lab block2

Group A20

Statement Of Contribution:

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PART ONE

QUESTION ONE

The code is given in the appendix.

Results are given below.

```
# QUESTION ONE PART ONE
mis_rate1 <- c()</pre>
for(i in 1:1000){
  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)</pre>
  y < -as.numeric(x1 < x2)
  trlabels<-as.factor(y)</pre>
  train_data <- as.data.frame(trdata)</pre>
  train_data <- dplyr::mutate(train_data,trlabels)</pre>
  Forest_1 <- randomForest::randomForest(trlabels~., data = train_data, ntree = 1, nodesize = 25, keep.f
  pre <- predict(Forest_1,newdata = train_data)</pre>
  misclassification_rate <- mean(pre!=trlabels)</pre>
  mis_rate1 <- c(mis_rate1,misclassification_rate)</pre>
mean_mis_rate1 <- mean(mis_rate1)</pre>
var_mis_rate1 <- var(mis_rate1)</pre>
# the mean and variable for misclassification rate when {\it B} = 1
mean_mis_rate1
## [1] 0.15419
var_mis_rate1
## [1] 0.003783527
# QUESTION ONE PART TWO
mis_rate10 <- c()</pre>
for(i in 1:1000){
```

```
x1<-runif(100)
  x2 \leftarrow runif(100)
  trdata<-cbind(x1,x2)
  y < -as.numeric(x1 < x2)
  trlabels<-as.factor(y)</pre>
  train_data <- as.data.frame(trdata)</pre>
  train_data <- dplyr::mutate(train_data,trlabels)</pre>
  Forest_10 <- randomForest::randomForest(trlabels~., data = train_data, ntree = 10, nodesize = 25, keep
  pre <- predict(Forest_1,newdata = train_data)</pre>
  misclassification_rate <- mean(pre!=trlabels)</pre>
  mis_rate10 <- c(mis_rate1, misclassification_rate)</pre>
mean_mis_rate10 <- mean(mis_rate10)</pre>
var_mis_rate10 <- var(mis_rate10)</pre>
# the mean and variable for misclassification rate when B = 10
mean mis rate10
## [1] 0.1542458
var_mis_rate10
## [1] 0.003782856
# QUESTION ONE PART THREE
mis rate100 <- c()
for(i in 1:1000){
  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)</pre>
  y < -as.numeric(x1 < x2)
  trlabels<-as.factor(y)</pre>
  train_data <- as.data.frame(trdata)</pre>
  train_data <- dplyr::mutate(train_data,trlabels)</pre>
  Forest_100 <- randomForest::randomForest(trlabels~., data = train_data, ntree = 100, nodesize = 25, ke
  pre <- predict(Forest_1,newdata = train_data)</pre>
  misclassification_rate <- mean(pre!=trlabels)</pre>
  mis_rate100 <- c(mis_rate1,misclassification_rate)</pre>
mean_mis_rate100 <- mean(mis_rate100)</pre>
var_mis_rate100 <- var(mis_rate100)</pre>
# the mean and variable for misclassification rate when B = 10
mean_mis_rate100
```

[1] 0.1542657

```
var_mis_rate100
```

[1] 0.003785485

QUESTION TWO

The code is given in the appendix.

Results are given below.

```
# 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)</pre>
  train_data <- as.data.frame(trdata)</pre>
  train_data <- dplyr::mutate(train_data,trlabels)</pre>
  Forest_1 <- randomForest::randomForest(trlabels ~., data = train_data, ntree = 1, nodesize = 25, keep.f
  pre <- predict(Forest_1,newdata = train_data)</pre>
  misclassification_rate <- mean(pre!=trlabels)</pre>
  mis_rate1 <- c(mis_rate1,misclassification_rate)</pre>
}
mean_mis_rate1 <- mean(mis_rate1)</pre>
var_mis_rate1 <- var(mis_rate1)</pre>
# the mean and variable for misclassification rate when B = 1
mean_mis_rate1
## [1] 0.07121
var_mis_rate1
## [1] 0.01237381
# QUESTION two PART TWO
mis_rate10 <- c()</pre>
for(i in 1:1000){
  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)</pre>
  y < -as.numeric(x1 < 0.5)
  trlabels<-as.factor(y)</pre>
  train data <- as.data.frame(trdata)</pre>
  train_data <- dplyr::mutate(train_data,trlabels)</pre>
  Forest_10 <- randomForest::randomForest(trlabels~., data = train_data, ntree = 10, nodesize = 25, keep
```

```
pre <- predict(Forest_1,newdata = train_data)</pre>
  misclassification_rate <- mean(pre!=trlabels)</pre>
  mis_rate10 <- c(mis_rate1, misclassification_rate)</pre>
}
mean_mis_rate10 <- mean(mis_rate10)</pre>
var_mis_rate10 <- var(mis_rate10)</pre>
# the mean and variable for misclassification rate when B = 10
mean_mis_rate10
## [1] 0.07155844
var mis rate10
## [1] 0.01248297
# QUESTION tWO PART THREE
mis rate100 <- c()
for(i in 1:1000){
  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)</pre>
  y < -as.numeric(x1 < 0.5)
  trlabels<-as.factor(y)</pre>
  train_data <- as.data.frame(trdata)</pre>
  train_data <- dplyr::mutate(train_data,trlabels)</pre>
  Forest_100 <- randomForest::randomForest(trlabels~., data = train_data, ntree = 100, nodesize = 25, ke
  pre <- predict(Forest_1,newdata = train_data)</pre>
  misclassification_rate <- mean(pre!=trlabels)</pre>
  mis_rate100 <- c(mis_rate1,misclassification_rate)</pre>
}
mean_mis_rate100 <- mean(mis_rate100)</pre>
var_mis_rate100 <- var(mis_rate100)</pre>
# the mean and variable for misclassification rate when B = 10
mean_mis_rate100
## [1] 0.07137862
var_mis_rate100
## [1] 0.0123899
QUESTION THREE
```

The code is given in the appendix.

Results are given below.

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

```
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)</pre>
  train_data <- as.data.frame(trdata)</pre>
  train_data <- dplyr::mutate(train_data,trlabels)</pre>
  Forest_1 <- randomForest::randomForest(trlabels ~., data = train_data, ntree = 1, nodesize = 12, keep.f
  pre <- predict(Forest_1,newdata = train_data)</pre>
  misclassification_rate <- mean(pre!=trlabels)</pre>
  mis_rate1 <- c(mis_rate1,misclassification_rate)</pre>
mean_mis_rate1 <- mean(mis_rate1)</pre>
var_mis_rate1 <- var(mis_rate1)</pre>
# the mean and variable for misclassification rate when B = 1
mean mis rate1
## [1] 0.14995
var_mis_rate1
## [1] 0.006740238
# QUESTION THREE PART TWO
mis rate10 \leftarrow c()
for(i in 1:1000){
  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)</pre>
  y<-as.numeric(((x1<0.5 \& x2<0.5)|(x1>0.5 \& x2>0.5)))
  trlabels<-as.factor(y)</pre>
  train_data <- as.data.frame(trdata)</pre>
  train_data <- dplyr::mutate(train_data,trlabels)</pre>
  Forest_10 <- randomForest::randomForest(trlabels~., data = train_data, ntree = 10, nodesize = 12, keep
  pre <- predict(Forest_1,newdata = train_data)</pre>
  misclassification_rate <- mean(pre!=trlabels)</pre>
  mis_rate10 <- c(mis_rate1,misclassification_rate)</pre>
mean_mis_rate10 <- mean(mis_rate10)</pre>
var_mis_rate10 <- var(mis_rate10)</pre>
# the mean and variable for misclassification rate when B = 10
mean_mis_rate10
```

[1] 0.1500999

```
var_mis_rate10
## [1] 0.00675599
# QUESTION THREE PART THREE
mis_rate100 <- c()
for(i in 1:1000){
  x1<-runif(100)
  x2<-runif(100)
  trdata<-cbind(x1,x2)</pre>
  y<-as.numeric(((x1<0.5 & x2<0.5)|(x1>0.5 & x2>0.5)))
  trlabels<-as.factor(y)</pre>
  # QUESTION ONE
  train_data <- as.data.frame(trdata)</pre>
  train_data <- dplyr::mutate(train_data,trlabels)</pre>
  Forest_100 <- randomForest::randomForest(trlabels~., data = train_data, ntree = 100, nodesize = 12, ke
  pre <- predict(Forest_1,newdata = train_data)</pre>
  misclassification_rate <- mean(pre!=trlabels)</pre>
  mis_rate100 <- c(mis_rate1, misclassification_rate)</pre>
}
mean_mis_rate100 <- mean(mis_rate100)</pre>
var_mis_rate100 <- var(mis_rate100)</pre>
# the mean and variable for misclassification rate when {\it B} = 10 \,
mean_mis_rate100
## [1] 0.1501598
var_mis_rate100
```

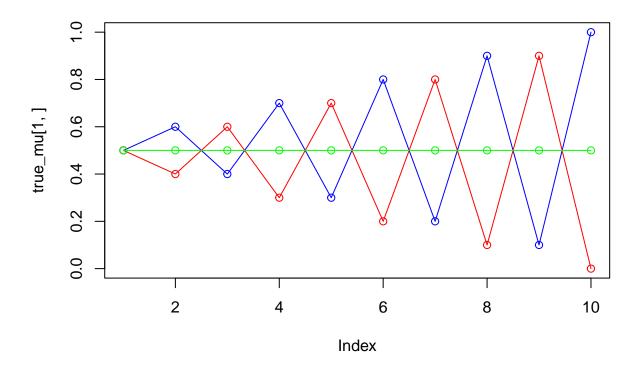
QUESTION THREE

[1] 0.006777574

1. From the first two calculations, we can see the misclasification rate decreases first and then increases as the number of trees increases.

2. Mixture Models

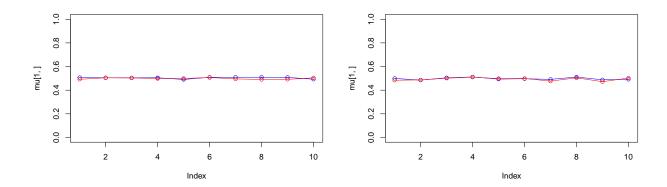
For implementing the EM algorithm for Bernoulli mixture model First we generate a π and μ of a Bernoulli mixture model

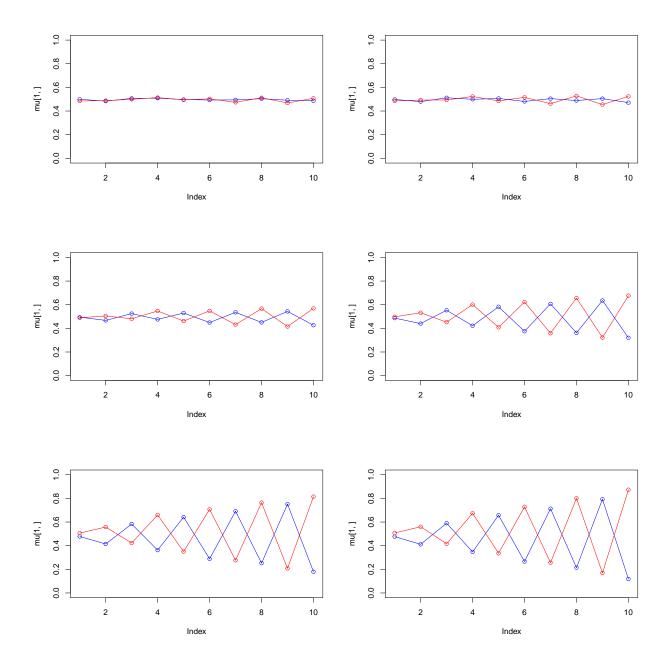


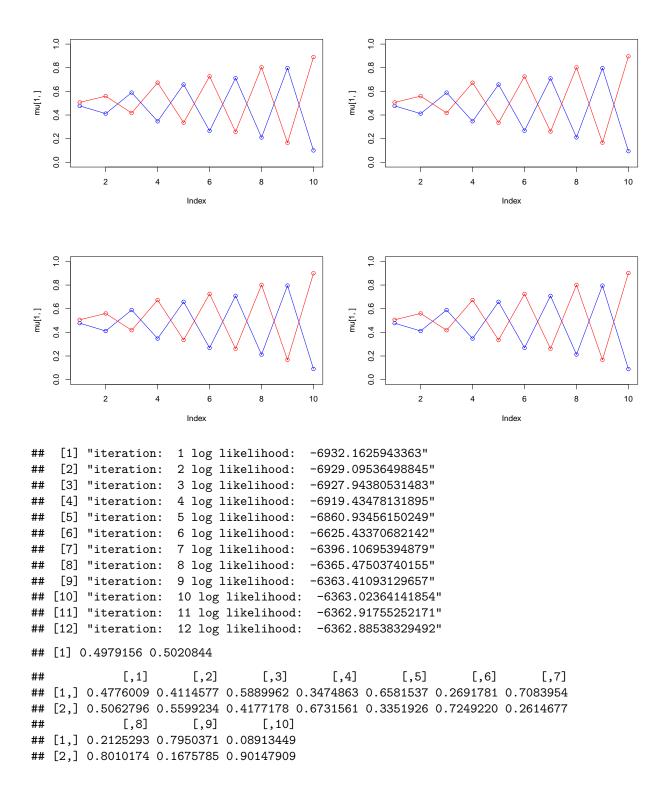
And the plot above shows the 3 μ s we are using to generate data set x, with a same $\pi = \frac{1}{3}$ for each μ , and of course with a Dimension = 10.

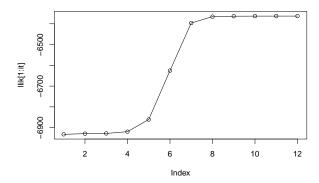
```
[1] 0.5052178 0.4947822
                        [,2]
                                  [,3]
                                             [,4]
                                                       [,5]
                                                                  [,6]
                                                                           [,7]
##
             [,1]
   [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.









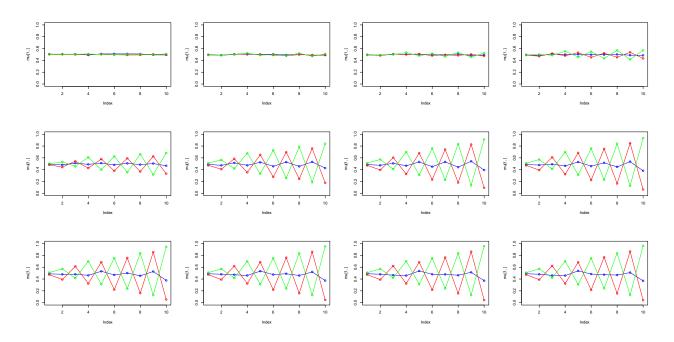
[3,] 0.5040348 0.4955050 0.5088683

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 μ s are symmetrical to the 0.5 axis.

And for every iteration the predicted μ is closer and closer to the $true~\mu$. 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.

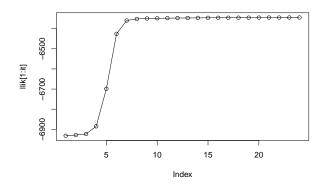
```
[1] 0.3359578 0.3290183 0.3350239
##
               [,1]
                          [,2]
                                      [,3]
                                                 [,4]
                                                             [,5]
                                                                        [,6]
                                                                                    [,7]
##
   \hbox{\tt [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
```

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 log likelihood:
                                          -6425.806406635"
##
       "iteration:
       "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 log likelihood:
##
   [13] "iteration:
                                          -6346.8026280888"
   [14] "iteration:
                     14 log likelihood:
                                          -6346.45328398564"
   [15] "iteration:
                      15 log likelihood:
                                          -6346.15273441616"
   [16] "iteration:
                     16 log likelihood:
                                          -6345.89062787433"
                     17 log likelihood:
##
   [17] "iteration:
                                          -6345.66037682444"
   [18] "iteration:
                      18 log likelihood:
                                          -6345.45729529842"
   [19] "iteration:
                      19 log likelihood:
                                          -6345.2777404626"
   [20] "iteration:
                      20 log likelihood:
                                          -6345.11870927259"
       "iteration:
                      21 log likelihood:
                                          -6344.97764443873"
   [21]
   [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
##
                                 [,3]
##
             [,1]
                        [,2]
                                            [,4]
                                                      [,5]
                                                                           [,7]
                                                                 [,6]
## [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

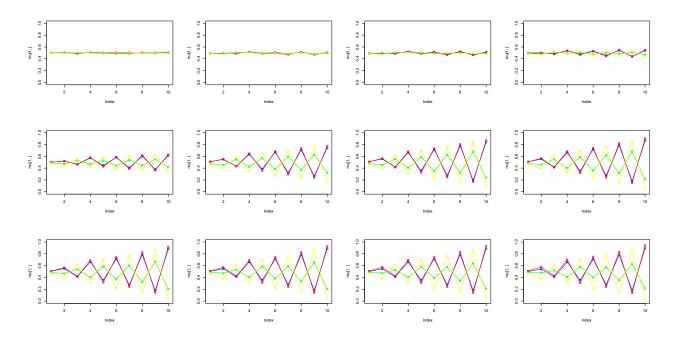


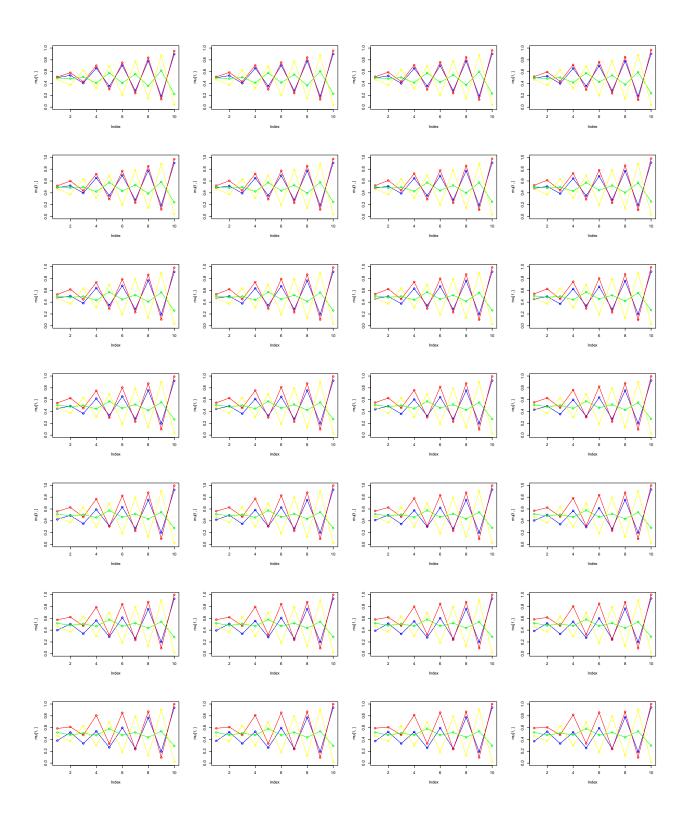
We can see that the log-likelihood rises rapidly during iteration 4-7, its also clearly shown by μ values plot. Then from final result we can see that it predict the true values well, especially in comparison with following M=4.

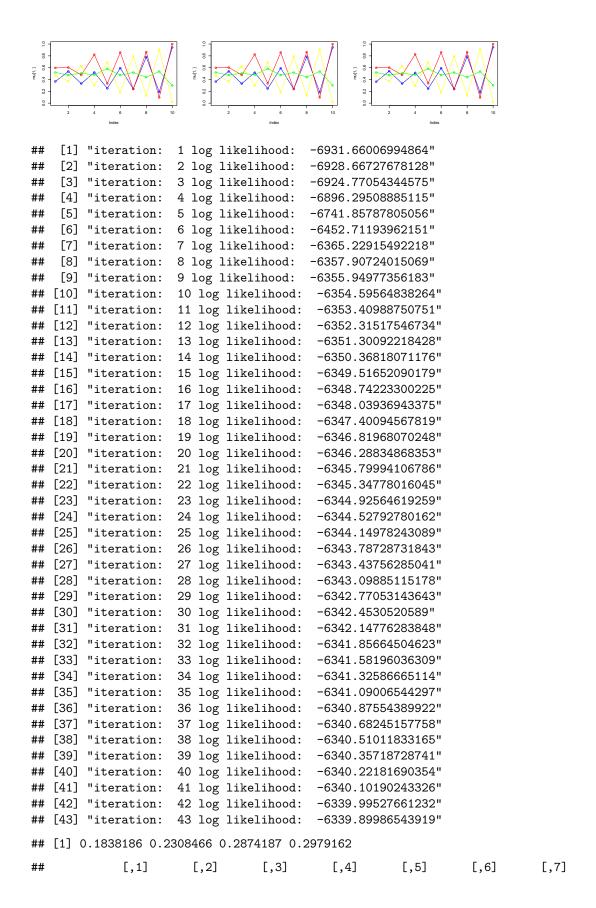
```
## [1] 0.2518811 0.2466783 0.2511809 0.2502598
```

```
[,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
```

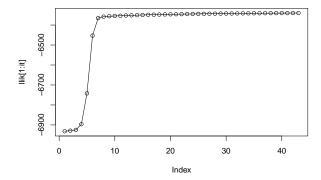
Then we change M to 4, again generate a π and μ under M = 4 as the start point for our model.







```
## [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
## [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</pre>
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)</pre>
  for(d in 1:D) {
    x[i,d] <- rbinom(1,1,true_mu[m,d])</pre>
  } }
set.seed(1234567890)
M <- 2 # number of clusters
w \leftarrow matrix(nrow=n, ncol=M) \# weights ; p(y = m | xi, thetaHat)
pi <- vector(length = M) # mixing coefficients</pre>
```

```
mu <- matrix(nrow=M, ncol=D) # conditional distributions</pre>
llik <- vector(length = max_it) # log likelihood of the EM iterations</pre>
# Random initialization of the parameters
pi \leftarrow runif(M, 0.49, 0.51)
pi <- pi / sum(pi)
for(m in 1:M) {
 mu[m,] <- runif(D,0.49,0.51)
}
рi
mu
set.seed(1234567890)
iterLog <- vector(length = max_it)</pre>
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 \leftarrow 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</pre>
      # print(paste(i,m,d,pxi))
    for (m in 1:M) {
      bernXMum <- 1
      for (d in 1:D) {
        bernXMum \leftarrow 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 \leftarrow bernXMum * (mu[m,d]^x[i,d]) * (1-mu[m,d])^(1-x[i,d])
      }
      pxi <- pxi + pi[m] * bernXMum</pre>
    llik[it] <- llik[it] + log(pxi)</pre>
  # Your code here
  iterLog[it] <- paste("iteration: ", it, "log likelihood: ", llik[it])</pre>
  flush.console()
  # Stop if the lok likelihood has not changed significantly
  stopFlag <- it > 1 && (llik[it] - llik[it - 1]) < min_change</pre>
  if(stopFlag) break
  #M-step: ML parameter estimation from the data and weights
  # pi mu
  pi <- apply(w, 2, mean)</pre>
  mu <- t(w) %*% x / colSums(w)</pre>
  # Your code here
}
print(iterLog[1:it])
рi
plot(llik[1:it], type="o")
set.seed(1234567890)
M <- 3 # number of clusters
w \leftarrow matrix(nrow=n, ncol=M) \# weights ; p(y = m | xi, thetaHat)
pi <- vector(length = M) # mixing coefficients</pre>
mu <- matrix(nrow=M, ncol=D) # conditional distributions</pre>
llik <- vector(length = max_it) # log likelihood of the EM iterations</pre>
# Random initialization of the parameters
pi \leftarrow runif(M, 0.49, 0.51)
pi <- pi / sum(pi)
for(m in 1:M) {
  mu[m,] \leftarrow runif(D,0.49,0.51)
рi
mu
iterLog <- vector(length = max_it)</pre>
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</pre>
      # print(paste(i,m,d,pxi))
    for (m in 1:M) {
      bernXMum <- 1
      for (d in 1:D) {
        bernXMum \leftarrow 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</pre>
  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</pre>
    llik[it] <- llik[it] + log(pxi)</pre>
  # Your code here
  iterLog[it] <- paste("iteration: ", it, "log likelihood: ", llik[it])</pre>
  flush.console()
  # Stop if the lok likelihood has not changed significantly
  stopFlag <- it > 1 && (llik[it] - llik[it - 1]) < min_change</pre>
  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)</pre>
  # Your code here
}
```

```
print(iterLog[1:it])
рi
plot(llik[1:it], type="o")
set.seed(1234567890)
M <- 4 # number of clusters
w \leftarrow matrix(nrow=n, ncol=M) \# weights ; p(y = m | xi, thetaHat)
pi <- vector(length = M) # mixing coefficients</pre>
mu <- matrix(nrow=M, ncol=D) # conditional distributions</pre>
llik <- vector(length = max_it) # log likelihood of the EM iterations</pre>
# Random initialization of the parameters
pi <- runif(M,0.49,0.51)</pre>
pi <- pi / sum(pi)
for(m in 1:M) {
  mu[m,] \leftarrow runif(D,0.49,0.51)
}
рi
mu
iterLog <- vector(length = max_it)</pre>
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</pre>
      # print(paste(i,m,d,pxi))
    for (m in 1:M) {
      bernXMum <- 1
      for (d in 1:D) {
        bernXMum \leftarrow 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</pre>
```

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