lab block2

Group A20

Statement Of Contribution:

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Assignment 2: NI Dongwei

1.ENSEMBLE METHODS

The code is given in the appendix.

Results are given below.

TASK ONE

The relevant code is added in Appendix

mean_mis_rate1 0.206625

mean_mis_rate10 0.137777

mean_mis_rate100 0.112063

var_mis_rate1 0.003044475

var_mis_rate10 0.000964694

var_mis_rate100 0.0008307177

TASK TWO

The relevant code is added in Appendix

mean_mis_rate1 0.09753

mean_mis_rate10 0.016116

mean_mis_rate100 0.006754

var_mis_rate1 0.01870012

var_mis_rate10 0.0006982528

var_mis_rate100 7.64119e-05

TASK THREE

The relevant code is added in Appendix

mean_mis_rate1 0.245286

mean_mis_rate10 0.120254

mean_mis_rate100 0.07359

var_mis_rate1 0.01369812

var_mis_rate10 0.002829063

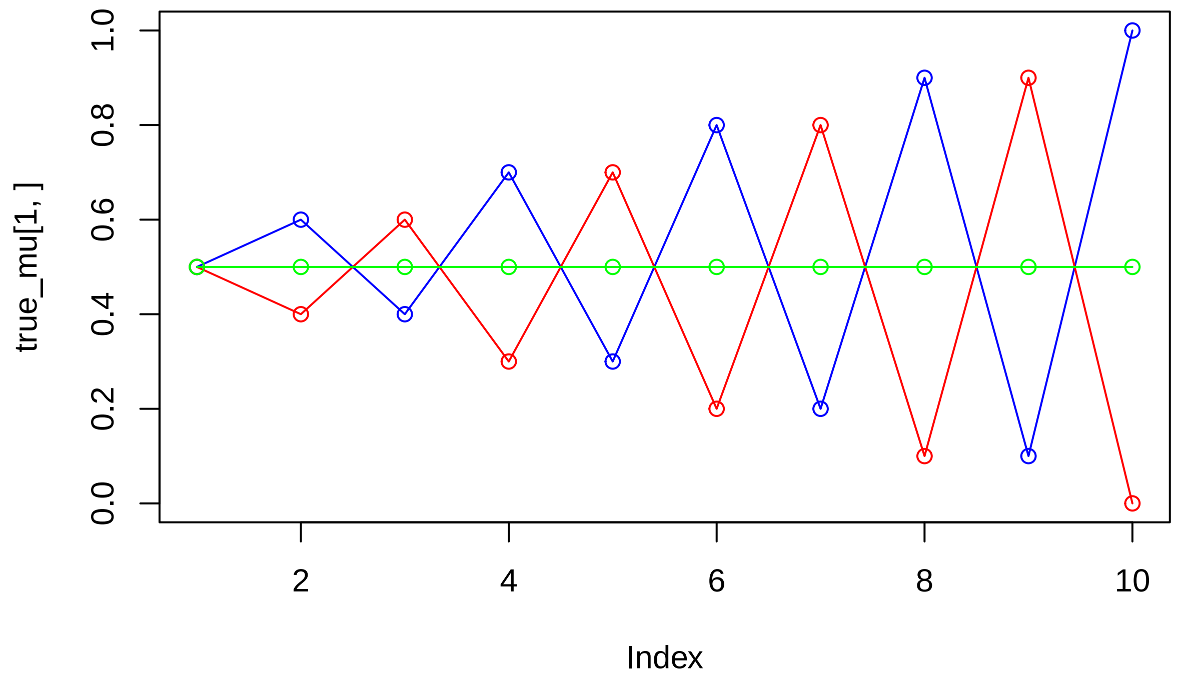
var_mis_rate100 0.001203491

TASK FOUR **1.What happens with the mean error rate when the number of trees in the random forest grows? Why?** From the above three situations, we can see that as the number of basic models increase, the mean error decreases. This is mainly because if there are only few and limited training data sets used for training, the model obtained just have little information about unseen and new data points. However, with more training data sets, the parameters learned contain more information of unseen data sets. When it is used to make predictions, the result would be more accurate.

The third dataset represents a slightly more complicated classification problem than the first one. Still, you should get better performance for it when using suffi-cient trees in the random forest. Explain why you get better performance.

2. Mixture Models

For implementing the EM algorithm for Bernoulli mixture model First we generate a π and μ of a Bernoulli mixture model

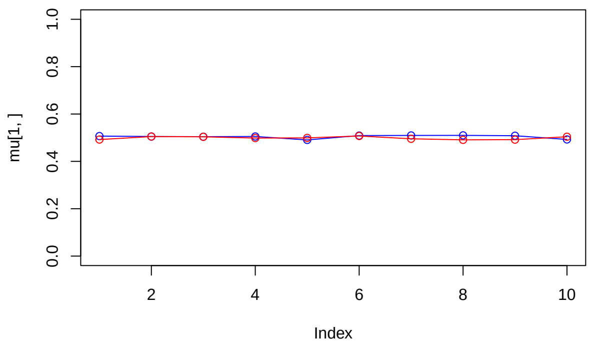


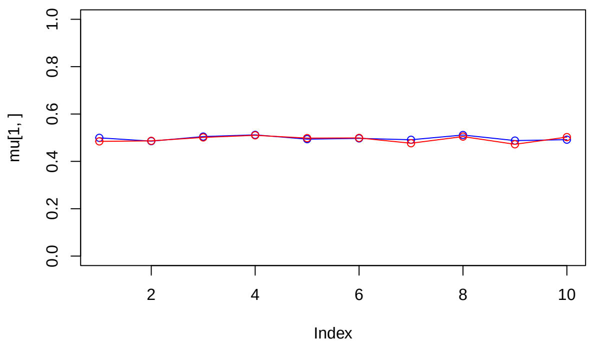
And the plot above shows the 3 μs we are using to generate data set x, with a same $\pi = \frac{1}{3}$ for each μ, and of course with a $Dimension = 10$.

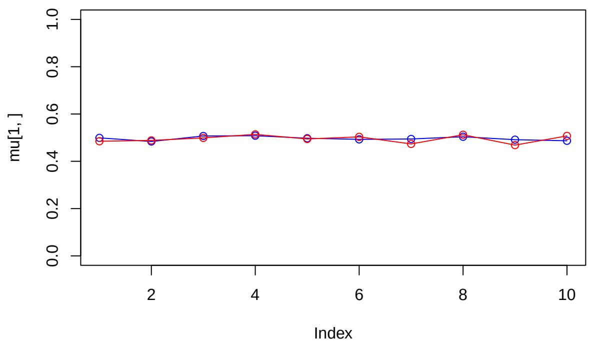
```
## [1] 0.5052178 0.4947822
```

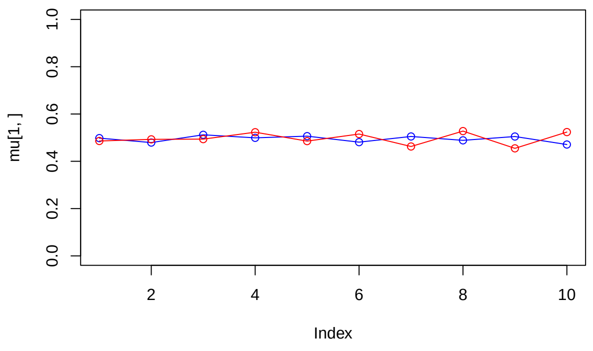
```
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]     [,7]
## [1,] 0.5068040 0.5049455 0.5041509 0.5051382 0.4905578 0.5089228 0.509453
## [2,] 0.4921113 0.5048207 0.5036886 0.4985467 0.4991731 0.5071384 0.495380
##           [,8]      [,9]     [,10]
## [1,] 0.5097480 0.5082991 0.4926313
## [2,] 0.4908757 0.4917657 0.5040657
```

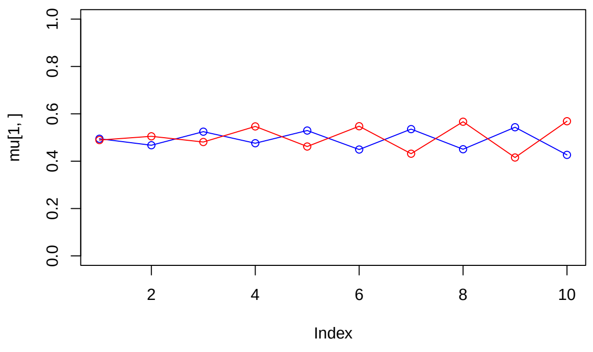
First we start with cluster M = 2. And we generate a π and μ under M = 2 as the start point for our model.

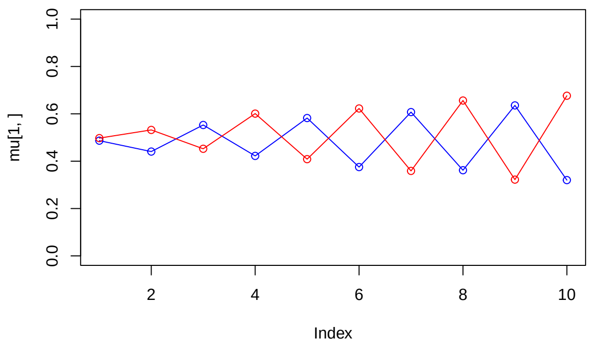


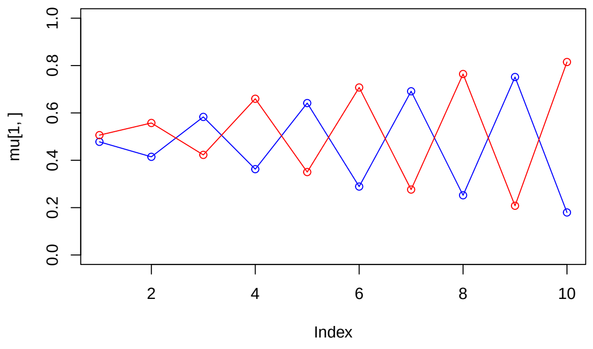


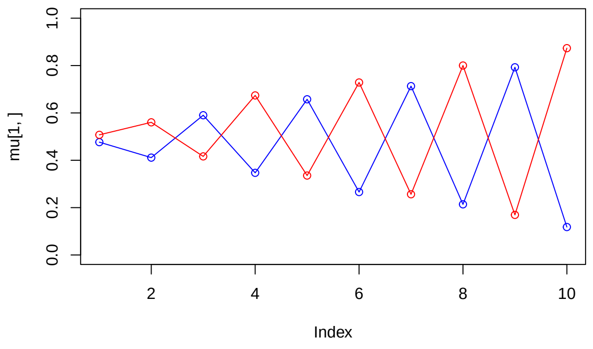


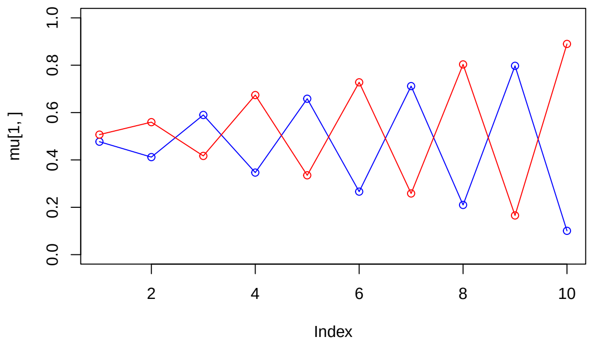


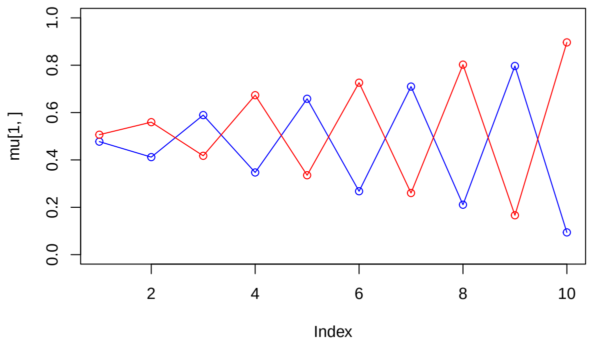


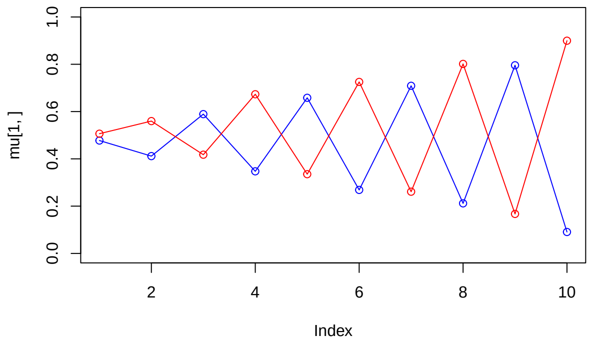


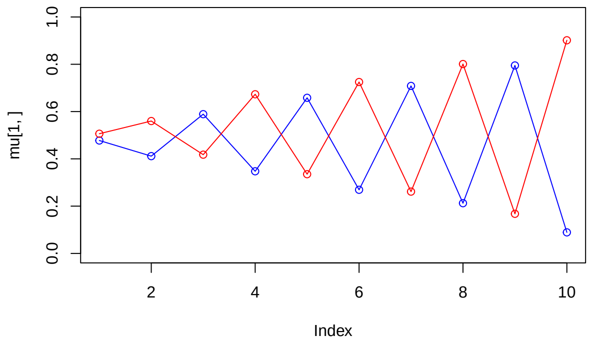






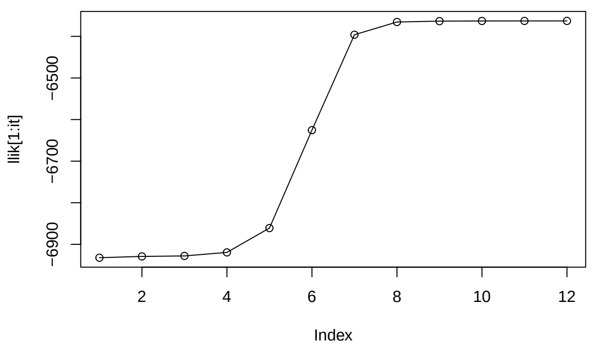






```
##  [1] "iteration:  1 log likelihood:  -6932.1625943363"
##  [2] "iteration:  2 log likelihood:  -6929.09536498845"
##  [3] "iteration:  3 log likelihood:  -6927.94380531483"
##  [4] "iteration:  4 log likelihood:  -6919.43478131895"
##  [5] "iteration:  5 log likelihood:  -6860.93456150249"
##  [6] "iteration:  6 log likelihood:  -6625.43370682142"
##  [7] "iteration:  7 log likelihood:  -6396.10695394879"
##  [8] "iteration:  8 log likelihood:  -6365.47503740155"
##  [9] "iteration:  9 log likelihood:  -6363.41093129657"
## [10] "iteration:  10 log likelihood:  -6363.02364141854"
## [11] "iteration:  11 log likelihood:  -6362.91755252171"
## [12] "iteration:  12 log likelihood:  -6362.88538329492"
## [1] 0.4979156 0.5020844
```

```
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]
## [1,] 0.4776009 0.4114577 0.5889962 0.3474863 0.6581537 0.2691781 0.7083954
## [2,] 0.5062796 0.5599234 0.4177178 0.6731561 0.3351926 0.7249220 0.2614677
##           [,8]      [,9]      [,10]
## [1,] 0.2125293 0.7950371 0.08913449
## [2,] 0.8010174 0.1675785 0.90147909
```

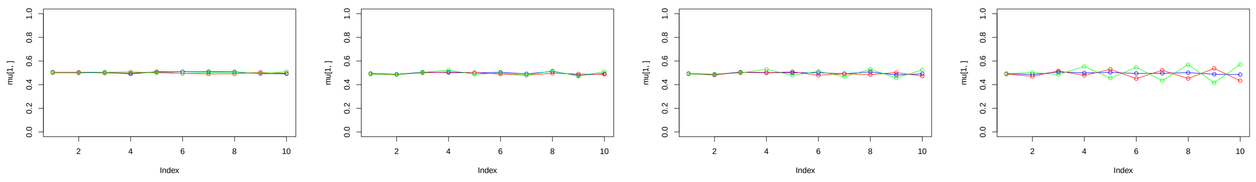


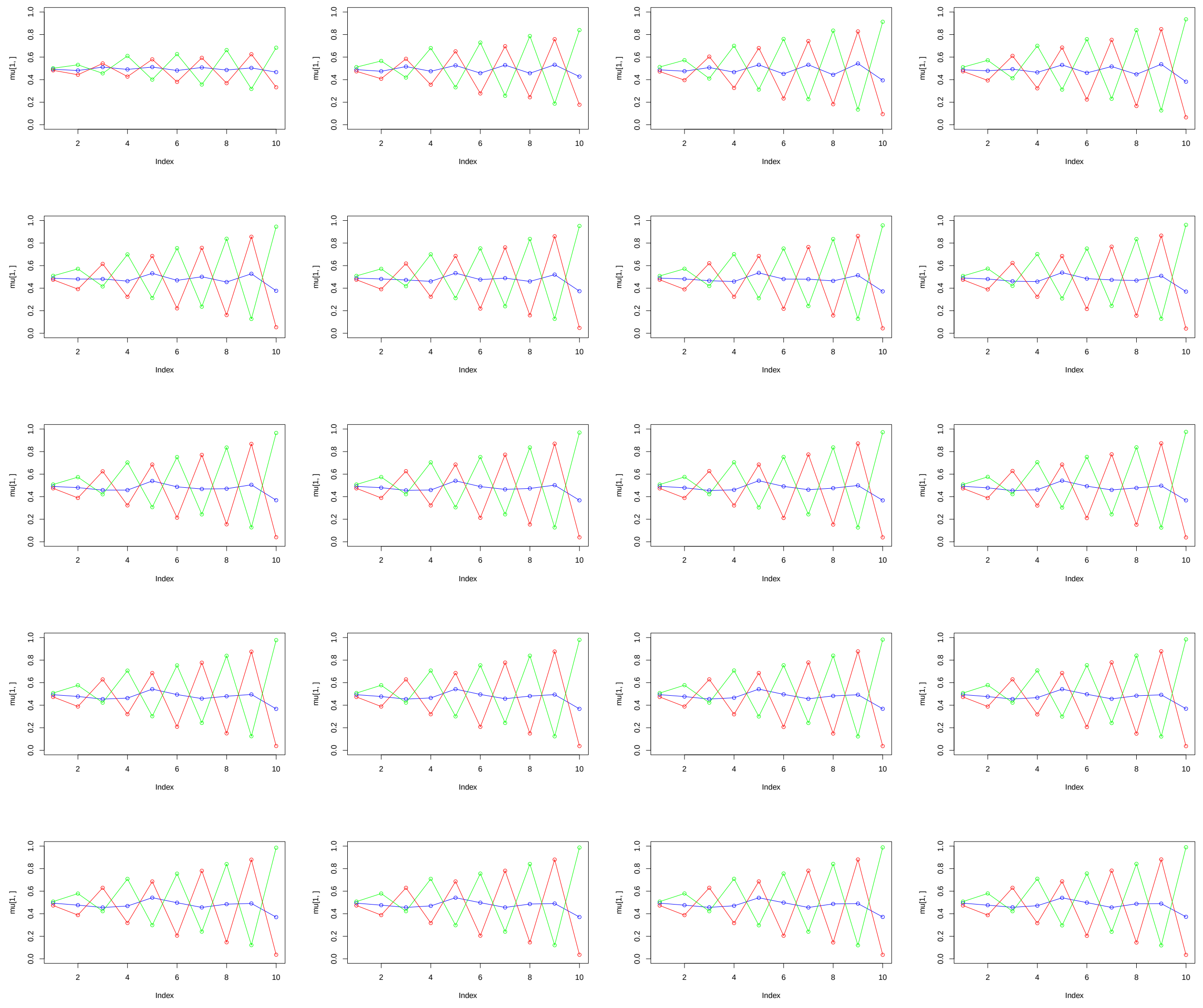
From the plots above. We can see that under this situation, μ which is equal to 0.5 every dimension seems did not being reflect. It might be that the other 2 μs are symmetrical to the 0.5 axis.
And for every iteration the predicted μ is closer and closer to the *true* μ. The rapidly raise of log-likelihood during iteration 5-7 is also reflect by the plot from significant changing of μ in corresponding iterations. The final predicted μ shows above is relatively close to the true value within around 10% differences.

```
## [1] 0.3359578 0.3290183 0.3350239
```

```
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]
## [1,] 0.5049455 0.5041509 0.5051382 0.4905578 0.5089228 0.5094530 0.5097480
## [2,] 0.5048207 0.5036886 0.4985467 0.4991731 0.5071384 0.4953800 0.4908757
## [3,] 0.4996279 0.4982070 0.5043346 0.5085042 0.4994862 0.4945702 0.5041462
##           [,8]      [,9]     [,10]
## [1,] 0.5082991 0.4926313 0.4921113
## [2,] 0.4917657 0.5040657 0.4956302
## [3,] 0.5040348 0.4955050 0.5088683
```

Then we goes to M = 3, again generate a π and μ under M = 3 as the start point for our model.

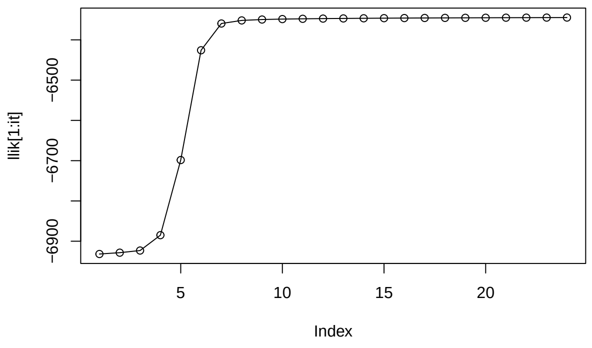




```
##  [1] "iteration:  1 log likelihood:  -6931.75122861544"
##  [2] "iteration:  2 log likelihood:  -6928.46695128332"
##  [3] "iteration:  3 log likelihood:  -6923.13091589768"
##  [4] "iteration:  4 log likelihood:  -6884.94468114899"
##  [5] "iteration:  5 log likelihood:  -6698.4237807576"
##  [6] "iteration:  6 log likelihood:  -6425.806406635"
##  [7] "iteration:  7 log likelihood:  -6359.4223002037"
##  [8] "iteration:  8 log likelihood:  -6351.74320723516"
##  [9] "iteration:  9 log likelihood:  -6349.54335699899"
## [10] "iteration:  10 log likelihood:  -6348.4434579416"
## [11] "iteration:  11 log likelihood:  -6347.73893891381"
## [12] "iteration:  12 log likelihood:  -6347.21907132148"
## [13] "iteration:  13 log likelihood:  -6346.8026280888"
## [14] "iteration:  14 log likelihood:  -6346.45328398564"
## [15] "iteration:  15 log likelihood:  -6346.15273441616"
## [16] "iteration:  16 log likelihood:  -6345.89062787433"
## [17] "iteration:  17 log likelihood:  -6345.66037682444"
## [18] "iteration:  18 log likelihood:  -6345.45729529842"
## [19] "iteration:  19 log likelihood:  -6345.2777404626"
## [20] "iteration:  20 log likelihood:  -6345.11870927259"
## [21] "iteration:  21 log likelihood:  -6344.97764443873"
## [22] "iteration:  22 log likelihood:  -6344.852335347"
## [23] "iteration:  23 log likelihood:  -6344.74086068395"
## [24] "iteration:  24 log likelihood:  -6344.64154880195"
```

```
## [1] 0.2663361 0.3438780 0.3897860
```

```
##           [,1]      [,2]     [,3]      [,4]      [,5]      [,6]      [,7]
## [1,] 0.4938980 0.4758006 0.457040 0.4711376 0.5411178 0.4986316 0.4555200
## [2,] 0.4728756 0.3874569 0.630045 0.3163584 0.6869103 0.2039956 0.7823031
## [3,] 0.5075751 0.5799061 0.422322 0.7099547 0.2967462 0.7569457 0.2402904
##           [,8]     [,9]      [,10]
## [1,] 0.4878804 0.489488 0.37258194
## [2,] 0.1446699 0.881597 0.03501224
## [3,] 0.8422855 0.119219 0.98958938
```

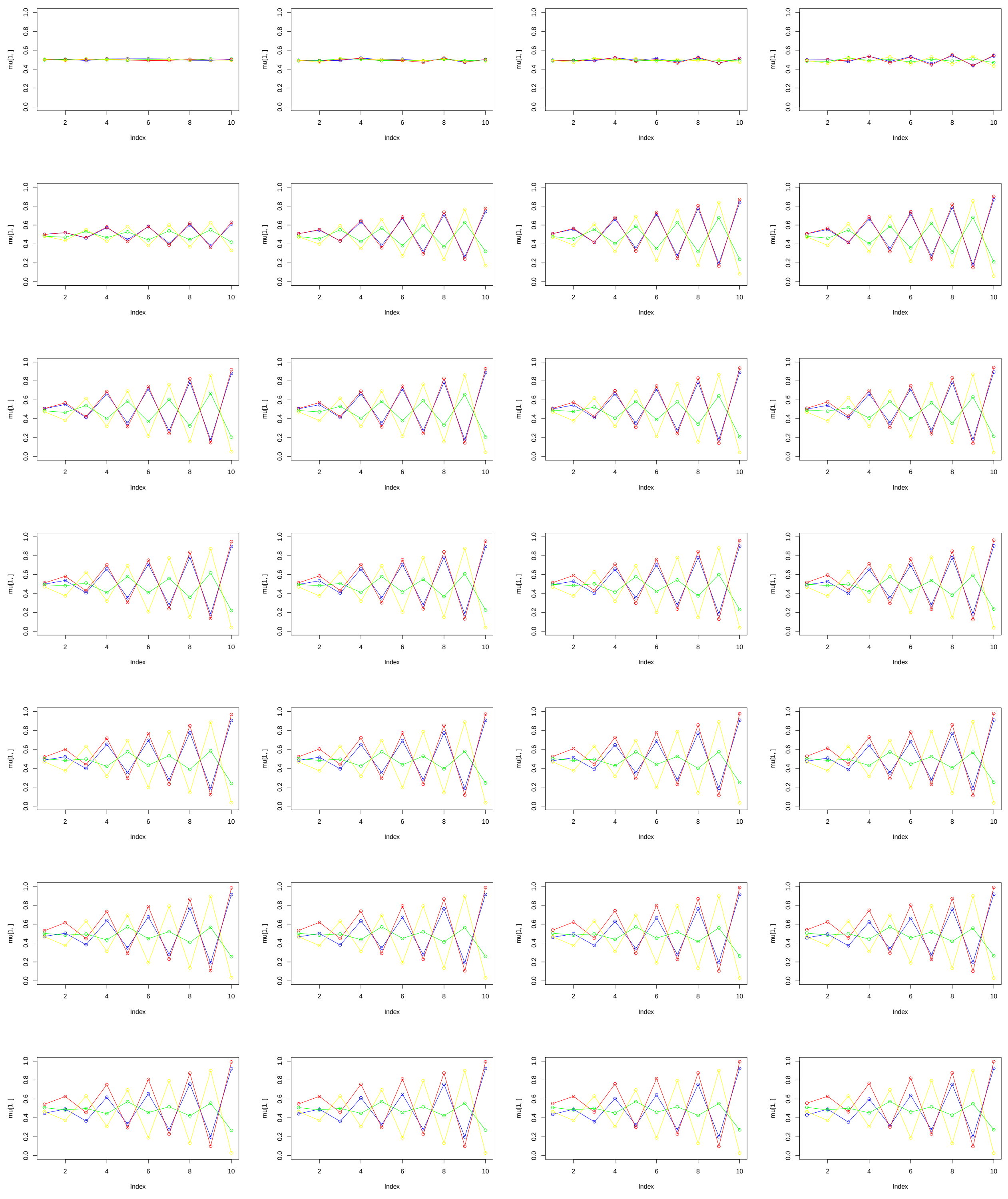


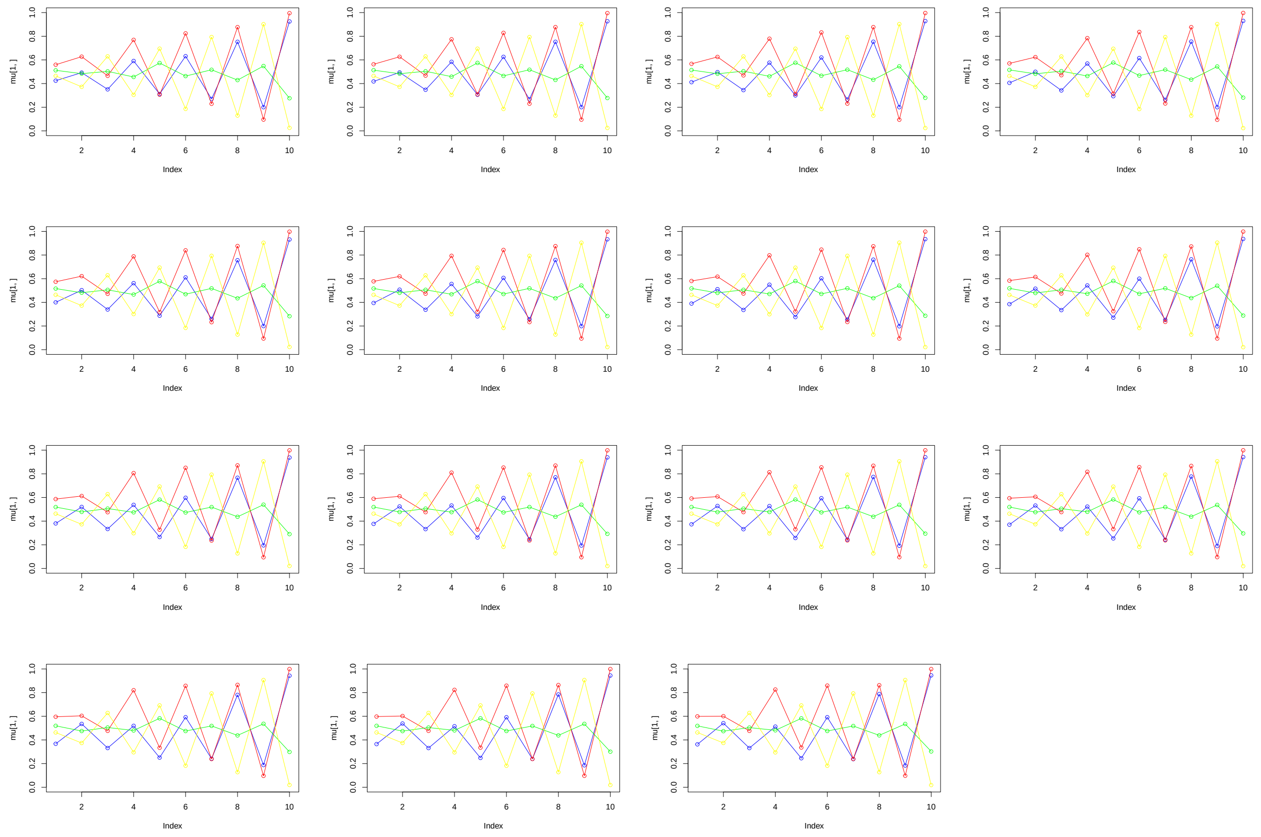
We can see that the log-likelihood rises rapidly during iteration 4-7, its also clearly shown by μ values plot. Then from final result we can see that it predict the true values well, especially in comparison with following M = 4.

```
## [1] 0.2518811 0.2466783 0.2511809 0.2502598
```

```
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]
## [1,] 0.5041509 0.5051382 0.4905578 0.5089228 0.5094530 0.5097480 0.5082991
## [2,] 0.5036886 0.4985467 0.4991731 0.5071384 0.4953800 0.4908757 0.4917657
## [3,] 0.4982070 0.5043346 0.5085042 0.4994862 0.4945702 0.5041462 0.5040348
## [4,] 0.5037389 0.4922173 0.5069624 0.5039756 0.5065369 0.5073122 0.5049473
##           [,8]      [,9]     [,10]
## [1,] 0.4926313 0.4921113 0.5048207
## [2,] 0.5040657 0.4956302 0.4996279
## [3,] 0.4955050 0.5088683 0.5072302
## [4,] 0.4943372 0.4951750 0.4940898
```

Then we change M to 4, again generate a π and μ under M = 4 as the start point for our model.

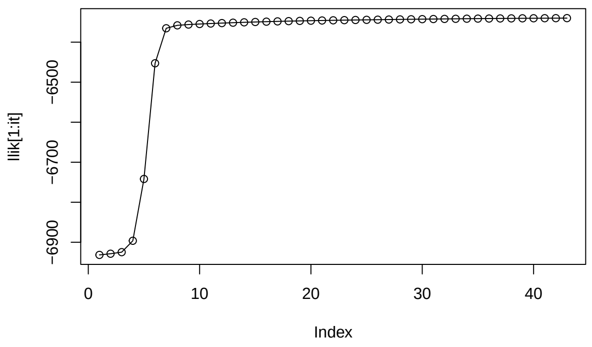

mu[1,]
Index



```
##  [1] "iteration:  1 log likelihood:  -6931.66006994864"
##  [2] "iteration:  2 log likelihood:  -6928.66727678128"
##  [3] "iteration:  3 log likelihood:  -6924.77054344575"
##  [4] "iteration:  4 log likelihood:  -6896.29508885115"
##  [5] "iteration:  5 log likelihood:  -6741.85787805056"
##  [6] "iteration:  6 log likelihood:  -6452.71193962151"
##  [7] "iteration:  7 log likelihood:  -6365.22915492218"
##  [8] "iteration:  8 log likelihood:  -6357.90724015069"
##  [9] "iteration:  9 log likelihood:  -6355.94977356183"
## [10] "iteration:  10 log likelihood:  -6354.59564838264"
## [11] "iteration:  11 log likelihood:  -6353.40988750751"
## [12] "iteration:  12 log likelihood:  -6352.31517546734"
## [13] "iteration:  13 log likelihood:  -6351.30092218428"
## [14] "iteration:  14 log likelihood:  -6350.36818071176"
## [15] "iteration:  15 log likelihood:  -6349.51652090179"
## [16] "iteration:  16 log likelihood:  -6348.74223300225"
## [17] "iteration:  17 log likelihood:  -6348.03936943375"
## [18] "iteration:  18 log likelihood:  -6347.40094567819"
## [19] "iteration:  19 log likelihood:  -6346.81968070248"
## [20] "iteration:  20 log likelihood:  -6346.28834868353"
## [21] "iteration:  21 log likelihood:  -6345.79994106786"
## [22] "iteration:  22 log likelihood:  -6345.34778016045"
## [23] "iteration:  23 log likelihood:  -6344.92564619259"
## [24] "iteration:  24 log likelihood:  -6344.52792780162"
## [25] "iteration:  25 log likelihood:  -6344.14978243089"
## [26] "iteration:  26 log likelihood:  -6343.78728731843"
## [27] "iteration:  27 log likelihood:  -6343.43756285041"
## [28] "iteration:  28 log likelihood:  -6343.09885115178"
## [29] "iteration:  29 log likelihood:  -6342.77053143643"
## [30] "iteration:  30 log likelihood:  -6342.4530520589"
## [31] "iteration:  31 log likelihood:  -6342.14776283848"
## [32] "iteration:  32 log likelihood:  -6341.85664504623"
## [33] "iteration:  33 log likelihood:  -6341.58196036309"
## [34] "iteration:  34 log likelihood:  -6341.32586665114"
## [35] "iteration:  35 log likelihood:  -6341.09006544297"
## [36] "iteration:  36 log likelihood:  -6340.87554389922"
## [37] "iteration:  37 log likelihood:  -6340.68245157758"
## [38] "iteration:  38 log likelihood:  -6340.51011833165"
## [39] "iteration:  39 log likelihood:  -6340.35718728741"
## [40] "iteration:  40 log likelihood:  -6340.22181690354"
## [41] "iteration:  41 log likelihood:  -6340.10190243326"
## [42] "iteration:  42 log likelihood:  -6339.99527661232"
## [43] "iteration:  43 log likelihood:  -6339.89986543919"
```

```
## [1] 0.1838186 0.2308466 0.2874187 0.2979162
```

```
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]
## [1,] 0.3627106 0.5416076 0.3311785 0.5125500 0.2451860 0.5918027 0.2376350
## [2,] 0.5991155 0.6005747 0.4768083 0.8260669 0.3357255 0.8593412 0.2392769
## [3,] 0.5188276 0.4740528 0.5042778 0.4812818 0.5823257 0.4755847 0.5177702
## [4,] 0.4628904 0.3744350 0.6280787 0.2945785 0.6916641 0.1817551 0.7930593
##           [,8]       [,9]      [,10]
## [1,] 0.7878580 0.18327423 0.94572455
## [2,] 0.8624625 0.09719753 0.99920005
## [3,] 0.4387190 0.53515949 0.30265960
## [4,] 0.1275007 0.90649071 0.01848283
```



We can see that after the rapid rising of log-likelihood, the iteration 8-15 seems still have a reasonable μ value, but then it falls into overfitting and the result μ and π values seems not so favorable.

```
# Code Appendix for part 2

set.seed(1234567890)
max_it <- 100 # max number of EM iterations
min_change <- 0.1 # min change in log lik between two consecutive iterations
```

```r
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 ; p(y)
true_mu <- matrix(nrow=3, ncol=D) # true conditional distributions ; p(xcol | y = Row)
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))
points(true_mu[2,], type="o", col="red")
points(true_mu[3,], type="o", col="green")
# Producing the training data x
for(i in 1:n) {
  m <- sample(1:3,1,prob=true_pi)
  for(d in 1:D) {
    x[i,d] <- rbinom(1,1,true_mu[m,d])
  } }

set.seed(1234567890)
M <- 2 # number of clusters
w <- matrix(nrow=n, ncol=M) # weights ; p(y = m | xi,thetaHat)
pi <- vector(length = M) # mixing coefficients
mu <- matrix(nrow=M, ncol=D) # conditional distributions
llik <- vector(length = max_it) # log likelihood of the EM iterations
# Random initialization of the parameters
pi <- runif(M,0.49,0.51)
pi <- pi / sum(pi)
for(m in 1:M) {
  mu[m,] <- runif(D,0.49,0.51)
}
pi
mu

set.seed(1234567890)
iterLog <- vector(length = max_it)
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 weights

  for (i in 1:n) {
    # px <- 0
    pxi <- 0
    for (m in 1:M) {
      bernXMum <- 1
      for (d in 1:D) {
        bernXMum <- bernXMum * (mu[m,d]^x[i,d]) * (1-mu[m,d])^(1-x[i,d])
        # print(paste(i,m,d,bernXMum))
      }
      pxi <- pxi + pi[m] * bernXMum
      # print(paste(i,m,d,pxi))
    }
    for (m in 1:M) {
      bernXMum <- 1
      for (d in 1:D) {
        bernXMum <- bernXMum * (mu[m,d]^x[i,d]) * (1-mu[m,d])^(1-x[i,d])
        # print(paste(i,m,d,bernXMum))
      }
      w[i,m] <- (bernXMum * pi[m]) / pxi
    }
    w[i, ] <- w[i,] /sum(w[i,])
  }


  # Your code here
  #Log likelihood computation.
  llik[it] <- 0
  for (i in 1:n) {
    pxi <- 0
    for (m in 1:M) {
      bernXMum <- 1
      for (d in 1:D) {
        bernXMum <- bernXMum * (mu[m,d]^x[i,d]) * (1-mu[m,d])^(1-x[i,d])
      }
      pxi <- pxi + pi[m] * bernXMum
    }
    llik[it] <- llik[it] + log(pxi)
  }


  # Your code here
  iterLog[it] <- paste("iteration: ", it, "log likelihood: ", llik[it])
  flush.console()
  # Stop if the lok likelihood has not changed significantly
  stopFlag <- it > 1 && (llik[it] - llik[it - 1]) < min_change
  if(stopFlag) break
  #M-step: ML parameter estimation from the data and weights
  # pi mu
  pi <- apply(w, 2, mean)
  mu <- t(w) %*% x / colSums(w)
  # Your code here
}
print(iterLog[1:it])
pi
mu
plot(llik[1:it], type="o")

set.seed(1234567890)
M <- 3 # number of clusters
w <- matrix(nrow=n, ncol=M) # weights ; p(y = m | xi,thetaHat)
pi <- vector(length = M) # mixing coefficients
mu <- matrix(nrow=M, ncol=D) # conditional distributions
```

```r
llik <- vector(length = max_it) # log likelihood of the EM iterations
# Random initialization of the parameters
pi <- runif(M,0.49,0.51)
pi <- pi / sum(pi)
for(m in 1:M) {
  mu[m,] <- runif(D,0.49,0.51)
}
pi
mu


iterLog <- vector(length = max_it)
for(it in 1:max_it) {
    # plotChoose <- c(1, 5, 6, 12, 24)
  # if (it == any(plotChoose)) {
    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 weights

  for (i in 1:n) {
    # px <- 0
    pxi <- 0
    for (m in 1:M) {
      bernXMum <- 1
      for (d in 1:D) {
        bernXMum <- bernXMum * (mu[m,d]^x[i,d]) * (1-mu[m,d])^(1-x[i,d])
        # print(paste(i,m,d,bernXMum))
      }
      pxi <- pxi + pi[m] * bernXMum
      # print(paste(i,m,d,pxi))
    }
    for (m in 1:M) {
      bernXMum <- 1
      for (d in 1:D) {
        bernXMum <- bernXMum * (mu[m,d]^x[i,d]) * (1-mu[m,d])^(1-x[i,d])
        # print(paste(i,m,d,bernXMum))
      }
      w[i,m] <- (bernXMum * pi[m]) / pxi
    }
    w[i, ] <- w[i,] /sum(w[i,])
  }


  # Your code here
  #Log likelihood computation.
  llik[it] <- 0
  for (i in 1:n) {
    pxi <- 0
    for (m in 1:M) {
      bernXMum <- 1
      for (d in 1:D) {
        bernXMum <- bernXMum * (mu[m,d]^x[i,d]) * (1-mu[m,d])^(1-x[i,d])
      }
      pxi <- pxi + pi[m] * bernXMum
    }
    llik[it] <- llik[it] + log(pxi)
  }


  # Your code here
  iterLog[it] <- paste("iteration: ", it, "log likelihood: ", llik[it])
  flush.console()
  # Stop if the lok likelihood has not changed significantly
  stopFlag <- it > 1 && (llik[it] - llik[it - 1]) < min_change
  if(stopFlag) break
  #M-step: ML parameter estimation from the data and weights
  # pi mu
  pi <- apply(w, 2, mean)
  mu <- t(w) %*% x / colSums(w)
  # Your code here
}

print(iterLog[1:it])
pi
mu
plot(llik[1:it], type="o")

set.seed(1234567890)
M <- 4 # number of clusters
w <- matrix(nrow=n, ncol=M) # weights ; p(y = m | xi,thetaHat)
pi <- vector(length = M) # mixing coefficients
mu <- matrix(nrow=M, ncol=D) # conditional distributions
llik <- vector(length = max_it) # log likelihood of the EM iterations
# Random initialization of the parameters
pi <- runif(M,0.49,0.51)
pi <- pi / sum(pi)
for(m in 1:M) {
  mu[m,] <- runif(D,0.49,0.51)
}
pi
mu


iterLog <- vector(length = max_it)
for(it in 1:max_it) {
  # plotChoose <- c(1, 15, 43)
  # if (it == any(plotChoose)) {
    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")
  # }
```

```r
Sys.sleep(0.5)
# E-step: Computation of the weights

for (i in 1:n) {
  # px <- 0
  pxi <- 0
  for (m in 1:M) {
    bernXMum <- 1
    for (d in 1:D) {
      bernXMum <- bernXMum * (mu[m,d]^x[i,d]) * (1-mu[m,d])^(1-x[i,d])
      # print(paste(i,m,d,bernXMum))
    }
    pxi <- pxi + pi[m] * bernXMum
    # print(paste(i,m,d,pxi))
  }
  for (m in 1:M) {
    bernXMum <- 1
    for (d in 1:D) {
      bernXMum <- bernXMum * (mu[m,d]^x[i,d]) * (1-mu[m,d])^(1-x[i,d])
      # print(paste(i,m,d,bernXMum))
    }
    w[i,m] <- (bernXMum * pi[m]) / pxi
  }
  w[i, ] <- w[i,] /sum(w[i,])
}


# Your code here
#Log likelihood computation.
llik[it] <- 0
for (i in 1:n) {
  pxi <- 0
  for (m in 1:M) {
    bernXMum <- 1
    for (d in 1:D) {
      bernXMum <- bernXMum * (mu[m,d]^x[i,d]) * (1-mu[m,d])^(1-x[i,d])
    }
    pxi <- pxi + pi[m] * bernXMum
  }
  llik[it] <- llik[it] + log(pxi)
}


# Your code here
iterLog[it] <- paste("iteration: ", it, "log likelihood: ", llik[it])
flush.console()
# Stop if the lok likelihood has not changed significantly
stopFlag <- it > 1 && (llik[it] - llik[it - 1]) < min_change
if(stopFlag) break
#M-step: ML parameter estimation from the data and weights
# pi mu
pi <- apply(w, 2, mean)
mu <- t(w) %*% x / colSums(w)
```

```
  # Your code here
}

print(iterLog[1:it])
pi
mu
plot(llik[1:it], type="o")
```

APPENDIX

```
set.seed(1234)
x1<-runif(1000)
x2<-runif(1000)
tedata<-cbind(x1,x2)
y<-as.numeric(x1<x2)
telabels<-as.factor(y)
test_data <- as.data.frame(tedata)
test_data <- dplyr::mutate(test_data,telabels)


# QUESTION ONE PART ONE
mis_rate1 <- c()
for(i in 1:1000){
  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)
  y<-as.numeric(x1<x2)
  trlabels<-as.factor(y)



  train_data <- as.data.frame(trdata)
  train_data <- dplyr::mutate(train_data,trlabels)
  Forest_1 <- randomForest::randomForest(trlabels~.,data = train_data, ntree = 1
                                         , nodesize = 25, keep.forest = TRUE)
  pre <- predict(Forest_1,newdata = test_data)
  misclassification_rate <- mean(pre!=telabels)
  mis_rate1 <- c(mis_rate1,misclassification_rate)
}

mean_mis_rate1 <- mean(mis_rate1)
var_mis_rate1 <- var(mis_rate1)

# the mean and variable for misclassification rate when B = 1
mean_mis_rate1
var_mis_rate1


# QUESTION ONE PART TWO
mis_rate10 <- c()
for(i in 1:1000){
  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)
  y<-as.numeric(x1<x2)
  trlabels<-as.factor(y)



  train_data <- as.data.frame(trdata)
  train_data <- dplyr::mutate(train_data,trlabels)
  Forest_10 <- randomForest::randomForest(trlabels~.,data = train_data, ntree =
                                          10, nodesize = 25, keep.forest = TRUE)
  pre <- predict(Forest_10,newdata = test_data)
  misclassification_rate <- mean(pre!=telabels)
  mis_rate10 <- c(mis_rate10,misclassification_rate)
}

mean_mis_rate10 <- mean(mis_rate10)
var_mis_rate10 <- var(mis_rate10)

# the mean and variable for misclassification rate when B = 10
mean_mis_rate10
var_mis_rate10





# QUESTION ONE PART THREE
mis_rate100 <- c()
for(i in 1:1000){

  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)
  y<-as.numeric(x1<x2)
  trlabels<-as.factor(y)



  train_data <- as.data.frame(trdata)
  train_data <- dplyr::mutate(train_data,trlabels)
  Forest_100 <- randomForest::randomForest(trlabels~.,data = train_data,
                        ntree = 100, nodesize = 25, keep.forest = TRUE)
  pre <- predict(Forest_100,newdata = test_data)
  misclassification_rate <- mean(pre!=telabels)
  mis_rate100 <- c(mis_rate100,misclassification_rate)
}

mean_mis_rate100 <- mean(mis_rate100)
var_mis_rate100 <- var(mis_rate100)

# the mean and variable for misclassification rate when B = 10
```

```r
mean_mis_rate100
var_mis_rate100


################################################################################
################################################################################

set.seed(1234)
x1<-runif(1000)
x2<-runif(1000)
tedata<-cbind(x1,x2)
y<-as.numeric(x1<0.5)
telabels<-as.factor(y)
test_data <- as.data.frame(tedata)
test_data <- dplyr::mutate(test_data,telabels)








# QUESTION TWO PART ONE
mis_rate1 <- c()
for(i in 1:1000){
  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)
  y<-as.numeric(x1<0.5)
  trlabels<-as.factor(y)



  train_data <- as.data.frame(trdata)
  train_data <- dplyr::mutate(train_data,trlabels)
  Forest_1 <- randomForest::randomForest(trlabels~.,data = train_data, ntree = 1
                                         , nodesize = 25, keep.forest = TRUE)
  pre <- predict(Forest_1,newdata = test_data)
  misclassification_rate <- mean(pre!=telabels)
  mis_rate1 <- c(mis_rate1,misclassification_rate)
}

mean_mis_rate1 <- mean(mis_rate1)
var_mis_rate1 <- var(mis_rate1)

# the mean and variable for misclassification rate when B = 1
mean_mis_rate1
var_mis_rate1


# QUESTION two PART TWO
mis_rate10 <- c()
for(i in 1:1000){
  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)
  y<-as.numeric(x1<0.5)
  trlabels<-as.factor(y)



  train_data <- as.data.frame(trdata)
  train_data <- dplyr::mutate(train_data,trlabels)
  Forest_10 <- randomForest::randomForest(trlabels~.,data = train_data,
                               ntree = 10, nodesize = 25, keep.forest = TRUE)
  pre <- predict(Forest_10,newdata = test_data)
  misclassification_rate <- mean(pre!=telabels)
  mis_rate10 <- c(mis_rate10,misclassification_rate)
}

mean_mis_rate10 <- mean(mis_rate10)
var_mis_rate10 <- var(mis_rate10)

# the mean and variable for misclassification rate when B = 10
mean_mis_rate10
var_mis_rate10


# QUESTION tWO PART THREE
mis_rate100 <- c()
for(i in 1:1000){

  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)
  y<-as.numeric(x1<0.5)
  trlabels<-as.factor(y)



  train_data <- as.data.frame(trdata)
  train_data <- dplyr::mutate(train_data,trlabels)
  Forest_100 <- randomForest::randomForest(trlabels~.,data = train_data,
                             ntree = 100, nodesize = 25, keep.forest = TRUE)
  pre <- predict(Forest_100,newdata = test_data)
  misclassification_rate <- mean(pre!=telabels)
  mis_rate100 <- c(mis_rate100,misclassification_rate)
}

mean_mis_rate100 <- mean(mis_rate100)
var_mis_rate100 <- var(mis_rate100)

# the mean and variable for misclassification rate when B = 10
mean_mis_rate100
var_mis_rate100
```

```r
################################################################################
################################################################################
################################################################################

set.seed(1234)
x1<-runif(1000)
x2<-runif(1000)
tedata<-cbind(x1,x2)
y<-as.numeric(((x1<0.5 & x2<0.5)|(x1>0.5 & x2>0.5)))
telabels<-as.factor(y)
test_data <- as.data.frame(tedata)
test_data <- dplyr::mutate(test_data,telabels)

# QUESTION THREE PART ONE
mis_rate1 <- c()
for(i in 1:1000){
  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)
  y<-as.numeric(((x1<0.5 & x2<0.5)|(x1>0.5 & x2>0.5)))
  trlabels<-as.factor(y)



  train_data <- as.data.frame(trdata)
  train_data <- dplyr::mutate(train_data,trlabels)
  Forest_1 <- randomForest::randomForest(trlabels~.,data = train_data,
                               ntree = 1, nodesize = 12, keep.forest = TRUE)
  pre <- predict(Forest_1,newdata = test_data)
  misclassification_rate <- mean(pre!=telabels)
  mis_rate1 <- c(mis_rate1,misclassification_rate)
}

mean_mis_rate1 <- mean(mis_rate1)
var_mis_rate1 <- var(mis_rate1)

# the mean and variable for misclassification rate when B = 1
mean_mis_rate1
var_mis_rate1



# QUESTION THREE PART TWO
mis_rate10 <- c()
for(i in 1:1000){

  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)
  y<-as.numeric(((x1<0.5 & x2<0.5)|(x1>0.5 & x2>0.5)))
  trlabels<-as.factor(y)
  train_data <- as.data.frame(trdata)
  train_data <- dplyr::mutate(train_data,trlabels)
  Forest_10 <- randomForest::randomForest(trlabels~.,data = train_data,
                              ntree = 10, nodesize = 12, keep.forest = TRUE)
  pre <- predict(Forest_10,newdata = test_data)
  misclassification_rate <- mean(pre!=telabels)
  mis_rate10 <- c(mis_rate10,misclassification_rate)
}

mean_mis_rate10 <- mean(mis_rate10)
var_mis_rate10 <- var(mis_rate10)

# the mean and variable for misclassification rate when B = 10
mean_mis_rate10
var_mis_rate10





# QUESTION THREE PART THREE
mis_rate100 <- c()
for(i in 1:1000){

  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)
  y<-as.numeric(((x1<0.5 & x2<0.5)|(x1>0.5 & x2>0.5)))
  trlabels<-as.factor(y)



  train_data <- as.data.frame(trdata)
  train_data <- dplyr::mutate(train_data,trlabels)
  Forest_100 <- randomForest::randomForest(trlabels~.,data = train_data,
                            ntree = 100, nodesize = 12, keep.forest = TRUE)
  pre <- predict(Forest_100,newdata = test_data)
  misclassification_rate <- mean(pre!=telabels)
  mis_rate100 <- c(mis_rate100,misclassification_rate)
}

mean_mis_rate100 <- mean(mis_rate100)
var_mis_rate100 <- var(mis_rate100)

# the mean and variable for misclassification rate when B = 10
mean_mis_rate100
var_mis_rate100
```