Lecture 7: Classification

October 24, 2017

Contents

Classification

- **Classification** is a supervised method which deals with prediction outcomes or **response variables that are qualitative, or categorical**.
- The task is to classify or **assign each observation to a category or a class.**
- Examples of classification problems include:
  - predicting what medical condition or disease a patient has base on their symptoms,
  - determining cell types based on their gene expression profiles (single cell RNA-seq data).
  - detecting fraudulent transactions based on the transaction history

Logistic Regression

Logistic Regression

- Logistic regression is actually used for **classification**, and not regression tasks, $Y \in \{0, 1\}$.
- The name **regression** comes from the fact that the method **fits a linear function to a continuous quantity, the log odds of the response**.

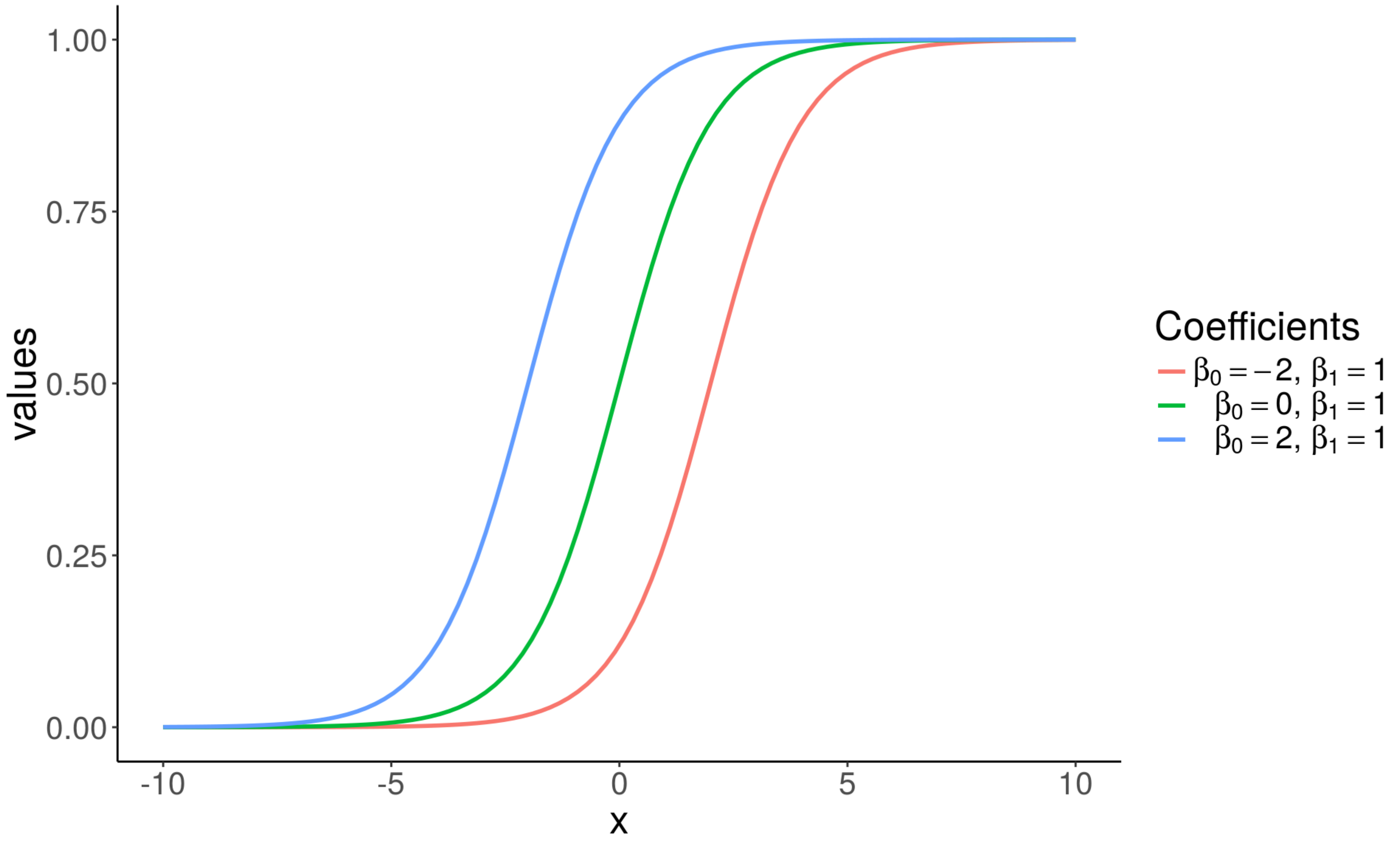
$$p = P[Y = 1 \mid X]$$

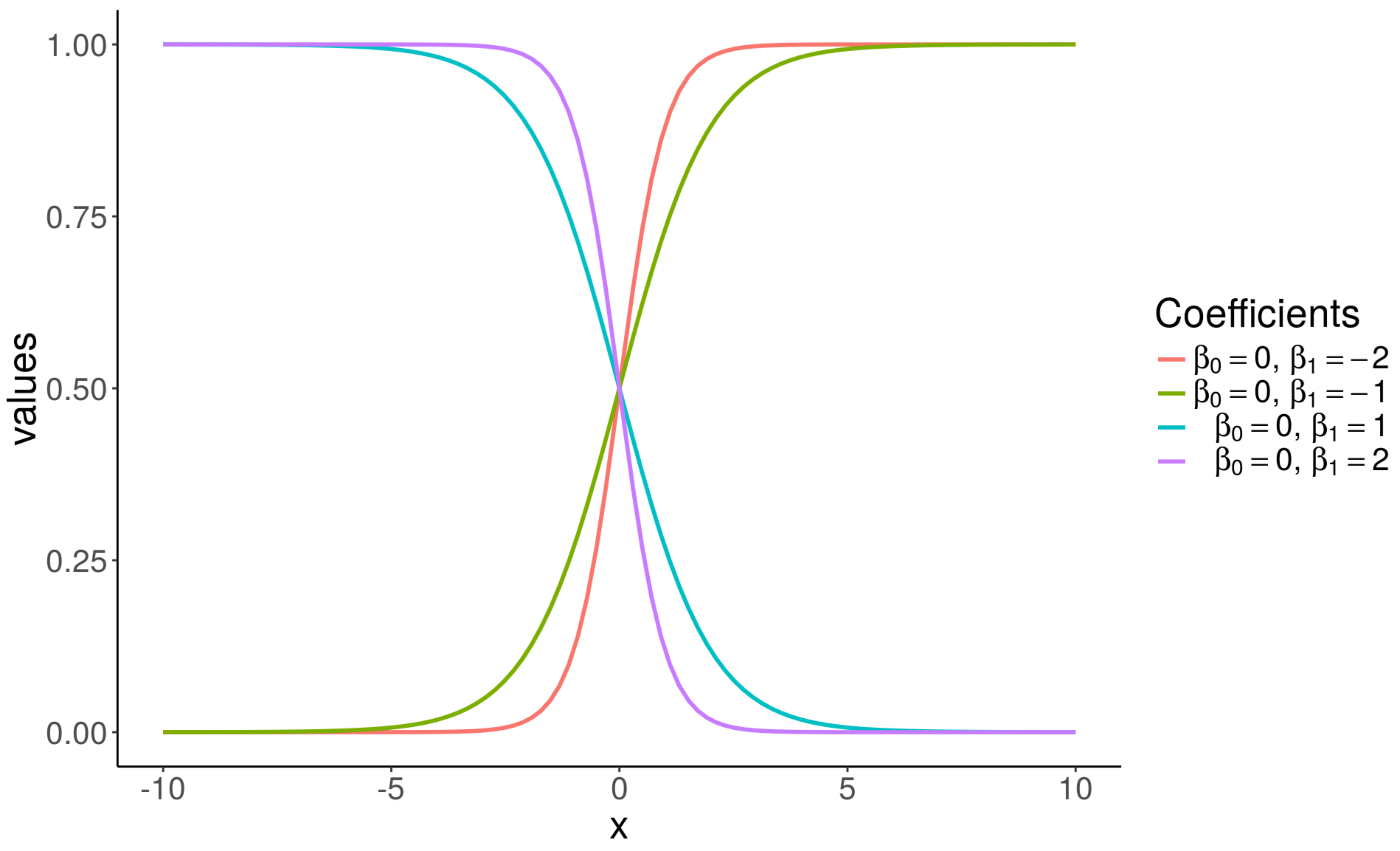
$$\log\left(\frac{p}{1-p}\right) = X\beta = \beta_0 + \beta_1^T x$$

- The method performs **binary classification** (k = 2), but can be generalized to handle $k > 2$ classes (**multinomial logistic regression**).

$$
\begin{aligned}
g(p) &= \log\left(\frac{p}{1-p}\right), && \text{(logit a link function)} \\
g^{-1}(\eta) &= \frac{1}{1+e^{-\eta}}, && \text{(logistic function)} \\
\eta &= X\beta, && \text{(linear predictor)}
\end{aligned}
$$

$$
\begin{aligned}
E[Y] &= P[Y=1 \mid X=x] && \text{(probability of outcome)} \\
&= p = g^{-1}(\eta) \\
&= \frac{1}{1+e^{-X\beta}}
\end{aligned}
$$


values
1.00
0.75
0.50
0.25
0.00
-10
-5
0
5
10
x
Coefficients
$\beta_0 = -2,\ \beta_1 = 1$
$\beta_0 = 0,\ \beta_1 = 1$
$\beta_0 = 2,\ \beta_1 = 1$



values
1.00
0.75
0.50
0.25
0.00
-10
-5
0
5
10
x
Coefficients
$\beta_0 = 0,\ \beta_1 = -2$
$\beta_0 = 0,\ \beta_1 = -1$
$\beta_0 = 0,\ \beta_1 = 1$
$\beta_0 = 0,\ \beta_1 = 2$

Grad School Admissions

Suppose we would like to predict students' admission to graduate school basec their GRE, GPA, and the rank of their undergraduate institution.

```
admissions <- read.csv("https://stats.idre.ucla.edu/stat/data/binary.csv" )
admissions <- tbl_df(admissions)
admissions
```

```
## # A tibble: 400 x 4
##    admit   gre   gpa  rank
##    <int> <int> <dbl> <int>
##  1     0   380  3.61     3
##  2     1   660  3.67     3
##  3     1   800  4.00     1
##  4     1   640  3.19     4
##  5     0   520  2.93     4
##  6     1   760  3.00     2
##  7     1   560  2.98     1
##  8     0   400  3.08     2
##  9     1   540  3.39     3
## 10     0   700  3.92     2
## # ... with 390 more rows
```

```r
summary(admissions)
```

```
##      admit             gre             gpa             rank      
##  Min.   :0.0000   Min.   :220.0   Min.   :2.260   Min.   :1.000  
##  1st Qu.:0.0000   1st Qu.:520.0   1st Qu.:3.130   1st Qu.:2.000  
##  Median :0.0000   Median :580.0   Median :3.395   Median :2.000  
##  Mean   :0.3175   Mean   :587.7   Mean   :3.390   Mean   :2.485  
##  3rd Qu.:1.0000   3rd Qu.:660.0   3rd Qu.:3.670   3rd Qu.:3.000  
##  Max.   :1.0000   Max.   :800.0   Max.   :4.000   Max.   :4.000  
```

```r
sapply(admissions, sd)
```

```
##       admit         gre         gpa        rank 
##   0.4660867 115.5165364   0.3805668   0.9444602 
```

Check that there are observations included in each subgroup, and whether the data is balanced:

```r
with(admissions, table(admit, rank))
```

```
##      rank
## admit  1  2  3  4
##     0 28 97 93 55
##     1 33 54 28 12
```

Logistic Regression in R

- In R logistic regression can be done using a function `glm()`.
- `glm` stands for Generalized Linear Model.
- The function can fit many other regression models. Use `?glm` to learn more.
- For cases with $k > 2$ classes, `multinom()` function from `nnet` package can be used. To see how go over this example.

Note that currently the column ‘admit’ and ‘rank’ in `admissions` are integers.

```r
sapply(admissions, class)
```

```
##     admit       gre       gpa      rank 
## "integer" "integer" "numeric" "integer" 
```

We convert the two columns to factors.

```r
admissions <- mutate(admissions,
  admit = factor(admit, levels = c(0, 1), labels = c("rejected", "admitted")),
  rank = factor(rank, levels = 1:4)
)
admissions
```

```
## # A tibble: 400 x 4
##       admit   gre   gpa   rank
##      <fctr> <int> <dbl> <fctr>
##  1 rejected   380  3.61      3
##  2 admitted   660  3.67      3
##  3 admitted   800  4.00      1
##  4 admitted   640  3.19      4
##  5 rejected   520  2.93      4
##  6 admitted   760  3.00      2
##  7 admitted   560  2.98      1
##  8 rejected   400  3.08      2
##  9 admitted   540  3.39      3
## 10 rejected   700  3.92      2
## # ... with 390 more rows
```

Split data

Divide data into train and test set so that we can evaluate the model accuracy l
on. Here we use 70%-30% split.

```r
set.seed(123456)
train.idx <- sample(nrow(admissions), 0.7*nrow(admissions))
train <- admissions[train.idx, ]
test <- admissions[-train.idx, ]
```

Fitting a logistic regression model

```r
fit.logit <- glm(admit ~ gre + gpa + rank, data = train,
                 family = "binomial")
```

- The first argument,
  `formula = admit ~ gre + gpa + rank`,
  specifies the linear predictor part, $\eta = X\beta$.
- You need to set the family to `family = "binomial"` equivalent to choosing a logistic regression, i.e. using **a logit link function** $g(\cdot)$ in a GLM model.

```r
summary(fit.logit)
```

```
##
## Call:
## glm(formula = admit ~ gre + gpa + rank, family = "binomial",
##     data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.4811  -0.8899  -0.6611   1.1862   2.0721
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.626928   1.333747  -2.719  0.00654 **
## gre          0.003061   0.001311   2.335  0.01953 *
## gpa          0.500902   0.386621   1.296  0.19512
## rank2       -0.502376   0.378062  -1.329  0.18391
## rank3       -0.980873   0.407041  -2.410  0.01596 *
## rank4       -1.237913   0.493217  -2.510  0.01208 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 350.14  on 279  degrees of freedom
## Residual deviance: 324.87  on 274  degrees of freedom
## AIC: 336.87
##
## Number of Fisher Scoring iterations: 4
```

Logistic regression **coefficients** for continuous predictors (covariates) give **the fold change in the odds of the outcome corresponding to a unit increase in th predictor**.

$$\beta_{cont} = \log\left(\frac{P[Y = 1 \mid X_{cont} = x + 1]}{P[Y = 1 \mid X_{cont} = x]}\right)$$

Categorical features (factors) are first converted to indicator variables and th the model fits separate coefficients for each level of the factor. Coefficients corresponding to a specific indicator variable give the increase/decrease in the odds of the outcome in case the observation is recorded with that level.

$$\beta_{facL} = \log\left(\frac{P[Y = 1 \mid X_{fac} = L]}{P[Y = 1 \mid X_{fac} \neq L]}\right)$$

```r
coef(fit.logit)
```

```
##  (Intercept)          gre          gpa        rank2        rank3 
## -3.626927707  0.003061239  0.500901628 -0.502375799 -0.980872661 
##        rank4 
## -1.237912642 
```

- For every unit increase in `gre`, the log odds of admitted (versus rejected) increases by ≈ 0.0030612.
- For every unit increase in `gpa`, the log odds increases by ≈ 0.5009016.
- There are three coefficients for the rank variable, e.g. a student attending a college with rank 2, one with rank 1 (base level), has the log admission odds decreased by ≈ -0.5023758.

You can get the confidence intervals for the coefficients with the `confint()` fuinction

```r
confint(fit.logit)
```

```
## Waiting for profiling to be done...
```

```
##                     2.5 %       97.5 %
## (Intercept) -6.3005033773 -1.055267675
## gre          0.0005270972  0.005682988
## gpa         -0.2517254914  1.269320820
## rank2       -1.2478927740  0.239891701
## rank3       -1.7887087854 -0.186990834
## rank4       -2.2410453972 -0.293855964
```

The 95% CI are away from zero which indicates significance.

Rank variable effect is given with three different coeffients.

We can sse `wald.test()` function from the `aod` package to test the overall e

of 'rank'.

```r
# install.packages(aod)
library(aod)
wald.test(b = coef(fit.logit), Sigma = vcov(fit.logit), Terms = 4:6)
```

```
## Wald test:
## ----------
##
## Chi-squared test:
## X2 = 8.8, df = 3, P(> X2) = 0.033
```

- `b` supplies the coefficients,
- `Sigma` supplies the variance covariance matrix of the error terms,
- `Terms` indices of the coefficients to be tested; here 4, 5, and 6, corresponding to 'rank'.

The p-value indicates that the overall effect of rank is statistically significant.

Predictions

Predictions can be computed using `predict()` function, with the argument `type = "response"`. Otherwise, the default will compute predictions on th
scale of the linear predictors.

```r
# Must have the same column names as the variables in the model
newStudents <- data.frame(gre = c(670, 790, 550),
                          gpa = c(3.56, 4.00, 3.87),
                          rank = factor(c(1, 2, 2)))

# The output is the probability of admissions for each of the new students.
newStudents <- newStudents %>%
  mutate(
    pred.prob.admit = predict(fit.logit, newdata = newStudents,
                              type = "response"),
    admit = factor(pred.prob.admit < 0.5, levels = c(TRUE, FALSE),
                   labels = c("rejected", "admitted"))
  )
newStudents
```

```
##   gre  gpa rank pred.prob.admit    admit
## 1 670 3.56    1       0.5516432 admitted
## 2 790 4.00    2       0.5726525 admitted
## 3 550 3.87    2       0.3758659 rejected
```

Test Set Predictions

```
pred.prob.admit <- predict(fit.logit, newdata = test, type = "response")
admit <- factor(pred.prob.admit < 0.5, levels = c(TRUE, FALSE),
                labels = c("rejected", "admitted"))
(confusion.matrix <- table(pred = admit, true = test$admit))
```

```
##            true
## pred        rejected admitted
##   rejected        80       34
##   admitted         2        4
```

```
# Accuracy
sum(diag(confusion.matrix))/nrow(test)
```

```
## [1] 0.7
```

Exercise

- Go to the “Lec7_Exercises.Rmd” file, which can be downloaded from the class website under the Lecture tab.
- Complete Exercise 1.

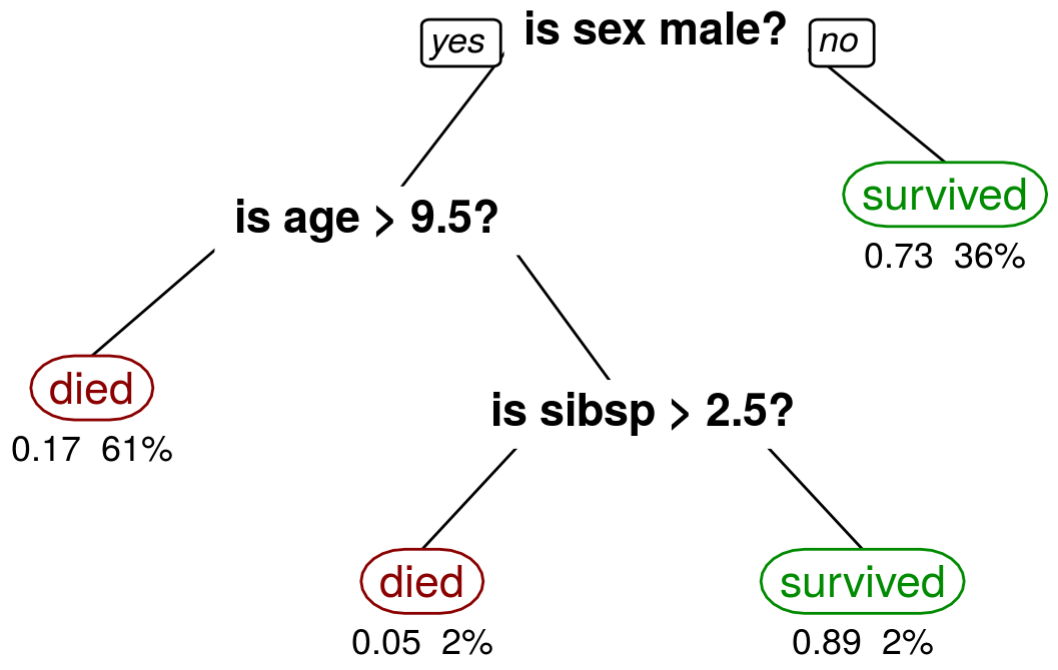
Random Forest

Random Forest

- Random Forest is **an ensemble learning method based on classification and regression trees, CART,** proposed by Breinman in 2001.
- RF can be used to perform **both classification and regression**.
- RF models are robust as they **combine predictions calculated from a large number of decision trees (a forest).**
- Details on RF can be found in Chapter 8 of ISL and Chapter 15 ESL; also a good write-up can also be found here

Decision trees

- Cool visualization explaining what decision trees are: link
- Decision tree on classification of Titanic Survivors:



Tree bagging Algorithm

Suppse we have an input data matrix, $X \in \mathbb{R}^{N \times p}$ and a response vector, $Y \in \mathbb{F}$

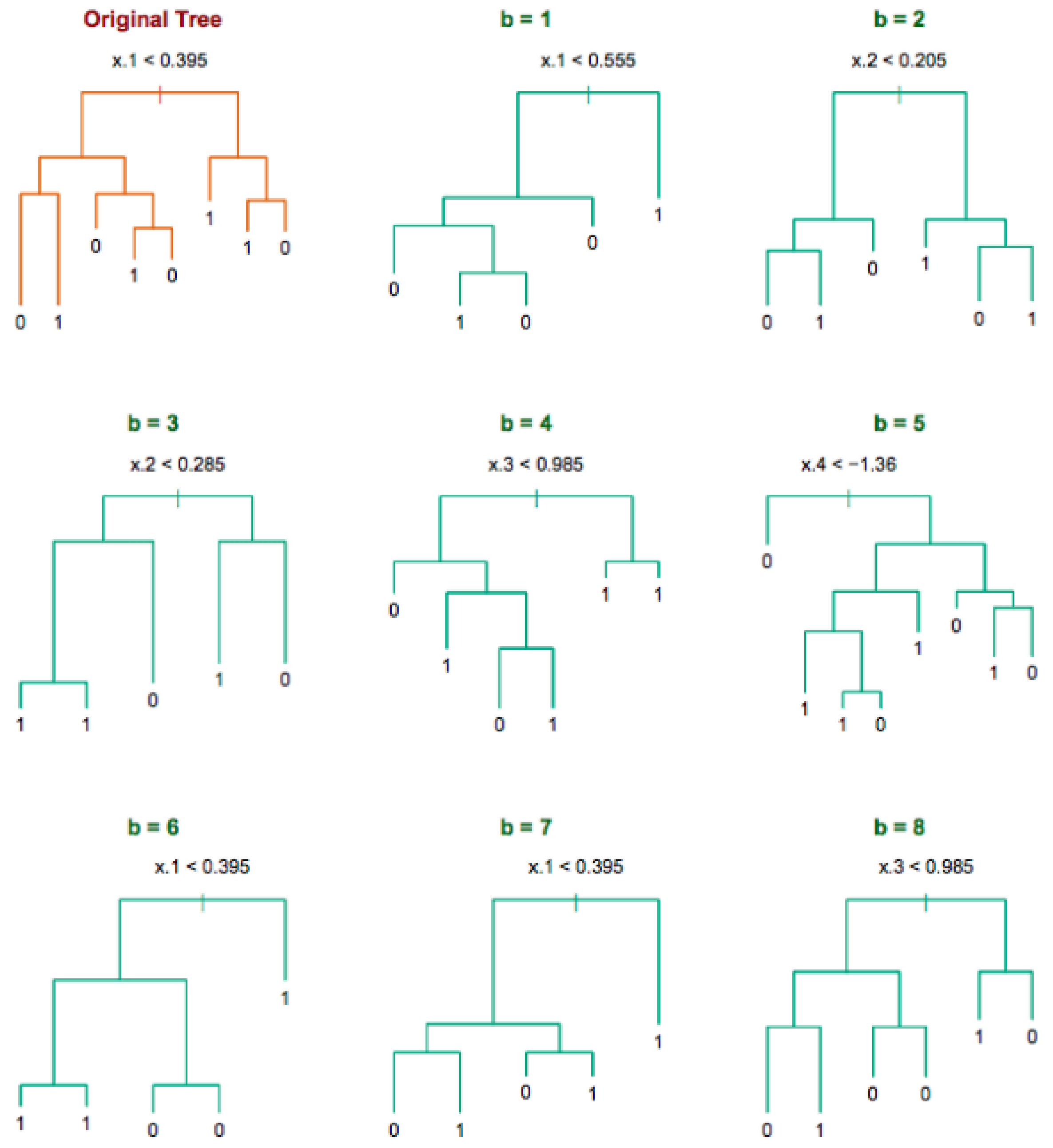
For b = 1, 2, …, B:

1. Generate a random subset of the data (X_b, Y_b) contatining $n < N$
   observations sampled with replacement.
2. Train a decision tree T_b on (X_b, Y_b)
3. Predict the outcome for $N - n$ unseen (complement) samples (X_b', Y_b')

Afterwards, combine predictions from all decision trees and compute the aver
predicted outcome .

Averaging over a collection of decision trees makes the predictions more stal

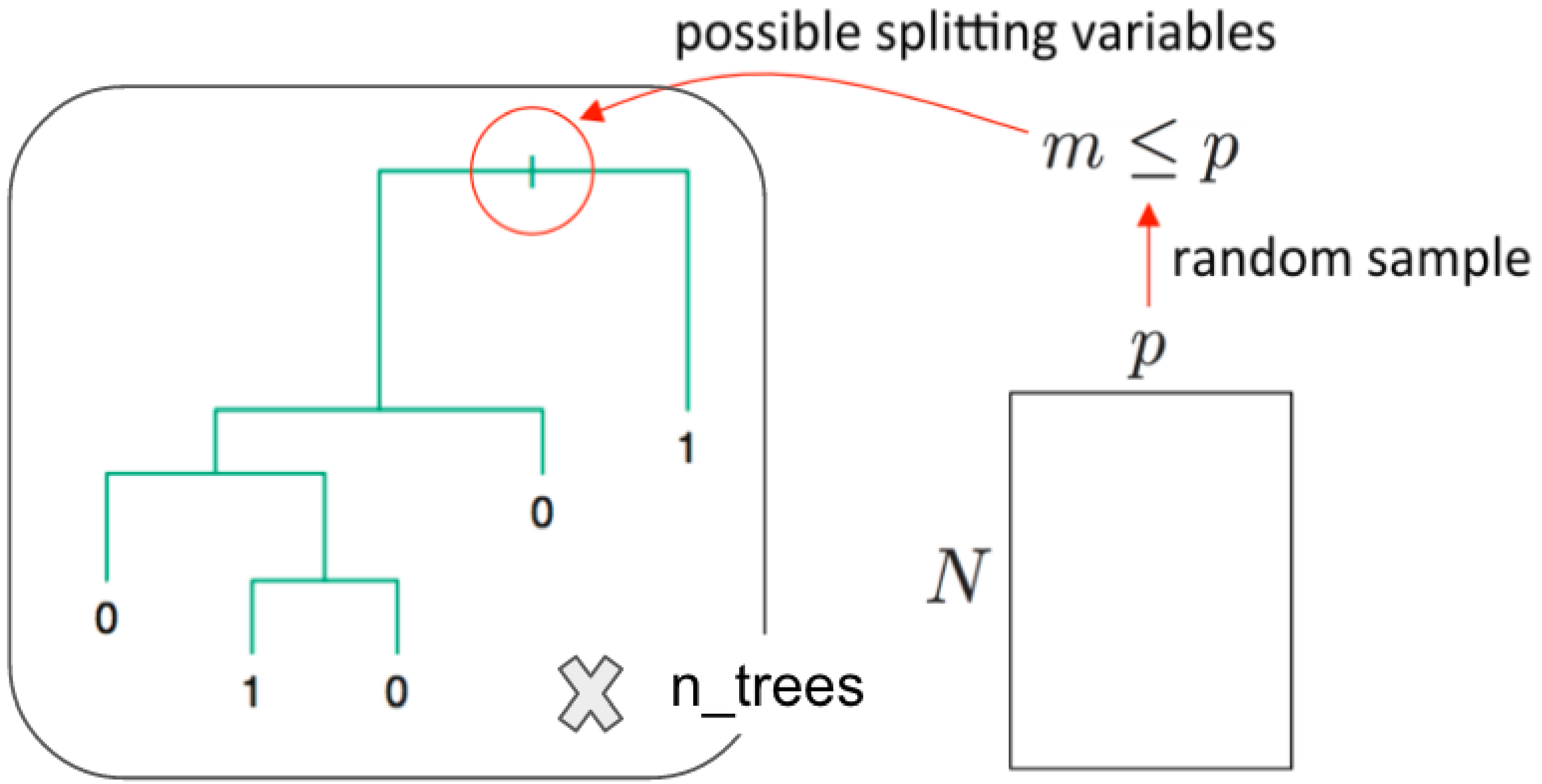
Decision trees for bootrap samples

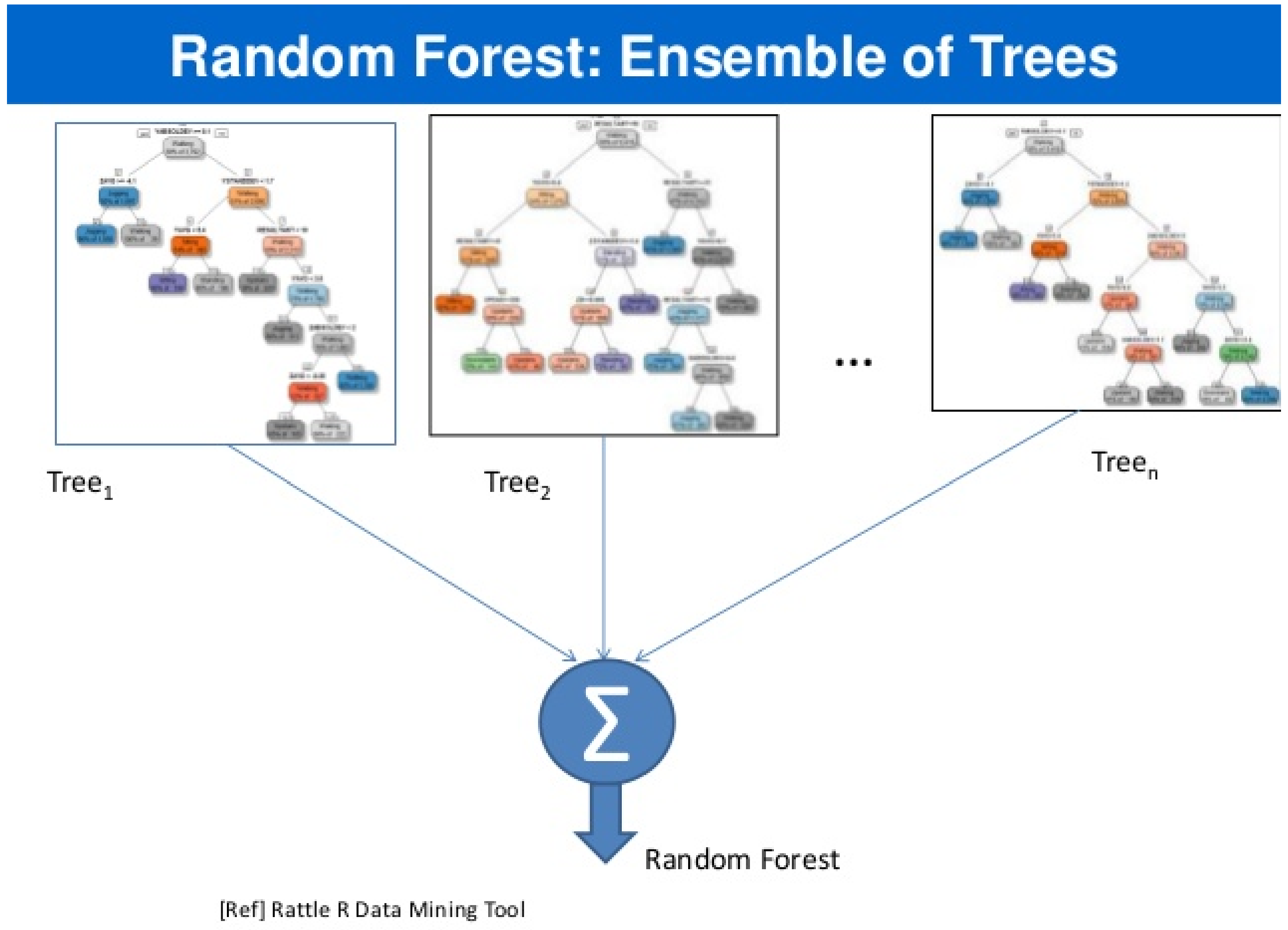


Source: Chapter 8 ESL

Random Forest Characteristics

- Random forests differ in only one way from tree bagging: it uses a modified tree learning algorithm sometimes called **feature bagging**.
- At each candidate split in the learning process, **only a random subset of the features is included in a pool** from which the variables can be selected for splitting the branch.
- Introducing **randomness** into the candidate splitting variables, **reduces correlation between the generated trees.**


possible splitting variables
$m \leq p$
random sample
p
N
n_trees
0
1
0
1
0
0


Random Forest: Ensemble of Trees
Tree_1
Tree_2
...
Tree_n
Σ
Random Forest
[Ref] Rattle R Data Mining Tool

Source: link

Wine Quality

UCI ML Repo includes two datasets on red and white variants of the Portugues
"Vinho Verde" wine. The datasets contain information on physicochemical and sensory characteristics of the wine quality score.

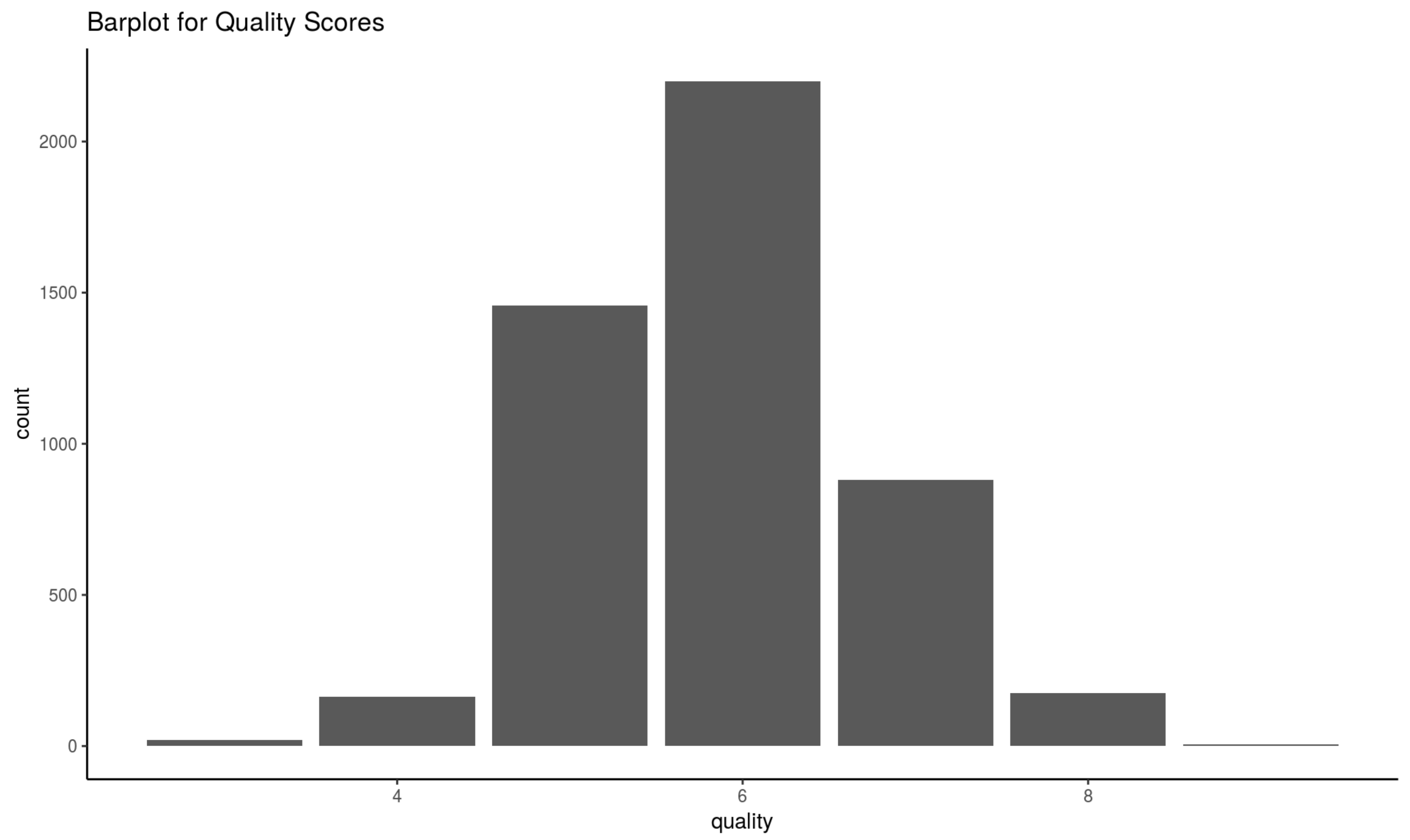
We will use the white wines dataset to classify wines according to their quality classes.

```
url <- 'https://archive.ics.uci.edu/ml/machine-learning-databases/wine-quality/w:
wines <- tbl_df(read.csv(url, sep = ";"))
print(wines, n = 6)
```

```
## # A tibble: 4,898 x 12
##   fixed.acidity volatile.acidity citric.acid residual.sugar chlorides
##           <dbl>            <dbl>       <dbl>          <dbl>     <dbl>
## 1           7.0             0.27        0.36           20.7     0.045
## 2           6.3             0.30        0.34            1.6     0.049
## 3           8.1             0.28        0.40            6.9     0.050
## 4           7.2             0.23        0.32            8.5     0.058
## 5           7.2             0.23        0.32            8.5     0.058
## 6           8.1             0.28        0.40            6.9     0.050
## # ... with 4,892 more rows, and 7 more variables:
## #   free.sulfur.dioxide <dbl>, total.sulfur.dioxide <dbl>, density <dbl>,
## #   pH <dbl>, sulphates <dbl>, alcohol <dbl>, quality <int>
```

Class Frequency

```r
ggplot(wines, aes(x = quality)) +
  geom_bar() + theme_classic() +
  ggtitle("Barplot for Quality Scores" )
```



The classes are ordered and not balanced (munch more normal wines than excellent/poor ones).

To make things easier, we will wines into **"good", "average" and "bad"** categorie

The new classes will be more balanced, and it will be easier to fit the model.

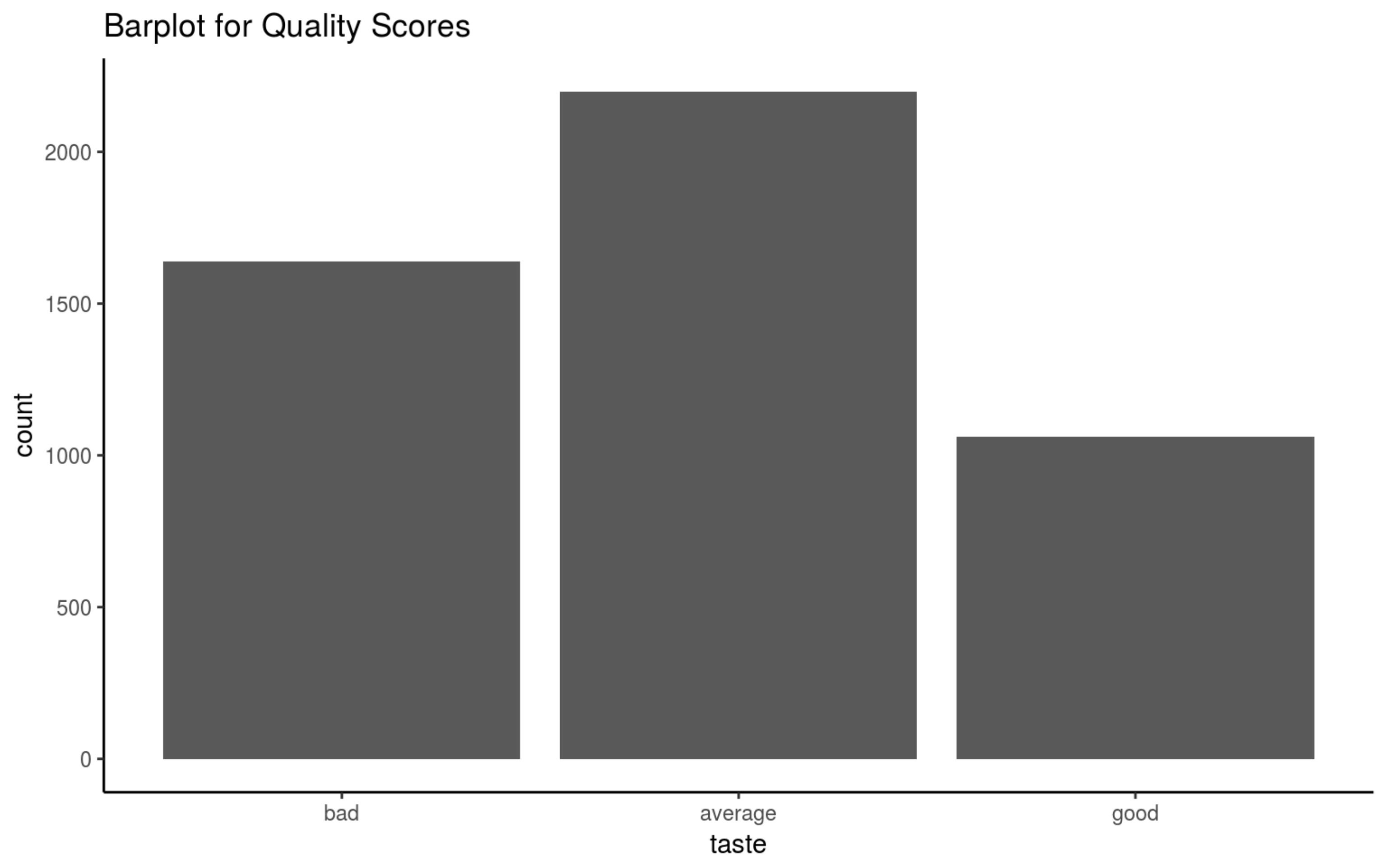
```
qualClass <- function(quality) {
  if(quality > 6) return("good")
  if(quality < 6) return("bad")
  return("average")
}
wines <- mutate(wines, taste = sapply(quality, qualClass),
         taste = factor(taste, levels = c("bad", "average", "good")))
wines
```

```
## # A tibble: 4,898 x 13
##    fixed.acidity volatile.acidity citric.acid residual.sugar chlorides
##            <dbl>            <dbl>       <dbl>          <dbl>     <dbl>
##  1           7.0             0.27        0.36           20.7     0.045
##  2           6.3             0.30        0.34            1.6     0.049
##  3           8.1             0.28        0.40            6.9     0.050
##  4           7.2             0.23        0.32            8.5     0.058
##  5           7.2             0.23        0.32            8.5     0.058
##  6           8.1             0.28        0.40            6.9     0.050
##  7           6.2             0.32        0.16            7.0     0.045
##  8           7.0             0.27        0.36           20.7     0.045
##  9           6.3             0.30        0.34            1.6     0.049
## 10           8.1             0.22        0.43            1.5     0.044
## # ... with 4,888 more rows, and 8 more variables:
## #   free.sulfur.dioxide <dbl>, total.sulfur.dioxide <dbl>, density <dbl>,
## #   pH <dbl>, sulphates <dbl>, alcohol <dbl>, quality <int>, taste <fctr>
```

```r
table(wines$quality)
```

```
##
##    3    4    5    6    7    8    9
##   20  163 1457 2198  880  175    5
```

```r
ggplot(wines, aes(x = taste)) +
  geom_bar() + theme_classic() +
  ggtitle("Barplot for Quality Scores")
```



Splitting data

We include 60% of the data in a train set and the remaining into a test set.

```r
set.seed(123)
train.idx <-  sample(nrow(wines), 0.6 * nrow(wines))
train <- wines[train.idx, ]
test <- wines[-train.idx, ]
dim(train)
```

```
## [1] 2938   13
```

```r
dim(test)
```

```
## [1] 1960   13
```

Random Forest in R

In R there is a convenient function `randomForest` from `randomForest` pacl

```
# install.packages("randomForest")
library(randomForest)
```

```
## randomForest 4.6-12
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
##
## Attaching package: 'randomForest'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
## The following object is masked from 'package:ggplot2':
##
##     margin
```

```
rf.wines <- randomForest(taste ~ . - quality, data = train,
                         mtry = 6, ntree = 600, importance = TRUE)
```

- Note that in the formula '`taste ~ . - quality`' means we include all features EXCEPT for 'quality' (the response variable).

- `mtry` - the number of variables randomly sampled as candidates at each split. Defaults: for classification – $\sqrt{p}$ and for regression – $p/3$, where p is number of all variables in the model.
- `ntree` - the number of trees in the forest.
- `importance` - whether importance of predictors be computed.

Observe, that RF is good at distinguishing “bad” wines from“good” wines, but st
struggles when it comes to “average” wines.

```
rf.wines
```

```
##
## Call:
##  randomForest(formula = taste ~ . - quality, data = train, mtry = 6,      ntre
##                Type of random forest: classification
##                      Number of trees: 600
## No. of variables tried at each split: 6
##
##         OOB estimate of  error rate: 30.12%
## Confusion matrix:
##         bad average good class.error
## bad     677     278   18   0.3042138
## average 228     971  117   0.2621581
## good     20     224  405   0.3759630
```

Model Accuracy

- You should always evaluate your model's performance on a test set, which was set aside and not observed by the method at all.
- In case of RF, performance on train and test set should be similar; this is because the method averages predictions computed by individual trees for observations unseen by the tree.
- Inspect the confusion matrix to asses the model accuracy.

```
pred <- predict(rf.wines, newdata = test)
(confusion.mat <- table(pred, truth = test$taste))
```

```
##          truth
## pred       bad average good
##   bad      476     131    9
##   average  178     661  151
##   good      13      90  251
```

```
(rf.accuracy <- sum(diag(confusion.mat)) / nrow(test))
```

```
## [1] 0.7081633
```

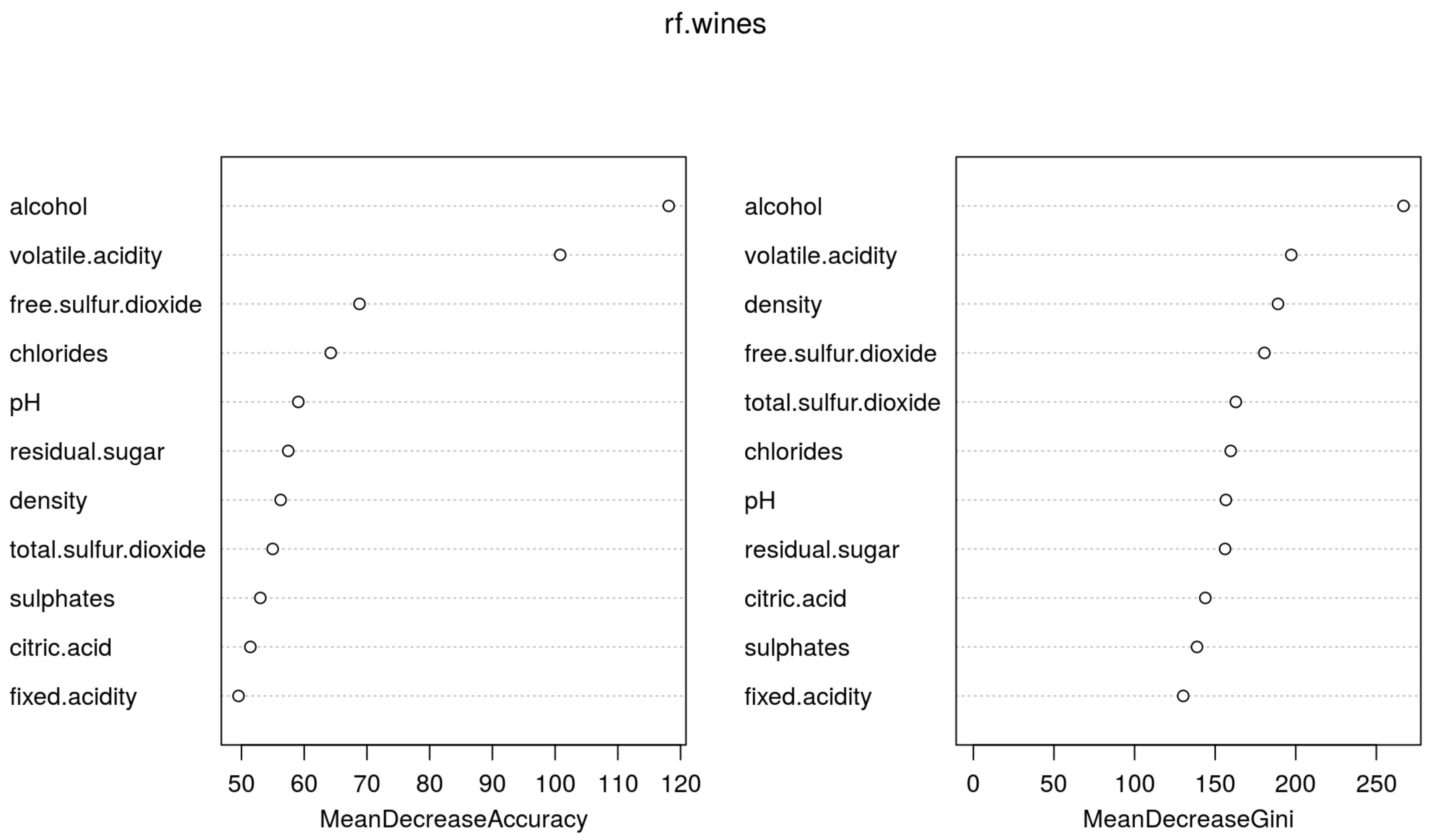
https://stats.stackexchange.com/questions/197827/how-to-interpret-mean-decrease-in-accuracy-and-mean-decrease-gini-in-random-fore

```r
## Look at variable importance:
importance(rf.wines)
```

```
##                           bad  average     good MeanDecreaseAccuracy
## fixed.acidity        31.61926 25.98041 36.16006             49.52878
## volatile.acidity     65.62247 53.90561 78.14410            100.81170
## citric.acid          29.32895 30.59606 42.66566             51.41656
## residual.sugar       34.76200 36.22169 34.11017             57.45461
## chlorides            38.82683 24.70974 59.44965             64.23190
## free.sulfur.dioxide  51.67186 35.52296 44.81158             68.81886
## total.sulfur.dioxide 29.64474 25.20661 44.60063             54.97681
## density              32.81271 26.11959 44.55753             56.24973
## pH                   37.88014 26.46448 46.75563             59.06318
## sulphates            28.53080 28.27934 42.38525             53.00674
## alcohol              88.94843 39.38382 96.90979            118.11452
##                      MeanDecreaseGini
## fixed.acidity                130.1805
## volatile.acidity             197.2117
## citric.acid                  143.9020
## residual.sugar               156.1524
## chlorides                    159.6429
## free.sulfur.dioxide          180.5619
## total.sulfur.dioxide         162.8233
## density                      188.9939
## pH                           156.6557
## sulphates                    138.7374
## alcohol                      266.9109
```

What seems to be the conclusion? What are the characteristics that are predic of the wine quality score?

```
varImpPlot(rf.wines)
```



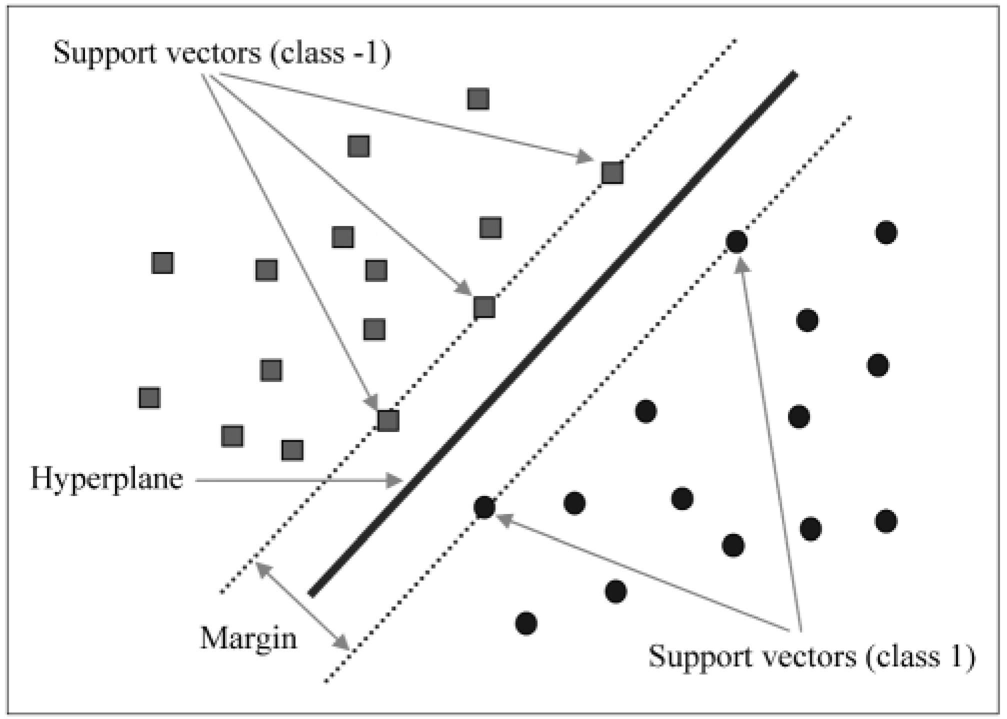
Exercise

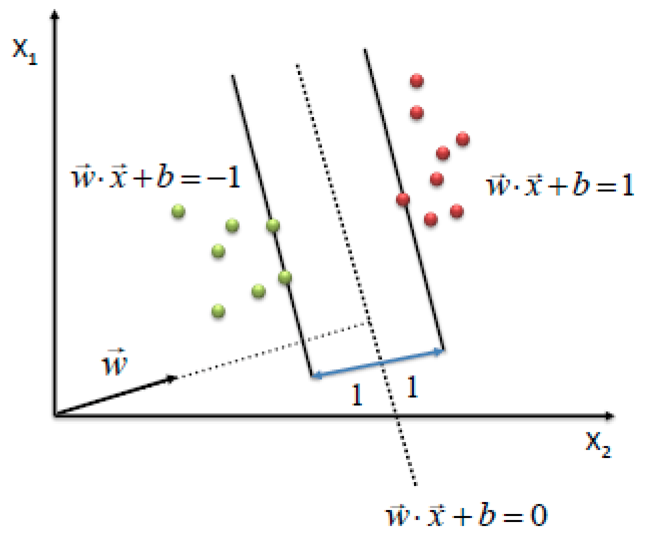
- Go to the “Lec7_Exercises.Rmd” file, which can be downloaded from the class website under the Lecture tab.
- Complete Exercise 2.

Support Vector Machines

Suport Vector Machines (SVM)

- Method invented by Vladimir N. Vapnik and Alexey Ya. Chervonenkis in 1963.
- The idea is to find the best hyperplane sepparating observations from 2 different classes, where the best means the one that represents the largest separation or margin.
- The Andrew Ng's CS229 lecture and notes are good resources to learn about principles of SVMs.
- More details can also be found in Chapter 9 ISL and Chapter 12 ESL




X_1
X_2
$\vec{w}\cdot\vec{x}+b=-1$
$\vec{w}\cdot\vec{x}+b=1$
$\vec{w}$
1
1
$\vec{w}\cdot\vec{x}+b=0$

$$\boxed{\max \frac{2}{\|w\|}}$$

$s.t.$
$(w\cdot x+b)\geq 1, \forall x$ of class 1
$(w\cdot x+b)\leq -1, \forall x$ of class 2

SVM Problem

$$\max_{w,b} \quad \frac{2}{\|w\|}$$
$$s.t.\ \ \forall i: \ \ y_i(w \cdot x_i + b) \geq 1$$

which can be converted to:

$$\min_{w,b} \quad \frac{1}{2}\|w\|^2$$
$$s.t.\ \ \forall i: \ \ y_i(w \cdot x_i + b) \geq 1$$

SVM Problem

Sometimes the data is not linearly separable, and regularization/soft-margin w better:

$$\min_{w,b} \frac{1}{2}\|w\|^2 + C\sum_{i=1}^{n}\xi_i$$

$$s.t.\ \ \forall i :\ \ y_i(w \cdot x_i + b) \geq 1 - \xi_i$$

$$\xi_i \geq 0$$

Lagrangian:

$$\mathcal{L}(w, b, \xi, \alpha, r) = \frac{1}{2}w^T w + C\sum_{i=1}^{n}\xi_i - \sum_{i=1}^{n} r_i\xi_i$$

n

$$- \sum_{i=1} \alpha_i \left[y_i(w \cdot x_i + b) - 1 + \xi_i\right]$$

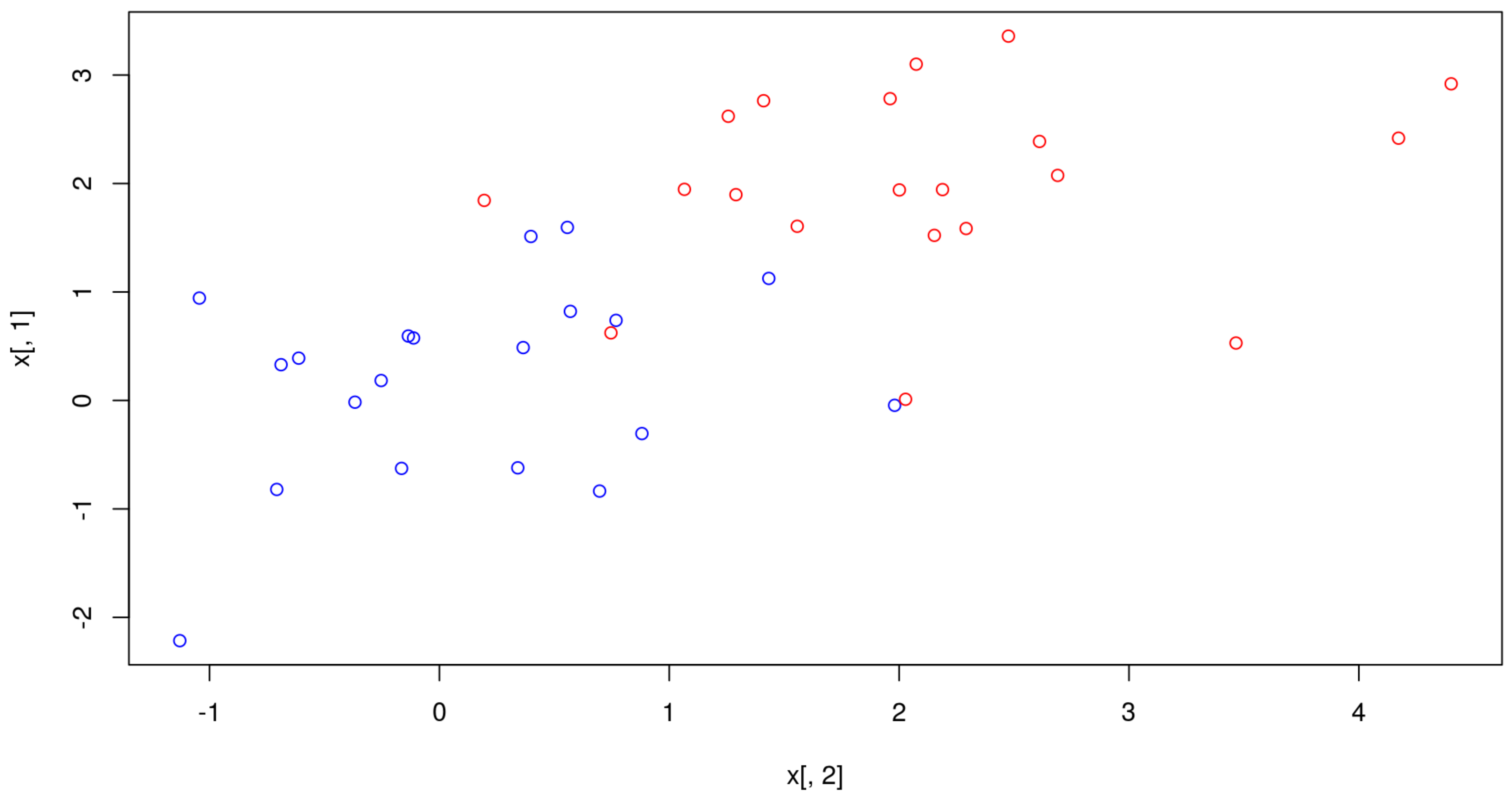
SVM Example

We will do a simple example from the ISL computing SVM on a simulated data:

```r
set.seed(1)
x <- matrix(rnorm(40*2), ncol=2)
y <- c(rep(-1,20), rep(1,20))
x[y == 1, ] <- x[y == 1, ] + 2
dat <- data.frame(x = x, y=as.factor(y))
head(dat)
```

```
##          x.1        x.2  y
## 1 -0.6264538 -0.1645236 -1
## 2  0.1836433 -0.2533617 -1
## 3 -0.8356286  0.6969634 -1
## 4  1.5952808  0.5566632 -1
## 5  0.3295078 -0.6887557 -1
## 6 -0.8204684 -0.7074952 -1
```

```
plot(x[, 2], x[, 1], col=(3-y))
```



SVM in R

You can use the `e1071` package to perform svm in R.

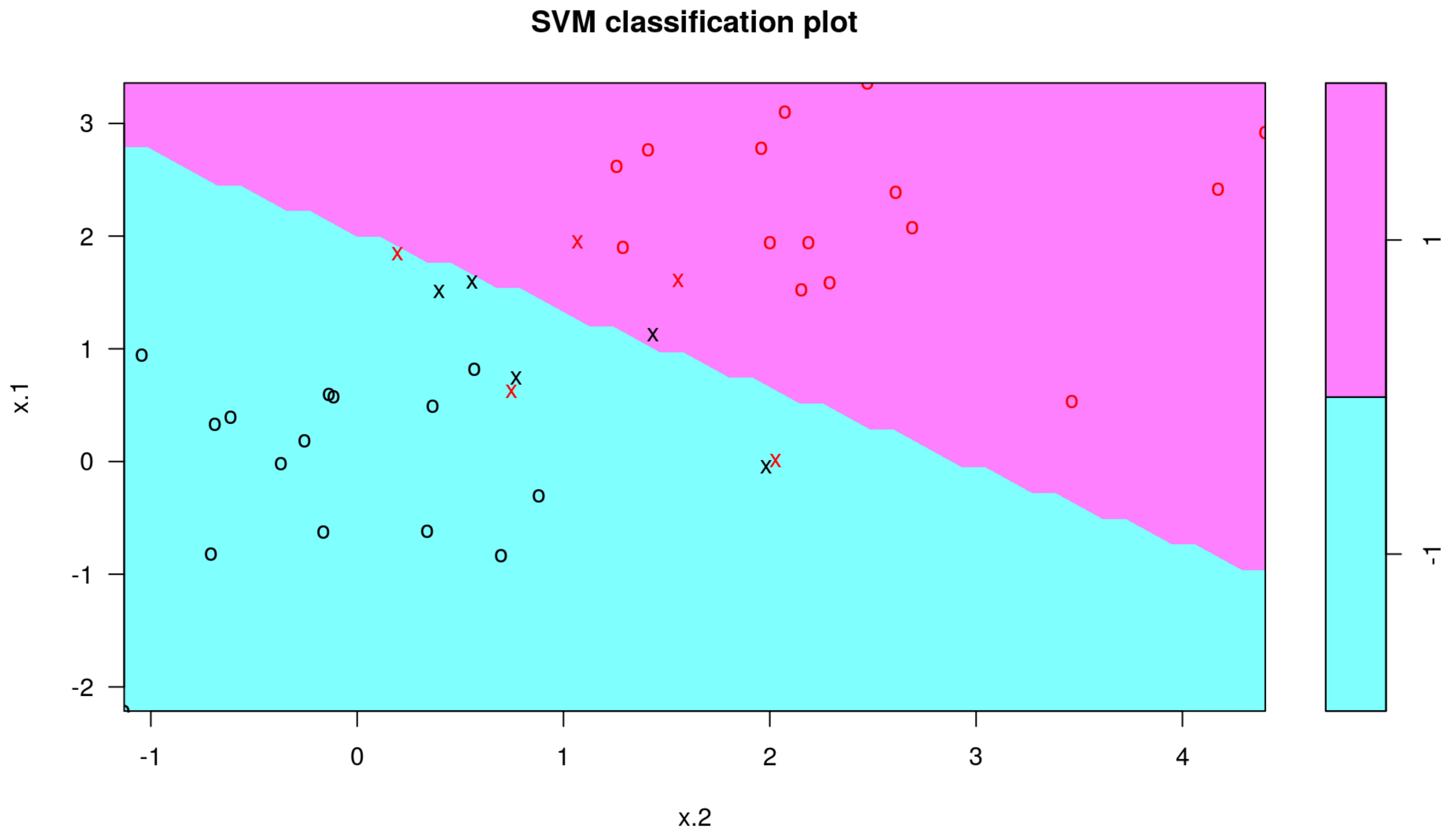
```r
library(e1071)
# Set scale to be FALSE otherwise by default x is scaled to zero mean and unit va
svmfit <- svm(y ~ ., data=dat, kernel="linear", cost = 10, scale=FALSE)
summary(svmfit)
```

```
##
## 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:  10
##
##  ( 5 5 )
##
##
## Number of Classes:  2
##
## Levels:
##  -1 1
```

```r
svmfit$index
```

```
##  [1]  4  8 11 15 16 24 27 34 35 37
```

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



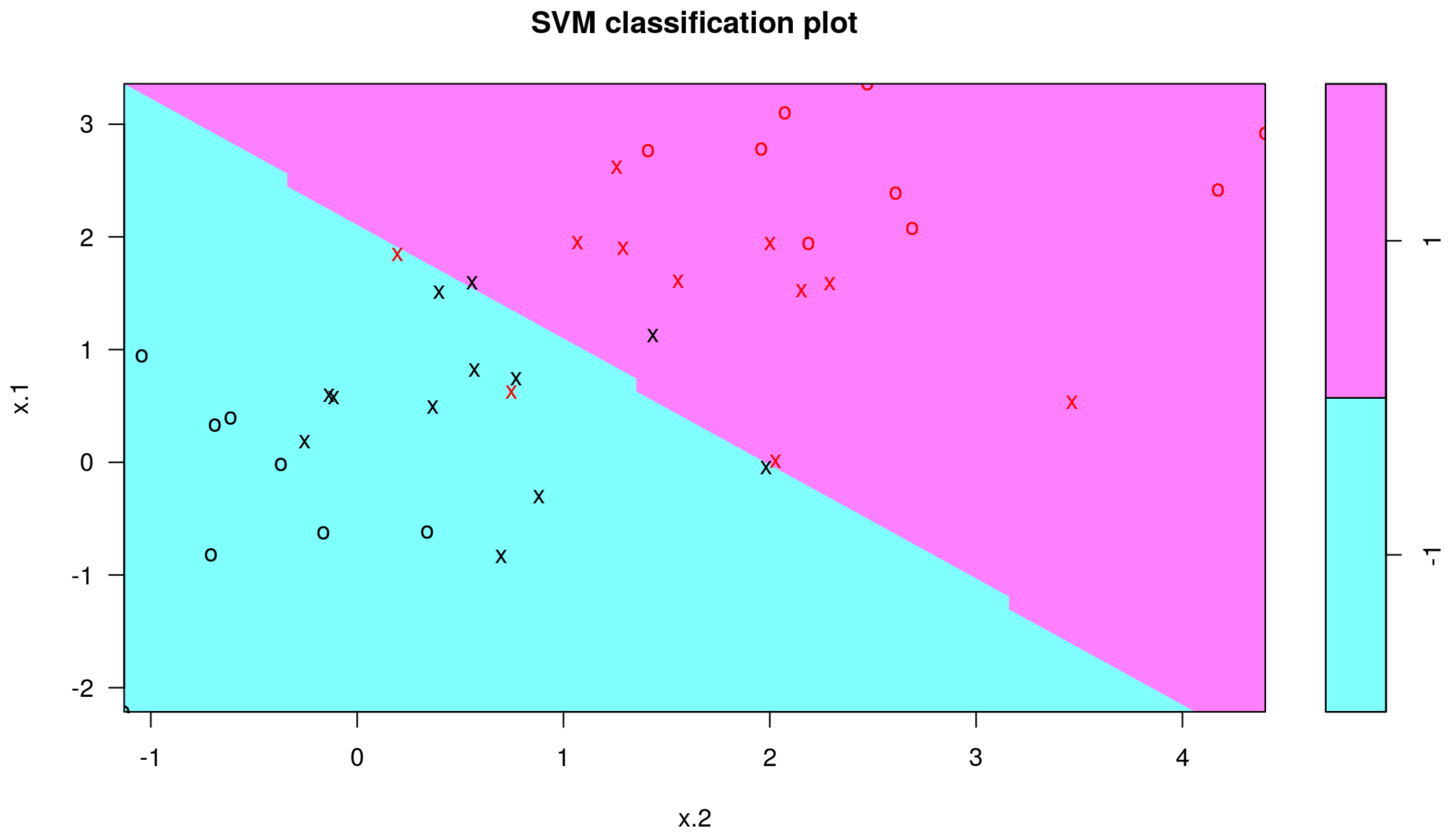
```
svmfit <- svm(y~., data=dat, kernel="linear", cost=0.05, scale=FALSE)
svmfit$index
```

```
##  [1]  2  3  4  7  8  9 10 11 15 16 19 20 24 25 27 28 29 32 34 35 36 37 38
```

```
summary(svmfit)
```

```
##
## Call:
## svm(formula = y ~ ., data = dat, kernel = "linear", cost = 0.05,
##     scale = FALSE)
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  linear
##        cost:  0.05
##       gamma:  0.5
##
## Number of Support Vectors:  23
##
##  ( 12 11 )
##
##
## Number of Classes:  2
##
## Levels:
##  -1 1
```

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

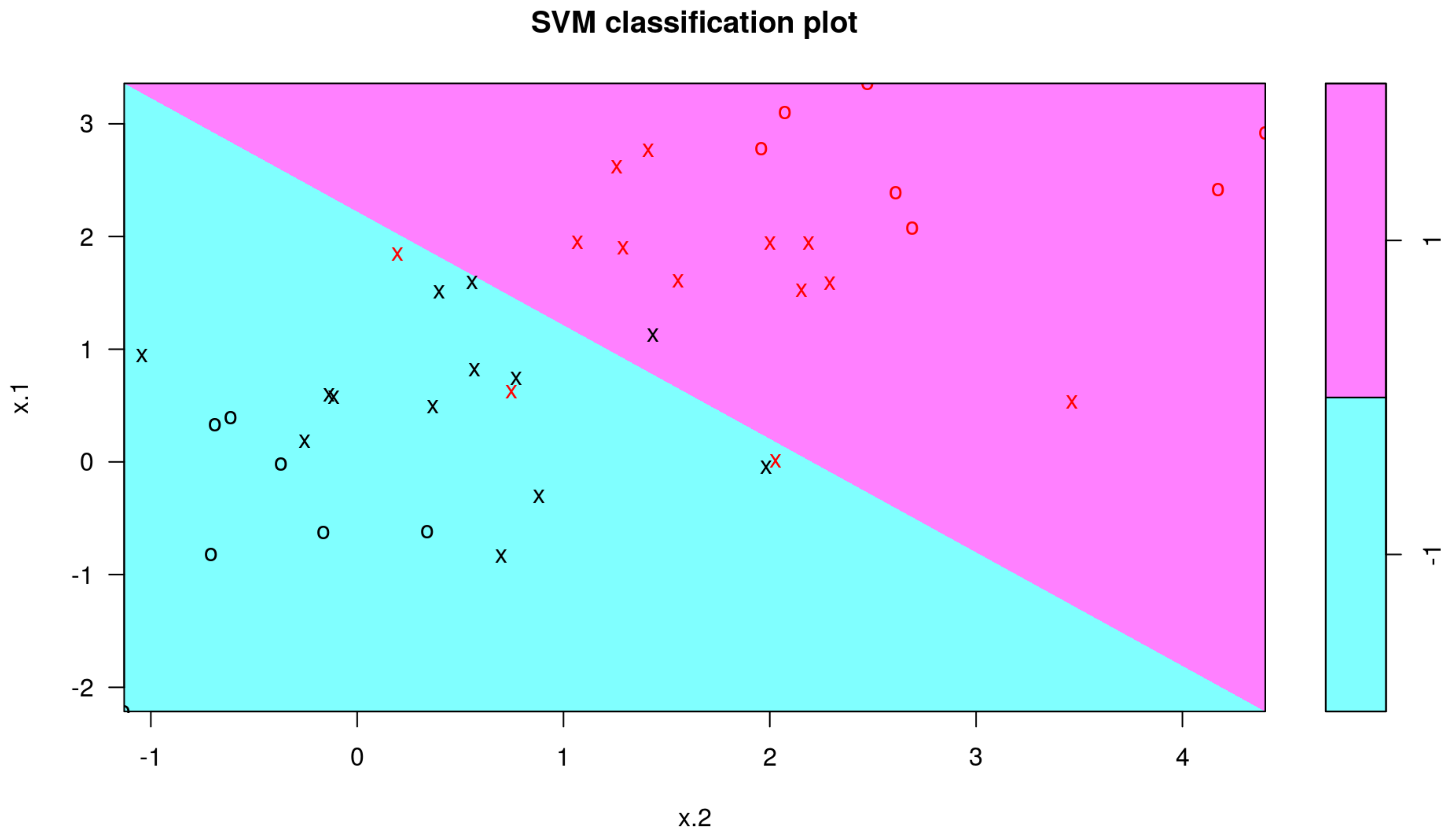


To find a best choice of the tuning parameter “C” use the `tune()` function

```r
set.seed(1)
tune.out <-  tune(svm,y ~ ., data=dat, kernel="linear",
                  ranges=list(cost=c(0.001, 0.01, 0.05, 0.1, 1,5,10,20)))
summary(tune.out)
```

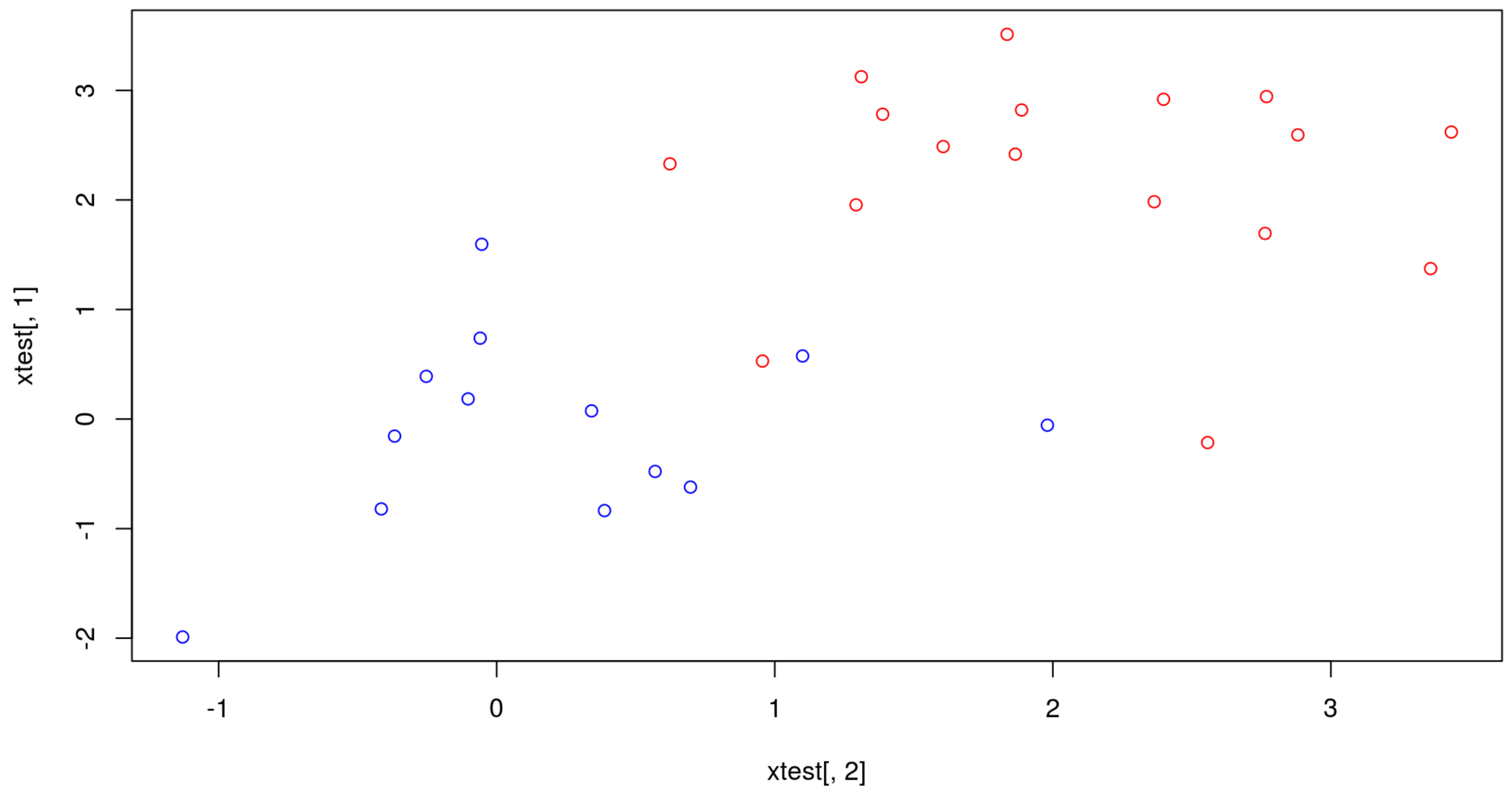
```
##
## Parameter tuning of 'svm':
##
## - sampling method: 10-fold cross validation
##
## - best parameters:
##  cost
##  0.05
##
## - best performance: 0.1
##
## - Detailed performance results:
##    cost error dispersion
## 1 1e-03 0.625  0.2946278
## 2 1e-02 0.450  0.2581989
## 3 5e-02 0.100  0.1290994
## 4 1e-01 0.125  0.1767767
## 5 1e+00 0.150  0.1748015
## 6 5e+00 0.125  0.1317616
## 7 1e+01 0.125  0.1317616
## 8 2e+01 0.125  0.1317616
```

```
bestmod <- tune.out$best.model
plot(bestmod, dat)
```



We build a new test dataset from a similar model as we did for the train data.

```
set.seed(1)
xtest <- matrix(rnorm(30*2), ncol=2)
ytest <- sample(c(-1,1), 30, rep=TRUE)
xtest[ytest == 1, ] <- xtest[ytest == 1,] + 2
testdat <- data.frame(x = xtest, y = as.factor(ytest))
plot(xtest[, 2], xtest[, 1], col=(3-ytest))
```



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

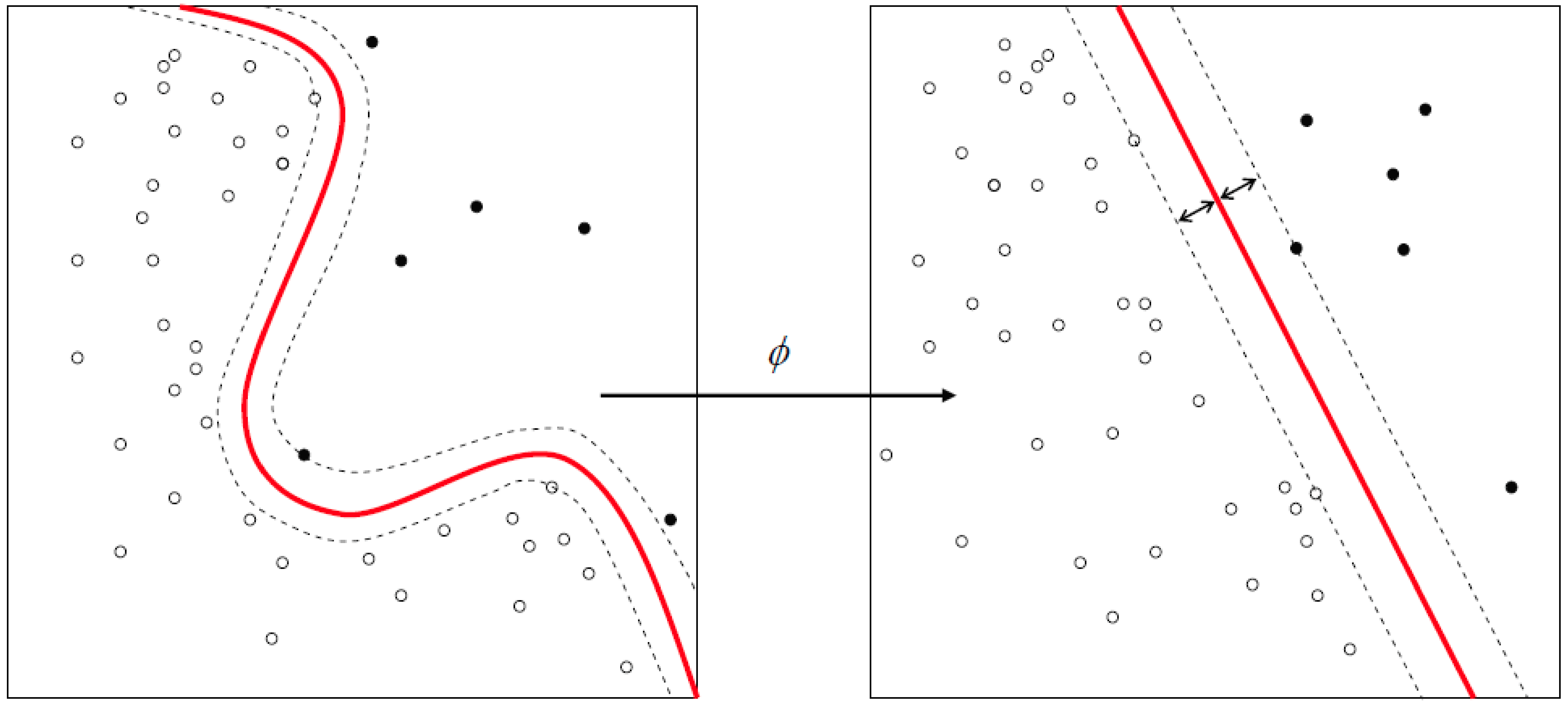
```
##          truth
## predict -1  1
##      -1 13  1
##      1   0 16
```

And for the non-tuned model we have:

```r
svmfit <- svm(y~., data=dat, kernel = "linear", cost=10, scale = FALSE)
ypred <- predict(svmfit, testdat)
table(predict = ypred, truth = testdat$y)
```

```
##          truth
## predict -1  1
##      -1 13  2
##      1   0 15
```

Kernel SVM

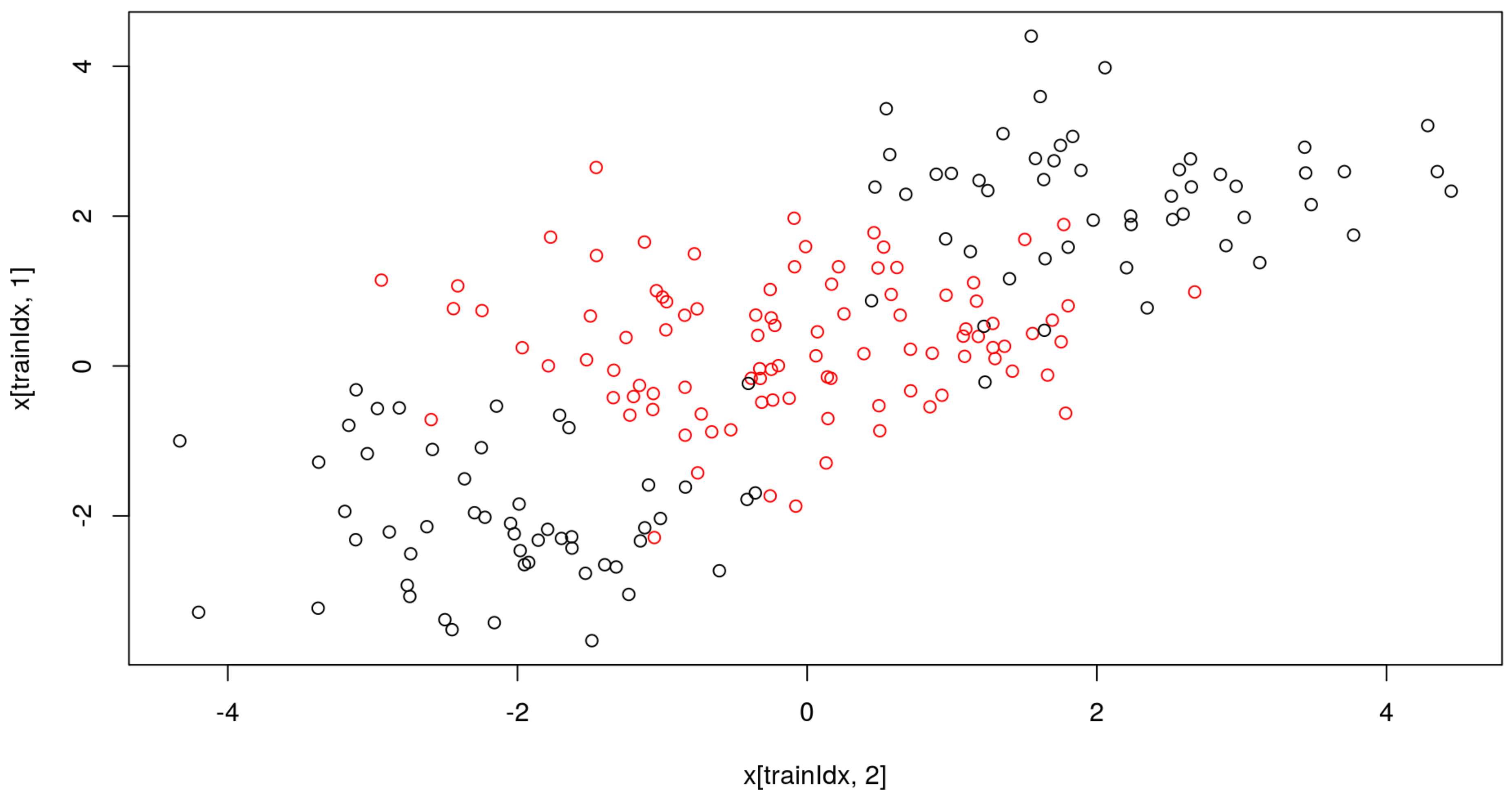


Kernel SVM Example

Now suppose we have non-linearly separable data:

```r
set.seed(1)
# Generate 200 points
x <- matrix(rnorm(400*2), ncol=2)
x[1:100,] <- x[1:100,] + 2
x[101:200,] <- x[101:200, ] - 2
y <- c(rep(1,200), rep(2,200))
dat <- data.frame(x = x, y = as.factor(y))
# Let a random half be a training set
trainIdx <- sample(400, 200)
```

```r
plot(x[trainIdx, 2], x[trainIdx, 1], col=y[trainIdx])
```

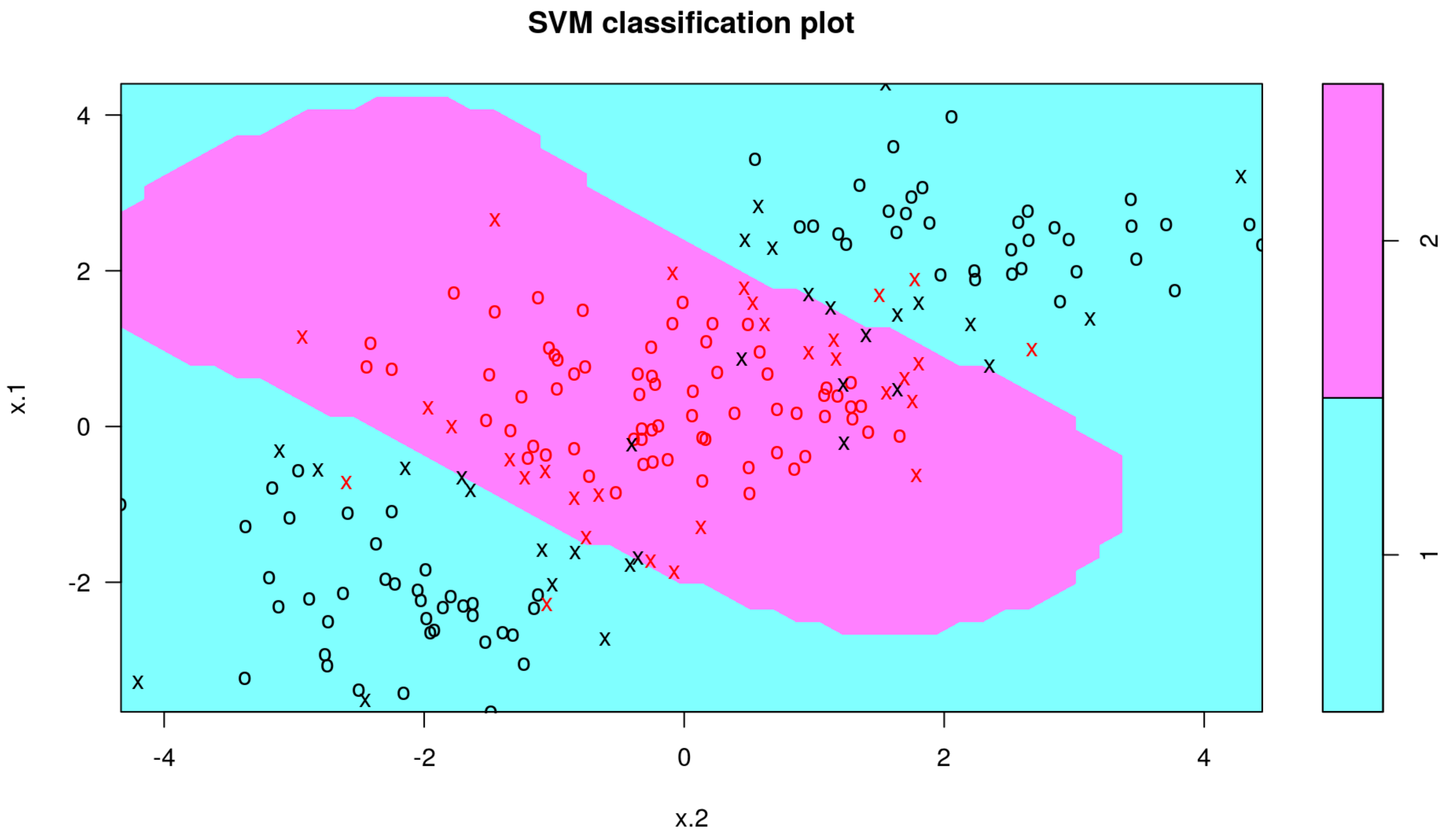


We will use the SVM with **a radial kernel**. Note that here we can additionally specify the `gamma` parameter for the radial function:

```
svmfit <- svm(y~., data=dat[trainIdx,], kernel = "radial",  gamma=1, cost=1)
table(true = dat[-trainIdx,"y"], pred=predict(svmfit, newdata = dat[-trainIdx,
```

```
##      pred
## true  1  2
##    1 81 16
##    2 11 92
```

```r
plot(svmfit, dat[trainIdx,])
```

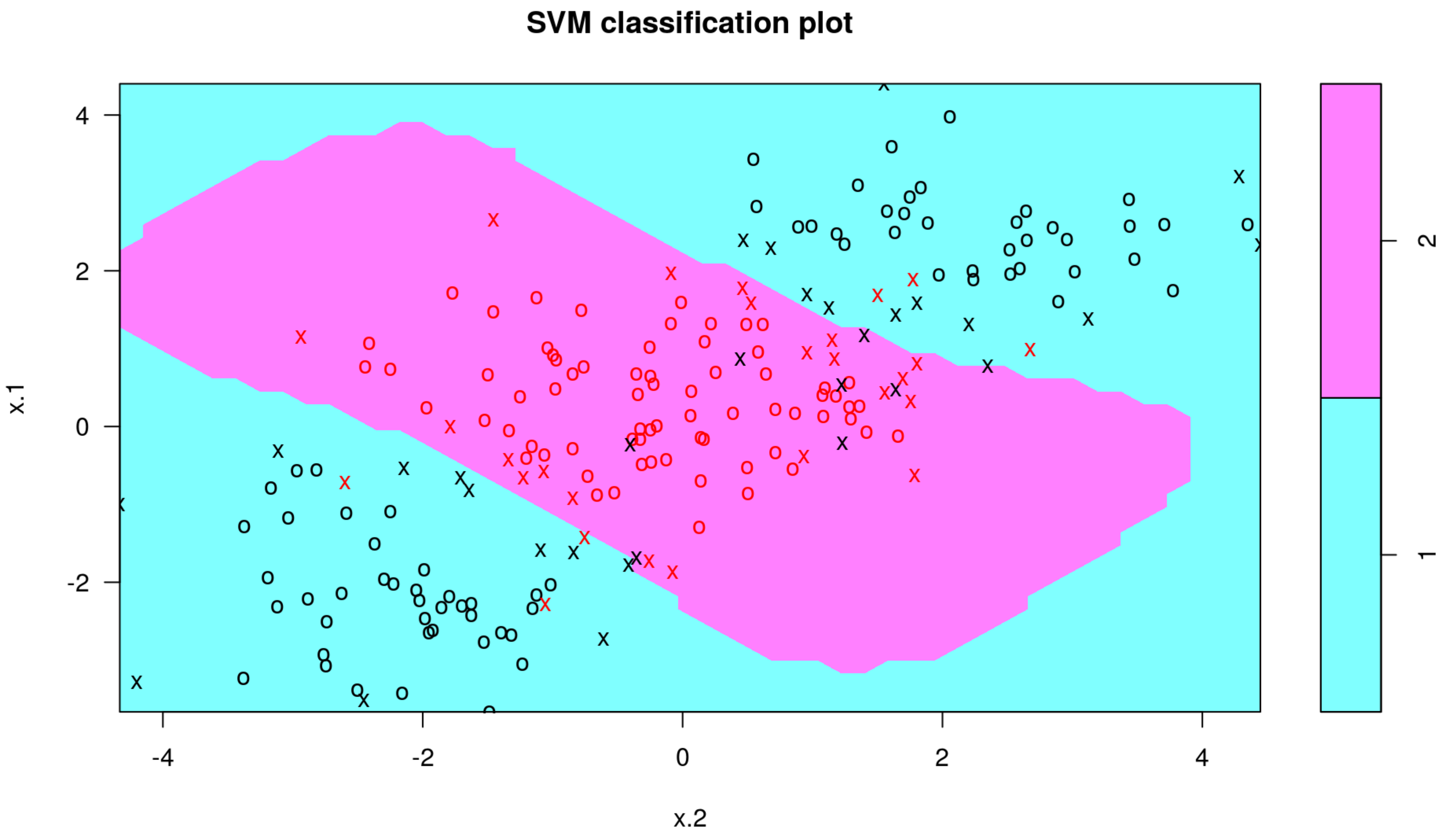


We can tune both `gamma` and `cost` parameters:

```
tune.out <- tune(svm, y~., data=dat[trainIdx,], kernel="radial",
              ranges=list(cost=seq(0.01, 15, length.out = 10),
                          gamma=seq(0.01, 5, length.out = 5)))
table(true = dat[-trainIdx,"y"],
      pred = predict(tune.out$best.model, newdata = dat[-trainIdx,]))
```

```
##      pred
## true  1  2
##    1 84 13
##    2 12 91
```

```r
plot(tune.out$best.model, dat[trainIdx,])
```


SVM classification plot
x.1
x.2