath** (Hastie 2004) provides an algorithm that fits the entire path of the SVM solution.

The package **e1071**

The package **e1071** contains the `svm` function used for SVMs. To install the package:

```
install.packages("e1071")
```

To load the package:

```
library(e1071)
```

The main function is:

```
svm(formula, data, scale=TRUE,
    kernel=linear or polynomial or radial or sigmoid,
    degree=3, gamma=1/n, coef0=0, cost=1, ...)
```

Consult the vignette:

https://cran.r-project.org/web/packages/e1071/vignettes/svmdoc.pdf

Example 1

Let's first download some Train data.

```
url <- "https://raw.githubusercontent.com/rdaymedellin/
tutoriales_Rday_2019/master/Machine%20Learning/blobs_train.txt"
Train <- read.table(url, sep=";", header=TRUE)
```

Exploring the dimensions and the content of Train dataset.

```
dim(Train)
```

```
## [1] 400   3
```

```
Train[199:202, ]  # Four middle observations
```

```
##                x1        x2     y
## 199 -0.0004792237 0.2484083 Pop 1
## 200 -1.3730953800 1.8877677 Pop 1
## 201  2.5548979647 0.2001338 Pop 2
## 202  2.9806430286 0.4338085 Pop 2
```

Example 1

You tell svm that the kernel is linear, the tune-in parameter cost is 10, and scale equals FALSE.

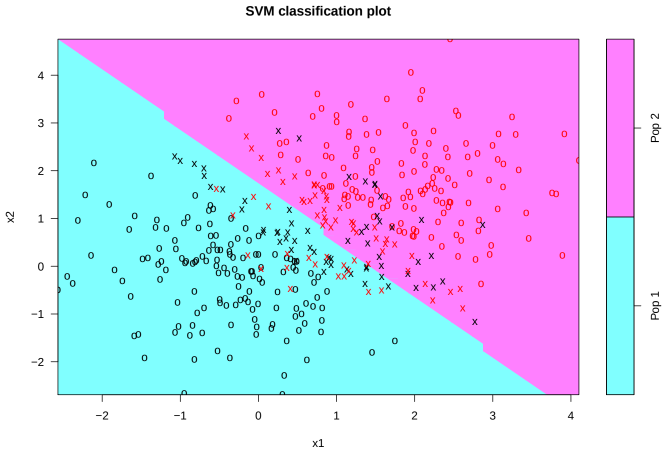
```
svm_lin <- svm(y ~ x1 + x2, data=Train, kernel="linear", scale=FALSE)
print(svm_lin)
```

```
##
## Call:
## svm(formula = y ~ x1 + x2, data = Train, kernel = "linear", scale = FALSE)
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  linear
##        cost:  1
##
## Number of Support Vectors:  123
```

Example 1

There's a plot function for SVM that shows the decision boundary.

```
plot(x=svm_lin, data=Train, formula=x2~x1,
     color.palette = cm.colors,
     symbolPalette=c('black', 'red'))
```



Example 1

To classify observations we can use the `predict` function.

```
pred_lin <- predict(object=svm_lin, newdata=Train[, -3])
```

To obtain the Confusion Matrix we can use:

```
tabla <- table(Predictions=pred_lin, True=Train$y)
tabla
```

```
##            True
## Predictions Pop 1 Pop 2
##       Pop 1   173    19
##       Pop 2    27   181
```

To obtain the accuracy we can use:

```
sum(diag(tabla)) / sum(tabla)
```

```
## [1] 0.885
```

Example 1

Download the `Test` dataset.

```
url <- "https://raw.githubusercontent.com/rdaymedellin/
tutoriales_Rday_2019/master/Machine%20Learning/blobs_test.txt"
Test <- read.table(url, sep=";", header=TRUE)
```

Exploring the dimensions and the content of `Train` dataset.

```
dim(Test)
```

```
## [1] 100   3
```

```
Test[49:52, ]  # Four middle observations
```

```
##            x1         x2     y
## 49 -1.4132094 -0.7593428 Pop 1
## 50 -1.3746188 -0.4218237 Pop 1
## 51  2.0752031  1.2803257 Pop 2
## 52  0.9922126  0.8767329 Pop 2
```

Example 1

To classify new observations using the information in the Test dataset we can use the predict function.

```
pred_lin <- predict(object=svm_lin, newdata=Test)
```

To obtain the Confusion Matrix we can use:

```
tabla <- table(Predictions=pred_lin, True=Test$y)
tabla
```

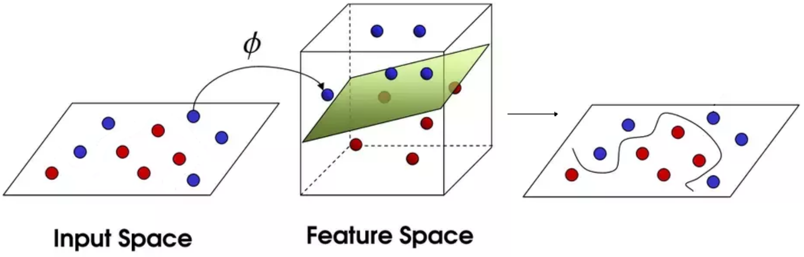
```
##            True
## Predictions Pop 1 Pop 2
##       Pop 1    40     3
##       Pop 2    10    47
```

To obtain the accuracy we can use:

```
sum(diag(tabla)) / sum(tabla)
```

```
## [1] 0.87
```

Kernels



See the next video:

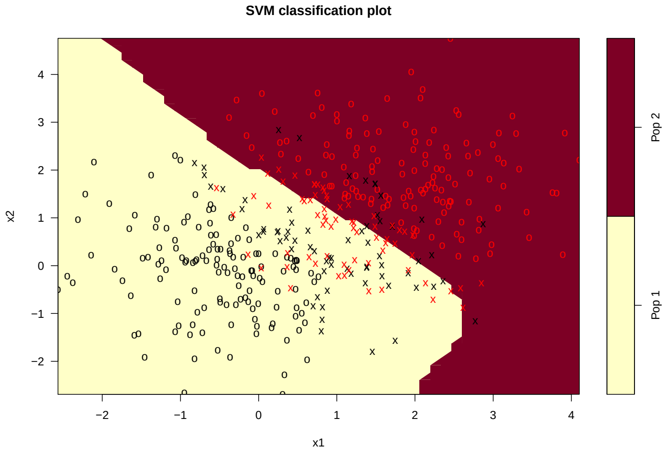
https://www.youtube.com/watch?v=3liCbRZPrZA

Kernels

- linear
- polynomial
- radial
- sigmoid

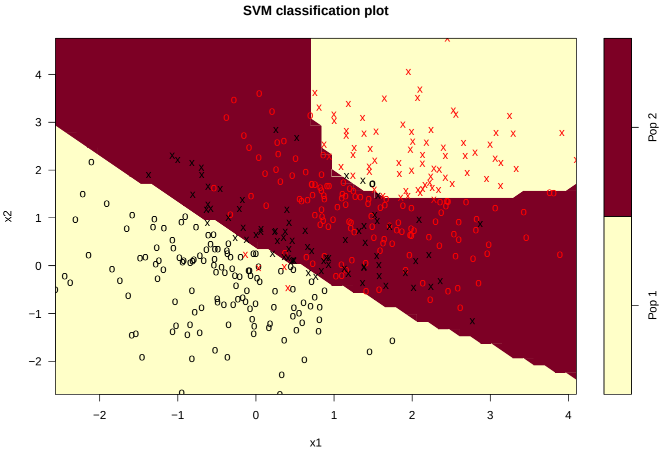
Example 1

```
svm_pol <- svm(y ~ ., data=Train, kernel="polynomial", scale=FALSE)
plot(x=svm_pol, data=Train, formula=x2~x1)
```



Example 1

```r
svm_sig <- svm(y ~ ., data=Train, kernel="sigmoid", scale=FALSE)
plot(x=svm_sig, data=Train, formula=x2~x1)
```



Example 1

Accuracy for each model.

```r
pred <- predict(object=svm_lin, newdata=Test)
tabla <- table(pred, Test$y)
sum(diag(tabla)) / sum(tabla)
```

```
## [1] 0.87
```

```r
pred <- predict(object=svm_pol, newdata=Test)
tabla <- table(pred, Test$y)
sum(diag(tabla)) / sum(tabla)
```

```
## [1] 0.89
```

```r
pred <- predict(object=svm_sig, newdata=Test)
tabla <- table(pred, Test$y)
sum(diag(tabla)) / sum(tabla)
```

```
## [1] 0.53
```

What is inside svm object?

What is the class of `svm_lin`?

```
class(svm_lin)
```

```
## [1] "svm.formula" "svm"
```

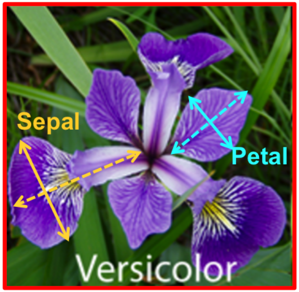
What is inside `svm_lin`?

```
names(svm_lin)
```

```
##  [1] "call"            "type"            "kernel"
##  [4] "cost"            "degree"          "gamma"
##  [7] "coef0"           "nu"              "epsilon"
## [10] "sparse"          "scaled"          "x.scale"
## [13] "y.scale"         "nclasses"        "levels"
## [16] "tot.nSV"         "nSV"             "labels"
## [19] "SV"              "index"           "rho"
## [22] "compprob"        "probA"           "probB"
## [25] "sigma"           "coefs"           "na.action"
## [28] "fitted"          "decision.values" "terms"
```

Example with iris

Could be used sepal length and sepal width to predict the Species?



```r
head(iris)
```

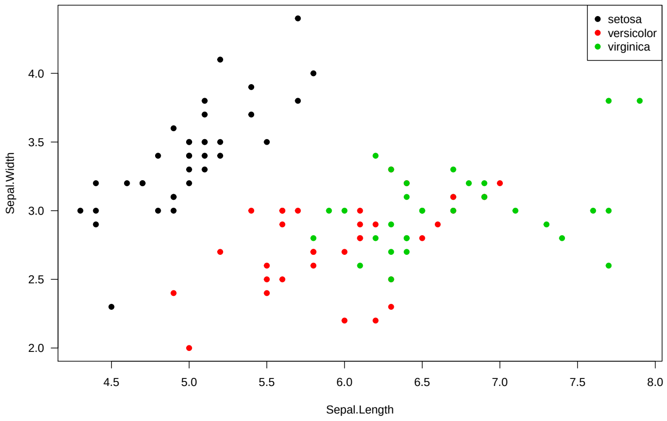
```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

Example iris

We can split the original data into `Train` and `Test`.

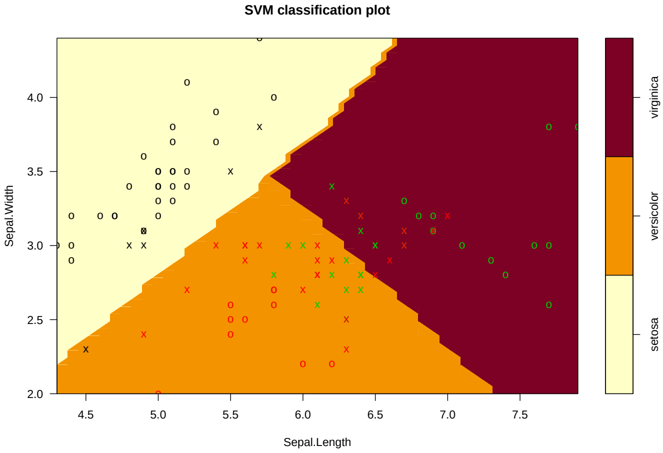
```
indices <- sample(1:150, size=100)
Train <- iris[indices, c(1, 2, 5)]
Test  <- iris[-indices, c(1, 2, 5)]
```

Example iris



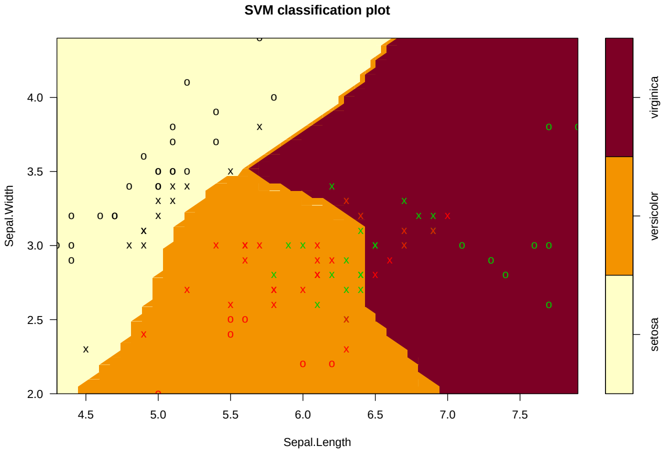
Example iris

```
iris1 <- svm(Species ~  Sepal.Width + Sepal.Length,
             data=Train, kernel="linear", scale=TRUE)
plot(iris1, Train)
```



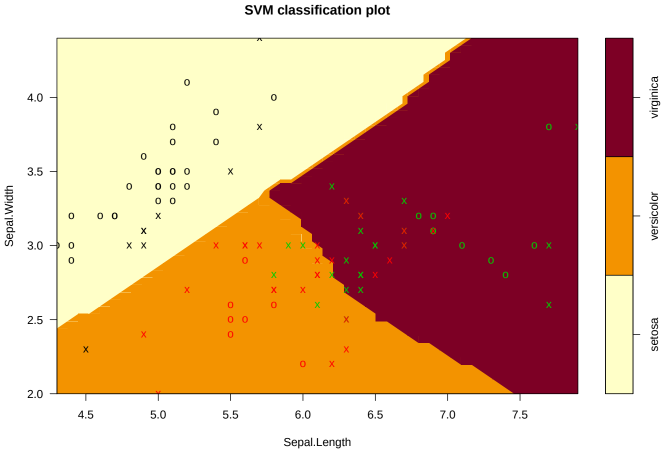
Example iris

```
iris2 <- svm(Species ~  Sepal.Width + Sepal.Length,
             data=Train, kernel="polynomial", scale=TRUE)
plot(iris2, Train)
```



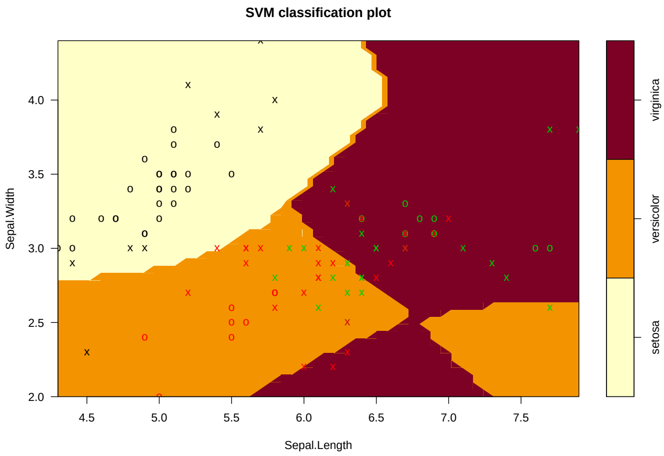
Example iris

```
iris3 <- svm(Species ~  Sepal.Width + Sepal.Length,
             data=Train, kernel="radial", scale=TRUE)
plot(iris3, Train)
```



Example iris

```r
iris4 <- svm(Species ~  Sepal.Width + Sepal.Length,
             data=Train, kernel="sigmoid", cost=1, scale=TRUE)
plot(iris4, Train)
```



other arguments for `svm`

- degree: parameter needed for kernel of type polynomial (default: 3).
- gamma: parameter needed for all kernels except linear (default: 1/(data dimension)).
- cost: cost of constraints violation (default: 1)—it is the ‘C’-constant of the regularization term in the Lagrange formulation.
- gamma: Kernel coefficient for ‘rbf’, ‘poly’ and ‘sigmoid’. Higher the value of gamma, will try to exact fit the as per training data set i.e. generalization error and cause over-fitting problem.

Pros and Cons associated with SVM

Pros:

- It works really well with clear margin of separation.
- It is effective in high dimensional spaces.
- It is effective in cases where number of dimensions is greater than the number of samples.
- It uses a subset of training points in the decision function (called support vectors), so it is also memory efficient.

Cons:

- It doesn't perform well, when we have large data set because the required training time is higher.
- It also doesn't perform very well, when the data set has more noise i.e. target classes are overlapping.
- SVM doesn't directly provide probability estimates, these are calculated using an expensive five-fold cross-validation. It is related SVC method of Python scikit-learn library.