Introduction to Machine Learning

Lab 2 Block 2

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Assignment 1a

Assumptions:

$$\mathbf{E}\left[\epsilon^{b}(x)\right] = 0,$$

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

Prove:

$$E_X [(f_{bag}(x) - h(x))^2] = \frac{1}{B} [\frac{1}{B} E_X [(f^b(x) - h(x))^2]]$$

We know:

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

Proof:

$$\begin{split} \mathbf{E}_{X} \left[(f_{bag}(x) - h(x))^{2} \right] &= \\ \mathbf{E}_{X} \left[(\frac{1}{B} \sum_{b} f^{b}(x) - h(x))^{2} \right] &= \\ \mathbf{E}_{X} \left[(\frac{1}{B} \sum_{b} \epsilon^{b}(x))^{2} \right] &= \\ \frac{1}{B^{2}} \mathbf{E}_{X} \left[(\epsilon^{1}(x))^{2} + 2\epsilon^{1}(x)\epsilon^{2}(x) + \dots + 2\epsilon^{b-1}(x)\epsilon^{b}(x) + (\epsilon^{b}(x))^{2} \right] &= \\ \frac{1}{B^{2}} \left(\mathbf{E}_{X} \left[(\epsilon^{1}(x))^{2} \right] + 2\mathbf{E}_{X} \left[\epsilon^{1}(x)\epsilon^{2}(x) \right] + \dots + 2\mathbf{E}_{X} \left[\epsilon^{b-1}(x)\epsilon^{b}(x) \right] + \mathbf{E}_{X} \left[(\epsilon^{b}(x))^{2} \right] \right) &= \\ \frac{1}{B^{2}} \sum_{b} \mathbf{E}_{X} \left[(\epsilon^{b}(x) - h(x))^{2} \right] &= \\ \frac{1}{B} \left[\frac{1}{B} \mathbf{E}_{X} \left[(f^{b}(x) - h(x))^{2} \right] \right] \end{split}$$

Assignment 1b

Assignment 2a

1

#> [1] 37.10301

2

#> [1] 40.19377

3

Assignment 2b

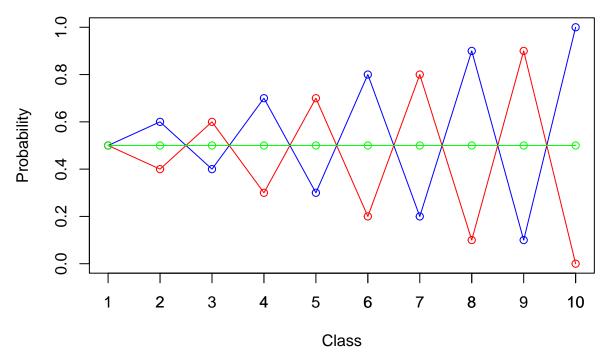
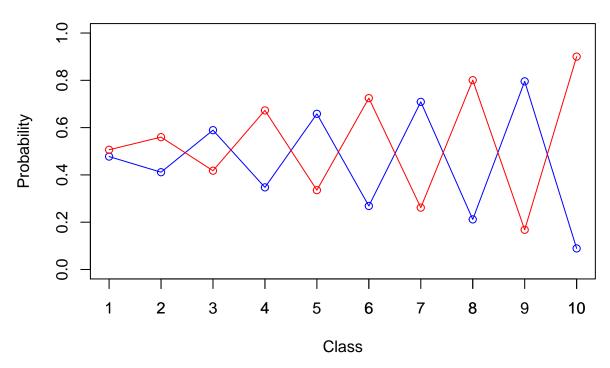


Figure 1: The true probabilities of the multinomal distributions.



 $Figure\ 2:\ The\ estimated\ probabilities\ of\ the\ multinomal\ distributions.$

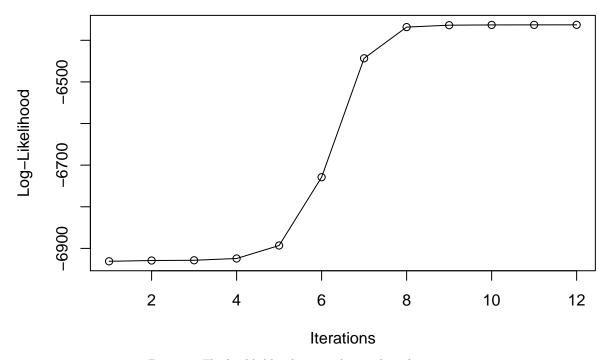


Figure 3: The log-likelihood versus the number of iterations.

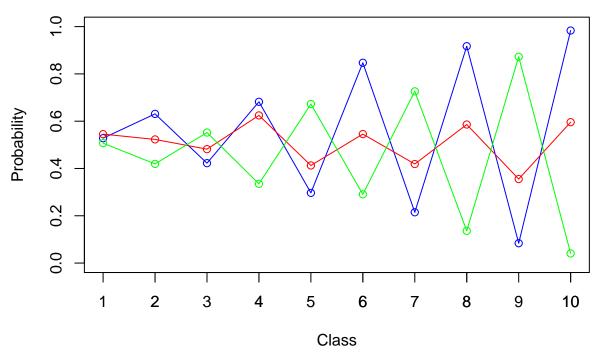


Figure 4: The estimated probabilities of the multinomal distributions.

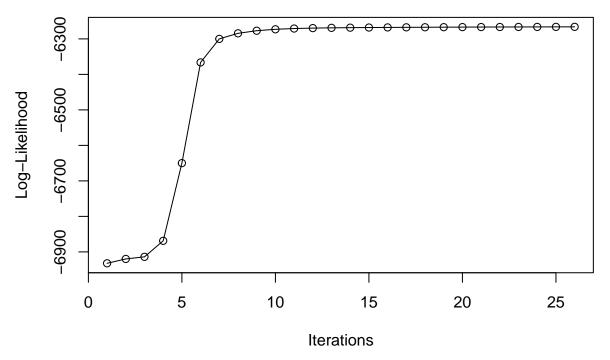


Figure 5: The log-likelihood versus the number of iterations.

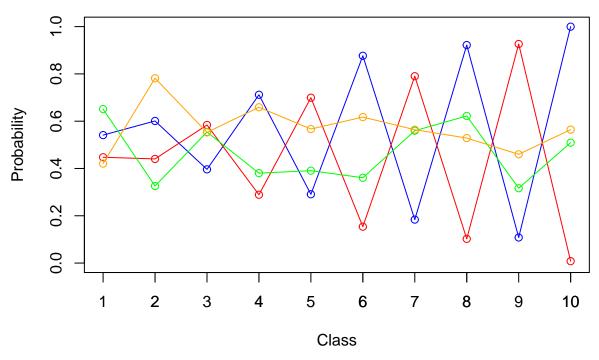


Figure 6: The estimated probabilities of the multinomal distributions.

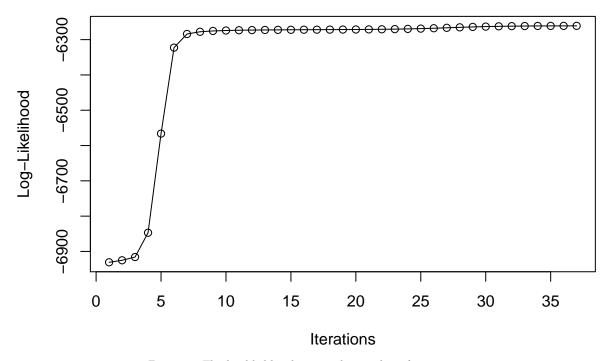
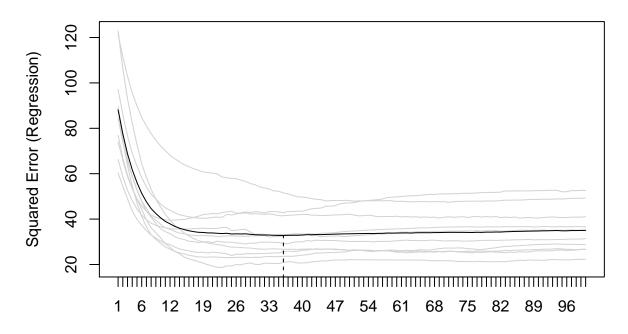


Figure 7: The log-likelihood versus the number of iterations.

Assignment 3a

1

10-fold kfold



Number of boosting iterations

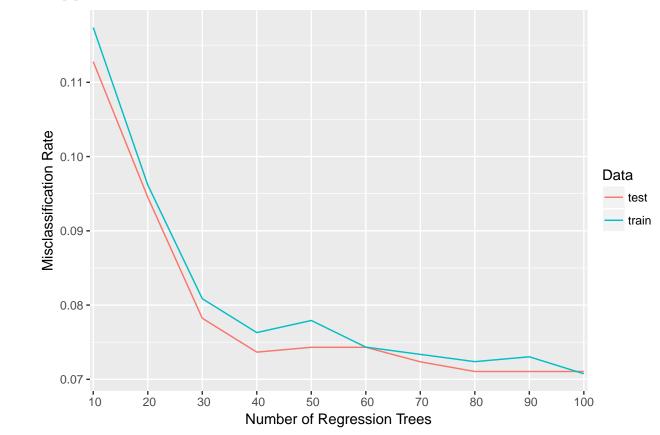
2

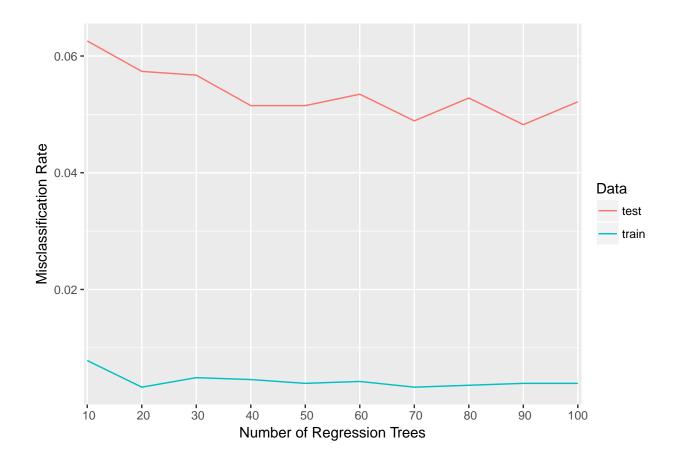
#> [1] 961.3727

#> [1] 1505.612

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





Appendix

Code for Assignment 1b

```
set.seed(1234567890)
max_it <- 100 # max number of EM iterations</pre>
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
K <- 3 # number of quessed components
## true mixing coefficients
true_pi <- vector(length=3)</pre>
true_pi <- c(1/3, 1/3, 1/3)
## true conditional distributions
true_mu <- matrix(nrow=3, ncol=D)</pre>
true_mu[1,] \leftarrow c(0.5, 0.6, 0.4, 0.7, 0.3, 0.8, 0.2, 0.9, 0.1, 1)
true_mu[2,] \leftarrow c(0.5, 0.4, 0.6, 0.3, 0.7, 0.2, 0.8, 0.1, 0.9, 0)
x_given_mu <- function(x, mu) {</pre>
    x_mu <- matrix(1, nrow=nrow(x), ncol=nrow(mu))</pre>
    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_mu[n, k] \leftarrow x_mu[n, k] * prob
        }
    }
    x_mu
}
expectation.step <- function(x, x_given_mu, pi) {</pre>
    z <- matrix(nrow=nrow(x), ncol=length(pi))</pre>
    for (n in 1:N) {
        denominator <- sum(pi * x_given_mu[n,])</pre>
        for (k in 1:K) {
            nominator <- pi[k] * x_given_mu[n, k]</pre>
            z[n, k] <- nominator / denominator</pre>
        }
    }
    z
}
```

```
loglikelihood.wrong <- function(x, mu, pi, z) {</pre>
    llik <- 0
    for (n in 1:N) {
        for (k in 1:K) {
            summation <- 0
            for (i in 1:D) {
                llik \leftarrow llik + z[n, k] * (log(pi[k]) + summation)
    }
    llik
}
loglikelihood <- function(x, x_given_mu, pi) {</pre>
    llik <- 0
    for (n in 1:N) {
        inner_summation <- 0
        for (k in 1:K) {
            inner_summation <- inner_summation + pi[k] * x_given_mu[n, k]</pre>
        llik <- llik + log(inner_summation)</pre>
    }
    llik
}
maximization.step <- function(x, z) {</pre>
    pi <- vector(length=ncol(z))</pre>
    mu <- matrix(nrow=ncol(z), ncol=ncol(x))</pre>
    for (k in 1:K) {
        pi[k] \leftarrow sum(z[, k]) / nrow(x)
    for (k in 1:K) {
        denominator <- sum(z[, k])</pre>
        for (i in 1:D) {
            nominator \leftarrow sum(x[, i] * z[, k])
            mu[k, i] <- nominator / denominator</pre>
        }
    }
    list(pi=pi, mu=mu)
}
EM <- function(N, D, K, max_it, min_change, true_pi, true_mu) {</pre>
    ## Producing the training data
    x <- matrix(nrow=N, ncol=D)</pre>
```

```
for(n in 1:N) {
        k <- sample(1:3, 1, prob=true_pi)</pre>
        for(d in 1:D) {
            x[n, d] \leftarrow rbinom(1, 1, true_mu[k, d])
        }
    }
    z <- matrix(nrow=N, ncol=K) # fractional component assignments
    pi <- vector(length=K) # mixing coefficients</pre>
    mu <- matrix(nrow=K, ncol=D) # conditional distributions</pre>
    llik <- vector(length=max_it) # log likelihood of the EM iterations</pre>
    ## Random initialization of the paramters
    pi <- runif(K, 0.49, 0.51)
    pi <- pi / sum(pi)
    for(k in 1:K) {
        mu[k,] \leftarrow runif(D, 0.49, 0.51)
    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)
        x_mu <- x_given_mu(x, mu)</pre>
        ## E-step: Computation of the fractional component assignments
        z <- expectation.step(x, x_mu, pi)</pre>
        ## Log likelihood computation.
        llik[it] <- loglikelihood(x, x_mu, pi)</pre>
        ## 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</pre>
        ## M-step: ML parameter estimation from the data and fractional component assignments
        result <- maximization.step(x, z)
        pi <- result$pi
        mu <- result$mu
    }
    list(pi=pi, mu=mu, llik=llik, it=it)
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")
```

Code for Assignment 2a

```
library(tree)
data <- read.csv2("../data/bodyfatregression.csv")</pre>
names(data) <- c("Waist", "Weight", "Bodyfat")</pre>
set.seed(1234567890)
train_idx <- sample(nrow(data), floor(nrow(data) * (2 / 3)))</pre>
train <- data[train_idx,]</pre>
test <- data[-train_idx,]</pre>
set.seed(1234567890)
tree_count <- 100
test_errors <- rep(0, tree_count)</pre>
for (i in 1:tree_count) {
    newdata <- train[sample(nrow(train), replace=TRUE),]</pre>
    fit <- tree(Bodyfat ~ ., data=newdata, split="deviance")</pre>
    test_error <- mean((predict(fit, test) - test$Bodyfat)^2)</pre>
    test_errors[i] <- test_error</pre>
}
mean(test_errors)
tree_count <- 100
fold_count <- 3</pre>
test_errors <- matrix(0, nrow=tree_count, ncol=fold_count)</pre>
set.seed(1234567890)
folds <- suppressWarnings(split(1:nrow(data), f=1:fold_count))</pre>
for (j in 1:fold_count) {
    train <- data[-folds[[j]],]</pre>
    test <- data[folds[[j]],]</pre>
    for (i in 1:tree_count) {
        newdata <- train[sample(nrow(train), replace=TRUE),]</pre>
        fit <- tree(Bodyfat ~ ., data=newdata, split="deviance")</pre>
        test_error <- mean((predict(fit, test) - test$Bodyfat)^2)</pre>
        test_errors[i, j] <- test_error</pre>
    }
}
mean(test_errors)
bagging.regtrees <- function(formula, data, newdata, b) {</pre>
    predictions <- matrix(0, nrow=nrow(newdata), ncol=b)</pre>
    trees <- list()</pre>
    for (i in 1:b) {
         bootstrap_sample <- data[sample(nrow(data), replace=TRUE),]</pre>
```

```
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) {</pre>
```

Code for Assignment 2b

```
set.seed(1234567890)
max_it <- 100 # max number of EM iterations</pre>
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
K <- 3 # number of guessed components
## true mixing coefficients
true_pi <- vector(length=3)</pre>
true_pi <- c(1/3, 1/3, 1/3)
## true conditional distributions
true_mu <- matrix(nrow=3, ncol=D)</pre>
true_mu[1,] \leftarrow c(0.5, 0.6, 0.4, 0.7, 0.3, 0.8, 0.2, 0.9, 0.1, 1)
true_mu[2,] \leftarrow c(0.5, 0.4, 0.6, 0.3, 0.7, 0.2, 0.8, 0.1, 0.9, 0)
x_given_mu <- function(x, mu) {</pre>
    x_mu <- matrix(1, nrow=nrow(x), ncol=nrow(mu))</pre>
    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_mu[n, k] \leftarrow x_mu[n, k] * prob
        }
    }
    x_{mu}
}
expectation.step <- function(x, x_given_mu, pi) {</pre>
    z <- matrix(nrow=nrow(x), ncol=length(pi))</pre>
    for (n in 1:N) {
        denominator <- sum(pi * x_given_mu[n,])</pre>
```

```
for (k in 1:K) {
             nominator <- pi[k] * x_given_mu[n, k]</pre>
             z[n, k] <- nominator / denominator</pre>
        }
    }
    z
}
loglikelihood.wrong <- function(x, mu, pi, z) {</pre>
    llik <- 0
    for (n in 1:\mathbb{N}) {
         for (k in 1:K) {
             summation <- 0
             for (i in 1:D) {
                  summation <- summation + x[n, i] * log(mu[k, i]) + (1 - x[n, i]) * log(1 - mu[k, i])
             llik \leftarrow llik + z[n, k] * (log(pi[k]) + summation)
        }
    }
    llik
}
loglikelihood <- function(x, x_given_mu, pi) {</pre>
    llik <- 0
    for (n in 1:N) {
         inner_summation <- 0
         for (k in 1:K) {
             inner_summation <- inner_summation + pi[k] * x_given_mu[n, k]</pre>
        llik <- llik + log(inner_summation)</pre>
    }
    llik
}
maximization.step <- function(x, z) {</pre>
    pi <- vector(length=ncol(z))</pre>
    mu <- matrix(nrow=ncol(z), ncol=ncol(x))</pre>
    for (k in 1:K) {
         pi[k] \leftarrow sum(z[, k]) / nrow(x)
    for (k in 1:K) {
         denominator <- sum(z[, k])</pre>
         for (i in 1:D) {
             nominator \leftarrow sum(x[, i] * z[, k])
             mu[k, i] <- nominator / denominator</pre>
         }
```

```
list(pi=pi, mu=mu)
}
EM <- function(N, D, K, max_it, min_change, true_pi, true_mu) {
    ## Producing the training data
    x <- matrix(nrow=N, ncol=D)
    for(n in 1:N) {
        k <- sample(1:3, 1, prob=true_pi)</pre>
        for(d in 1:D) {
            x[n, d] <- rbinom(1, 1, true_mu[k, d])
        }
    }
    z <- matrix(nrow=N, ncol=K) # fractional component assignments</pre>
    pi <- vector(length=K) # mixing coefficients</pre>
    mu <- matrix(nrow=K, ncol=D) # conditional distributions</pre>
    llik <- vector(length=max_it) # log likelihood of the EM iterations</pre>
    ## Random initialization of the paramters
    pi <- runif(K, 0.49, 0.51)
    pi <- pi / sum(pi)</pre>
    for(k in 1:K) {
        mu[k,] \leftarrow runif(D, 0.49, 0.51)
    }
    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)
        x_mu <- x_given_mu(x, mu)</pre>
        ## E-step: Computation of the fractional component assignments
        z <- expectation.step(x, x_mu, pi)</pre>
        ## Log likelihood computation.
        llik[it] <- loglikelihood(x, x_mu, pi)</pre>
        ## 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</pre>
        ## M-step: ML parameter estimation from the data and fractional component assignments
        result <- maximization.step(x, z)
        pi <- result$pi
```

```
mu <- result$mu
    }
    list(pi=pi, mu=mu, llik=llik, it=it)
plot(true_mu[1,], type="o", col="blue", ylim=c(0,1),
     xlab="Class", ylab="Probability")
axis(side=1, at=c(1:D))
points(true_mu[2,], type="o", col="red")
points(true_mu[3,], type="o", col="green")
K <- 2
result <- EM(N, D, K, max_it, min_change, true_pi, true_mu)
mu <- result$mu
pi <- result$pi
llik <- result$llik
it <- result$it</pre>
plot(mu[1,], type="o", col="blue", ylim=c(0,1),
     xlab="Class", ylab="Probability")
axis(side=1, at=c(1:D))
points(mu[2,], type="o", col="red")
plot(llik[1:it], type="o", xlab="Iterations",
     ylab="Log-Likelihood")
K <- 3
result <- EM(N, D, K, max_it, min_change, true_pi, true_mu)
mu <- result$mu
pi <- result$pi
llik <- result$llik
it <- result$it</pre>
plot(mu[1,], type="o", col="blue", ylim=c(0,1),
     xlab="Class", ylab="Probability")
axis(side=1, at=c(1:D))
points(mu[2,], type="o", col="red")
points(mu[3,], type="o", col="green")
plot(llik[1:it], type="o", xlab="Iterations",
     ylab="Log-Likelihood")
result <- EM(N, D, K, max_it, min_change, true_pi, true_mu)</pre>
mu <- result$mu
pi <- result$pi
llik <- result$llik
it <- result$it</pre>
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")
points(mu[4,], type="o", col="orange")
plot(llik[1:it], type="o", xlab="Iterations",
     ylab="Log-Likelihood")
```

Code for Assignment 3a

```
library(mboost)
data <- read.csv2(".../data/bodyfatregression.csv")</pre>
fit <- blackboost(Bodyfat percent ~ Waist cm + Weight kg, data=data)</pre>
cvf <- cv(model.weights(fit), type="kfold")</pre>
cvm <- cvrisk(fit, folds=cvf, grid=1:100)</pre>
plot(cvm)
set.seed(1234567890)
train_idx <- sample(nrow(data), floor(nrow(data) * (2 / 3)))</pre>
train <- data[train_idx,]</pre>
test <- data[-train_idx,]</pre>
fit <- blackboost(Bodyfat_percent ~ Waist_cm + Weight_kg, data=train,</pre>
                    control=boost_control(mstop=mstop(cvm)))
test error <- sum((predict(fit, test) - test$Bodyfat percent)^2)</pre>
train_error <- sum((predict(fit, train) - train$Bodyfat_percent)^2)</pre>
test_error
train_error
```

Code for Assignment 4a

```
library(mboost)
library(randomForest)
library(ggplot2)
library(reshape2)
data <- read.csv2("../data/spambase.csv")</pre>
data$Spam <- as.factor(data$Spam)</pre>
set.seed(1234567890)
train_idx <- sample(nrow(data), floor(nrow(data) * (2 / 3)))</pre>
train <- data[train_idx,]</pre>
test <- data[-train_idx,]</pre>
tree_counts \leftarrow seq(10, 100, by=10)
test_errors <- rep(0, length(tree_counts))</pre>
train_errors <- rep(0, length(tree_counts))</pre>
for (i in 1:length(tree_counts)) {
    fit <- blackboost(Spam ~ ., data=train, family=AdaExp(),</pre>
                        control=boost control(mstop=tree counts[i]))
    test_error <- 1 - (sum(predict(fit, test, type="class") == test$Spam) / nrow(test))</pre>
    train_error <- 1 - (sum(predict(fit, train, type="class") == train$Spam) / nrow(train))</pre>
    test_errors[i] <- test_error</pre>
    train_errors[i] <- train_error</pre>
}
test_errors
```

```
train_errors
plot_data <- data.frame(Trees=tree_counts, test=test_errors, train=train_errors)</pre>
plot_data <- melt(plot_data, id="Trees", value.name="Error", variable.name="Data")</pre>
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))</pre>
train_errors <- rep(0, length(tree_counts))</pre>
for (i in 1:length(tree_counts)) {
    fit <- randomForest(Spam ~ ., data=train, ntree=tree_counts[i])</pre>
    test_error <- 1 - (sum(predict(fit, test, type="class") == test$Spam) / nrow(test))</pre>
    train_error <- 1 - (sum(predict(fit, train, type="class") == train$Spam) / nrow(train))</pre>
    test_errors[i] <- test_error</pre>
    train_errors[i] <- train_error</pre>
}
plot_data <- data.frame(Trees=tree_counts, test=test_errors, train=train_errors)</pre>
plot_data <- melt(plot_data, id="Trees", value.name="Error", variable.name="Data")</pre>
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)
```