Introduction to Machine Learning

Lab 2 Block 2

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Contents

Assignment 1a

Assumptions:

$$\mathrm{E}\left[\epsilon^b(x)\right] = 0,$$
$$\forall_{i,j}, i \neq j : \mathrm{E}\left[\epsilon^i(x)\epsilon^j(x)\right] = 0$$

Prove:

$$\mathrm{E}_x\left[(f_{bag}(x) - h(x))^2\right] = \frac{1}{B}\left[\frac{1}{B}\mathrm{E}\left[(\epsilon^b(x))^2\right]\right]$$

We know:

$$f^b(x) = h(x) + \epsilon^b(x)$$

Proof:

$$\mathrm{E}_x\left[(f_{bag}(x) - h(x))^2\right] =$$
$$\mathrm{E}_x\left[(\frac{1}{B}\sum_b f^b(x) - h(x))^2\right] =$$
$$\mathrm{E}_x\left[(\frac{1}{B}\sum_b \epsilon^b(x))^2\right] =$$
$$\frac{1}{B^2}\mathrm{E}_x\left[(\epsilon^1(x))^2 + \epsilon^1(x)\epsilon^2(x) + \cdots + (\epsilon^b(x))^2\right] =$$
$$\frac{1}{B^2}\left(\mathrm{E}_x\left[(\epsilon^1(x))^2\right] + \mathrm{E}_x\left[\epsilon^1(x)\epsilon^2(x)\right] + \cdots + \mathrm{E}_x\left[(\epsilon^b(x))^2\right]\right) =$$
$$\frac{1}{B^2}\sum_b \mathrm{E}_x\left[(\epsilon^b(x))^2\right] =$$
$$\frac{1}{B^2}\sum_b \mathrm{E}_x\left[(f^b(x) - h(x))^2\right]$$

Assignment 1b

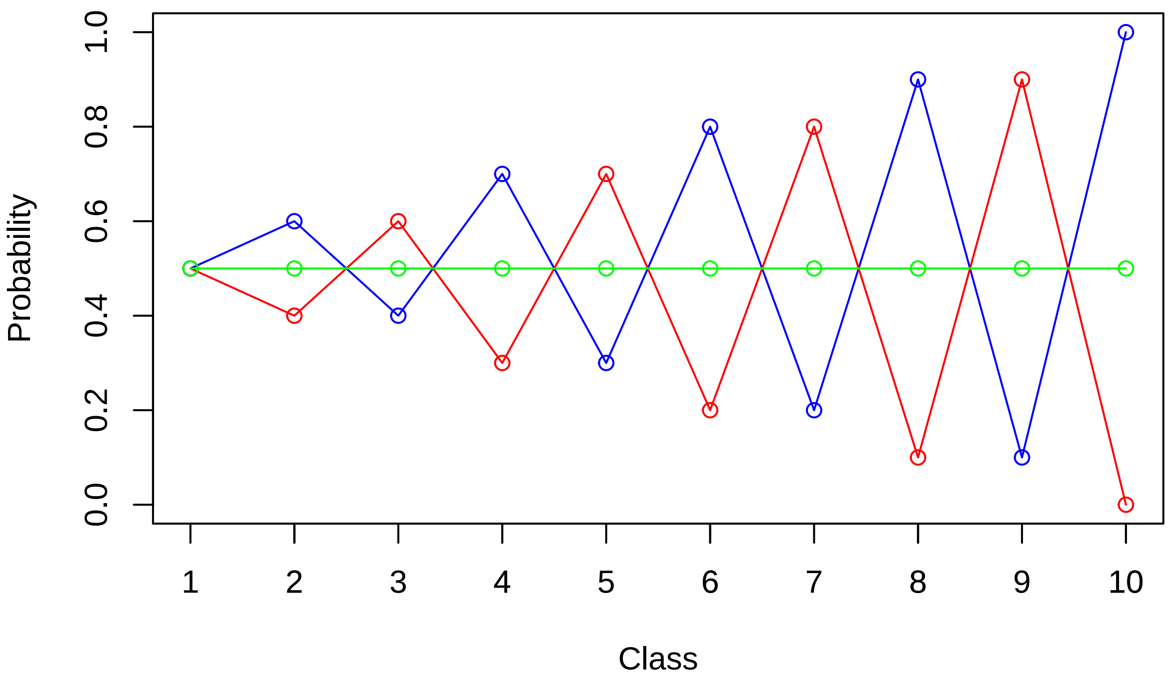


Figure 1: The true probabilities of the multinomal distributions.

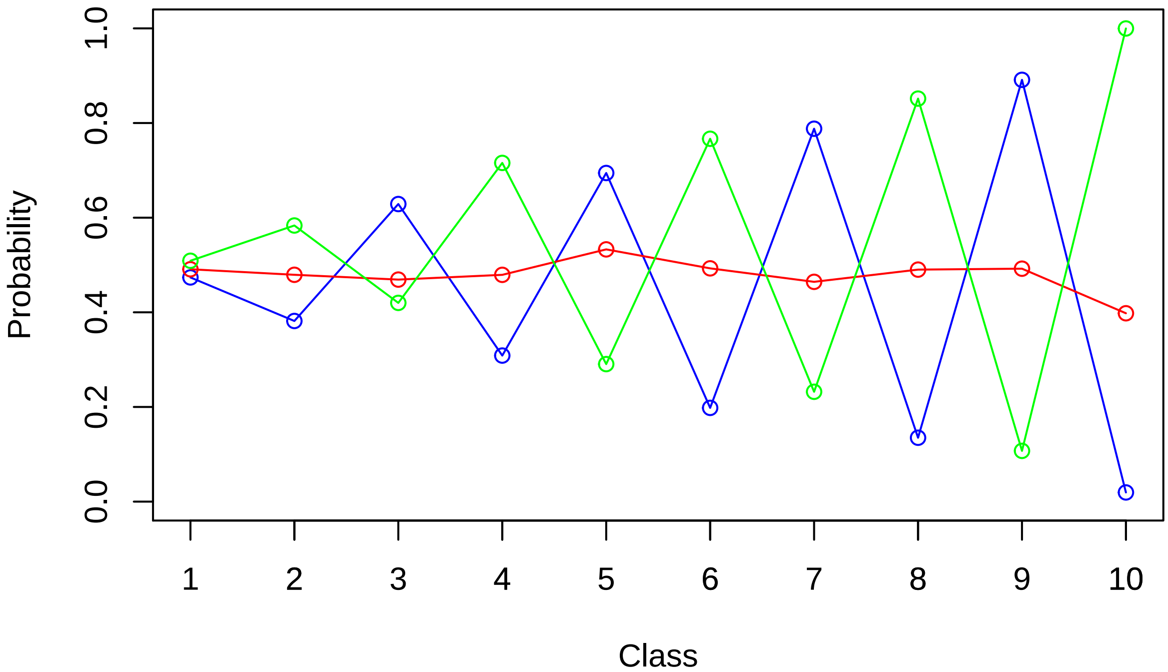


Figure 2: The estimated probabilities of the multinomal distributions.

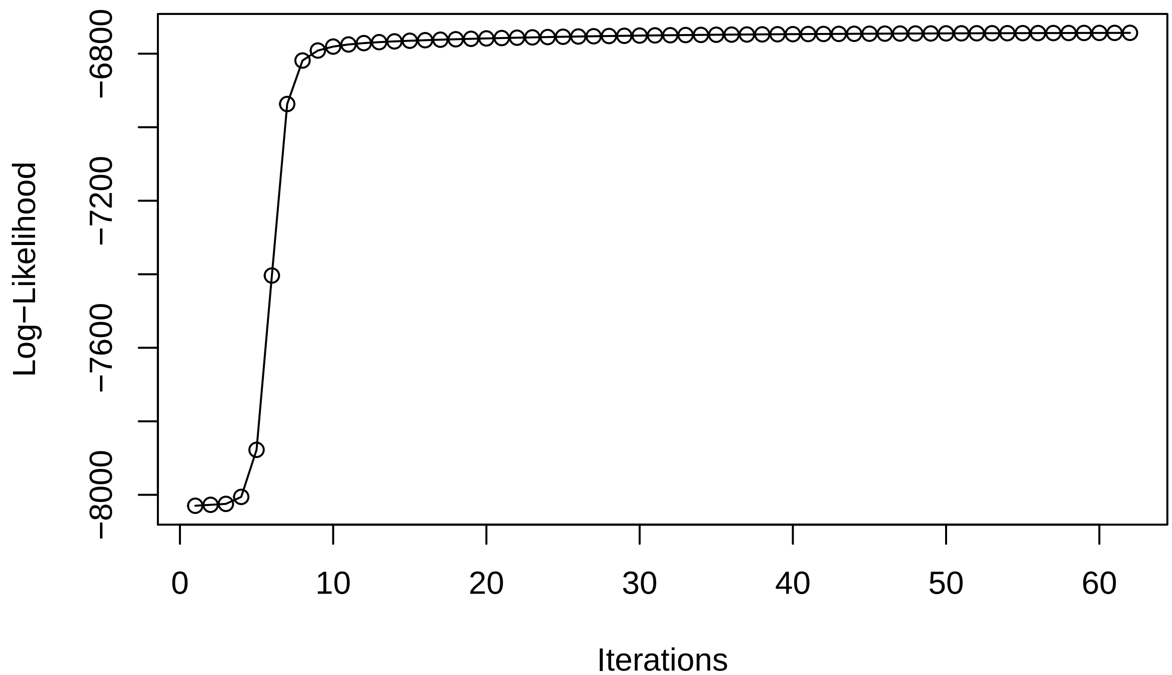


Figure 3: The log-likelihood versus the number of iterations.

Assignment 2a

1

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

2

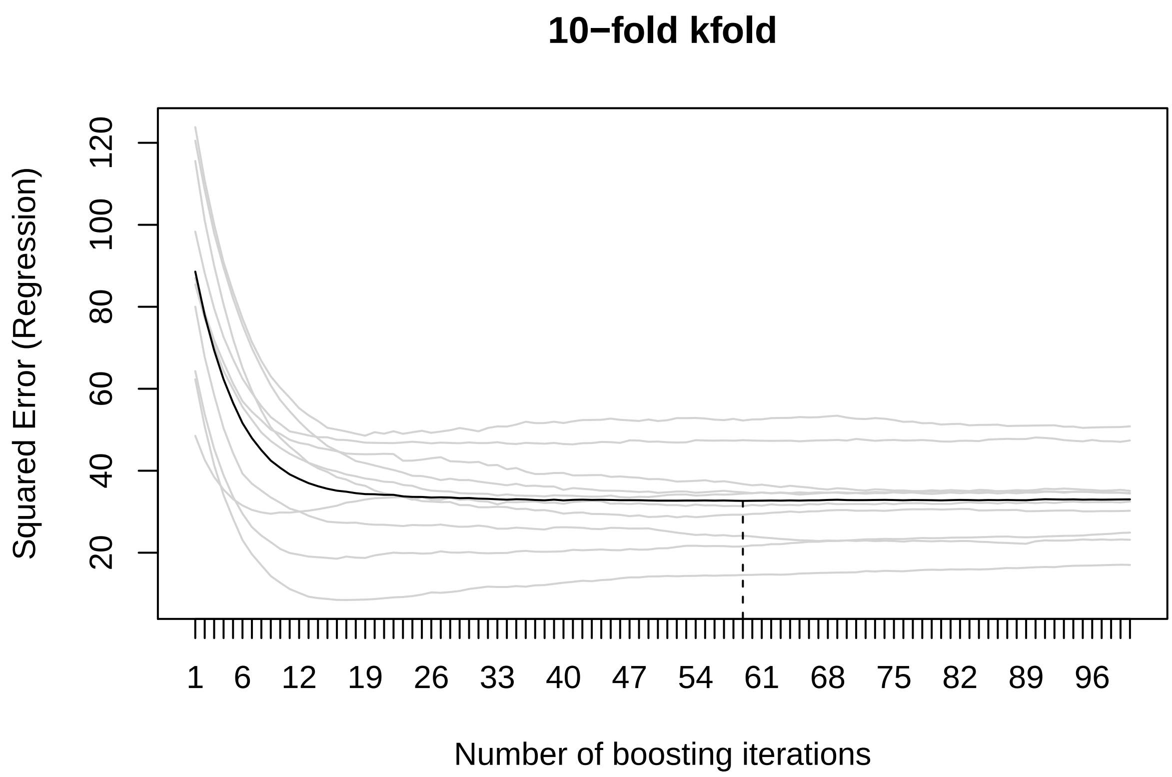
```
#> [1] 40.19377
```

3

Assignment 2b

Assignment 3a

1

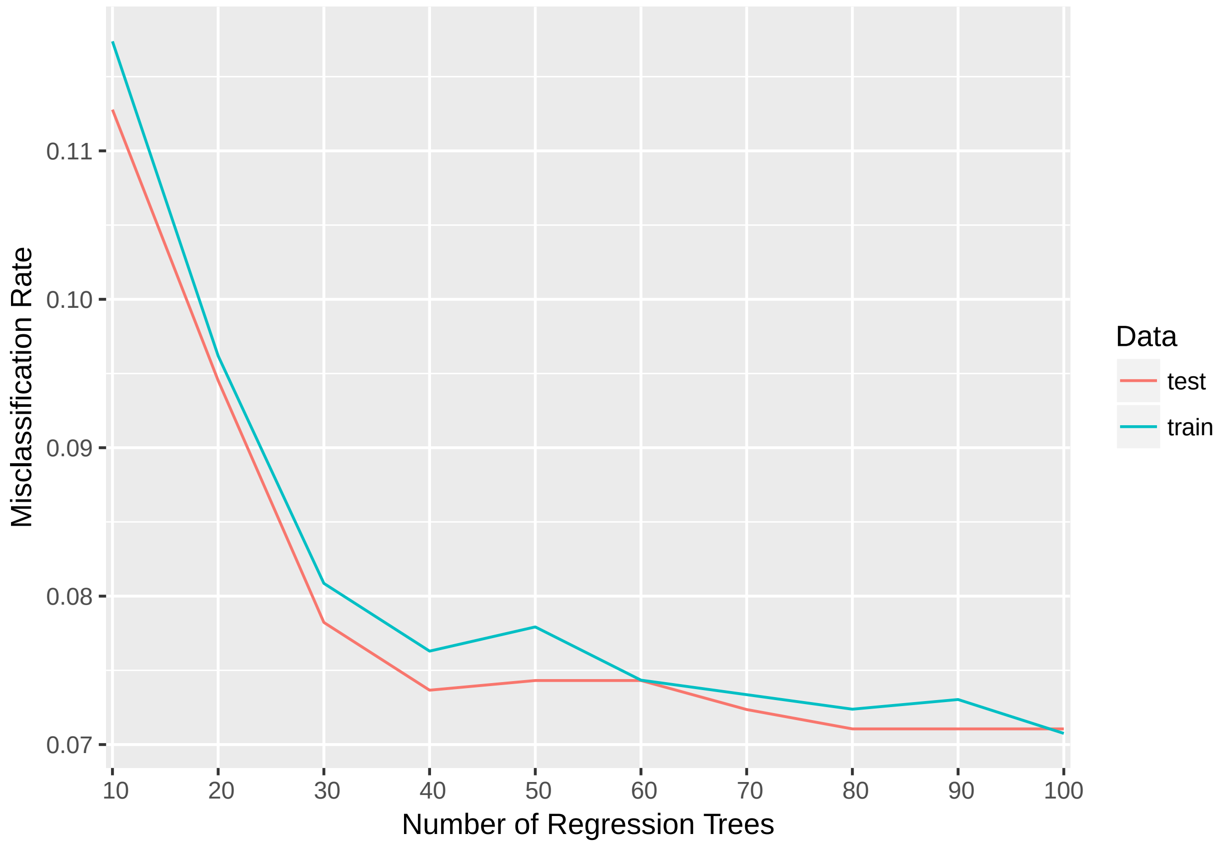


2

```
#> [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
```



0.06
0.04
0.02
Misclassification Rate
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) {
                prob <-  mu[k, i]^x[n, i] * (1 - mu[k, i])^(1 - x[n, i])
                x_given_mu[n, k] <- x_given_mu[n, k] * prob
            }
        }
    }

    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
}

maximization.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])
            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 <- maximization.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

```
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

```
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

```
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
}
```

```r
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)
```