Introduction to Machine Learning

Lab 2 Block 2

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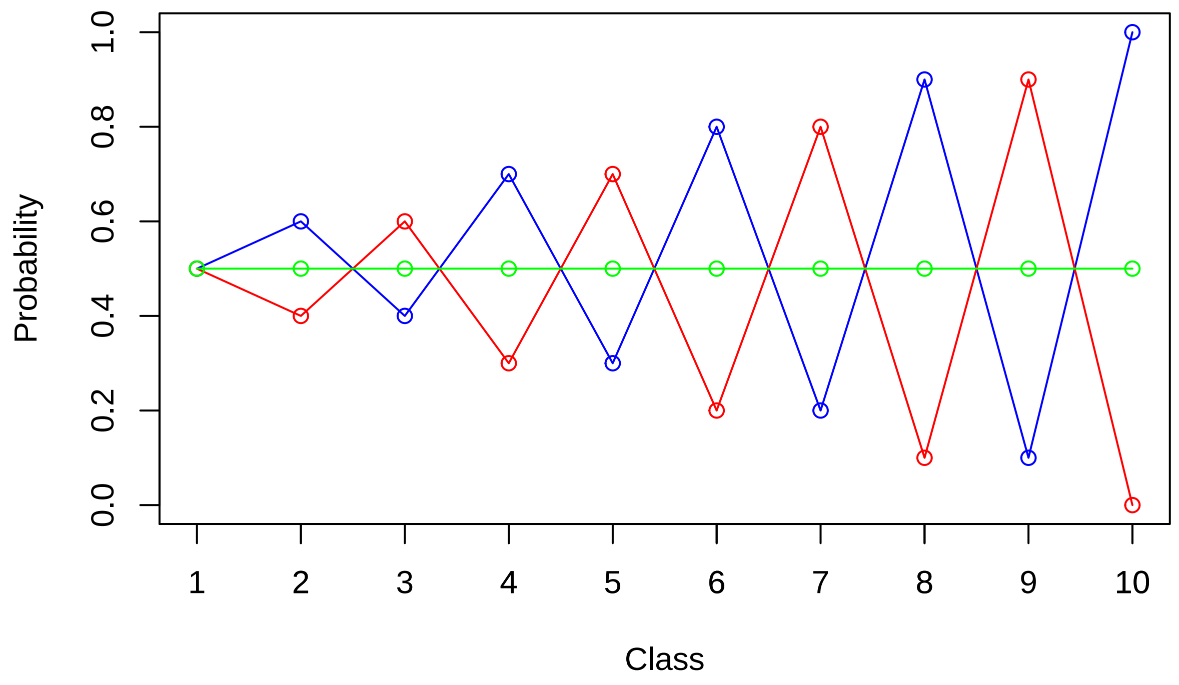


Figure 1: The true probabilities of the multinomal distributions.

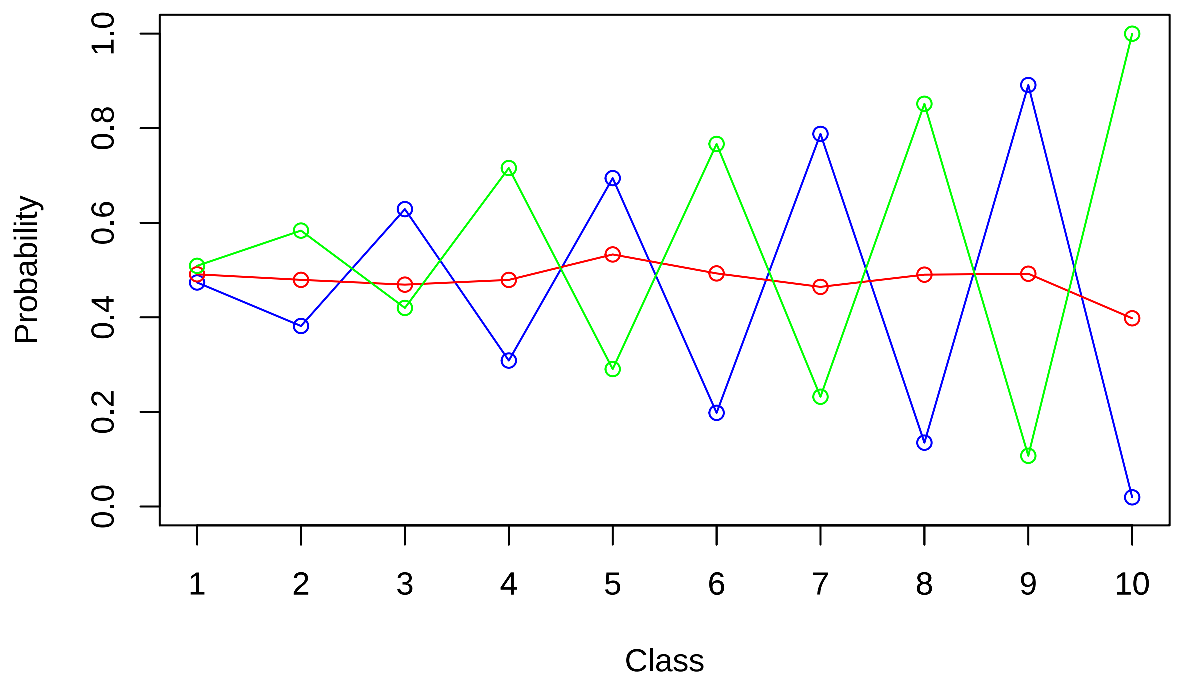


Figure 2: The estimated probabilities of the multinomal distributions.

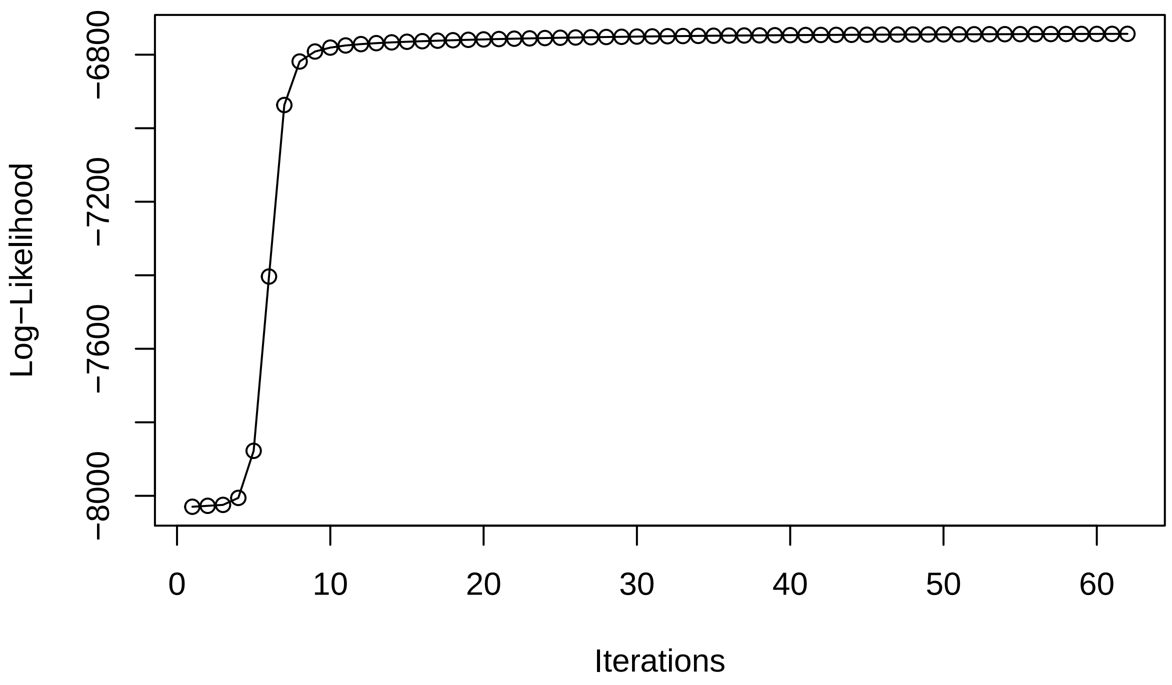


Figure 3: The log-likelihood versus the number of iterations.

Assignment 2a

1

```
#> [1] 37.10301
```

2

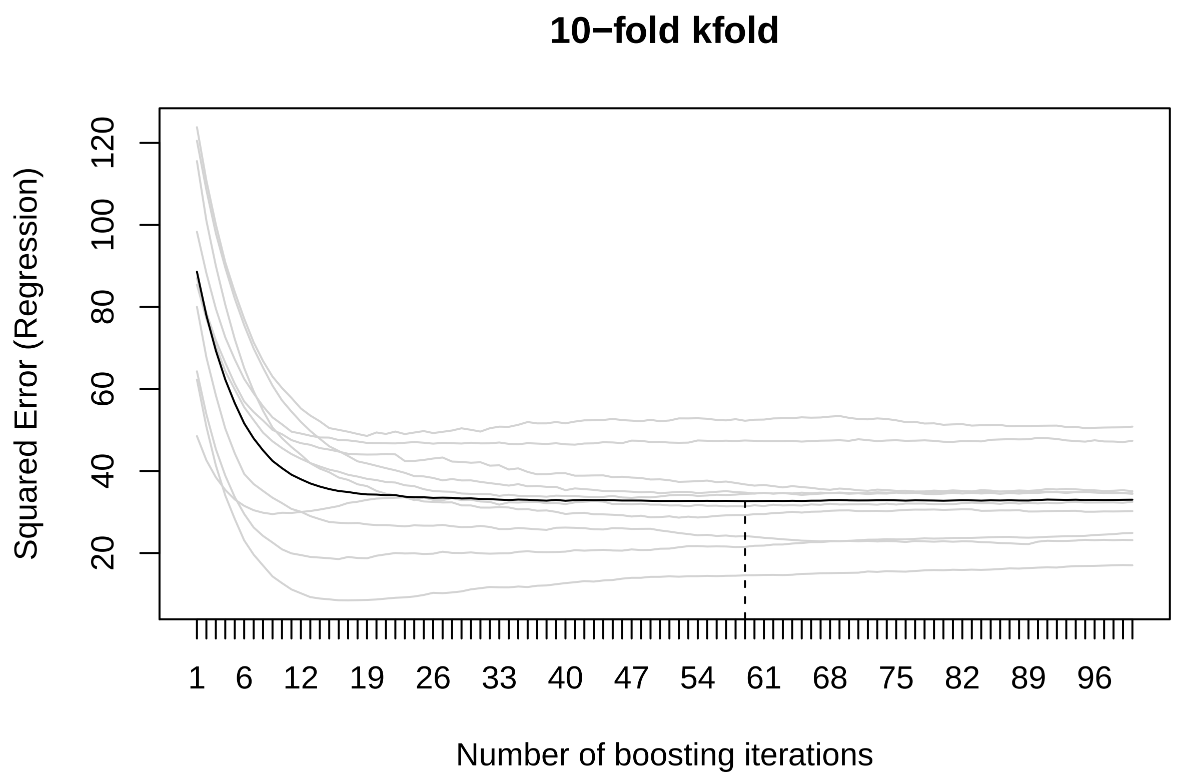
```
#> [1] 40.19377
```

3

Assignment 2b

Assignment 3a

1

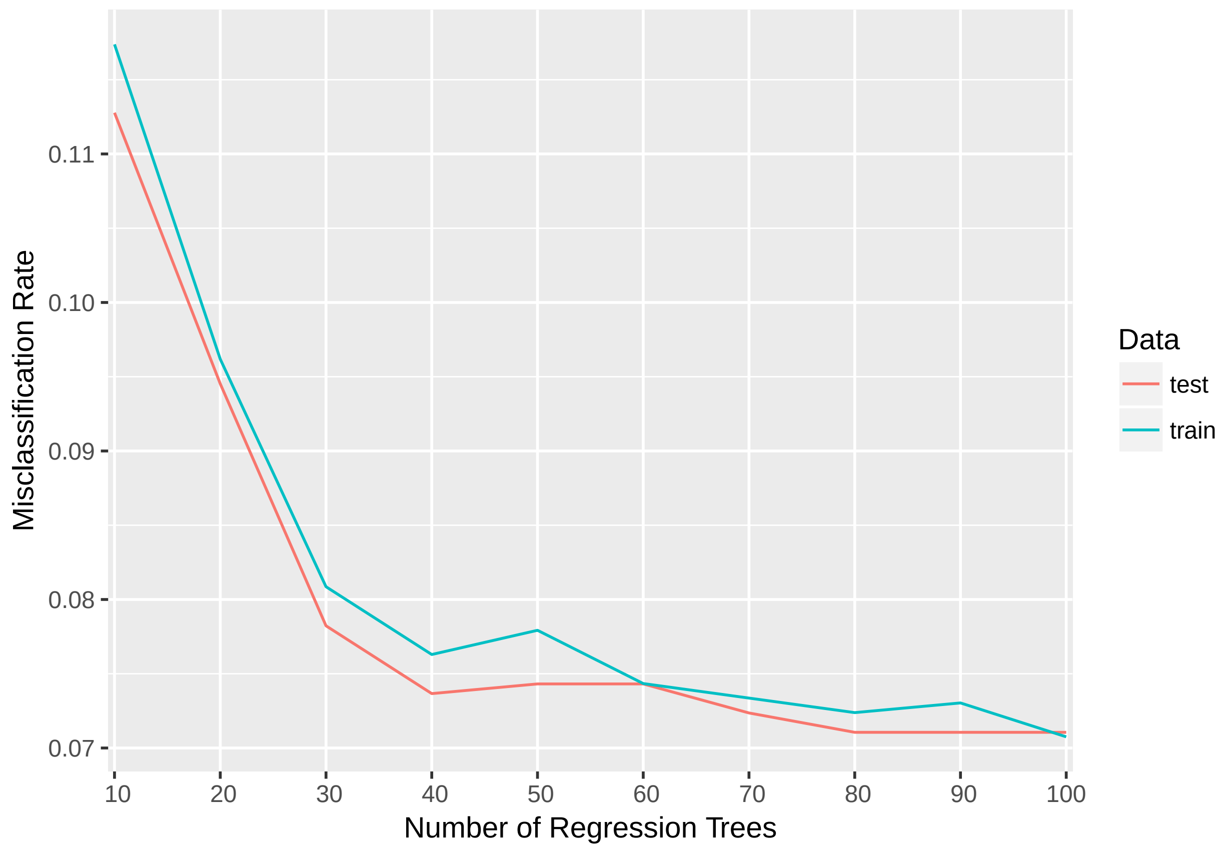


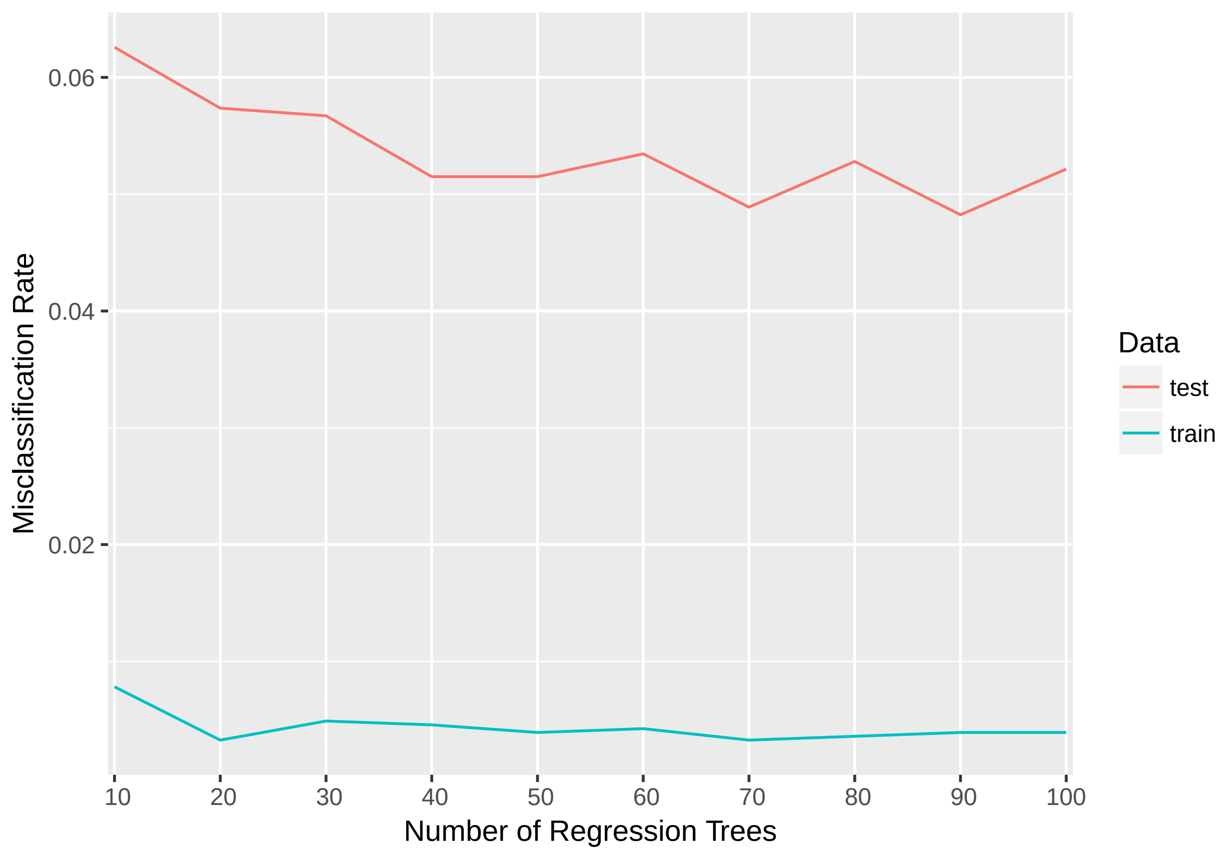
2

```
#> [1] 1037.719
#> [1] 1295.767
```

Assignment 4a

```
#>  [1] 0.11277705 0.09452412 0.07822686 0.07366362 0.07431551 0.07431551
#>  [7] 0.07235984 0.07105606 0.07105606 0.07105606
#>  [1] 0.11737855 0.09618520 0.08086078 0.07629605 0.07792631 0.07433975
#>  [7] 0.07336159 0.07238344 0.07303554 0.07075318
```




Misclassification Rate
0.06
0.04
0.02
10
20
30
40
50
60
70
80
90
100
Number of Regression Trees
Data
test
train

Appendix

Code for Assignment 1a

Code for Assignment 1b

```r
set.seed(1234567890)

max_it <- 100 # max number of EM iterations
min_change <- 0.1 # min change in log likelihood between two consecutive EM iterations

N <- 1000 # number of training points
D <- 10 # number of dimensions

## true mixing coefficients
true_pi <- vector(length=3)
true_pi <- c(1/3, 1/3, 1/3)

## true conditional distributions
true_mu <- matrix(nrow=3, ncol=D)
true_mu[1,] <- c(0.5, 0.6, 0.4, 0.7, 0.3, 0.8, 0.2, 0.9, 0.1, 1)
true_mu[2,] <- c(0.5, 0.4, 0.6, 0.3, 0.7, 0.2, 0.8, 0.1, 0.9, 0)
true_mu[3,] <- c(0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5)

## Producing the training data
x <- matrix(nrow=N, ncol=D)

for(n in 1:N) {
    k <- sample(1:3, 1, prob=true_pi)
    for(d in 1:D) {
        x[n, d] <- rbinom(1, 1, true_mu[k, d])
    }
}

K <- 3 # number of guessed components
z <- matrix(nrow=N, ncol=K) # fractional component assignments
pi <- vector(length=K) # mixing coefficients
mu <- matrix(nrow=K, ncol=D) # conditional distributions
llik <- vector(length=max_it) # log likelihood of the EM iterations

## Random initialization of the paramters
pi <- runif(K, 0.49, 0.51)
pi <- pi / sum(pi)
for(k in 1:K) {
    mu[k,] <- runif(D, 0.49, 0.51)
}
plot(true_mu[1,], type="o", col="blue", ylim=c(0,1),
     xlab="Class", ylab="Probability")
axis(side=1, at=c(1:D))
points(true_mu[2,], type="o", col="red")
points(true_mu[3,], type="o", col="green")
expectation.step <- function(x, mu, pi) {
    x_given_mu <- matrix(1, nrow=N, ncol=length(pi))
    for (n in 1:N) {
        for (k in 1:K) {
            for (i in 1:D) {
                x_given_mu[n, k] <- x_given_mu[n, k] * mu[k, i]^x[n, i] * (1 - mu[k, i])^(1 - x[n, i])
            }
        }
    }

    z <- matrix(nrow=nrow(x), ncol=length(pi))

    for (n in 1:N) {
        denominator <- sum(pi * x_given_mu[n,])

        for (k in 1:K) {
            nominator <- pi[k] * x_given_mu[n, k]

            z[n, k] <- nominator / denominator
        }
    }

    z
}

loglikelihood <- function(x, mu, pi, z) {
    llik <- 0
    for (n in 1:N) {
        for (k in 1:K) {
            summation <- 0
            ## conditional <- 1
            for (i in 1:D) {
                summation <- summation + x[n, i] * log(mu[k, i]) + (1 - x[n, i]) * log(1 - mu[k, i])
                ## conditional <- conditional * mu[k, i]^x[n, i] * (1 - mu[k, i])^(1 - x[n, i])
            }
            llik <- llik + z[n, k] * (log(pi[k]) + summation)
            ## llik[it] <- llik[it] + pi[k] * conditional
        }
    }

    llik
}

maximize.step <- function(x, z) {
    pi <- vector(length=ncol(z))
    mu <- matrix(nrow=ncol(z), ncol=ncol(x))

    for (k in 1:K) {
        pi[k] <- sum(z[, k]) / nrow(x)
    }

    for (k in 1:K) {
        denominator <- sum(z[, k])
        for (i in 1:D) {
            nominator <- sum(x[, i] * z[, k])
```

```r
            mu[k, i] <- nominator / denominator
        }
    }

    list(pi=pi, mu=mu)
}

for(it in 1:max_it) {
    ## plot(mu[1,], type="o", col="blue", ylim=c(0,1))
    ## points(mu[2,], type="o", col="red")
    ## points(mu[3,], type="o", col="green")
    ## points(mu[4,], type="o", col="yellow")
    ## Sys.sleep(0.5)

    ## E-step: Computation of the fractional component assignments
    z <- expectation.step(x, mu, pi)

    ## Log likelihood computation.
    llik[it] <- loglikelihood(x, mu, pi, z)

    ## cat("iteration: ", it, "log likelihood: ", llik[it], "\n")
    ## flush.console()

    ## Stop if the lok likelihood has not changed significantly
    if (it > 1 && abs(llik[it] - llik[it-1]) < min_change) break

    ## M-step: ML parameter estimation from the data and fractional component assignments
    result <- maximize.step(x, z)
    pi <- result$pi
    mu <- result$mu
}
plot(mu[1,], type="o", col="blue", ylim=c(0,1),
     xlab="Class", ylab="Probability")
axis(side=1, at=c(1:D))
points(mu[2,], type="o", col="red")
points(mu[3,], type="o", col="green")
plot(llik[1:it], type="o", xlab="Iterations",
     ylab="Log-Likelihood")
```

Code for Assignment 2a

```r
library(tree)

data <- read.csv2("../data/bodyfatregression.csv")
names(data) <- c("Waist", "Weight", "Bodyfat")
set.seed(1234567890)
train_idx <- sample(nrow(data), floor(nrow(data) * (2 / 3)))
train <- data[train_idx,]
test <- data[-train_idx,]

set.seed(1234567890)
```

```r
tree_count <- 100
test_errors <- rep(0, tree_count)

for (i in 1:tree_count) {
    newdata <- train[sample(nrow(train), replace=TRUE),]
    fit <- tree(Bodyfat ~ ., data=newdata, split="deviance")

    test_error <- mean((predict(fit, test) - test$Bodyfat)^2)
    test_errors[i] <- test_error
}

mean(test_errors)
tree_count <- 100
fold_count <- 3
test_errors <- matrix(0, nrow=tree_count, ncol=fold_count)

set.seed(1234567890)

folds <- suppressWarnings(split(1:nrow(data), f=1:fold_count))

for (j in 1:fold_count) {
    train <- data[-folds[[j]],]
    test <- data[folds[[j]],]

    for (i in 1:tree_count) {
        newdata <- train[sample(nrow(train), replace=TRUE),]
        fit <- tree(Bodyfat ~ ., data=newdata, split="deviance")

        test_error <- mean((predict(fit, test) - test$Bodyfat)^2)
        test_errors[i, j] <- test_error
    }
}

mean(test_errors)
bagging.regtrees <- function(formula, data, newdata, b) {
    predictions <- matrix(0, nrow=nrow(newdata), ncol=b)
    trees <- list()

    for (i in 1:b) {
        bootstrap_sample <- data[sample(nrow(data), replace=TRUE),]
        fit <- tree(formula, data=bootstrap_sample, split="deviance")
        trees[[i]] <- fit
        predictions[, i] <- predict(fit, newdata)
    }

    list(trees=trees, predictions=rowMeans(predictions))
}
cv.regtrees <- function(formula, data, newdata, b, k) {

}
```

Code for Assignment 2b

Code for Assignment 3a

```r
library(mboost)

data <- read.csv2("../data/bodyfatregression.csv")

fit <- blackboost(Bodyfat_percent ~ Waist_cm + Weight_kg, data=data)

cvf <- cv(model.weights(fit), type="kfold")
cvm <- cvrisk(fit, folds=cvf, grid=1:100)
plot(cvm)
set.seed(1234567890)
train_idx <- sample(nrow(data), floor(nrow(data) * (2 / 3)))
train <- data[train_idx,]
test <- data[-train_idx,]

fit <- blackboost(Bodyfat_percent ~ Waist_cm + Weight_kg, data=train,
                  control=boost_control(mstop=mstop(cvm)))
test_error <- sum((predict(fit, test) - test$Bodyfat_percent)^2)
train_error <- sum((predict(fit, train) - train$Bodyfat_percent)^2)

test_error
train_error
```

Code for Assignment 4a

```r
library(mboost)
library(randomForest)
library(ggplot2)
library(reshape2)

data <- read.csv2("../data/spambase.csv")
data$Spam <- as.factor(data$Spam)

set.seed(1234567890)
train_idx <- sample(nrow(data), floor(nrow(data) * (2 / 3)))
train <- data[train_idx,]
test <- data[-train_idx,]
tree_counts <- seq(10, 100, by=10)
test_errors <- rep(0, length(tree_counts))
train_errors <- rep(0, length(tree_counts))

for (i in 1:length(tree_counts)) {
    fit <- blackboost(Spam ~ ., data=train, family=AdaExp(),
                      control=boost_control(mstop=tree_counts[i]))
    test_error <- 1 - (sum(predict(fit, test, type="class") == test$Spam) / nrow(test))
    train_error <- 1 - (sum(predict(fit, train, type="class") == train$Spam) / nrow(train))
    test_errors[i] <- test_error
    train_errors[i] <- train_error
}
```

```
test_errors
train_errors
plot_data <- data.frame(Trees=tree_counts, test=test_errors, train=train_errors)
plot_data <- melt(plot_data, id="Trees", value.name="Error", variable.name="Data")

ggplot(plot_data) +
    xlab("Number of Regression Trees") +
    ylab("Misclassification Rate") +
    geom_line(aes(x=Trees, y=Error, color=Data)) +
    scale_x_discrete(limits=tree_counts)
test_errors <- rep(0, length(tree_counts))
train_errors <- rep(0, length(tree_counts))

for (i in 1:length(tree_counts)) {
    fit <- randomForest(Spam ~ ., data=train, ntree=tree_counts[i])
    test_error <- 1 - (sum(predict(fit, test, type="class") == test$Spam) / nrow(test))
    train_error <- 1 - (sum(predict(fit, train, type="class") == train$Spam) / nrow(train))
    test_errors[i] <- test_error
    train_errors[i] <- train_error
}
plot_data <- data.frame(Trees=tree_counts, test=test_errors, train=train_errors)
plot_data <- melt(plot_data, id="Trees", value.name="Error", variable.name="Data")

ggplot(plot_data) +
    xlab("Number of Regression Trees") +
    ylab("Misclassification Rate") +
    geom_line(aes(x=Trees, y=Error, color=Data)) +
    scale_x_discrete(limits=tree_counts)
```