Classification

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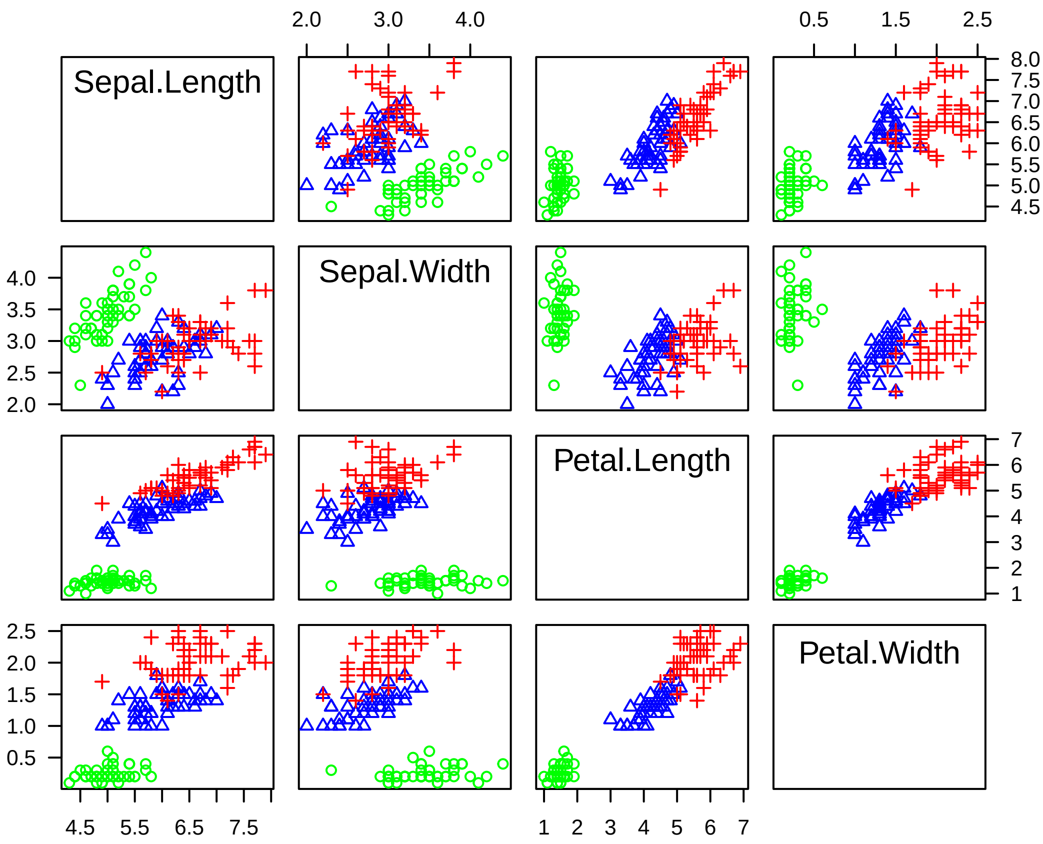
Iris Data

```
data(iris)
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
```

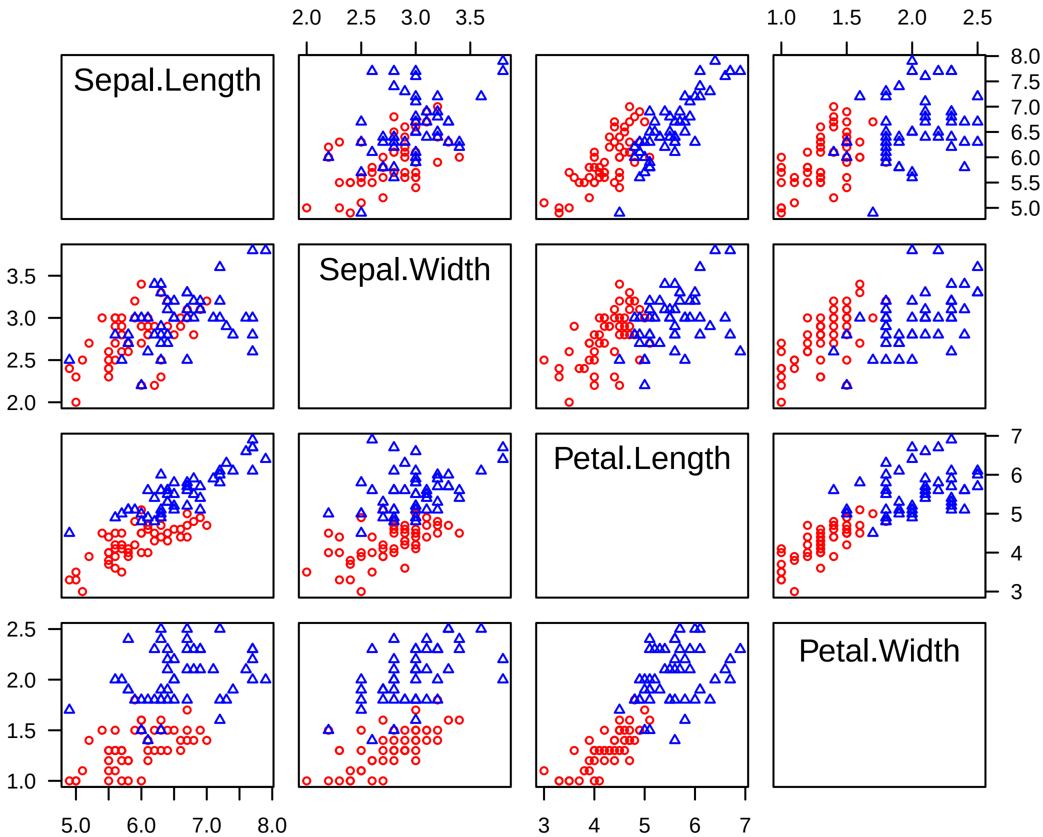
```
attach(iris) # Eliminates the need to code "iris$" when declaring variable names
library(car)

# Scatterplot Matrix
par(las = 1)
scatterplotMatrix(~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width | Species,
                  col = c("green", "blue", "red"), diagonal = F,
                  smooth = F, regLine = F, legend = F)
```



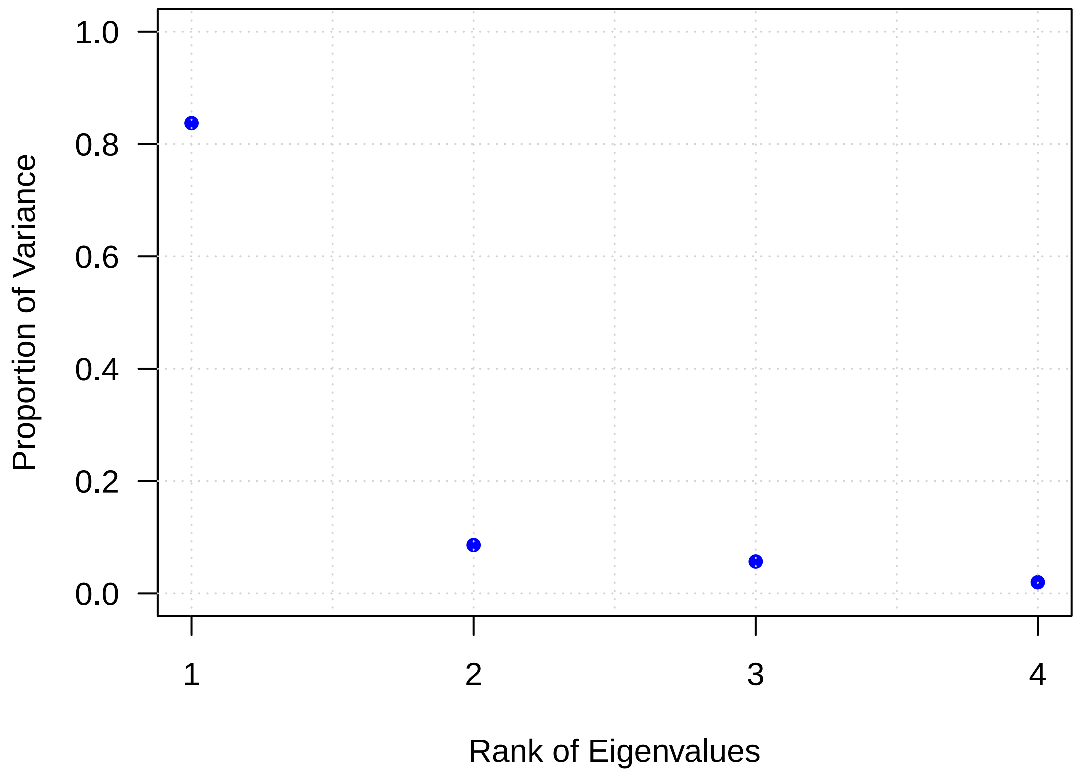
Binary Classification

```r
# Scatterplot Matrix
irisv = iris[51:150, ]
irisv$Species <- factor(irisv$Species)
attach(irisv)
par(las = 1)
scatterplotMatrix(~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width | Species,
                  col = c("red", "blue"), diagonal = F,
                  smooth = F, regLine = F, legend = F, cex = 0.75)
```

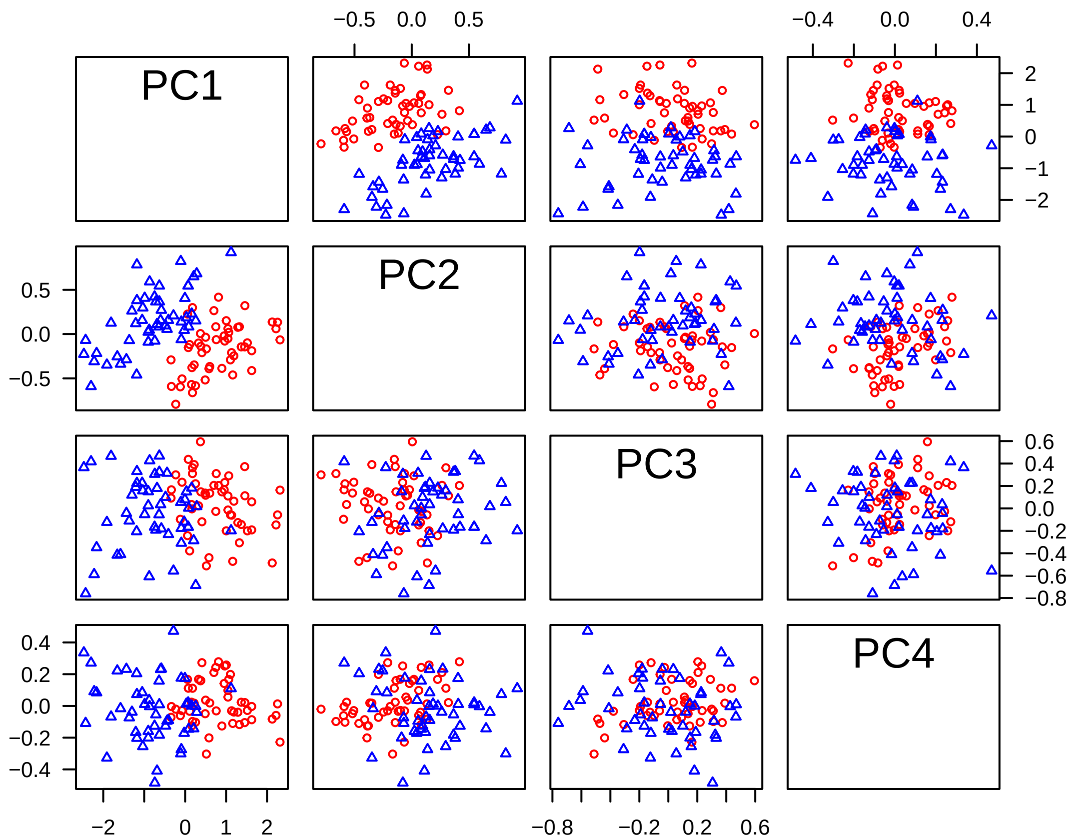


Principal Component Analysis (PCA)

```
# PCA
pca <- prcomp(irisv[, 1:4])
Z <- pca$x
lambda <- pca$sdev^2 # Eigenvalues
par(las = 1)
plot(1:4, lambda / sum(lambda), xaxt = "n", las = 1, xlab = "Rank of Eigenvalues",
     ylab = "Proportion of Variance", pch = 16, col = "blue", cex = 1, ylim = c(0, 1))
grid(); axis(1, at = 1:4)
```




```r
# Scatterplot Matrix
scatterplotMatrix(~ Z | Species, col = c("red", "blue"), diagonal = F, smooth = F,
                  regLine = F, legend = F, cex = 0.75)
```



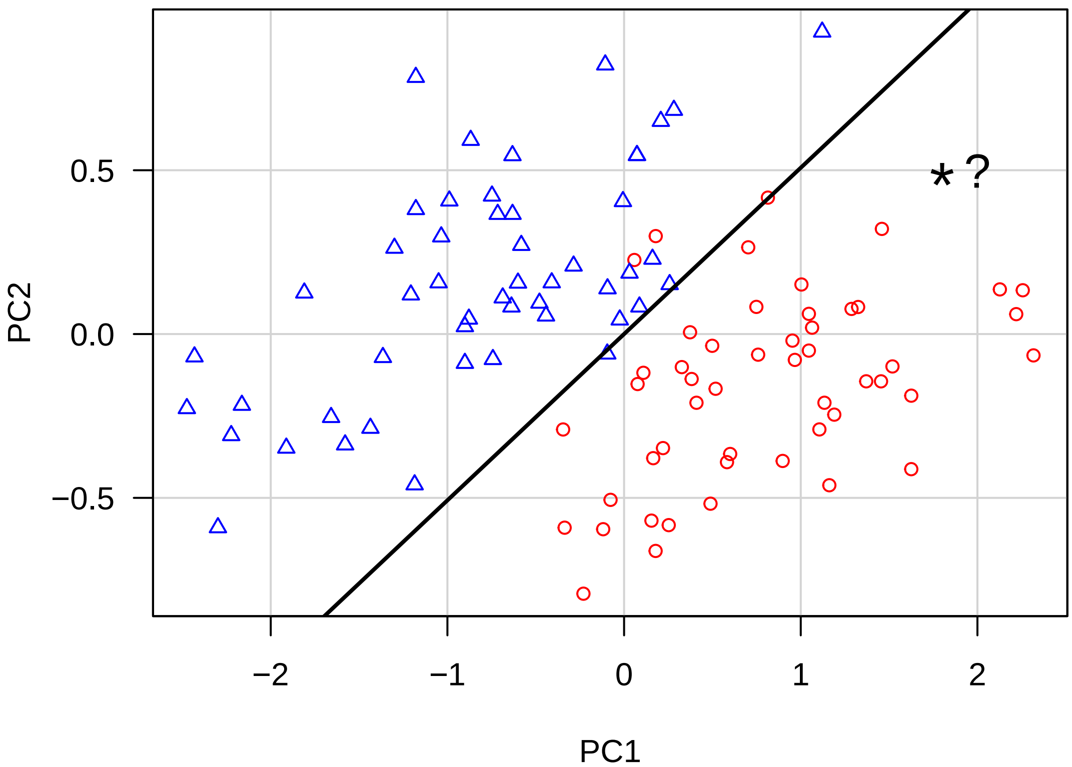
Linear Discriminant Analysis (LDA)

```
# LDA
library(MASS)
par(las = 1)
scatterplot(PC2 ~ PC1 | Species , Z, smooth = F, regLine = F, legend = F, cex = 0.85,
            col = c("red", "blue"))
fit <- lda(Species ~ Z[, 1:2])
fit # Shows Results
```

```
## Call:
## lda(Species ~ Z[, 1:2])
##
## Prior probabilities of groups:
## versicolor  virginica
##        0.5        0.5
##
## Group means:
##            Z[, 1:2]PC1 Z[, 1:2]PC2
## versicolor   0.7930189  -0.1607571
## virginica   -0.7930189   0.1607571
```

```
##
## Coefficients of linear discriminants:
##                 LD1
## Z[, 1:2]PC1 -1.553249
## Z[, 1:2]PC2  3.060560
```

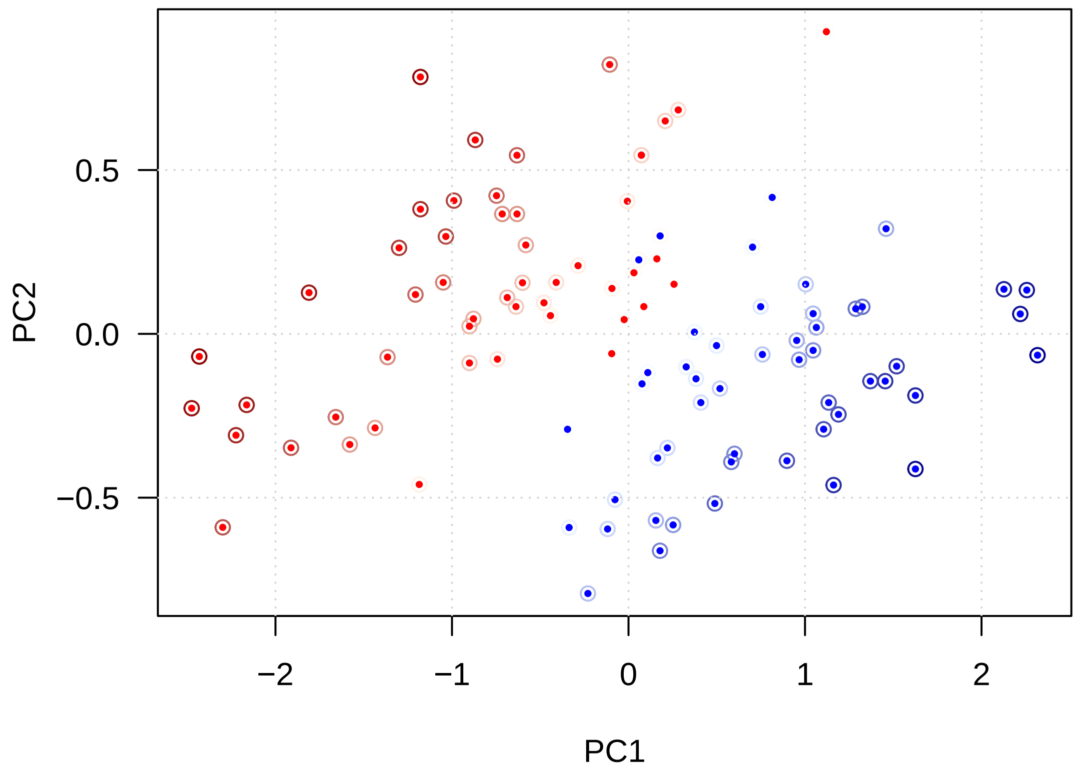
```r
abline(0, -fit$scaling[1] / fit$scaling[2], pch = 5, lwd = 2)
points(2, 0.5, pch = "?", cex = 1.5)
points(1.8, 0.5, pch = "*", cex = 2)
```



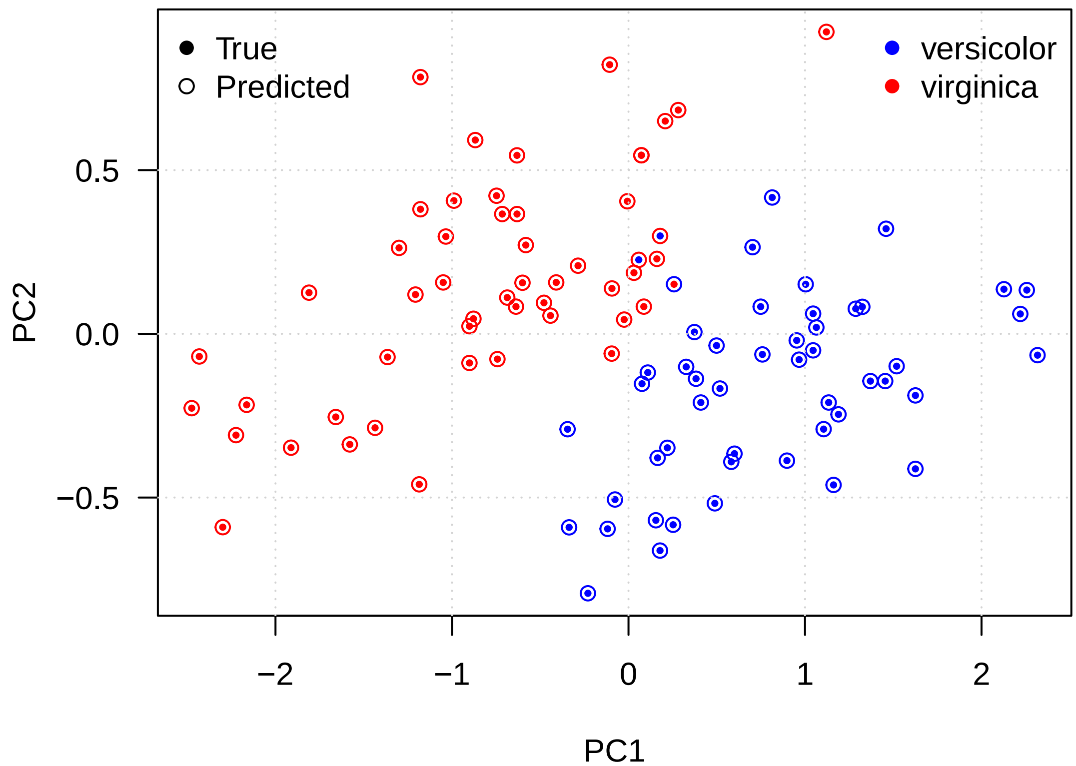
Logistic Regression

```r
# Logistic Regression Plot
logfit <- glm(irisv$Species ~ Z[, 1:2], family = binomial) # GLM = Generalized Linear Model
logpred <- predict(logfit, type = "response")
library(fields)
cols <- two.colors(n = 100, "darkblue", "darkred")
order <- order(logpred)
predCol <- ifelse(logpred <= 0.5, "blue", "red")
Col <- rep(c("blue", "red"), each = 50)
```

```r
plot(Z[order, 1:2], col = cols, pch = 1, las = 1)
points(Z[order, 1:2], col = Col[order], pch = 16, cex = 0.5)
grid()
```




```r
# Logistic Regression Plot
plot(Z[, 1:2], col = predCol, pch = 1, las = 1)
points(Z[, 1:2], col = Col, pch = 16, cex = 0.5)
grid()
legend("topleft", legend = c("True", "Predicted"), pch = c(16, 1), bty = "n")
legend("topright", legend = c("versicolor", "virginica"),
       col = c("blue", "red"), pch = 16, bty = "n")
```




```
# Logistic Regression Matrix
logisticPred <- ifelse(logpred <= 0.5, "versicolor", "virginica")
table(irisv$Species, logisticPred)
```

```
##             logisticPred
##              versicolor virginica
##   versicolor         48         2
##   virginica           1        49
```

LDA vs. QDA

```
# Treat Data as a Matrix
z = as.matrix(Z)

lda <- lda(irisv$Species ~ Z[, 1:2]) # LDA = Linear Discriminant Analysis
qda <- qda(irisv$Species ~ Z[, 1:2]) # QDA = Quadratic Discriminant Analysis

fit.LDA = predict(lda)$class
table(irisv$Species, fit.LDA)
```

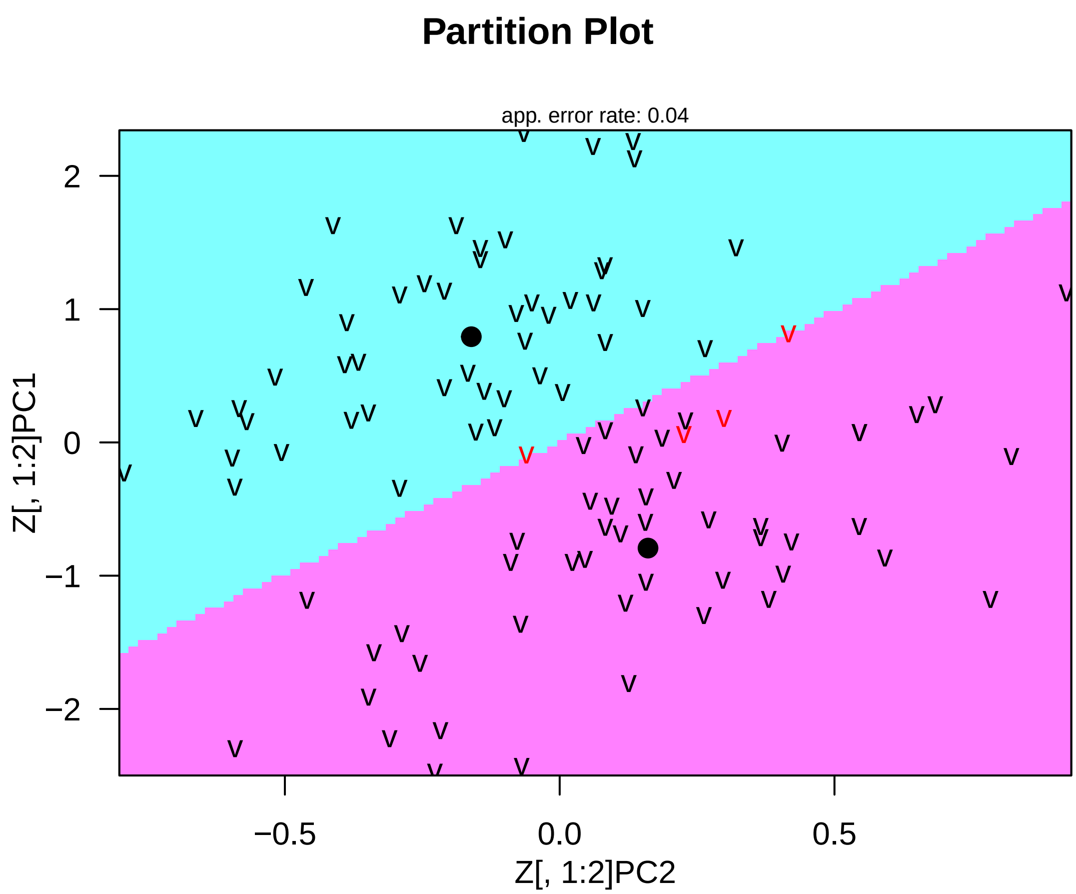
```
##             fit.LDA
```

```
##                versicolor virginica
##   versicolor          47         3
##   virginica            1        49
```

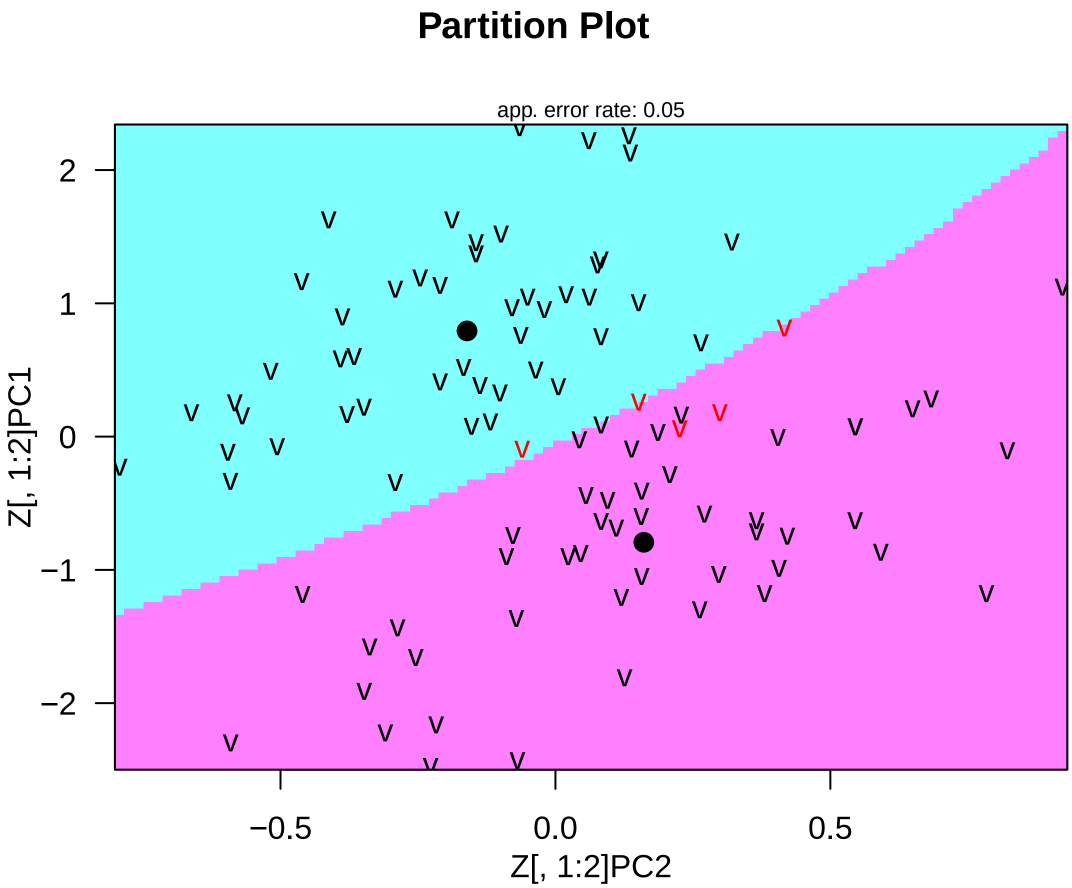
```
fit.QDA = predict(qda)$class
table(irisv$Species, fit.QDA)
```

```
##               fit.QDA
##                versicolor virginica
##   versicolor          47         3
##   virginica            2        48
```

```
# Show Results
library(klaR)
par(las = 1, mgp = c(2, 1, 0), mar = c(3.5, 3.5, 2, 1))
partimat(Species ~ Z[, 1:2], method = "lda")
```



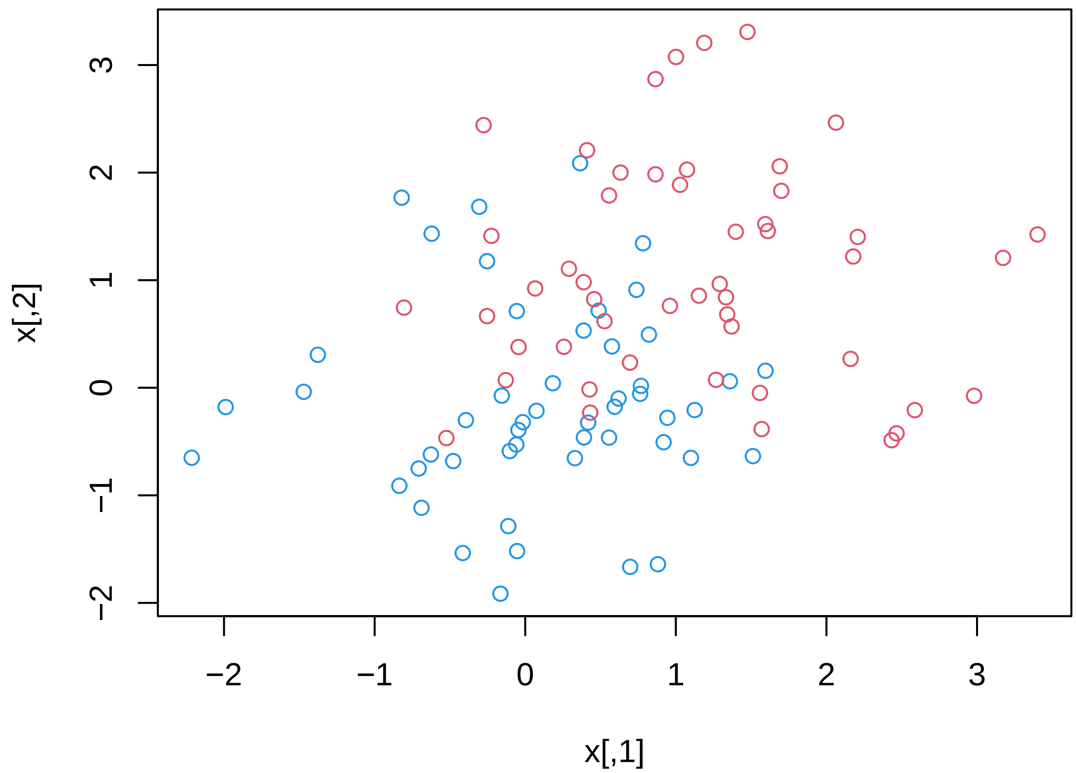

```
partimat(Species ~ Z[, 1:2], method = "qda")
```



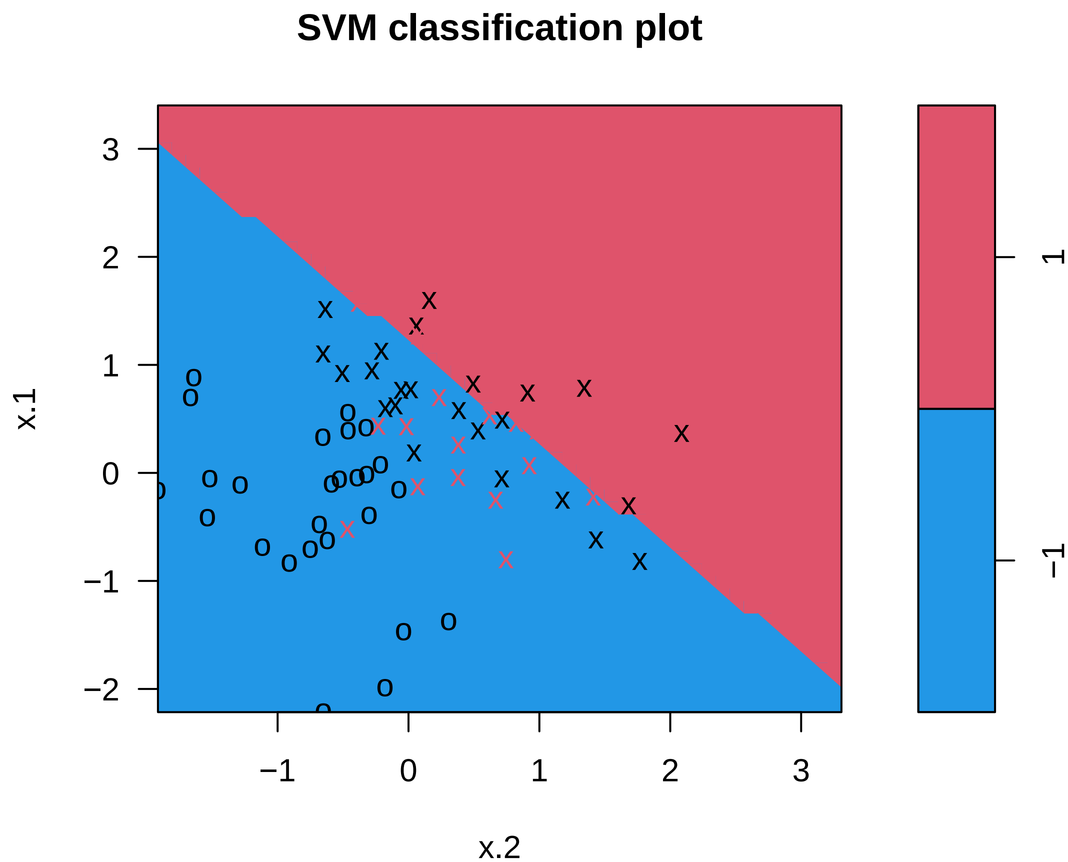
Support Vector Classifier

Here we demonstrate the use of the `svm()` function from the library `e1071` on a two-dimensional toy example so that we can visualize the resulting decision boundary. We begin by generating the observations, which belong to two classes and check whether the classes are linearly separable.

```
set.seed(1)
x <- matrix(rnorm (100 * 2), ncol = 2)
y <- c(rep(-1, 50), rep(1, 50))
x[y == 1, ] <- x[y == 1, ] + 1
plot(x, col = (3 - y))
```




```
dat <- data.frame(x = x, y = as.factor(y))
library(e1071)
svmfit <- svm(y ~ ., data = dat, kernel = "linear",
              cost = 10, scale = FALSE)
plot(svmfit, dat, col = c(4, 2))
```




```r
# Support Points
svmfit$index
```

```
##  [1]   2   4   6   7   8   9  10  11  13  15  18  19  20  21  22  25  26  31  33
## [20]  39  40  42  47  48  52  53  54  55  58  59  62  65  67  68  69  72  74  75
## [39]  81  84  88  89  90  91  96  97  98  99 100
```

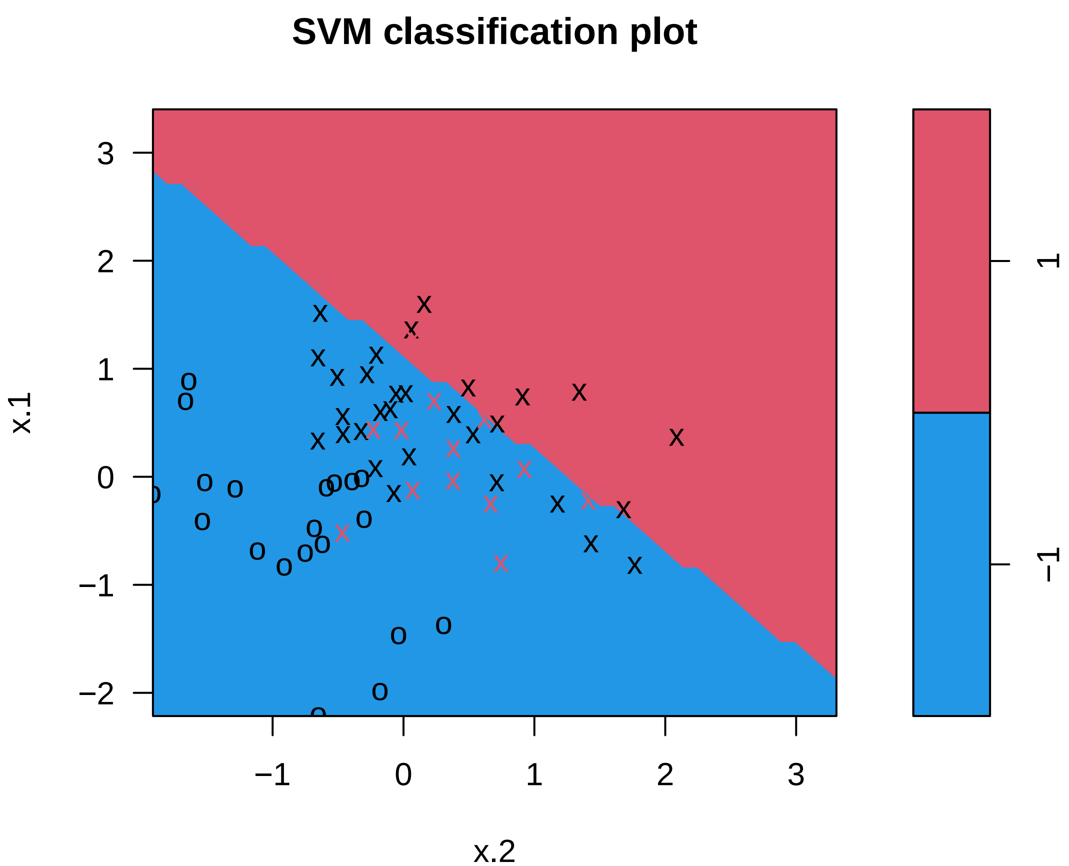
```r
# Summary
summary(svmfit)
```

```
##
## Call:
## svm(formula = y ~ ., data = dat, kernel = "linear", cost = 10, scale = FALSE)
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  linear
##        cost:  10
##
## Number of Support Vectors:  49
##
```

```
##  ( 24 25 )
##
##
## Number of Classes:  2
##
## Levels:
##  -1 1
```

Changing Cost to Allow for a Wider Margin

```r
svmfit <- svm(y ~ ., data = dat , kernel = "linear",
cost = 0.1, scale = FALSE)
plot(svmfit, dat, col = c(4, 2))
```




```r
svmfit$index
```

```
##  [1]   2   4   5   6   7   8   9  10  11  12  13  15  18  19  20  21  22  23  25
## [20]  26  27  30  31  33  39  40  42  44  47  48  52  53  54  55  58  59  62  65
## [39]  67  68  69  72  74  75  76  77  80  81  84  86  88  89  90  91  93  95  96
## [58]  97  98  99 100
```

Cross-Validation

The e1071 library includes a built-in function, tune(), to perform cross-validation. Here we compare SVMs with a linear kernel, using a range of values of the cost parameter.

```
set.seed(1)
tune.out <- tune(svm, y ~ ., data = dat , kernel = "linear",
ranges = list(cost = c(0.001 , 0.01, 0.1, 1, 5, 10, 100)))

summary(tune.out)
```

```
##
## Parameter tuning of 'svm':
##
## - sampling method: 10-fold cross validation
##
## - best parameters:
##  cost
##     5
##
## - best performance: 0.2
##
## - Detailed performance results:
##    cost error dispersion
## 1 1e-03  0.45 0.24152295
## 2 1e-02  0.24 0.10749677
## 3 1e-01  0.21 0.09944289
## 4 1e+00  0.21 0.08755950
## 5 5e+00  0.20 0.10540926
## 6 1e+01  0.20 0.10540926
## 7 1e+02  0.20 0.10540926
```

```
bestmod <- tune.out$best.model
summary(bestmod)
```

```
##
## Call:
## best.tune(METHOD = svm, train.x = y ~ ., data = dat, ranges = list(cost = c(0.001,
##     0.01, 0.1, 1, 5, 10, 100)), kernel = "linear")
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  linear
##        cost:  5
##
## Number of Support Vectors:  49
##
##  ( 24 25 )
##
##
## Number of Classes:  2
##
```

```
## Levels:
##  -1 1
```

Predcition

The `predict()` function can be used to predict the class label on a set of test observations, at any given value of the cost parameter.

```r
xtest <- matrix(rnorm (20 * 2), ncol = 2)
ytest <- sample(c(-1, 1), 20, rep = TRUE)
xtest[ytest == 1, ] <- xtest[ytest == 1, ] + 1
testdat <- data.frame(x = xtest, y = as.factor(ytest))

ypred <- predict(bestmod, testdat)
table(predict = ypred, truth = testdat$y)
```

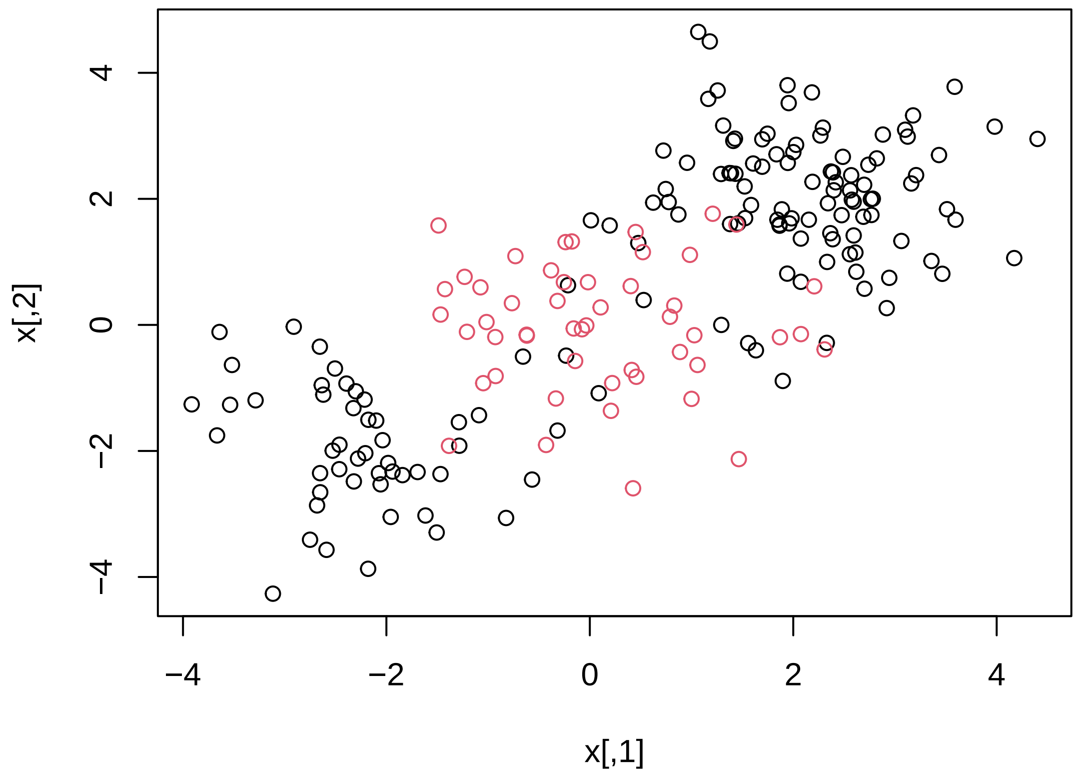
```
##        truth
## predict -1  1
##      -1  8  2
##      1   0 10
```

Support Vector Machine (SVM)

Generate Some Data with Non-Linear Class Boundary

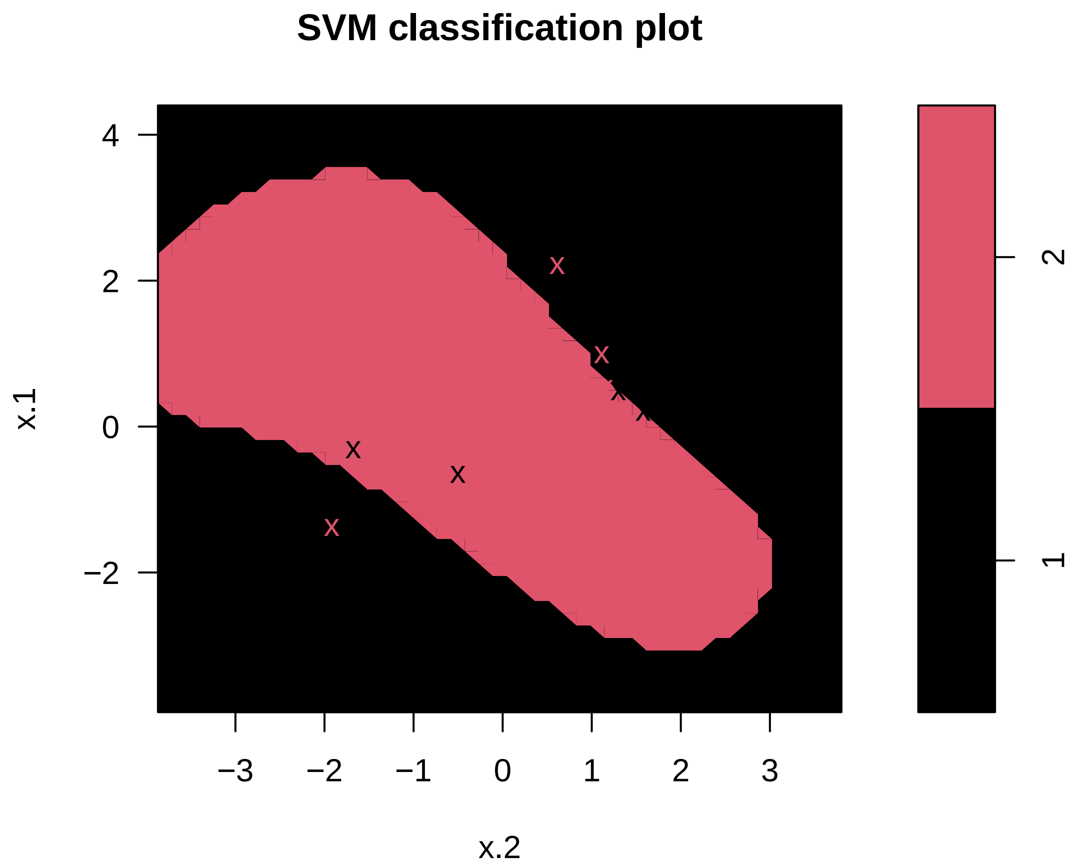
```r
set.seed (1)
x <- matrix(rnorm (200 * 2), ncol = 2)
x[1:100, ] <- x[1:100, ] + 2
x[101:150, ] <- x[101:150, ] - 2
y <- c(rep(1, 150) , rep(2, 50))
dat <- data.frame(x = x, y = as.factor(y))

plot(x, col = y)
```



Training

```
train <- sample (200, 100)
svmfit <- svm(y ~ ., data = dat[train, ], kernel = "radial",
gamma = 1, cost = 1)
plot(svmfit, dat[train, ], col = 1:2)
```

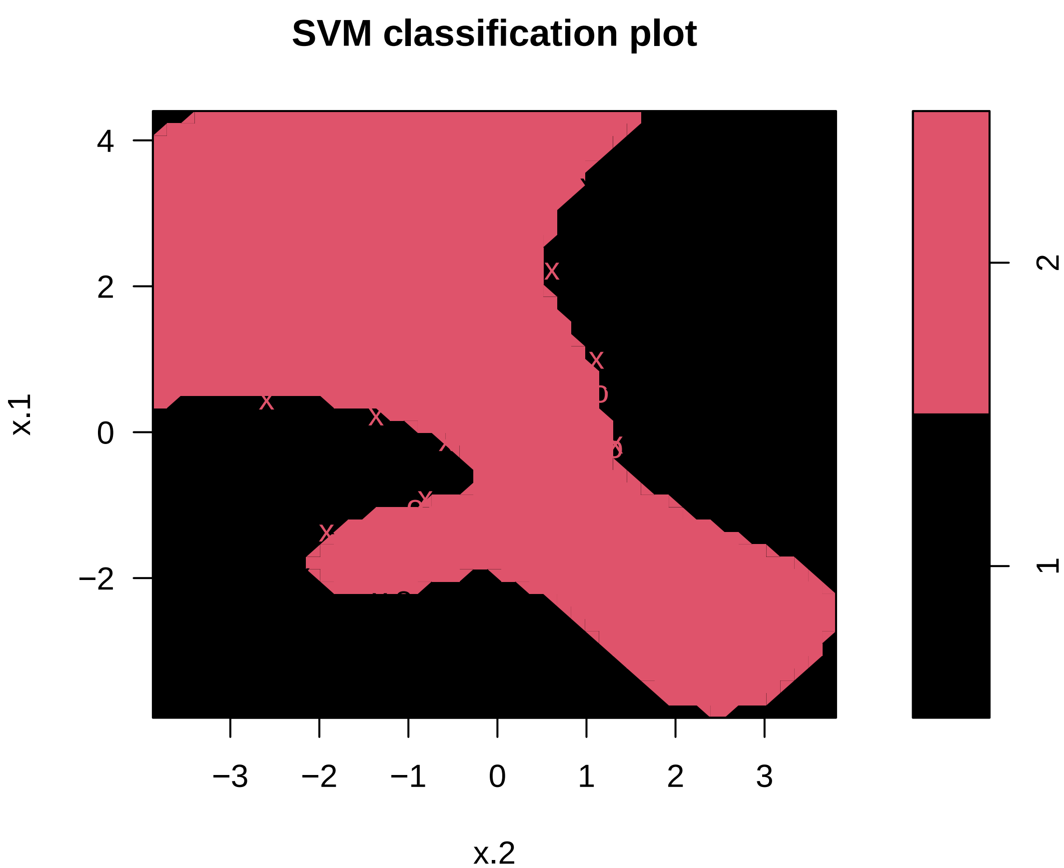



```r
summary(svmfit)
```

```
##
## Call:
## svm(formula = y ~ ., data = dat[train, ], kernel = "radial", gamma = 1,
##     cost = 1)
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  radial
##        cost:  1
##
## Number of Support Vectors:  31
##
##  ( 16 15 )
##
##
## Number of Classes:  2
##
## Levels:
##  1 2
```

Changing the Cost

```
svmfit <- svm(y ~ ., data = dat[train, ], kernel = "radial",
gamma = 1, cost = 1e5)
plot(svmfit, dat[train, ], col = 1:2)
```



Cross-Validation

```
set.seed(1)
tune.out <- tune(svm, y ~ ., data = dat[train, ],
                 kernel = "radial",
                 ranges = list(cost = c(0.1, 1, 10, 100, 1000),
                               gamma = c(0.5, 1, 2, 3, 4))
)
summary(tune.out)
```

```
##
## Parameter tuning of 'svm':
##
```

```
## - sampling method: 10-fold cross validation
##
## - best parameters:
##  cost gamma
##     1   0.5
##
## - best performance: 0.07
##
## - Detailed performance results:
##     cost gamma error dispersion
## 1  1e-01   0.5  0.26 0.15776213
## 2  1e+00   0.5  0.07 0.08232726
## 3  1e+01   0.5  0.07 0.08232726
## 4  1e+02   0.5  0.14 0.15055453
## 5  1e+03   0.5  0.11 0.07378648
## 6  1e-01   1.0  0.22 0.16193277
## 7  1e+00   1.0  0.07 0.08232726
## 8  1e+01   1.0  0.09 0.07378648
## 9  1e+02   1.0  0.12 0.12292726
## 10 1e+03   1.0  0.11 0.11005049
## 11 1e-01   2.0  0.27 0.15670212
## 12 1e+00   2.0  0.07 0.08232726
## 13 1e+01   2.0  0.11 0.07378648
## 14 1e+02   2.0  0.12 0.13165612
## 15 1e+03   2.0  0.16 0.13498971
## 16 1e-01   3.0  0.27 0.15670212
## 17 1e+00   3.0  0.07 0.08232726
## 18 1e+01   3.0  0.08 0.07888106
## 19 1e+02   3.0  0.13 0.14181365
## 20 1e+03   3.0  0.15 0.13540064
## 21 1e-01   4.0  0.27 0.15670212
## 22 1e+00   4.0  0.07 0.08232726
## 23 1e+01   4.0  0.09 0.07378648
## 24 1e+02   4.0  0.13 0.14181365
## 25 1e+03   4.0  0.15 0.13540064
```

```r
table(true = dat[-train, "y"],
      pred = predict(tune.out$best.model, newdata = dat[-train, ])
)
```

```
##     pred
## true  1  2
##    1 67 10
##    2  2 21
```