Group_A11:Block-2,Lab1

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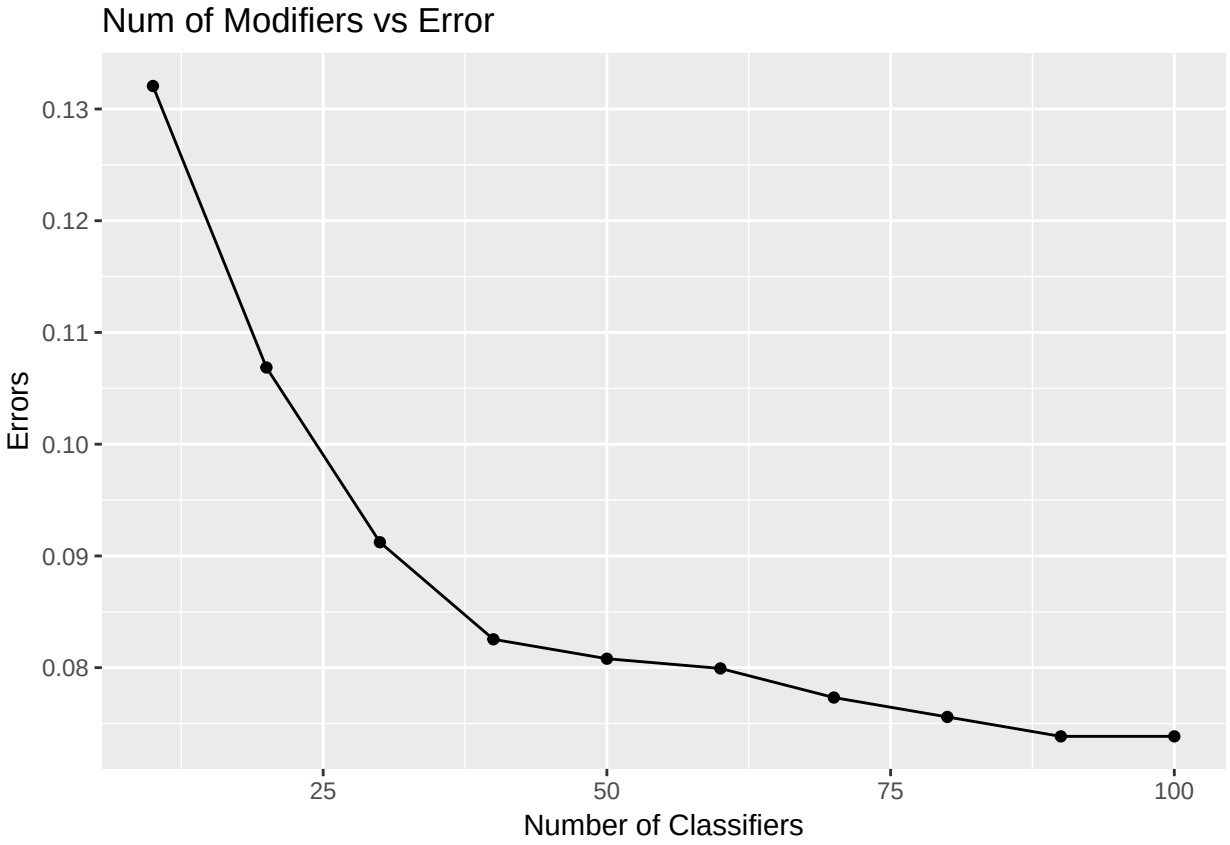
Assignment 1

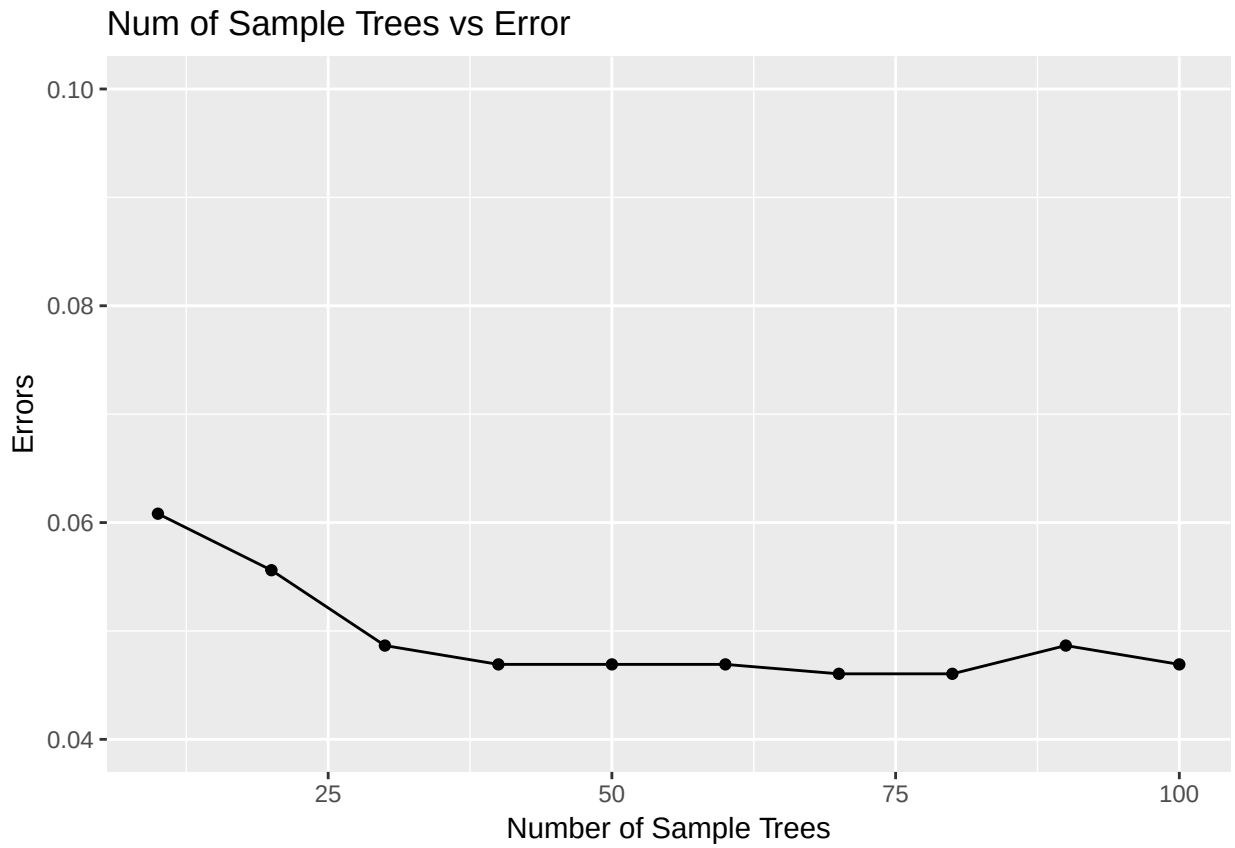
1 Ensemble Method

1 Adaboost

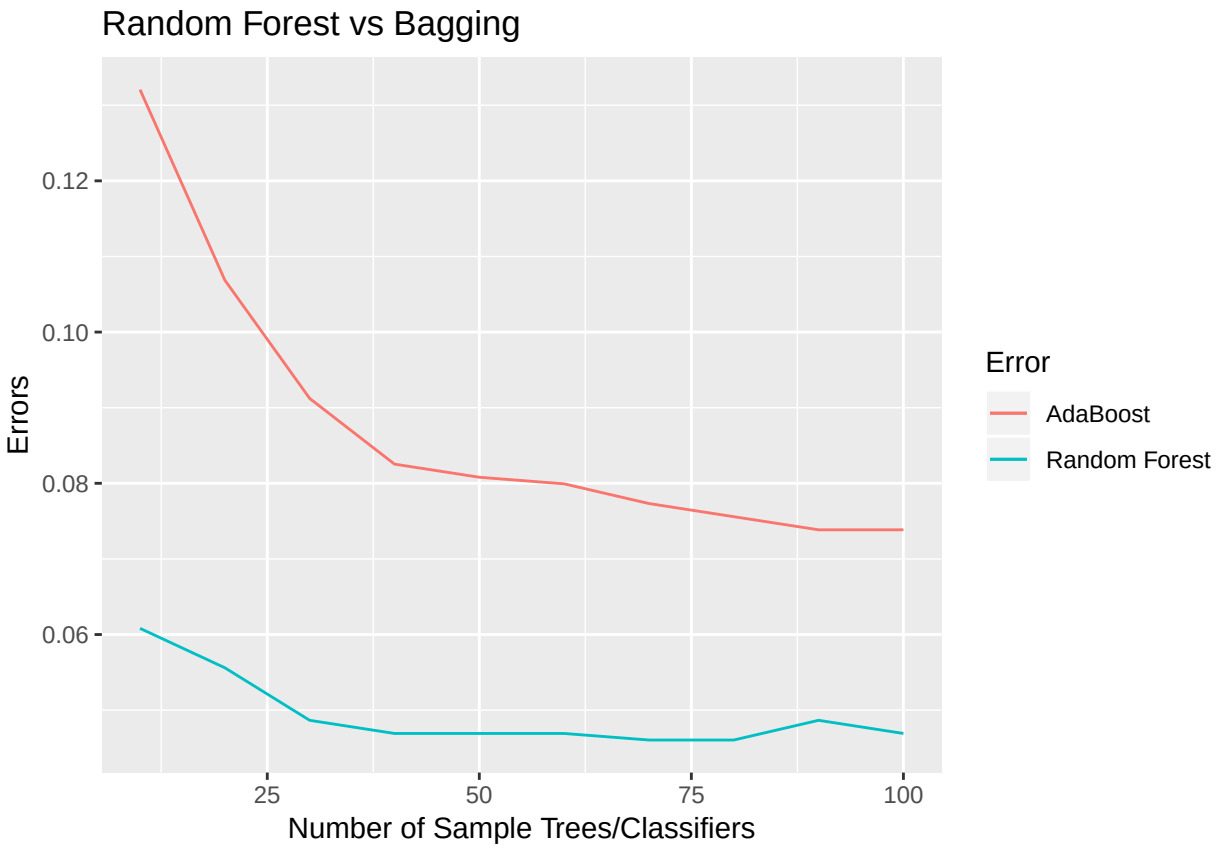
From the graph it can be seen that as the number of iteration increases, the adaboost model improves in accuracy. This is because, at each iteration the weights to those parameter is given more importance which predicts poorly. The updated weight is reflected in next iteration. So as the number of iterations increases the cumulative classifier predictiveness improves. Here the number of iteration consider for the classifier is 10,20..100 and the classfier is decision tree.



2 Random Forest



From the graph it can be seen that as the number of bagging increases, the error doesn't change much on a grand scale. Although, through midway around 50-75 sample trees the error reaches the lowest point and from there the error rate gradualy climbs up.



The plot shows the comparison between Ada Boost vs Random Forest for the same number of classifier/sampling. In this case Random Forest seems to perform better than Ada Boost.

Assignment 2

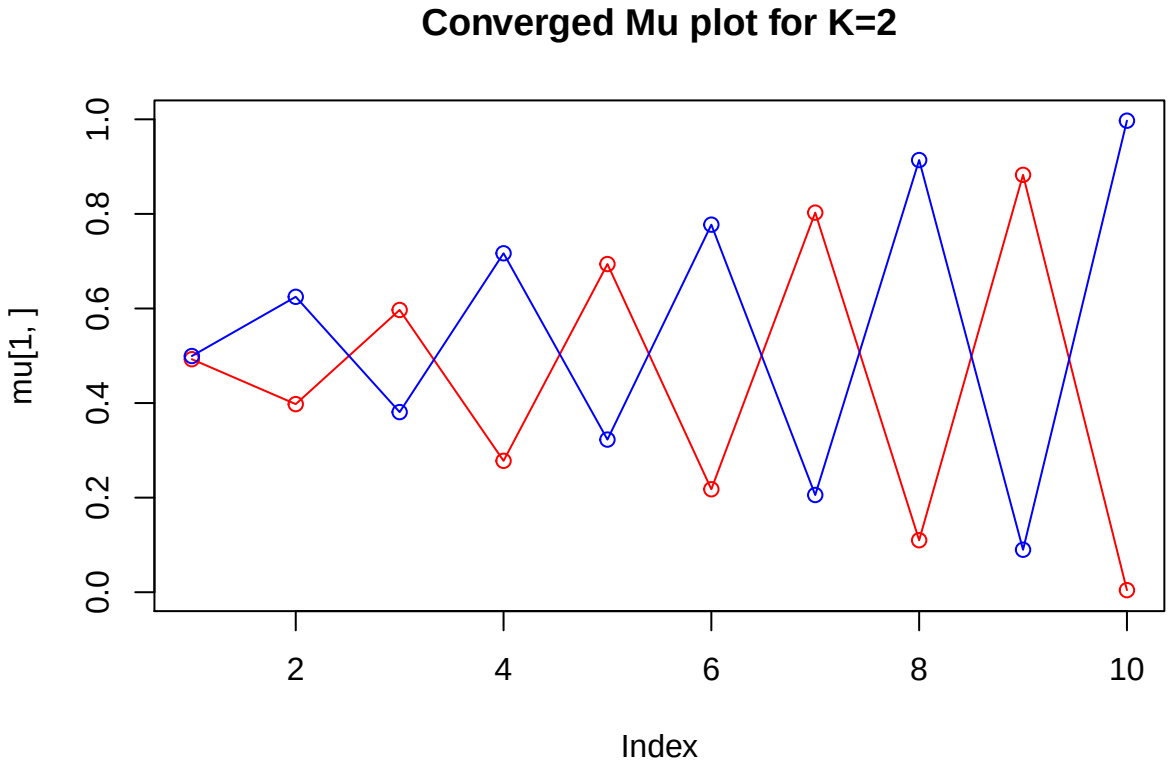
1 EM Function for Bernoulli Distribution

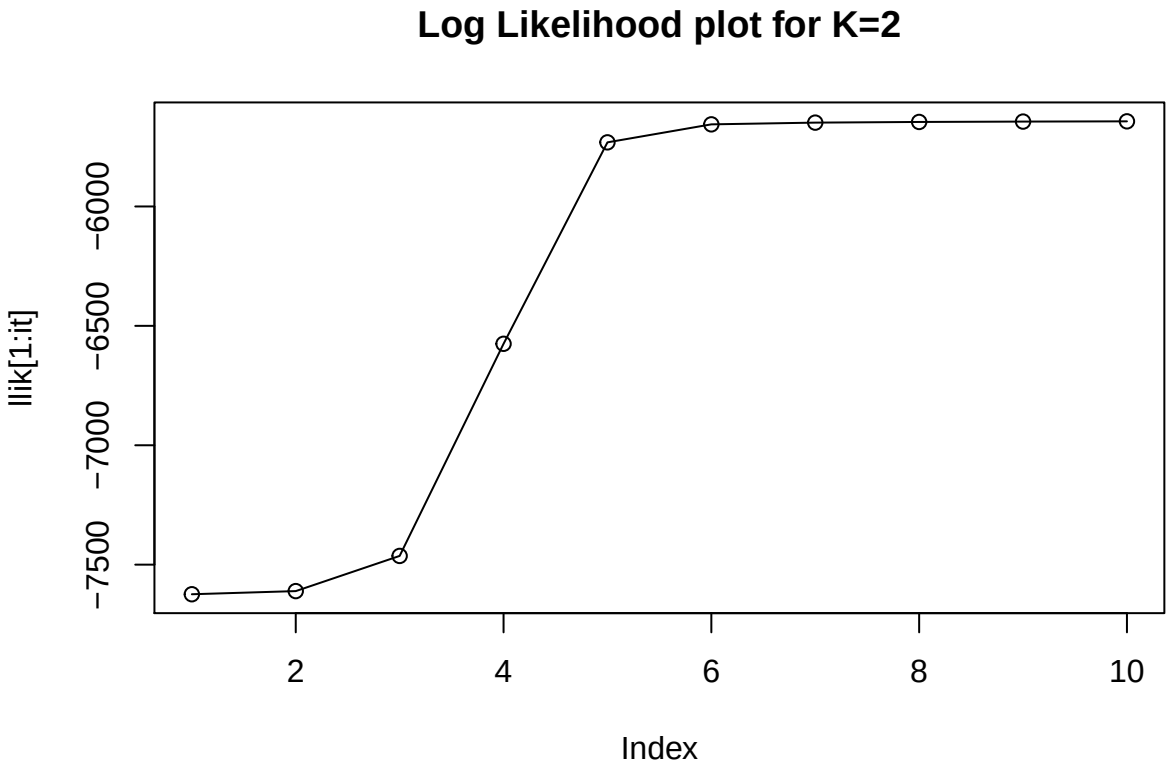
```
#Function for EM algorithm
em_alg = function(pi, mu, llik, min_change, maxit=100){
  old = 0
  for(it in 1:max_it) {
    # E-step: Computation of the fractional component assignments
    total <- matrix(0, nrow = nrow(x), ncol= 1)

    z = matrix(1, nrow = nrow(x), ncol = length(pi))
    for (i in 1:length(pi)) {
      for (j in 1:ncol(x)) {
        z[, i] = z[, i] * dbinom(x[ ,j], 1, mu[i,j])
      }
      z[, i] = z[, i] * pi[i]
      total= total + z[,i]
    }
    for(i in 1:length(pi)){
      z[,i] = z[,i]/total
    }

    # #Log likelihood computation.
    q = matrix(1, nrow = length(total), ncol = 1)
    for(i in 1:nrow(mu)){
      temp = matrix(1, nrow = nrow(x), ncol = 1)
      for(j in 1:ncol(x)){
        temp = temp*(mu[i,j]^x[,j])*((1-mu[i,j])^(1-x[,j]))
      }
      q = q * (temp*pi[i])^(z[,i])
    }

    llik[it] = sum(log(q))

    # Stop if the log likelihood has not changed significantly
    if(abs(old-llik[it])<min_change){
      break
    }
    else{
      old = llik[it]
    }

    #M-step: ML parameter estimation from the data and fractional component assignments
    new_pi = colSums(z)/nrow(x)
    new_mu = matrix(nrow = nrow(mu), ncol = ncol(mu))
    for (i in 1:length(pi)){
      nm = sum(z[,i])
      new_mu[i,] = colSums(x*z[,i])/nm
    }
    mu = new_mu
    pi = new_pi
  }
```

```
  return(list(pi, mu, llik, it))
}
```

2 K = 2


True Mu plot for K=2
true_mu[1,]
0.0
0.2
0.4
0.6
0.8
1.0
2
4
6
8
10
Index

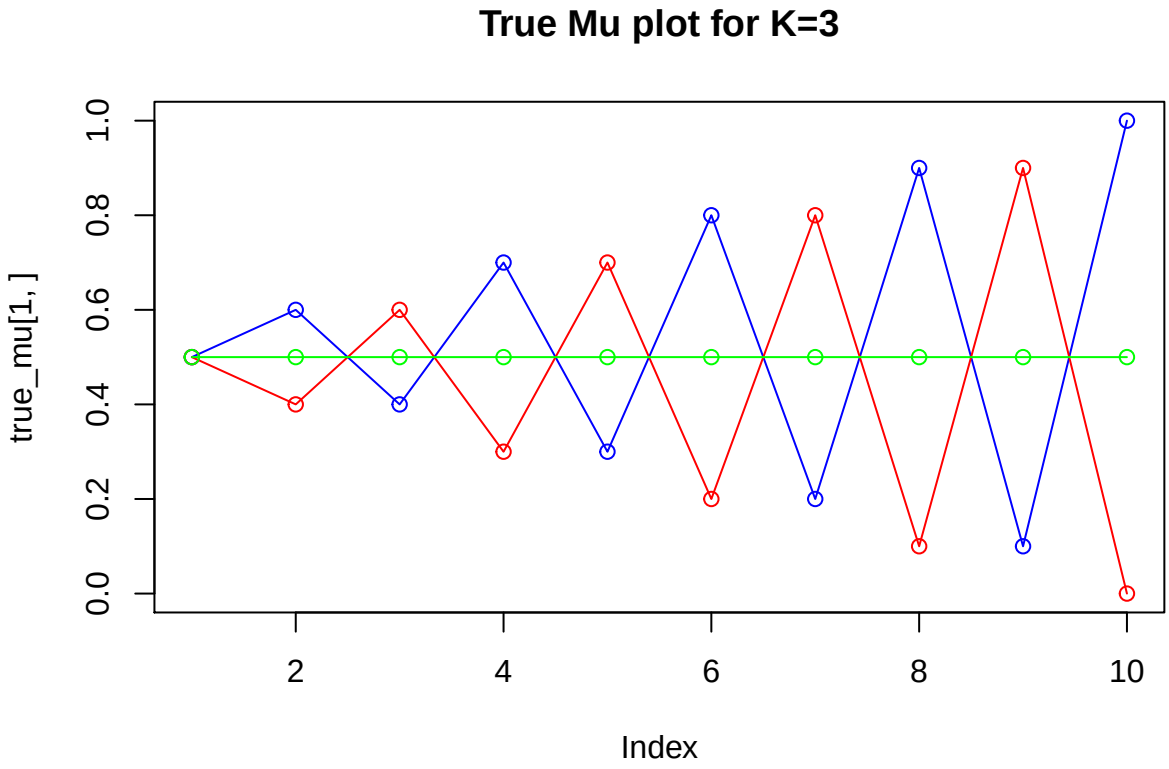

Converged Mu plot for K=2
mu[1,]
0.0
0.2
0.4
0.6
0.8
1.0
2
4
6
8
10
Index

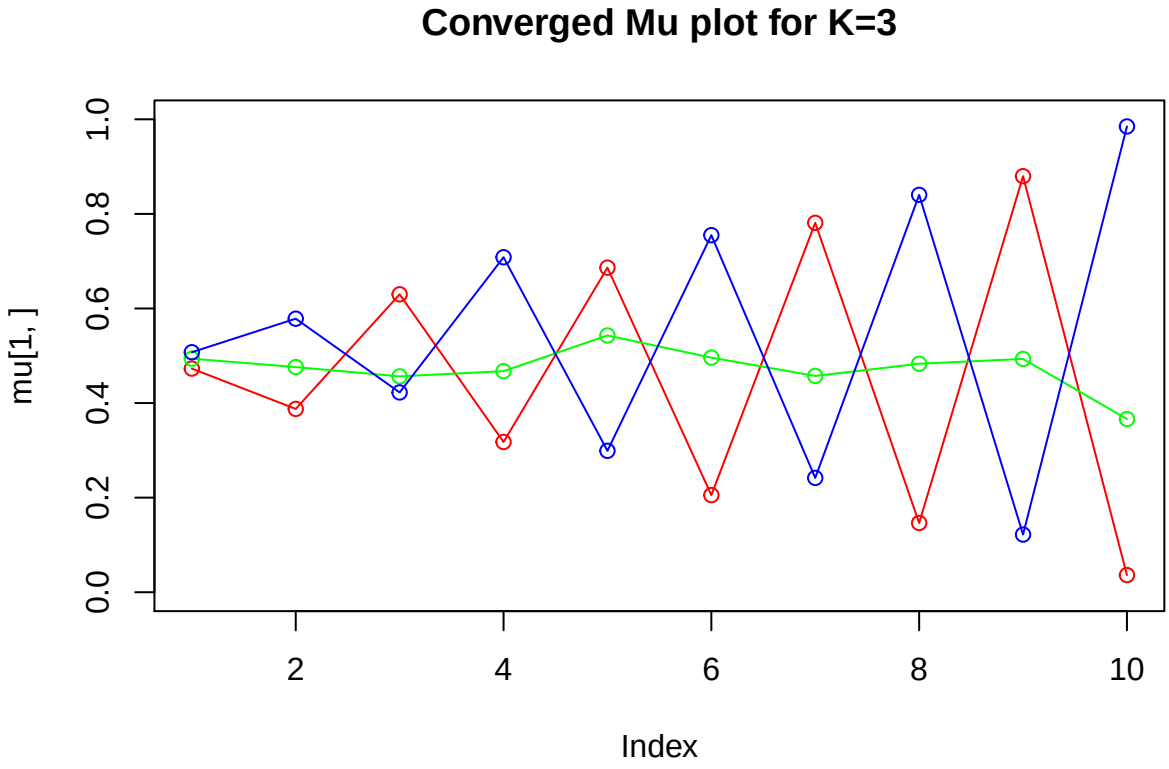


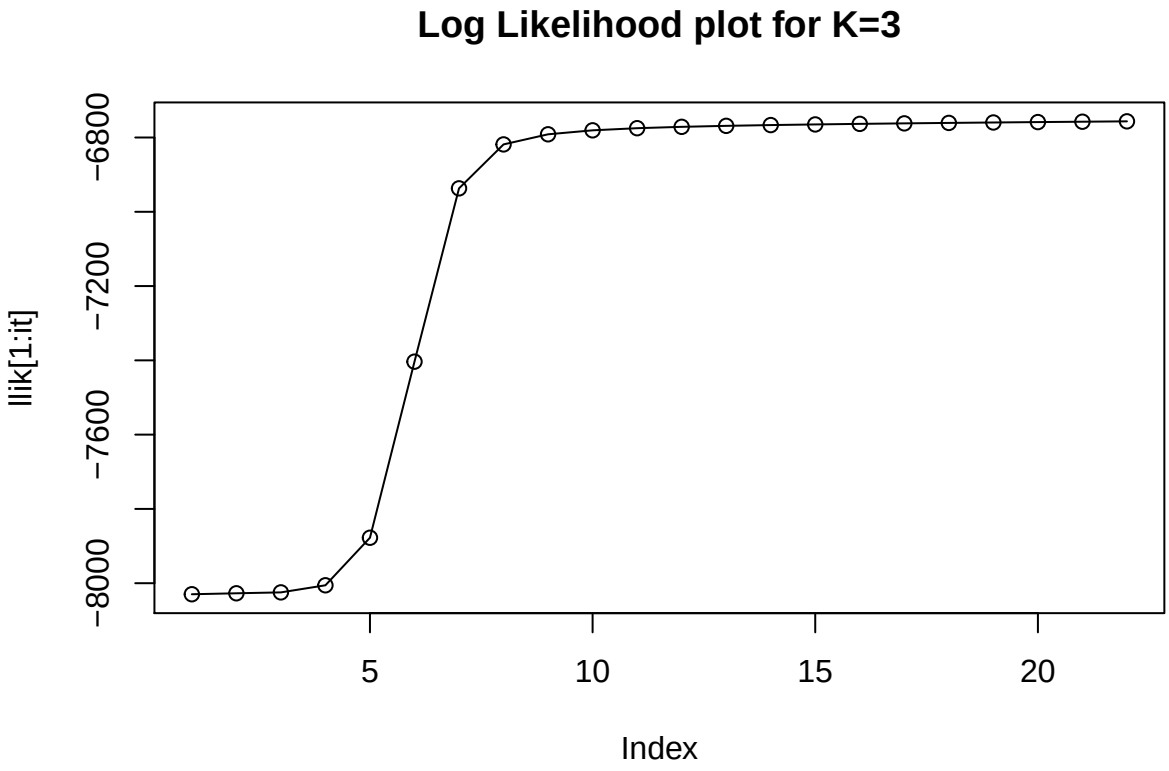

```
## Convergence at iteration:  10  with log likelihood:  -5643.615
```

For K=2 the EM algorithm's convergence is close to the true mu values. This is the reason we are getting very similar plots. The algorithm converged at iteration 10 with log likelihood value of "-5643.615". The minimum threshold value was 1.

3 K = 3


True Mu plot for K=3
true_mu[1,]
0.0
0.2
0.4
0.6
0.8
1.0
2
4
6
8
10
Index

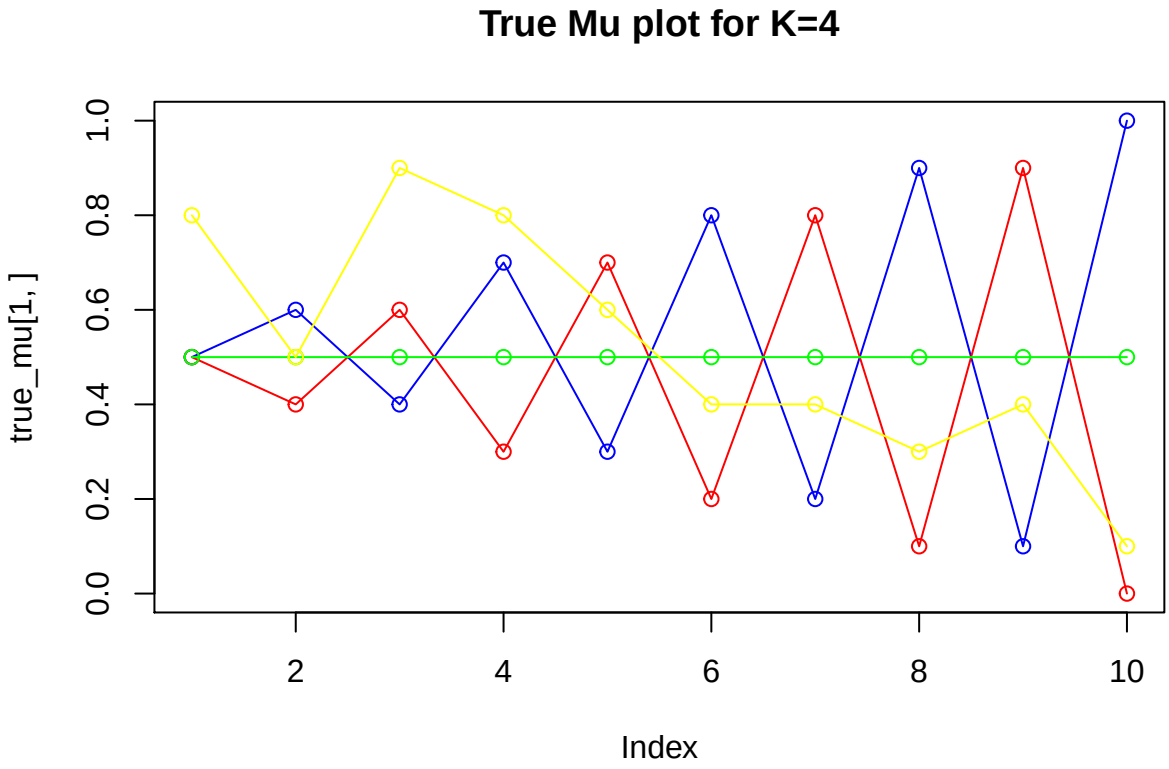

Converged Mu plot for K=3
mu[1,]
0.0
0.2
0.4
0.6
0.8
1.0
2
4
6
8
10
Index

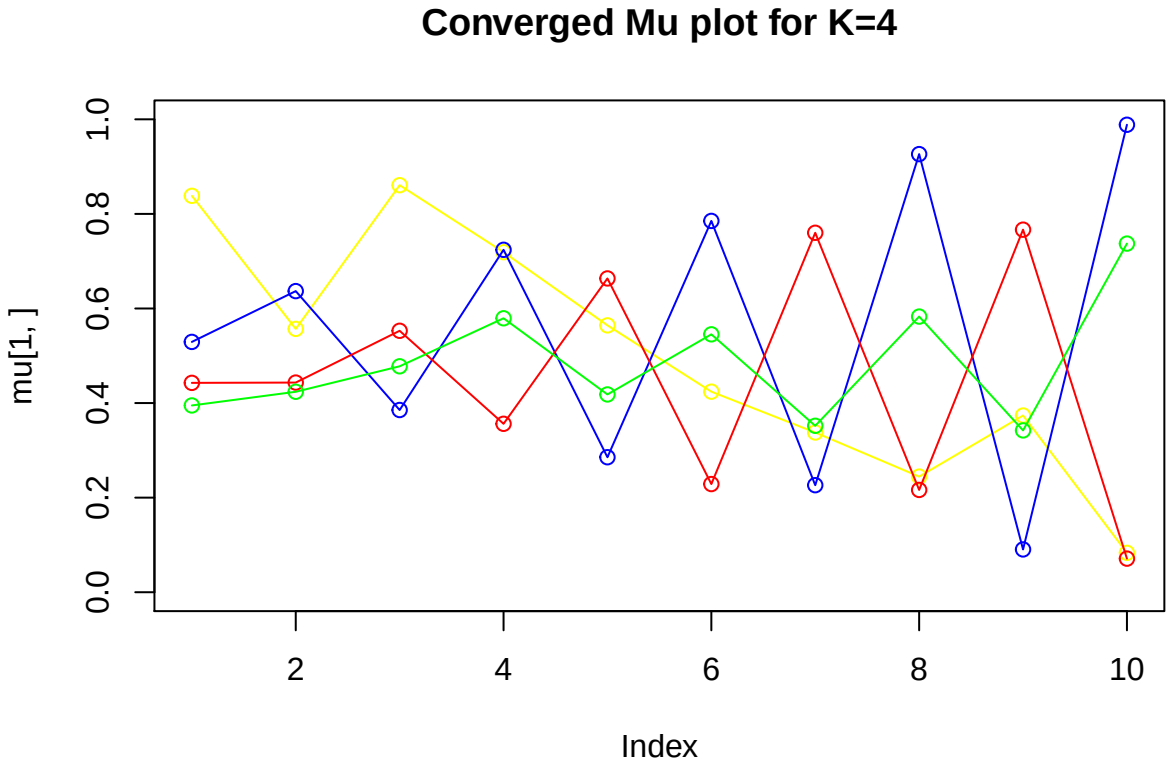


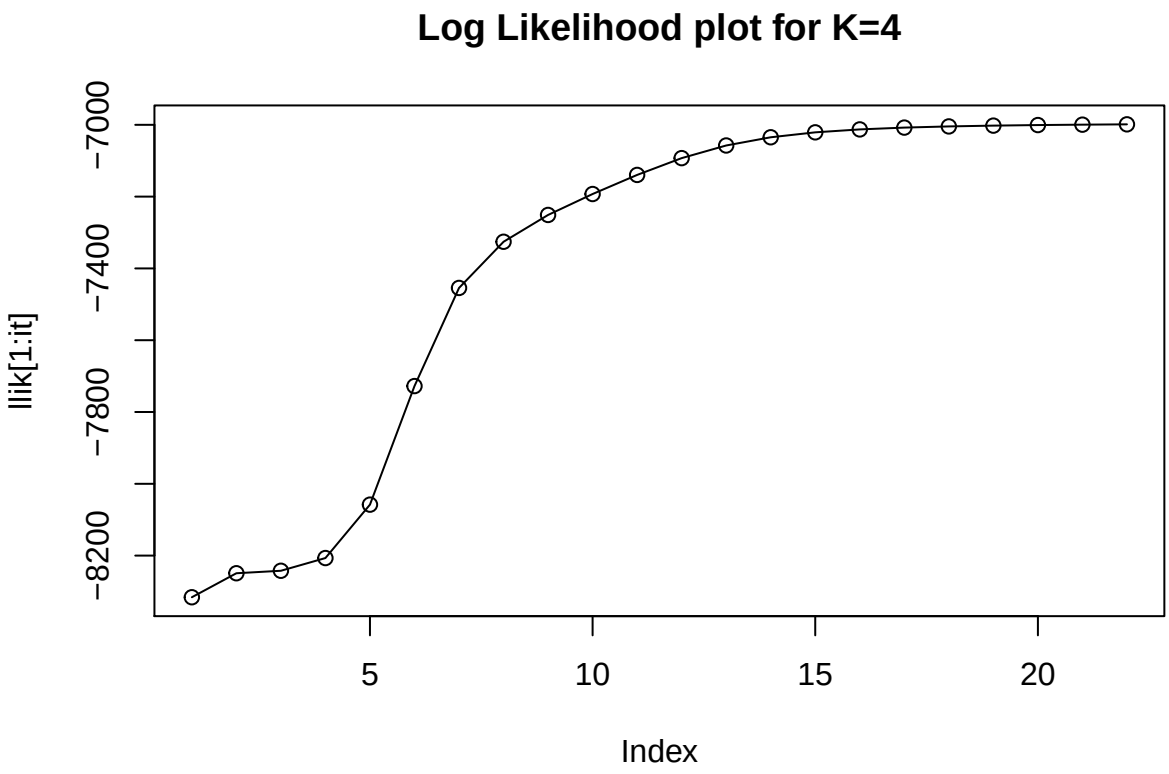

```
## Convergence at iteration:  22  with log likelihood:  -6756.521
```

For K to 3, the convergence is not exact. Since we had equal probabilities for all the rows of mu the convergence is switched between the rows. The algorithm converged at iteration 22 with log likelihood value of "-6756.521". The minimum threshold value was 1.

4 K = 4


True Mu plot for K=4
true_mu[1,]
0.0
0.2
0.4
0.6
0.8
1.0
2
4
6
8
10
Index


Converged Mu plot for K=4
mu[1,]
0.0
0.2
0.4
0.6
0.8
1.0
2
4
6
8
10
Index




```
## Convergence at iteration:  22  with log likelihood:  -6998.695
```

This is the convergence we get for K=4. Since the complexcity increases even more the convergence takes much more time, but it is a good approximation of the true model we had for mu. The algorithm converged at iteration 22 with log likelihood value of "-6998.695". The minimum threshold value was 1.

EM algorithm is famous for its conceptual simplicity and ease of implementation. Each iteration of the algorithm improves log likelihood. The rate of convergence is fast at first but slow down as you approach local optima. EM works best the missing imformation (K) is small and the dimensionality of the data(D) is not too large. EM can require many iterations, and higher dimensionality can dramatically slow down the E-Step.

Appendix

```
knitr::opts_chunk$set(
    echo = FALSE,
    message = FALSE,
    warning = FALSE
)
library(mboost)
library(randomForest)
library(ggplot2)
spambase <- read.csv2("spambase.csv")
spambase$Spam <- as.factor(spambase$Spam)
```

```
n=dim(spambase)[1]
set.seed(12345)
id=sample(1:n,floor(0.75*n))
spam_train=spambase[id,]
spam_test=spambase[-id,]

misclas_test <- c()
comp<-matrix(0,nrow=0,ncol=2)
colnames(comp) <- c("Classes","Error_ada")
for(i in seq(10,100,10)) {
    model_boost <-
        mboost::blackboost(
        Spam ~ .,
        data = spam_train,
        family = AdaExp(),
        control = boost_control(mstop = i)

        )
    predict_test<-predict(model_boost,newdata=spam_test,type="class")

    comp_test<-data.frame("Expected_Value"=spam_test$Spam,
                "Predicted_Value"=predict_test)
    pred<-table(comp_test)
    missclas_test<-(pred[2,1]+pred[1,2])/nrow(spam_test)
    comp <- rbind(comp,c(i,missclas_test))
}
comp<-as.data.frame(comp)

plot1 <- ggplot(comp,aes(Classes,Error_ada)) +geom_point() +
         geom_line() + xlab("Number of Classifiers") +
         ylab("Errors")+ggtitle("Num of Modifiers vs Error" )

plot1
comp_ran<-matrix(0,nrow=0,ncol=2)
colnames(comp_ran) <- c("Classes","Error_rf")
for(i in seq(10,100,10)) {

    set.seed(1234)
    model_rforest<-randomForest(Spam~.,data=spam_train,ntree=i)
    predict_test<-predict(model_rforest,newdata=spam_test,type="class")

    comp_test<-data.frame("Expected_Value"=spam_test$Spam,
                "Predicted_Value"=predict_test)
    pred<-table(comp_test)
    missclas_test<-(pred[2,1]+pred[1,2])/nrow(spam_test)
    comp_ran <- rbind(comp_ran,c(i,missclas_test))
}

comp_ran<-as.data.frame(comp_ran)

ggplot(comp_ran,aes(Classes,Error_rf)) +geom_point() + geom_line()+
  coord_cartesian(ylim=c(0.04,0.1)) + xlab("Number of Sample Trees") +
         ylab("Errors")+ggtitle("Num of Sample Trees vs Error" )
```

```
comp_data <- as.data.frame(merge(comp,comp_ran))
ggplot(comp_data,aes(x=Classes))+ geom_line(aes(y=Error_ada,color="blue")) +
          geom_line(aes(y=Error_rf,color="red")) +
          scale_color_discrete(name="Error",labels=c("AdaBoost","Random Forest"))+
          xlab("Number of Sample Trees/Classifiers") +ylab("Errors") +
            ggtitle("Random Forest vs Bagging" )


#Function for EM algorithm
em_alg = function(pi, mu, llik, min_change, maxit=100){
  old = 0
  for(it in 1:max_it) {
    # E-step: Computation of the fractional component assignments
    total <- matrix(0, nrow = nrow(x), ncol= 1)

    z = matrix(1, nrow = nrow(x), ncol = length(pi))
    for (i in 1:length(pi)) {
      for (j in 1:ncol(x)) {
        z[, i] = z[, i] * dbinom(x[ ,j], 1, mu[i,j])
      }
      z[, i] = z[, i] * pi[i]
      total= total + z[,i]
    }
    for(i in 1:length(pi)){
      z[,i] = z[,i]/total
    }

    # #Log likelihood computation.
    q = matrix(1, nrow = length(total), ncol = 1)
    for(i in 1:nrow(mu)){
      temp = matrix(1, nrow = nrow(x), ncol = 1)
      for(j in 1:ncol(x)){
        temp = temp*(mu[i,j]^x[,j])*((1-mu[i,j])^(1-x[,j]))
      }
      q = q * (temp*pi[i])^(z[,i])
    }

    llik[it] = sum(log(q))

    # Stop if the log likelihood has not changed significantly
    if(abs(old-llik[it])<min_change){
      break
    }
    else{
      old = llik[it]
    }

    #M-step: ML parameter estimation from the data and fractional component assignments
    new_pi = colSums(z)/nrow(x)
    new_mu = matrix(nrow = nrow(mu), ncol = ncol(mu))
```

```
    for (i in 1:length(pi)){
      nm = sum(z[,i])
      new_mu[i,] = colSums(x*z[,i])/nm
    }
    mu = new_mu
    pi = new_pi
  }
  return(list(pi, mu, llik, it))
}
##K=2
set.seed(1234567890)
max_it <- 100 # max number of EM iterations
min_change <- 1 # min change in log likelihood between two consecutive EM iterations
N=1000 # number of training points
D=10 # number of dimensions
x <- matrix(nrow=N, ncol=D) # training data
true_pi <- vector(length = 2) # true mixing coefficients
true_mu <- matrix(nrow=2, ncol=D) # true conditional distributions
true_pi=c(1/2,1/2)
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)
plot(true_mu[1,], type="o", col="blue", ylim=c(0,1), main = 'True Mu plot for K=2')
points(true_mu[2,], type="o", col="red")
# Producing the training data
for(n in 1:N) {
  k <- sample(1:2,1,prob=true_pi)
  for(d in 1:D) {
    x[n,d] <- rbinom(1,1,true_mu[k,d])
  }
}
K=2 # 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)
}
#Call the EM-algorithm function
ret = em_alg(pi, mu, llik, min_change)
pi = ret[[1]]
mu = ret[[2]]
llik = ret[[3]]
it = ret[[4]]
plot(mu[1,], type="o", col="red", ylim=c(0,1), main = 'Converged Mu plot for K=2')
points(mu[2,], type="o", col='blue')
plot(llik[1:it], type="o", main = 'Log Likelihood plot for K=2')
cat("Convergence at iteration: ", it, " with log likelihood: ", llik[it], "\n")
set.seed(1234567890)
max_it <- 100 # max number of EM iterations
```

```
min_change <- 1 # min change in log likelihood between two consecutive EM iterations
N=1000 # number of training points
D=10 # number of dimensions
x <- matrix(nrow=N, ncol=D) # training data
true_pi <- vector(length = 3) # true mixing coefficients
true_mu <- matrix(nrow=3, ncol=D) # true conditional distributions
true_pi=c(1/3,1/3,1/3)
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)
plot(true_mu[1,], type="o", col="blue", ylim=c(0,1), main = 'True Mu plot for K=3')
points(true_mu[2,], type="o", col="red")
points(true_mu[3,], type="o", col="green")
# Producing the training data
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)
}
#Call the EM-algorithm function
ret = em_alg(pi, mu, llik, min_change)
pi = ret[[1]]
mu = ret[[2]]
llik = ret[[3]]
it = ret[[4]]
cols = c('green', 'blue')
plot(mu[1,], type="o", col="red", ylim=c(0,1), main = 'Converged Mu plot for K=3')
for(i in 2:nrow(mu)){
  points(mu[i,], type="o", col=cols[i-1])
}
plot(llik[1:it], type="o", main = 'Log Likelihood plot for K=3')
cat("Convergence at iteration: ", it, " with log likelihood: ", llik[it], "\n")
##K=4
set.seed(1234567890)
max_it <- 100 # max number of EM iterations
min_change <- 1 # min change in log likelihood between two consecutive EM iterations
N=1000 # number of training points
D=10 # number of dimensions
x <- matrix(nrow=N, ncol=D) # training data
true_pi <- vector(length = 4) # true mixing coefficients
true_mu <- matrix(nrow=4, ncol=D) # true conditional distributions
```

```
true_pi=c(1/4,1/4,1/4,1/4)
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)
true_mu[4,]=c(0.8,0.5,0.9,0.8,0.6,0.4,0.4,0.3,0.4,0.1)
plot(true_mu[1,], type="o", col="blue", ylim=c(0,1), main = 'True Mu plot for K=4')
points(true_mu[2,], type="o", col="red")
points(true_mu[3,], type="o", col="green")
points(true_mu[4,], type="o", col="yellow")
# Producing the training data
for(n in 1:N) {
  k <- sample(1:4,1,prob=true_pi)
  for(d in 1:D) {
    x[n,d] <- rbinom(1,1,true_mu[k,d])
  }
}
K=4 # 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)
}
#Call the EM-algorithm function
ret = em_alg(pi, mu, llik, min_change)
pi = ret[[1]]
mu = ret[[2]]
llik = ret[[3]]
it = ret[[4]]
cols = c('blue', 'red', 'green')
plot(mu[1,], type="o", col="yellow", ylim=c(0,1), main = 'Converged Mu plot for K=4')
for(i in 2:nrow(mu)){
  points(mu[i,], type="o", col=cols[i-1])
}

plot(llik[1:it], type="o", main = 'Log Likelihood plot for K=4')
cat("Convergence at iteration: ", it, " with log likelihood: ", llik[it], "\n")
```