CS539 hw1

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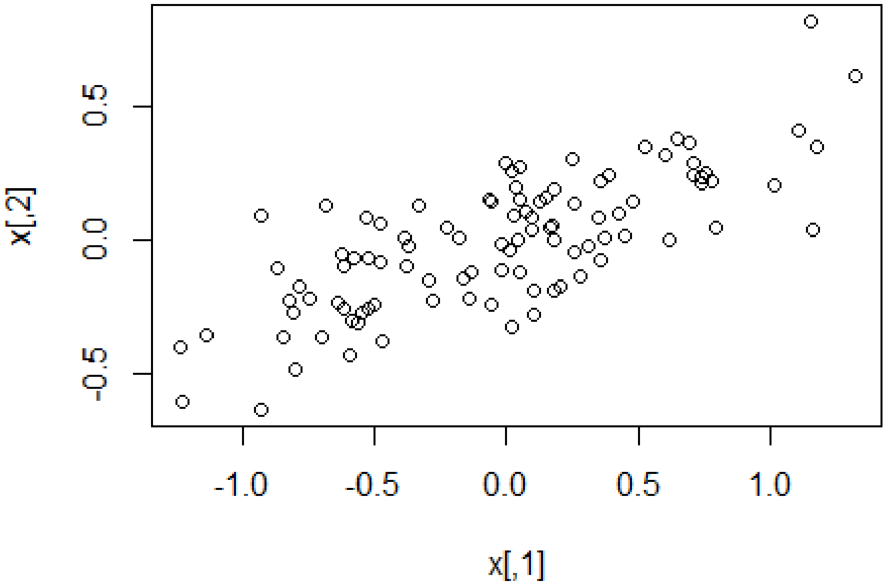
problem 1

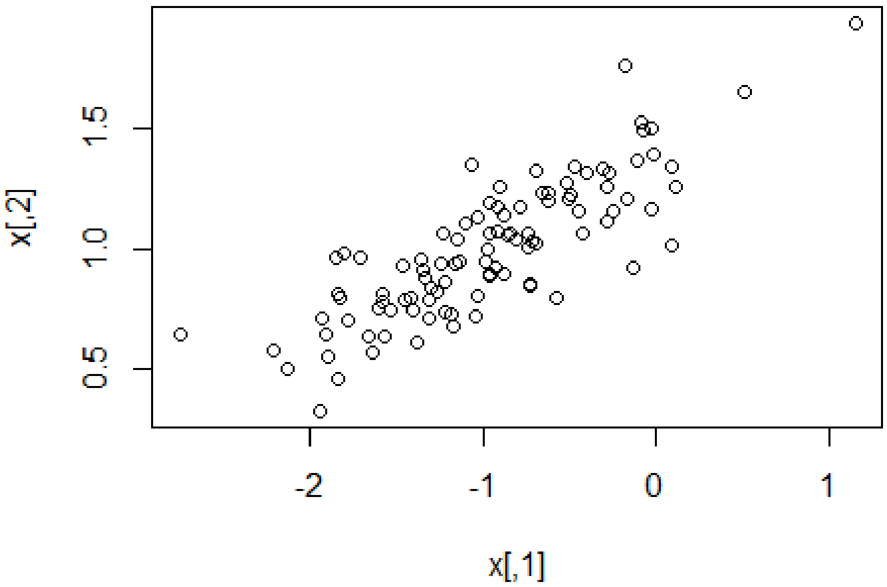
a)

```
X <- matrix(runif(2 * 2), 2, 2)
COV <- crossprod(X)
mu <- rep(0, 2)
library(MASS)
x <- mvrnorm(100, mu, COV)
plot(x)
```



b)

```
mu <- c(-1,1)
x <- mvrnorm(100, mu, COV)
plot(x)
```

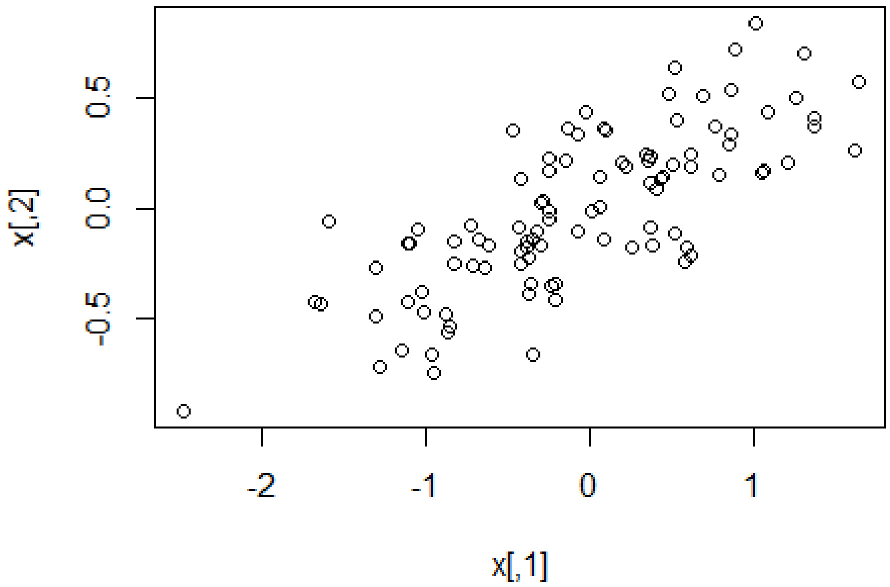


```
mu <- c(0,0)
```

The interval of x1 is moving left by about 1, and the interval of x2 is moving up by about 1.

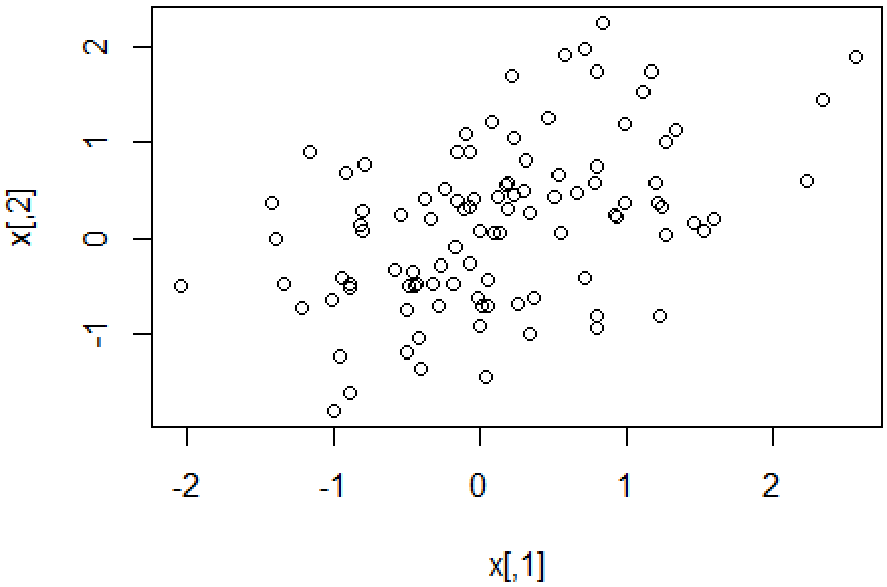
c)

```
COV <- 2*COV
x <- mvrnorm(100, mu, COV)
plot(x)
```



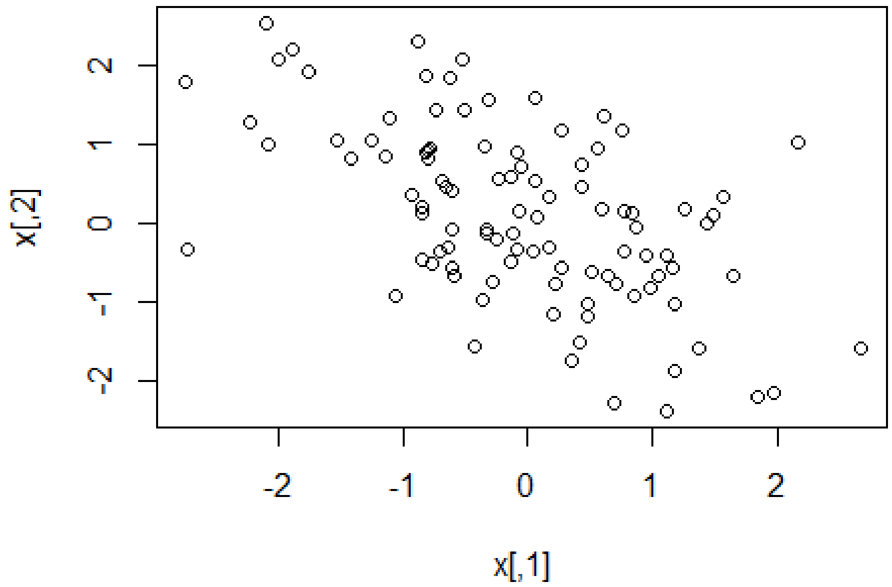
d)

```
COV <- matrix(c(1,0.5,0.5,1), nrow = 2, ncol = 2)
x <- mvrnorm(100, mu, COV)
plot(x)
```



e)

```
COV <- matrix(c(1,-0.5,-0.5,1), nrow = 2, ncol = 2)
x <- mvrnorm(100, mu, COV)
plot(x)
```

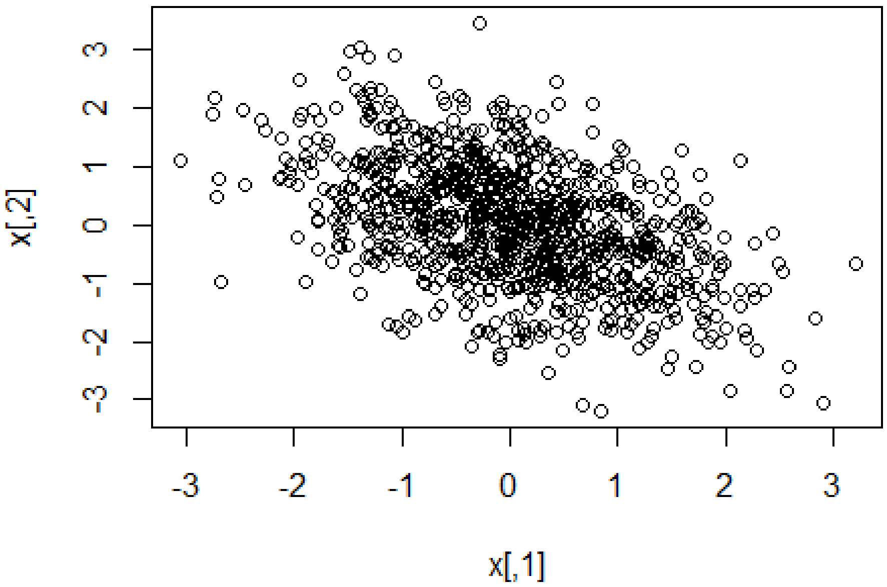


f)

```
X <- matrix(runif(2 * 2), 2, 2)
COV <- crossprod(X)
mu <- rep(0, 2)
x <- mvrnorm(100, mu, COV)
mean(x)

## [1] 0.003945048

cov(x)

##          [,1]     [,2]
## [1,] 1.910007 1.331396
## [2,] 1.331396 0.970151
```

g)

```
COV <- matrix(c(1,-0.5,-0.5,1), nrow = 2, ncol = 2)
x <- mvrnorm(1000, mu, COV)
plot(x)
```



h)

```
mean(x)

## [1] 0.01909849

cov(x)

##            [,1]      [,2]
## [1,]  0.9773492 -0.484074
## [2,] -0.4840740  1.036510
```

i)

```
x <- mvrnorm(10, mu, COV)
mean(x[,1])

## [1] 0.2690736

x <- mvrnorm(100, mu, COV)
mean(x[,1])

## [1] 0.01383696

x <- mvrnorm(1000, mu, COV)
mean(x[,1])

## [1] 0.01326269
```

Mean is tend to 0, as the more samples we have

j)

```
COV # the initial covariance we use to get the sample

##      [,1] [,2]
## [1,]  1.0 -0.5
## [2,] -0.5  1.0

x <- mvrnorm(10, mu, COV)
cov(x)

##           [,1]      [,2]
## [1,]  1.196858 -1.169756
## [2,] -1.169756  2.085406

x <- mvrnorm(100, mu, COV)
cov(x)

##           [,1]       [,2]
## [1,]  1.008264 -0.5121600
## [2,] -0.512160  0.9278948

x <- mvrnorm(1000, mu, COV)
cov(x)

##            [,1]       [,2]
## [1,]  0.9841772 -0.4980792
## [2,] -0.4980792  0.9746574
```

covariance is getting closer to the initial covariance, When we have more sample

problem 2

a)

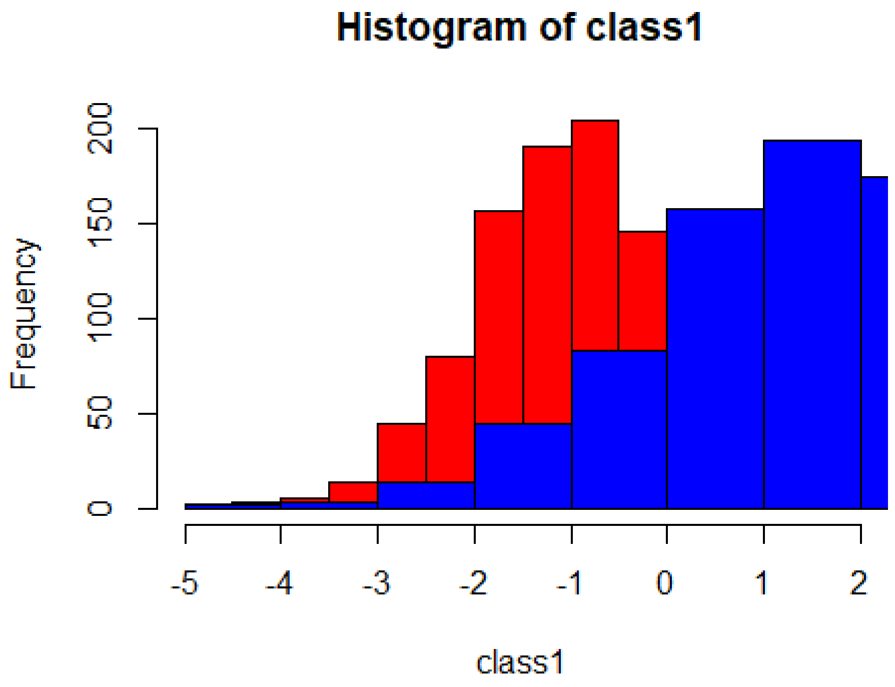
```
class1 <- rnorm(1000,-1,1)
```

b)

```
class2 <- rnorm(1000,2,2)
```

c)

```
hist(class1, col='red')
hist(class2, col='blue', add=TRUE)
```



d)

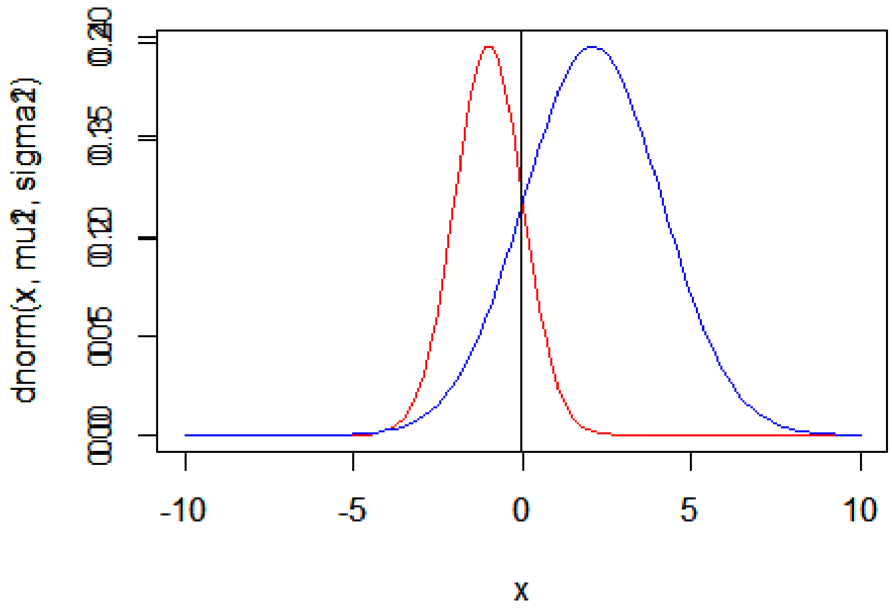
```
library(stats4)
library(methods)
options(warn = -1)
LL1 <- function(mu,sigma){
  -sum(log(dnorm(class1,mu,sigma)))
}
m1<-mle(LL1,start = list(mu=0,sigma=1))
m1

##
## Call:
## mle(minuslogl = LL1, start = list(mu = 0, sigma = 1))
##
## Coefficients:
##         mu       sigma
## -0.9980152  1.0034457

LL2 <- function(mu,sigma){
  R = dnorm(class2,mu,sigma)
  -sum(log(R))
}
m2<-mle(LL2,start = list(mu=0,sigma=1))
m2

##
## Call:
```

```
## mle(minuslogl = LL2, start = list(mu = 0, sigma = 1))
##
## Coefficients:
##       mu    sigma
## 2.082832 2.043154
```

```
options(warn = getOption("warn"))
```

e)

```
mu1 <- m1@coef[1]
sigma1<- m1@coef[2]
mu2<-m2@coef[1]
sigma2<-m2@coef[2]

x <- seq(-10, 10, length=100)
plot(x,dnorm(x,mu1,sigma1), type = "l",col = "red")
par(new=TRUE)
plot(x,dnorm(x,mu2,sigma2), type = "l",col="blue")
i = -2
while(round(dnorm(i,mu1,sigma1),5)!=round(dnorm(i,mu2,sigma2),5)){
  i=i+0.00001
}
par(new=TRUE)
abline(v=-0.014)
```

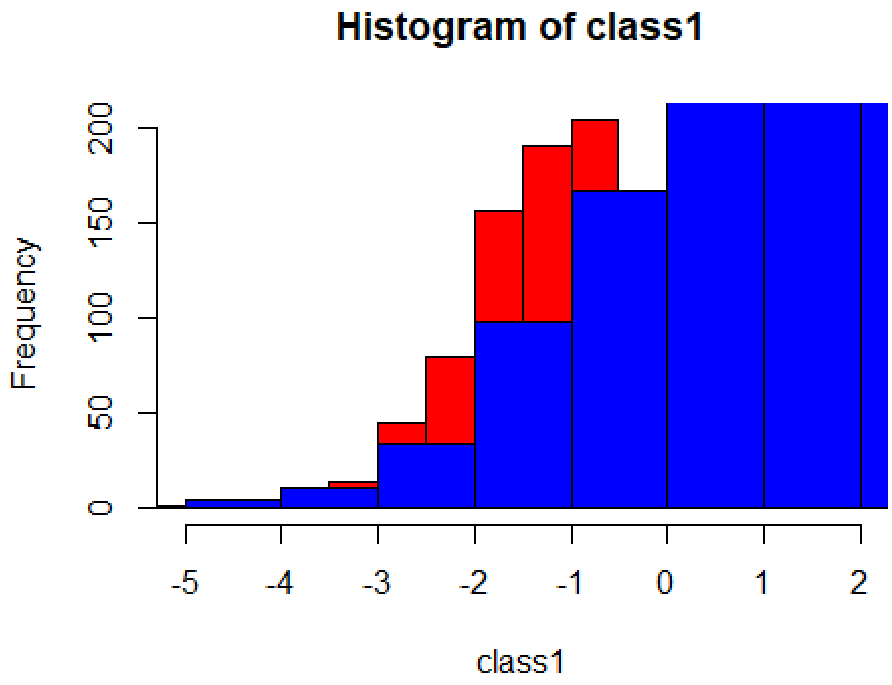


f)

both of the decision boundary of pdf and histogram are about 0

g)

```
class2 <- rnorm(2000,2,2)
#c
hist(class1, col='red')
hist(class2, col='blue', add=TRUE)
```

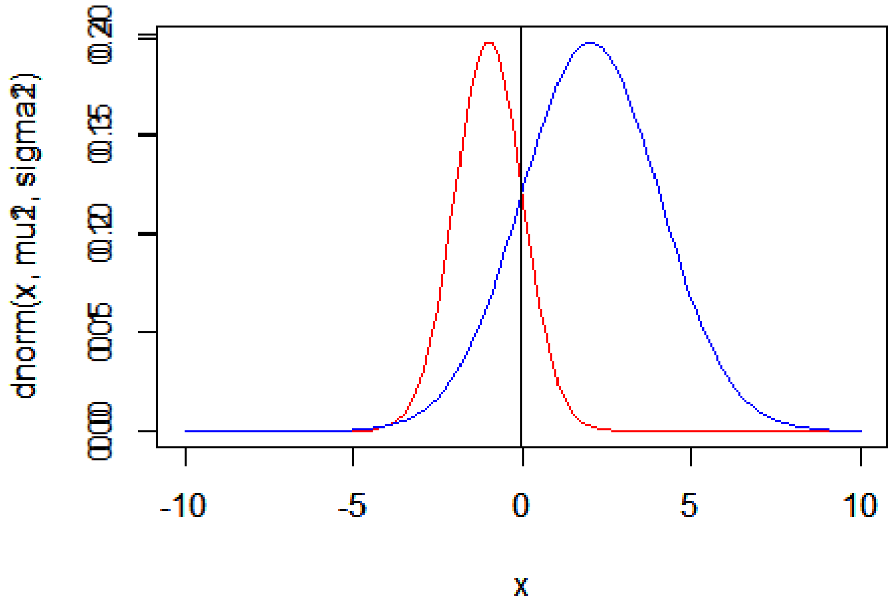


```
#d
options(warn = -1)
LL1 <- function(mu,sigma){
  -sum(log(dnorm(class1,mu,sigma)))
}
m1<-mle(LL1,start = list(mu=0,sigma=1))
m1

##
## Call:
## mle(minuslogl = LL1, start = list(mu = 0, sigma = 1))
##
## Coefficients:
##         mu      sigma
## -0.9980152  1.0034457
```

```r
LL2 <- function(mu,sigma){
  R = dnorm(class2,mu,sigma)
  -sum(log(R))
}
m2<-mle(LL2,start = list(mu=0,sigma=1))
m2
```

```
##
## Call:
## mle(minuslogl = LL2, start = list(mu = 0, sigma = 1))
##
## Coefficients:
##       mu    sigma
## 2.014727 2.036637
```

```r
options(warn = getOption("warn"))
#e
mu1 <- m1@coef[1]
sigma1<- m1@coef[2]
mu2<-m2@coef[1]
sigma2<-m2@coef[2]

x <- seq(-10, 10, length=100)
plot(x,dnorm(x,mu1,sigma1), type = "l",col = "red")
par(new=TRUE)
plot(x,dnorm(x,mu2,sigma2), type = "l",col="blue")
i = -2
while(round(dnorm(i,mu1,sigma1),5)!=round(dnorm(i,mu2,sigma2),5)){
  i=i+0.0001
}
par(new=TRUE)
abline(v=-0.016)
```



```
#f
```

Since there are more samples in class2, the decision boundary of histogram comes to -1, but the decision boundary of pdf does not change.

h)

```
library(MASS)
fitdistr(class1, densfun="normal")

##       mean           sd
##   -0.99793273    1.00348621
##  ( 0.03173302) ( 0.02243863)

class2 <- rnorm(1000,2,2)
fitdistr(class2, densfun="normal")

##       mean          sd
##   1.97822236   1.94124094
##  (0.06138743) (0.04340747)
```

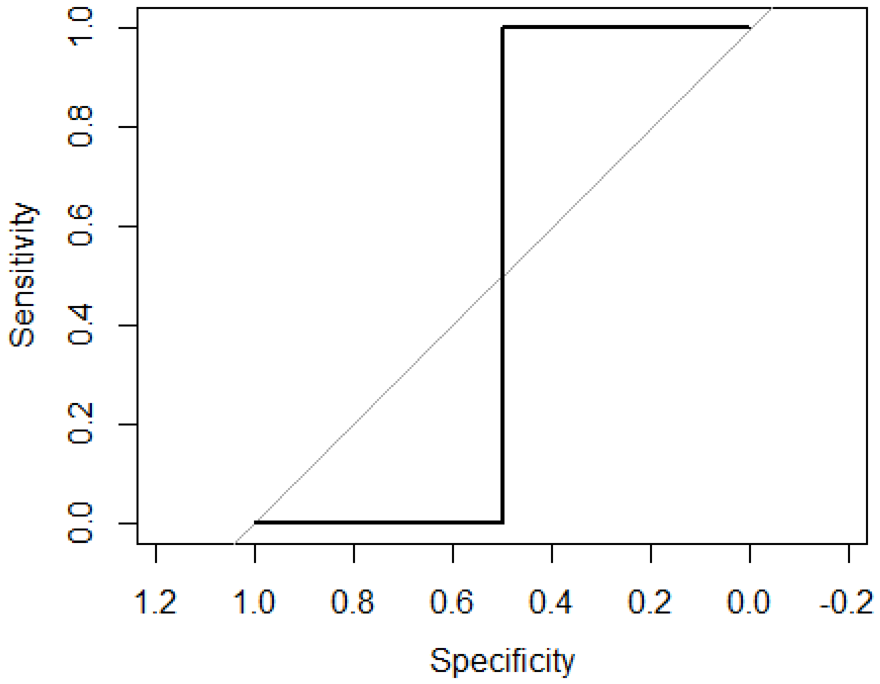
the error rate are on the second line.

```
library(MASS)
fitdistr(class1, densfun="normal")

##       mean           sd
##   -0.99793273    1.00348621
##  ( 0.03173302) ( 0.02243863)
```

```
class2 <- rnorm(2000,2,2)
fitdistr(class2, densfun="normal")

##       mean          sd
##   1.95616385   2.03949020
##  (0.04560439) (0.03224717)
```

i)

```
options(warn = -1)
df <- data.frame(class1,class2)
library(pROC)

## Type 'citation("pROC")' for a citation.

##
## 载入程辑包：'pROC'

## The following objects are masked from 'package:stats':
##
##     cov, smooth, var

roc(df$class1,df$class2,plot=TRUE)

## Setting levels: control = -4.6552738797062, case = -4.31843317823687

## Setting direction: controls < cases
```



```
##
## Call:
## roc.default(response = df$class1, predictor = df$class2, plot = TRUE)
##
## Data: df$class2 in 2 controls (df$class1 -4.6552738797062) < 2 cases
 (df$class1 -4.31843317823687).
## Area under the curve: 0.5

options(warn = getOption("warn"))
```

problem 3

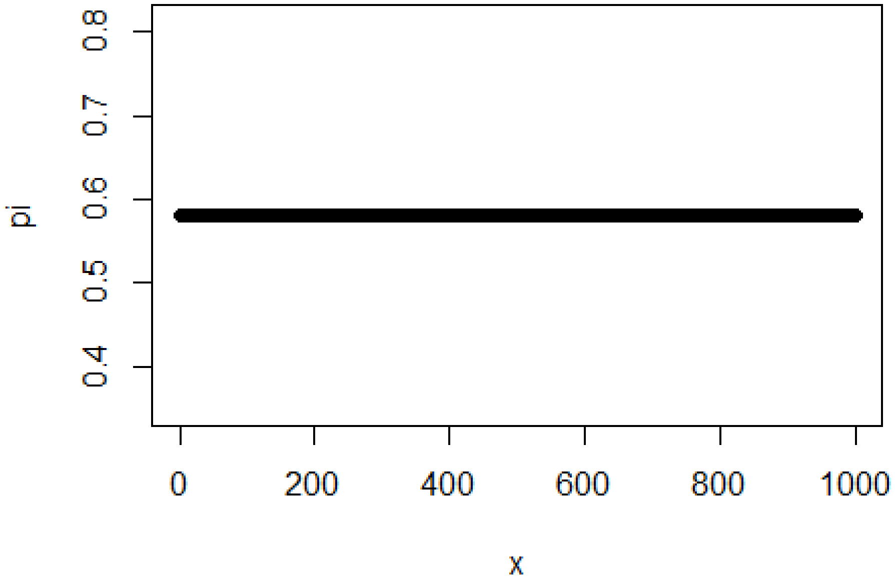
a)

```
library("Rlab")

## Rlab 2.15.1 attached.

##
## 载入程辑包：'Rlab'

## The following object is masked from 'package:MASS':
##
##     michelson

## The following objects are masked from 'package:stats':
##
##     dexp, dgamma, dweibull, pexp, pgamma, pweibull, qexp, qgamma,
##     qweibull, rexp, rgamma, rweibull

## The following object is masked from 'package:datasets':
##
##     precip

coin <- rbern(1000, 0.6)
```

##b)

```
options(warn = -1)
LL1 <- function(p){
  -sum(log(dbern(coin,p)))
}
m1<-mle(LL1,start = list(p=0.01))
m1@coef

##         p
## 0.5809974

LL <- function(n,p){
  -sum(log(dbern(rbern(n, 0.6),p)))
}
```

```
for(n in 1:1000){
  ll <- function(p){
    LL(n,p)
  }
  m1<-mle(LL1,start = list(p=0.01))
  pi[n]<-m1@coef
}

x<-seq(0, 1000, length=1000)
plot(x,pi)
```

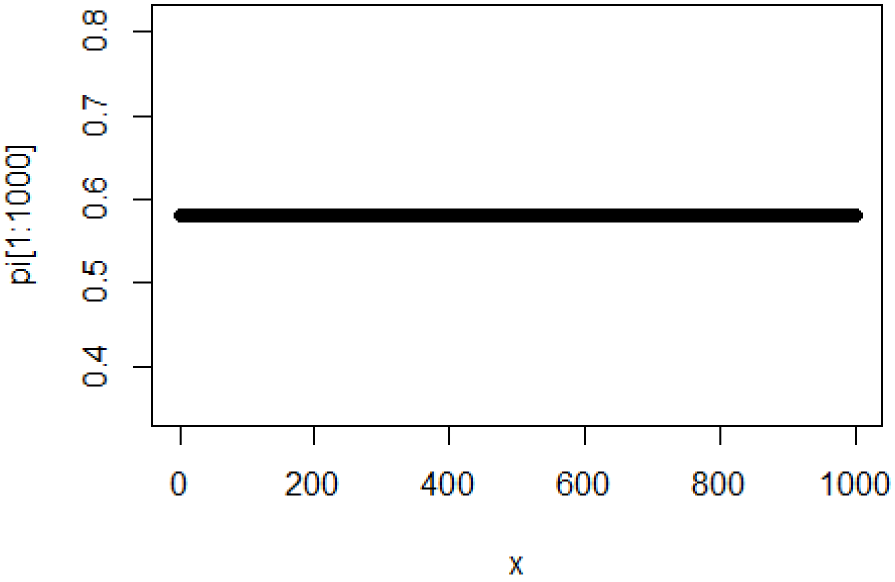


```
options(warn = getOption("warn"))
```

c)

```
coin2 <- rbern(1000, 0.6)
LL2 <- function(p){
  -sum(log(dbern(coin2,p)))
}
m2<-mle(LL2,start = list(p=0.01))
m2@coef

##         p
## 0.5999919

LL <- function(n,p){
  -sum(log(dbern(rbern(n, 0.6),p)))
}
```

```
for(n in 1:100){
  ll <- function(p){
    LL(n,p)
  }
  m1<-mle(LL1,start = list(p=0.01))
  pi[n]<-m1@coef
}
x<-seq(0, 1000, length=1000)
plot(x,pi[1:1000])
```

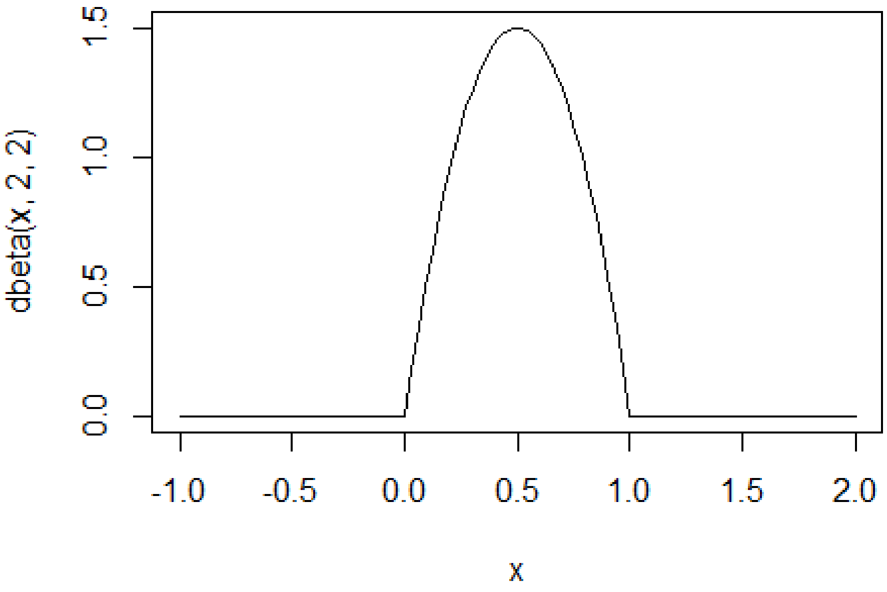


```
options(warn = getOption("warn"))
```

both P_{ML} from b) and c) are approximate and get close to 0.6,

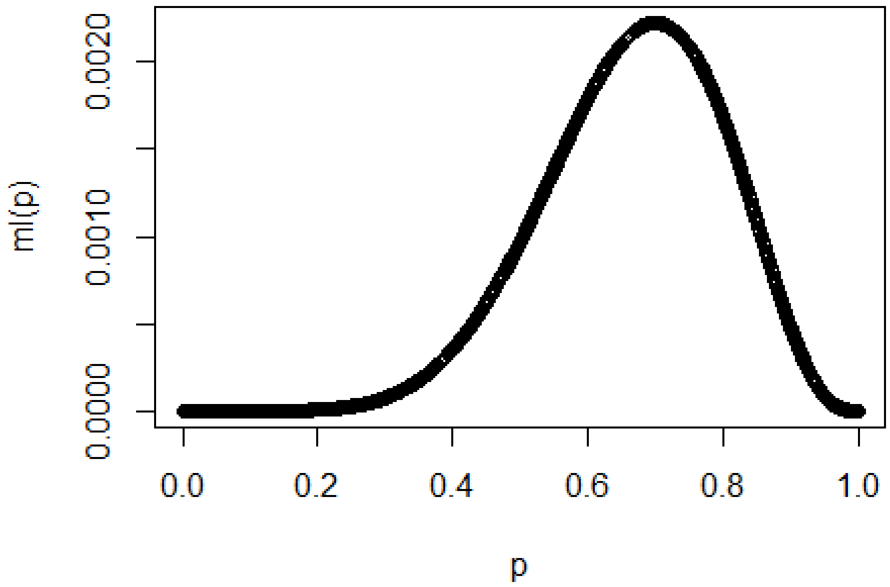
d)

```
x <- seq(-1, 2, length=100)
plot(x,dbeta(x, 2, 2), type = "l")
```



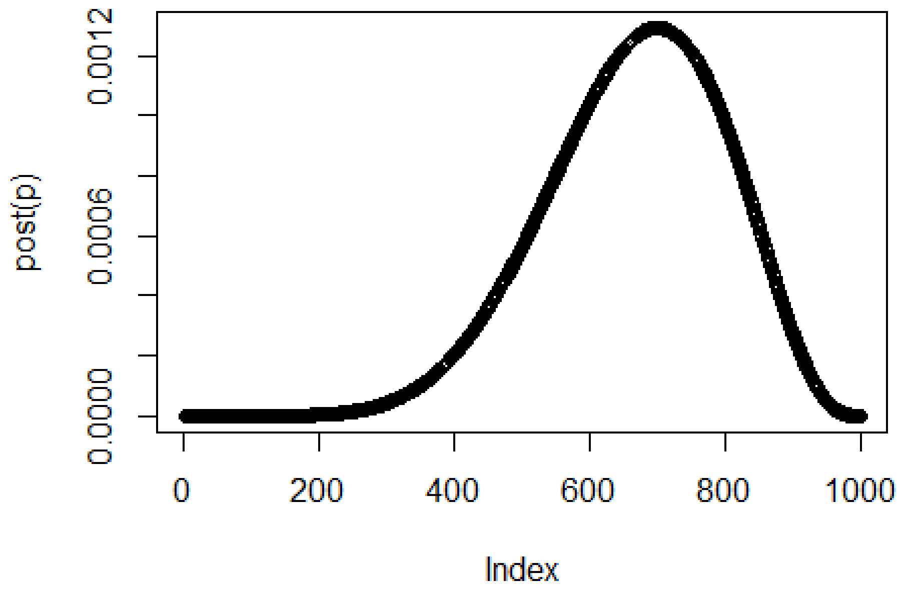
e)

```
p <- seq(0, 1, length=1000)
ml <- function(p){
  mult = 1
  for(i in 1:10){
    mult <- mult*p^coin[i]*(1-p)^(1-coin[i])
  }
  mult
}
plot(p,ml(p))
```



f)

```
post <- function(p){
  ml(p)*pi
}
plot(post(p))
```



Since the posterior is proportion to prior and likelihood, the curve is not change too much.

g)

```
max(post(p))

## [1] 0.001291883
```

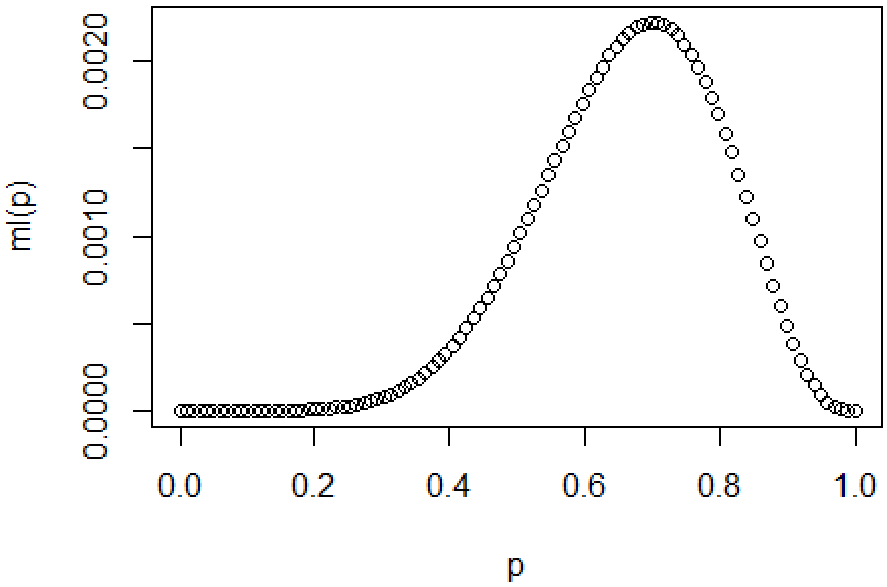
MAP is 6.915e-04

h)

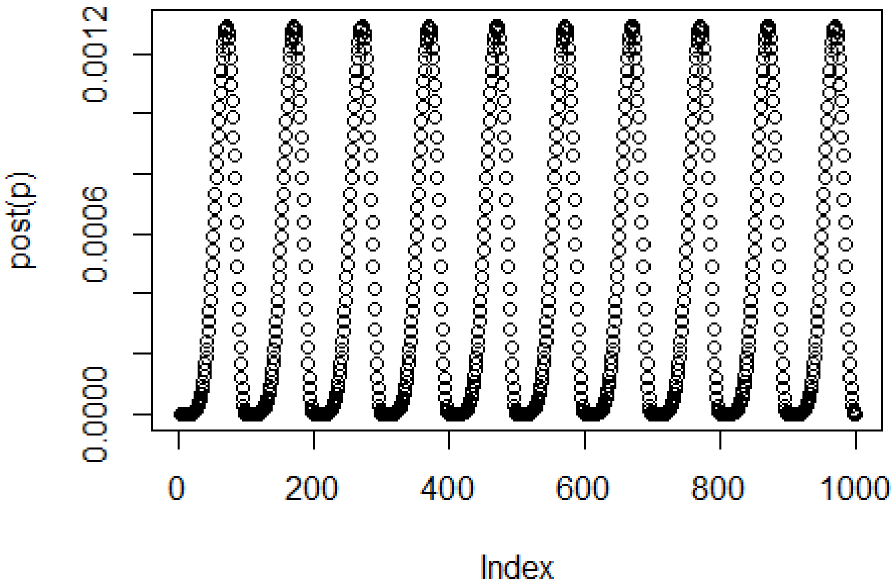
```
var(post(p))

## [1] 2.211729e-07
```

i)

```
p <- seq(0, 1, length=100)
ml <- function(p){
  mult = 1
  for(i in 1:10){
    mult <- mult*p^coin[i]*(1-p)^(1-coin[i])
  }
  mult
}
plot(p,ml(p))
```



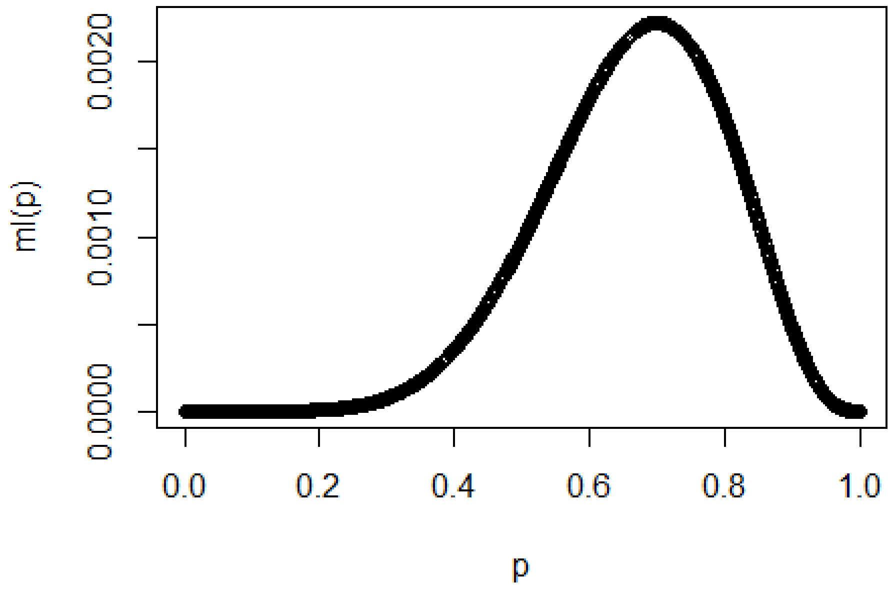
```
post <- function(p){
  ml(p)*pi
}
plot(post(p))
```



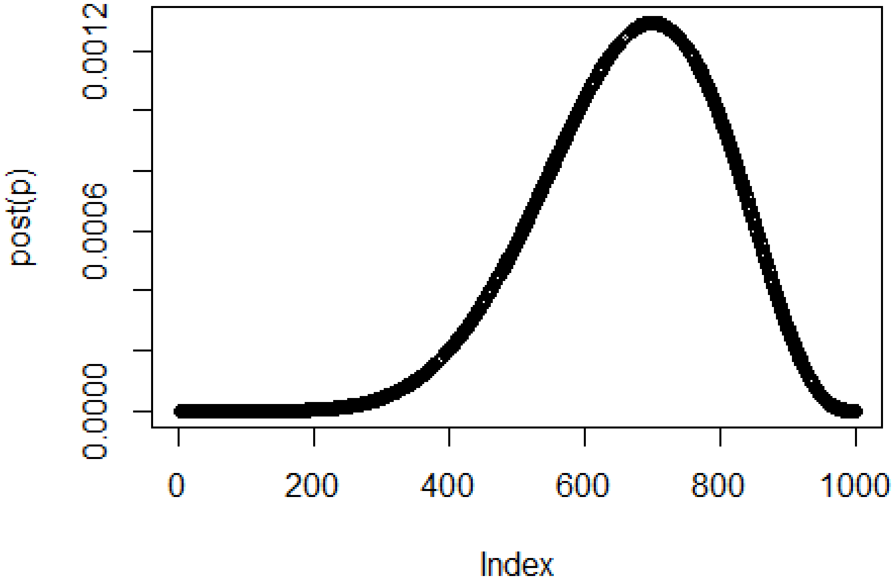
```
max(post(p))

## [1] 0.001291605

var(post(p))

## [1] 2.209082e-07
```

j)

```
p <- seq(0, 1, length=1000)
ml <- function(p){
  mult = 1
  for(i in 1:10){
    mult <- mult*p^coin[i]*(1-p)^(1-coin[i])
  }
  mult
}
plot(p,ml(p))
```



```
post <- function(p){
  ml(p)*pi
}
plot(post(p))
```



```
max(post(p))

## [1] 0.001291883

var(post(p))

## [1] 2.211729e-07
```

problem 4

a)

```
library(MASS)
pi1 <- 0.1
mu1 <- c(3, 2)
COV1 <- matrix(c(1,0,0,1), nrow = 2, ncol = 2)

pi2 <- 0.6
mu2 <- c(-5, -3)
COV2 <- matrix(c(2,-1,-1,3), nrow = 2, ncol = 2)

pi3<-0.3
COV3 <- matrix(c(6,3,3,3), nrow = 2, ncol = 2)
mu3 <- c(4, 2)
```

```
p <- pi1*mvrnorm(1000, mu1, COV1)+pi2*mvrnorm(1000, mu2, COV2)+pi3*mvrn
orm(1000, mu3, COV3)
```

b)

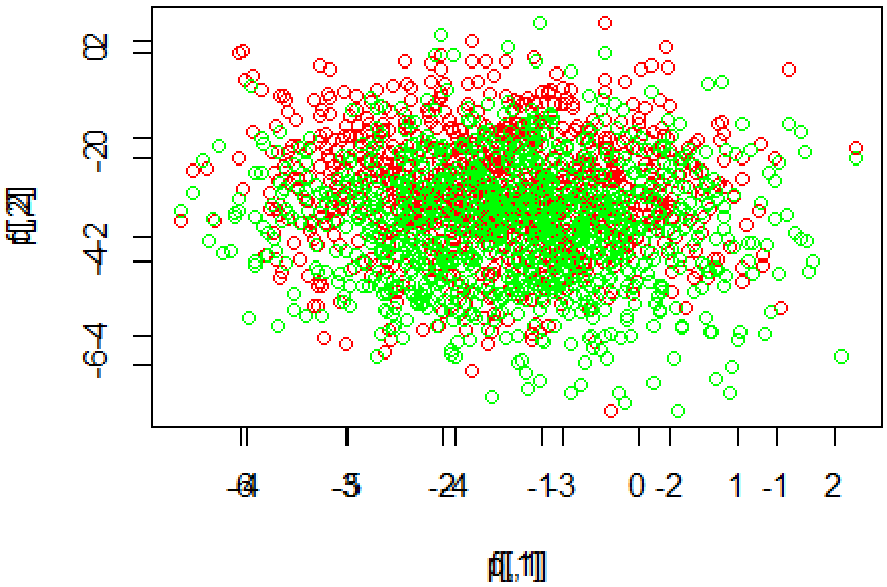
```
mean(p[1])

## [1] -3.523997

mean(p[2])

## [1] -3.288717

cov(p)

##             [,1]      [,2]
## [1,]  1.298926 -0.109365
## [2,] -0.109365  1.385695
```

c)

```
mu <- c(mean(p[1]),mean(p[2]))
COV <- cov(p)
f <- mvrnorm(1000, mu, COV)
```

d)

```
plot(p,col="red")
par(new=TRUE)
plot(f,col="green")
```



the mixture model have the same concentration area with multivariate normal distribution. The difference is that the mixture model have a more range.

e)

```
K3<-kmeans(p, centers = 3, nstart = 25)
str(K3)

## List of 9
##  $ cluster     : int [1:1000] 2 2 2 1 2 2 1 3 2 1 ...
##  $ centers     : num [1:3, 1:2] -2.239 -1.715 -0.166 -0.147 -2.185
 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:3] "1" "2" "3"
##   .. ..$ : NULL
##  $ totss       : num 2682
##  $ withinss    : num [1:3] 466 422 324
##  $ tot.withinss: num 1212
##  $ betweenss   : num 1470
##  $ size        : int [1:3] 368 348 284
##  $ iter        : int 3
##  $ ifault      : int 0
##  - attr(*, "class")= chr "kmeans"
```