lab block2

Group A20

Statement Of Contribution:

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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 0.205101

mean_mis_rate10 0.122574

mean_mis_rate100 0.077882

var_mis_rate1 0.002805146

var_mis_rate10 0.0008313639

var_mis_rate100 0.0004518479

TASK TWO

The relevant code is added in Appendix

mean_mis_rate1 0.093459

mean_mis_rate10 0.010777

mean_mis_rate100 0.006265

var_mis_rate1 0.01690613

var_mis_rate10 0.0001199092

var_mis_rate100 2.553328e-06

TASK THREE

The relevant code is added in Appendix

mean_mis_rate1 0.213347

mean_mis_rate10 0.077935

mean_mis_rate100 0.034172

var_mis_rate1 0.01461418

var_mis_rate10 0.001286011

var_mis_rate100 1.389431e-05

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.

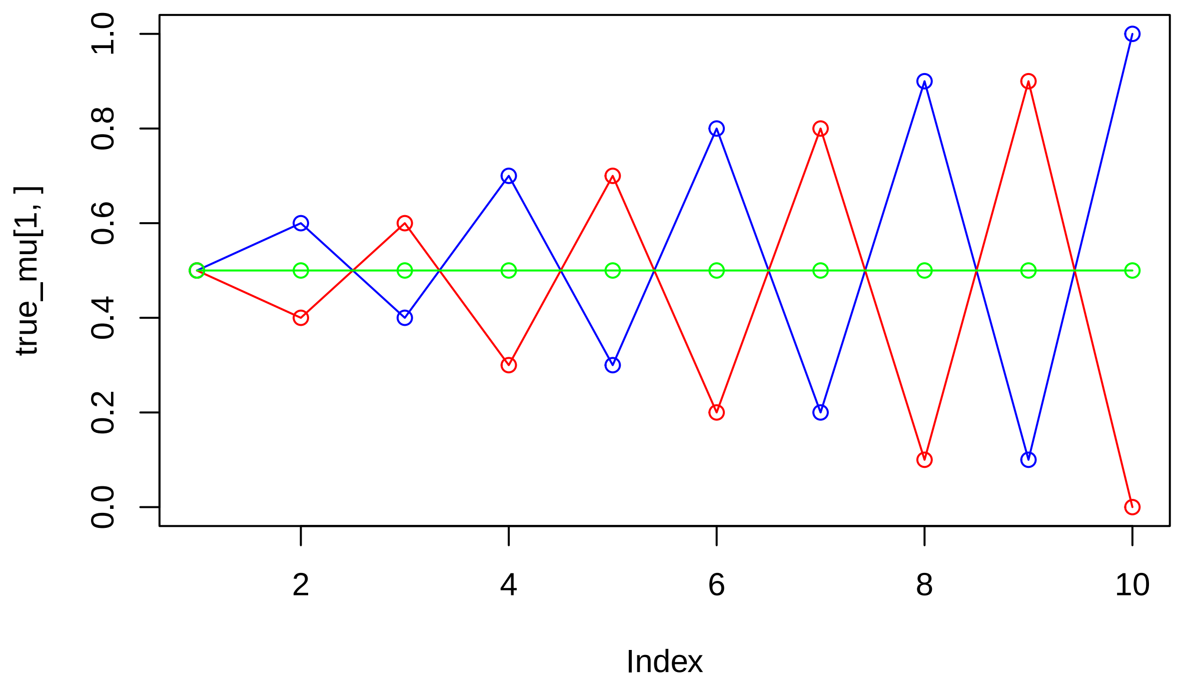
The third dataset represents a slightly more complicated classification problem than the first one. Still, you should get better performance for it when using suffi-cient trees in the random forest. Explain why you get better performance.

The smaller nodesize means that the decision tree tree is larger, in other words , the average of the predicted values from the decision tree in the random forest has smaller bias compared to the true values, and this will increase the variance of the distribution of the predicted values from the decision tree in the random forest. However, according to the relationship between the predicted values of the decision tree and the predicted values of the random forest, the effect of bagging can make the variance of the distribution of the predicted values of the random forest smaller, especially when B increases gradually. This is why, for the third data set, when B is 1, the prediction effect is not as good as the first set of predictions. This is because when B is 1 and the decision tree becomes complex, compared to the true value ,the bias of the mean of the distribution of the predicted values of the decision tree inside the random forest decreases and the variance increases, but the bagging effect of the random forest does not work well, so the prediction effect of the random forest is not very good. However, we notice that the effect of bagging is also improved when B increases. Accordingly, compared to the true value the bias of the mean value of the entire random forest prediction distribution is reduced. At the same time, the variance also decreases. In other words, the prediction accuracy of the individual random forest has been significantly improved. This also corresponds to the data.

2. Mixture Models

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

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



```r
# 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])
  } }
```

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 $Dimension = 10$.

```r
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
```

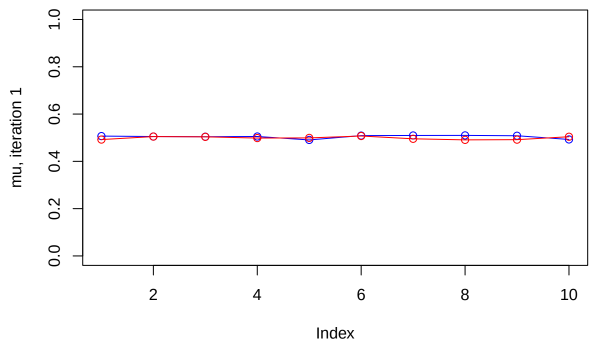
```
## [1] 0.5052178 0.4947822
```

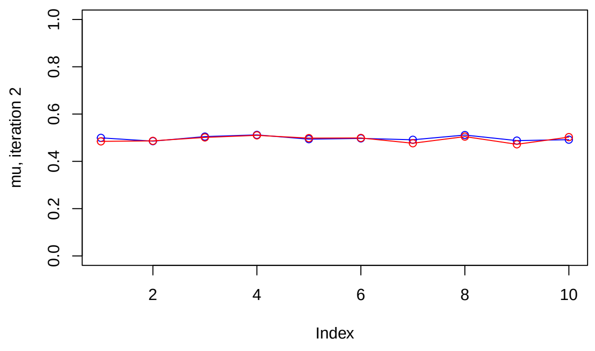
```
mu
```

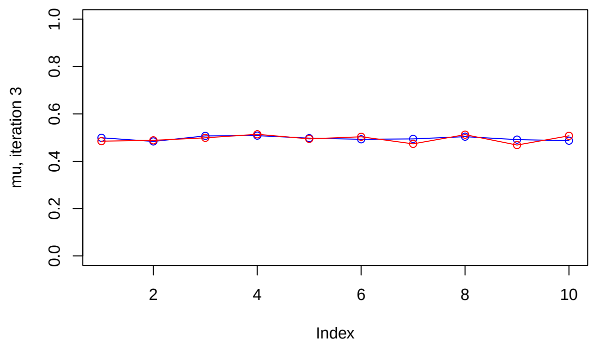
```
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]
## [1,] 0.5068040 0.5049455 0.5041509 0.5051382 0.4905578 0.5089228 0.509453
## [2,] 0.4921113 0.5048207 0.5036886 0.4985467 0.4991731 0.5071384 0.495380
##           [,8]      [,9]     [,10]
## [1,] 0.5097480 0.5082991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

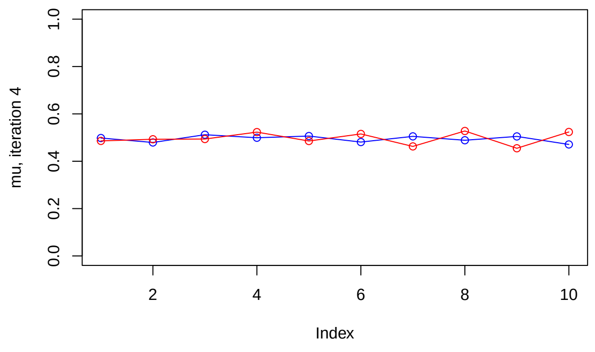
First we start with cluster M = 2. And we generate a π and μ under M = 2 as the start point for our model.

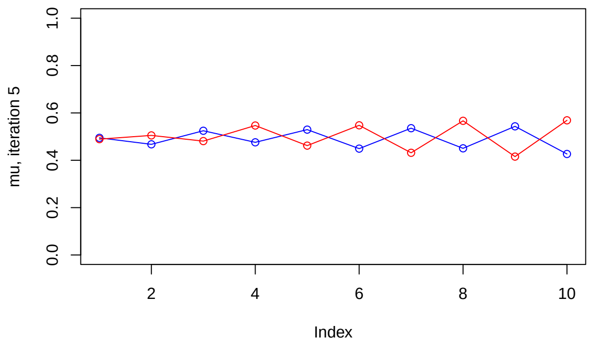
```
set.seed(1234567890)
iterLog <- vector(length = max_it)
for(it in 1:max_it) {
  plot(mu[1,], type="o", col="blue", ylim=c(0,1), ylab = paste("mu, iteration", it))
  points(mu[2,], type="o", col="red")
  # points(mu[3,], type="o", col="green")
  #points(mu[4,], type="o", col="yellow")
  Sys.sleep(0.5)
  # 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
}
```

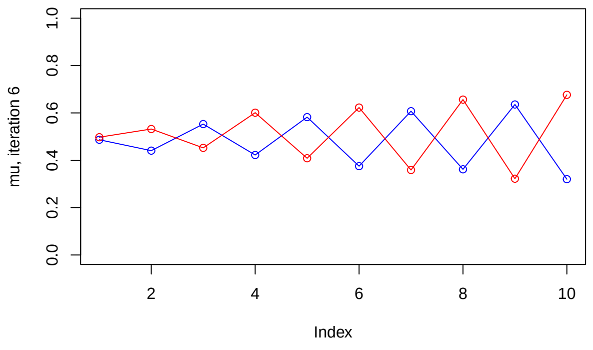


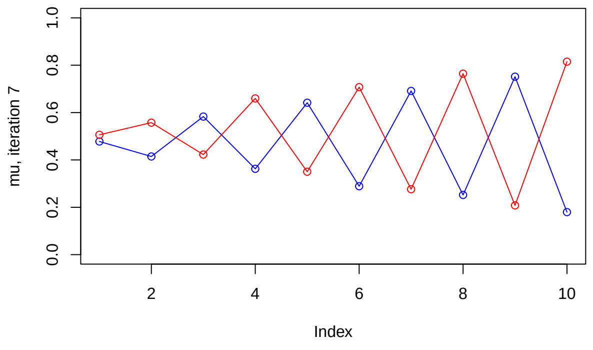


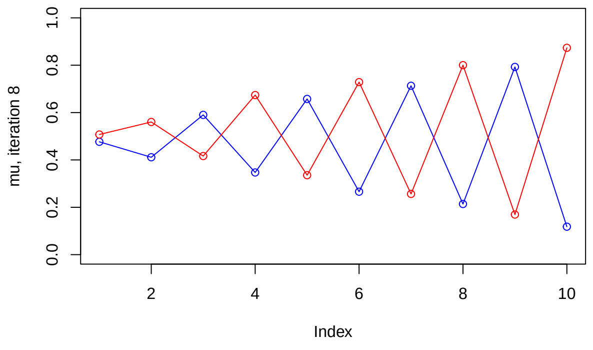


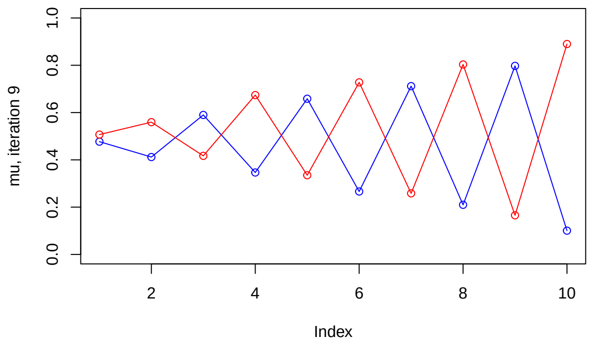


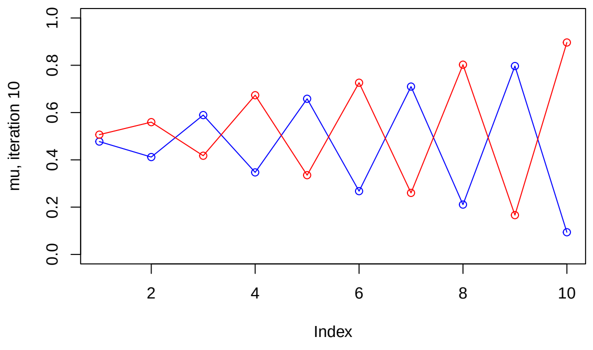

mu, iteration 5
Index

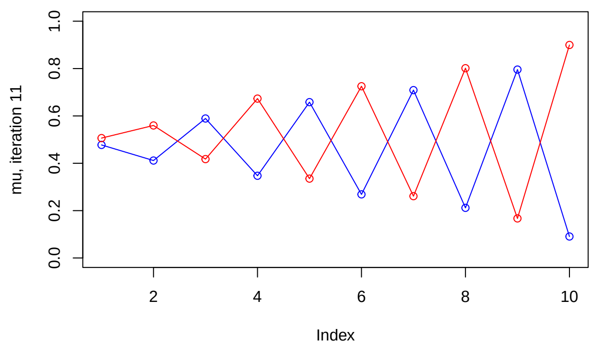

mu, iteration 6
Index

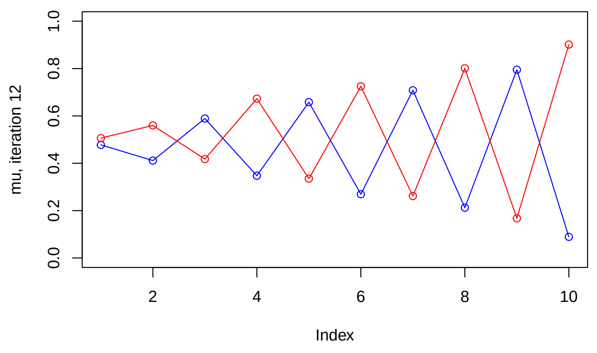

mu, iteration 7
Index


mu, iteration 8
Index


mu, iteration 9
Index


mu, iteration 10
Index





```
print(iterLog[1:it])
```

```
##  [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"
```

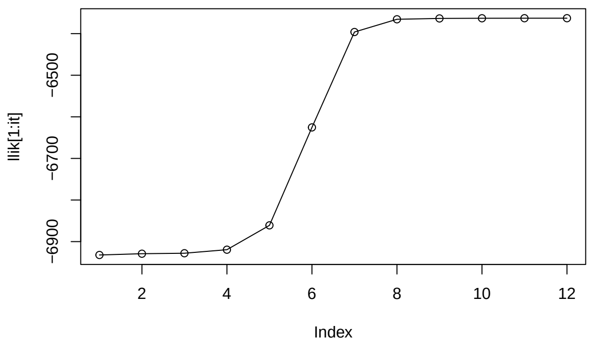
```
pi
```

```
## [1] 0.4979156 0.5020844
```

```
mu
```

```
##           [,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
```

```
plot(llik[1:it], type="o")
```



From the plots above, and comparing it with the plot of *ture* μ. We can see that under this situation, the red and blue *ture* μ is in a sense shown by the red and blue *predicted* μ. While the green *ture* μ, which is $p = 0.5$ in all dimensions, disappeared in the plot of *predicted* μ, and green *ture* μ's impact on dataset generation might be represented by the remaining 2 *predicted* μs. The rapidly raise of log-likelihood during iteration 5-7 is also reflect by the plot from significant changing of μ in corresponding iterations.

```
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
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
```

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

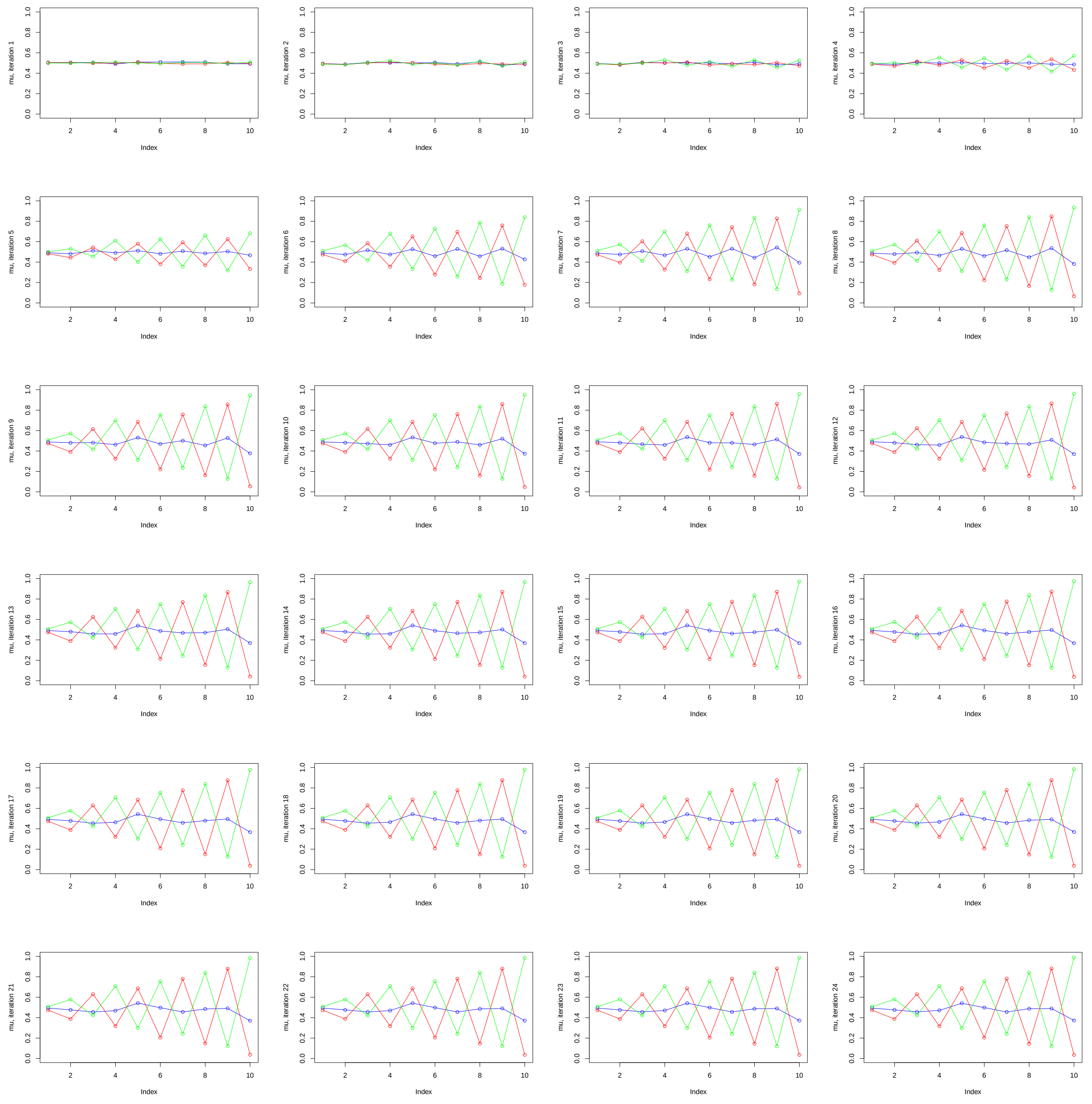
```
mu
```

```
##           [,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.

```
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), ylab = paste("mu, iteration", it))
    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])
```

```
##  [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"
```

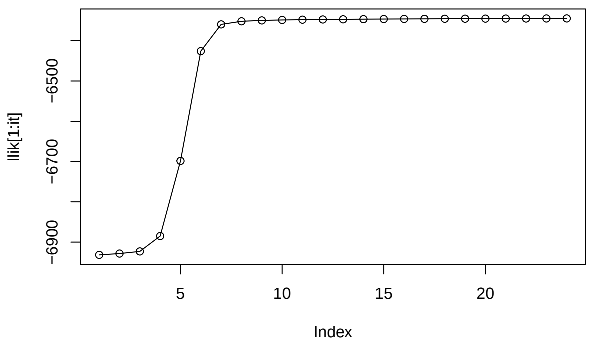
```
pi
```

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

```
mu
```

```
##           [,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
```

```
plot(llik[1:it], type="o")
```



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.

```
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
```

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

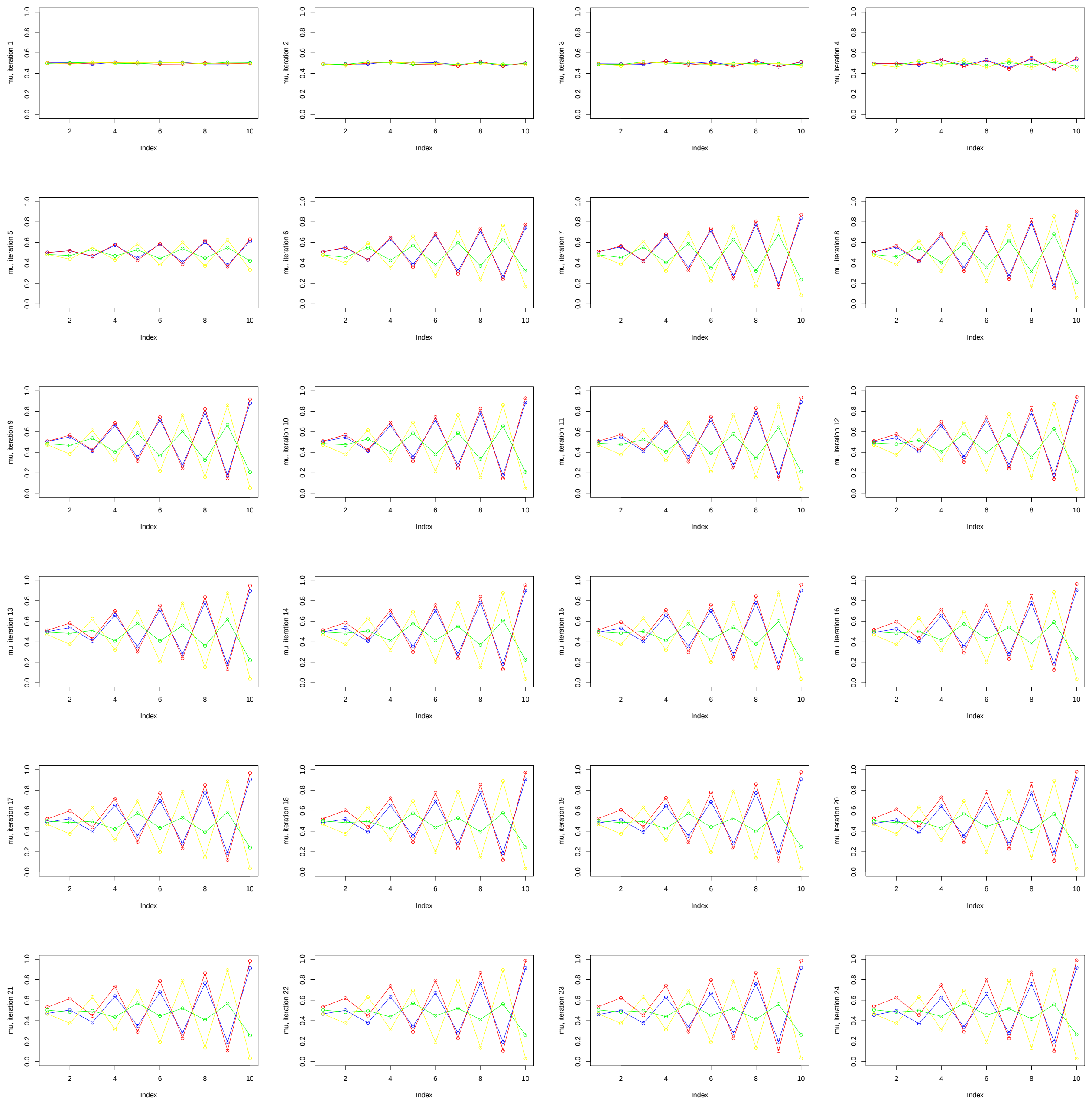
```
mu
```

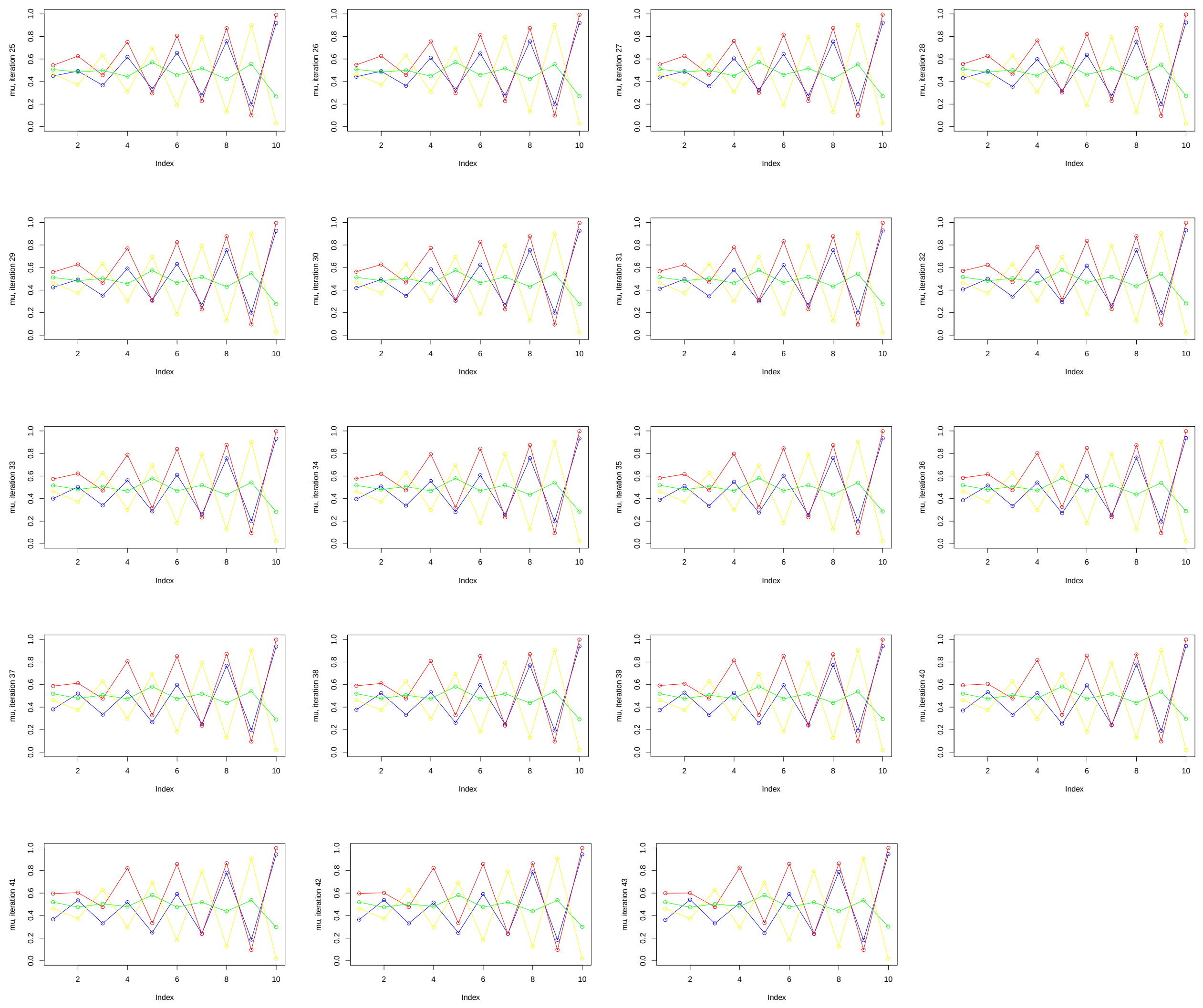
```
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]
## [1,] 0.5041509 0.5051382 0.4905578 0.5089228 0.5094530 0.5097480 0.5082991
## [2,] 0.5036886 0.4985467 0.4991731 0.5071384 0.4953800 0.4908757 0.4917657
## [3,] 0.4982070 0.5043346 0.5085042 0.4994862 0.4945702 0.5041462 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.

```
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), ylab = paste("mu, iteration", it))
    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])
```

```
##  [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"
```

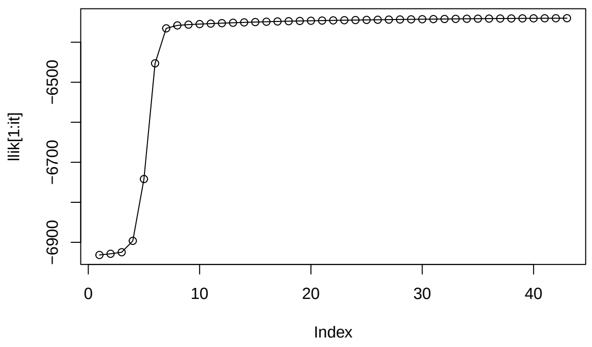
```
pi
```

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

```
mu
```

```
##           [,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
```

```
plot(llik[1:it], type="o")
```



We can see that after the rapid rising of log-likelihood, the iteration 8-15 seems still have a reasonable μ patterns, but then it falls into a pattern that harder to be interpreted. Seems the plot of *predicted* μs is no longer emulating the pattern of *true* μs, but trying to model the dataset in its own M=4 way.

```r
# 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
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)
}
```

```r
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), ylab = paste("mu, iteration", it))
  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
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)
```

```r
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")
  # }
  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

```r
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)



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)
```

```r
# QUESTION ONE PART ONE
mis_rate1 <- c()
for(i in 1:1000){

  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){

  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){

  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)
```

```r
var_mis_rate100 <- var(mis_rate100)

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

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)





# QUESTION TWO PART ONE
mis_rate1 <- c()
for(i in 1:1000){

  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){
  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){
  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



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

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)


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)
```

```r
train_data <- as.data.frame(trdata)
train_data <- dplyr::mutate(train_data,trlabels)

# QUESTION THREE PART ONE
mis_rate1 <- c()
for(i in 1:1000){

  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){

  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){

  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
```