Homework 5

Bin Dong

bindong2@illinois.edu

Question 1

```
rm(list=ls())
```

Implement K-means

```
library(ElemStatLearn)

nrow(zip.train)
```

```
## [1] 7291
```

```
ncol(zip.train)
```

```
## [1] 257
```

```
data <- zip.train
#data


customKmeans<-function(dataset=NA,k=NA, seed){
  if(is.na(dataset) || is.na(k)){
    stop("You must input valid parameters!!")
  }

  Eudist<-function(x,y){
    distance<-sqrt(sum((x-y)^2))
    return (distance)
  }

  set.seed(seed)

  rows.dataset<-nrow(dataset)
  continue.change=TRUE
  initPoint<-dataset[sample.int(rows.dataset,size = k),]
  formerPoint<-initPoint
  iterPoint<-matrix(0,nrow = k,ncol = ncol(dataset))


  error.matrix<-matrix(0,nrow=rows.dataset,ncol=k)
  while(continue.change){

    cluster.matrix<-matrix(0,nrow=rows.dataset,ncol=k)
```

```
    for(i in 1:rows.dataset){
      for(j in 1:k){
        error.matrix[i,j]<-Eudist(dataset[i,2:257],formerPoint[j,2:257])
      }
    }

    for(i in 1:rows.dataset){
      cluster.matrix[i,which.min(error.matrix[i,])]<-1
    }

    for(i in 1:k){
      iterPoint[i,]<-apply(dataset[which(cluster.matrix[,i] == 1),],2,"mean")
    }
    all.true<-c()

    for(i in 1:k){
      if(all(formerPoint[i,] == iterPoint[i,]) == T){
        all.true[i]<-TRUE
      }
    }
    formerPoint = iterPoint
    continue.change=ifelse(all(all.true) == T,F,T)
  }
  colnames(iterPoint)<-colnames(dataset)
  out=list()
  out[["centers"]]<-iterPoint
  out[["distance"]]<-error.matrix
  out[["cluster"]]<-rep(1,rows.dataset)
  for(i in 1:rows.dataset){
    out[["cluster"]][i]<-which(cluster.matrix[i,] == 1)
  }
  return <-out
}
```

One random initialization

```
out <- customKmeans(data, 5, 1)
result <- data.frame("data"=data, "cluster"=out$cluster)
cluster.count <- matrix(rep(0, 50), nrow=5, ncol=10)
for(i in 1:5)
{
  clusters <- subset(result, cluster==i);

  for(j in 0:9)
  {
    cluster.count[i, j+1] <- nrow(subset(clusters, data.1==j))
  }
}

print(cluster.count)
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
```

```
## [1,]  592    0  128  289   17  270  299    1   43    5
## [2,]  378    0   28    3    4   15   25    2    1    2
## [3,]   63 1005  456  103  206  140  319  230  190  154
## [4,]  133    0   41  137   38   47   20   48   21   20
## [5,]   28    0   78  126  387   84    1  364  287  463
```

In cluster 1, the most prevalent digits are: 0,3,6 In cluster 2, the most prevalent digits are: 0 In cluster 3, the most prevalent digits are: 1,2,6 In cluster 4, the most prevalent digits are: 0,3 In cluster 5, the most prevalent digits are: 9,4,7

Ten random initialization

```
for(seed in 1:10)
{
  out<-customKmeans(data, 5, seed);

  whole.data <- data.frame("distance"=out$distance, "cluster_result"=out$cluster, "data"=data)
  error <- 0;
  for(cluster in 1:5)
  {
    cluster.data <- subset(whole.data, cluster_result==cluster);
    error <- error+sum(cluster.data[,cluster]);
    pca <- prcomp(cluster.data[, (8:ncol(cluster.data))])

    summary(pca)

    #plot(x=dim[,1], y = dim[,2], col=cluster)

  }
  print(error)
}
```

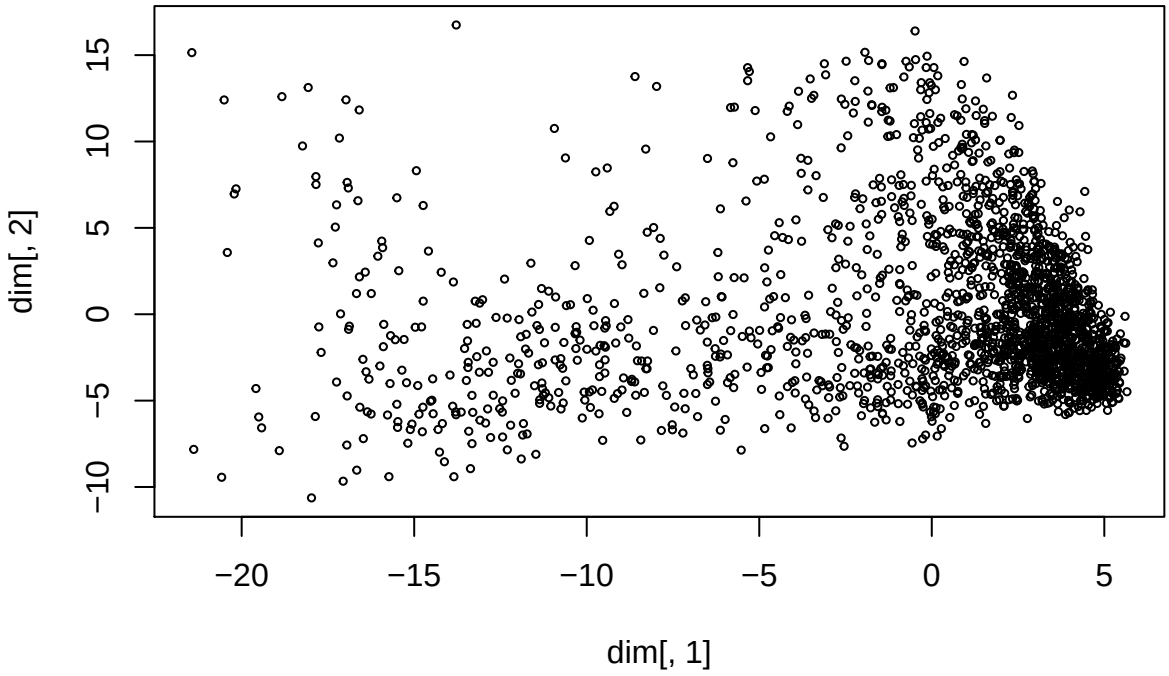
```
## [1] 85055.55
## [1] 88201.81
## [1] 105748.4
## [1] 85931.7
## [1] 91439.58
## [1] 86676.72
## [1] 81460.47
## [1] 90355.09
## [1] 102987.3
## [1] 87571.46
```

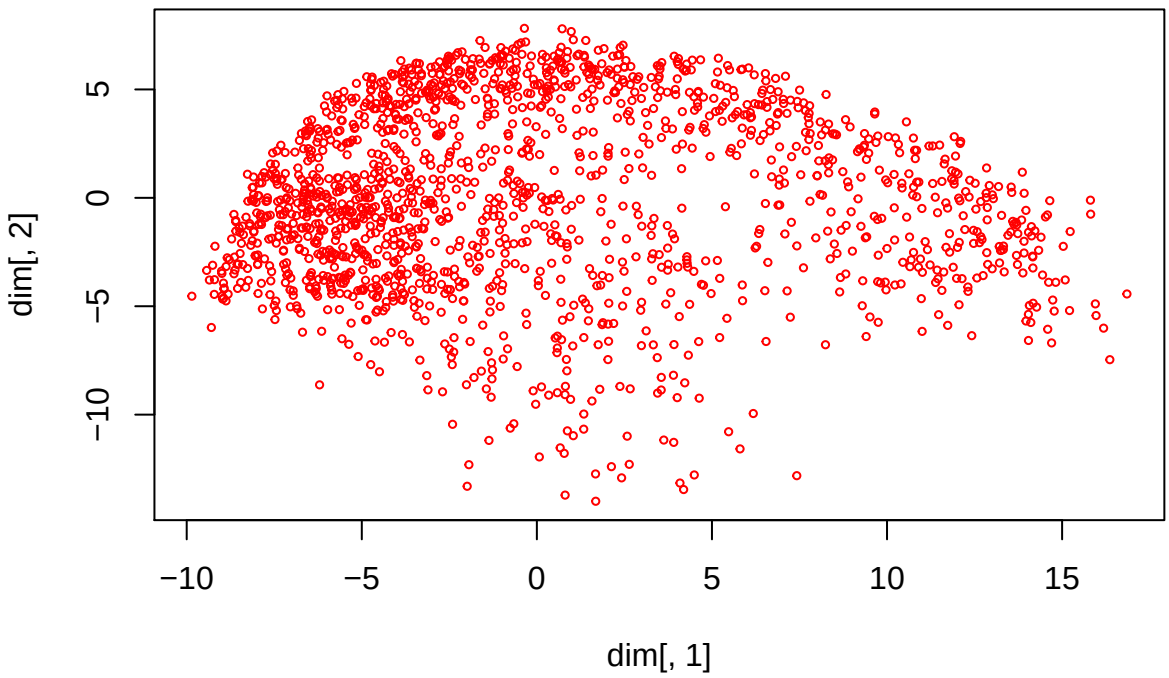
Best error occurs when seed is 7. Repeat to get plots:

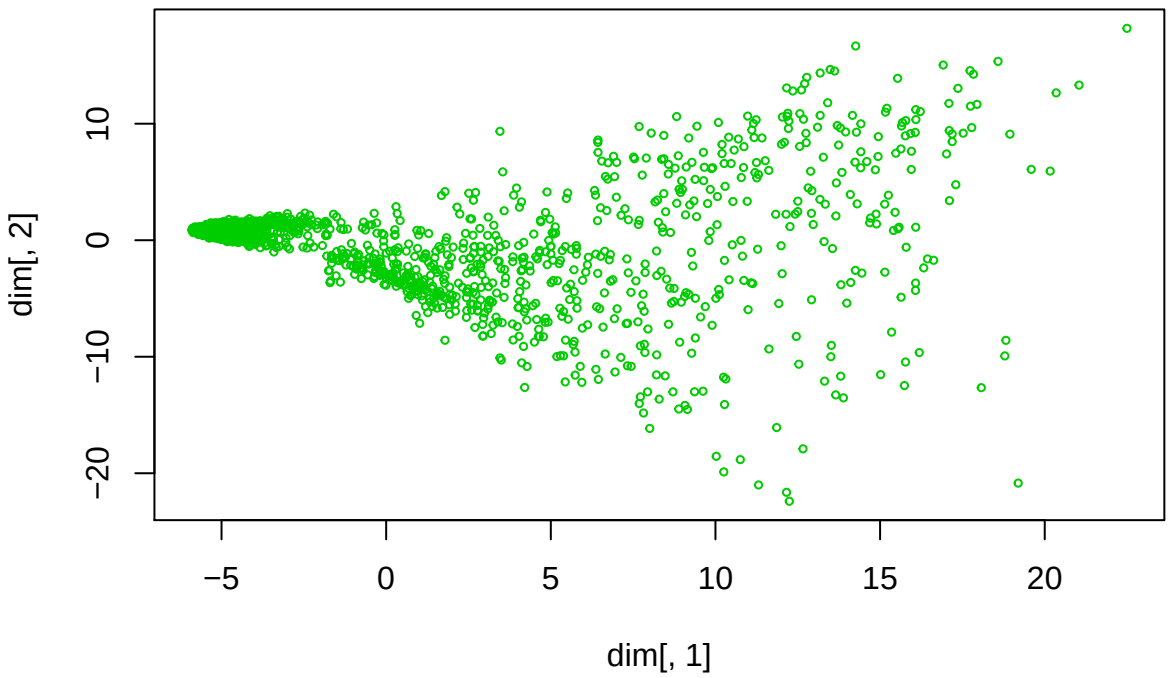
Plots

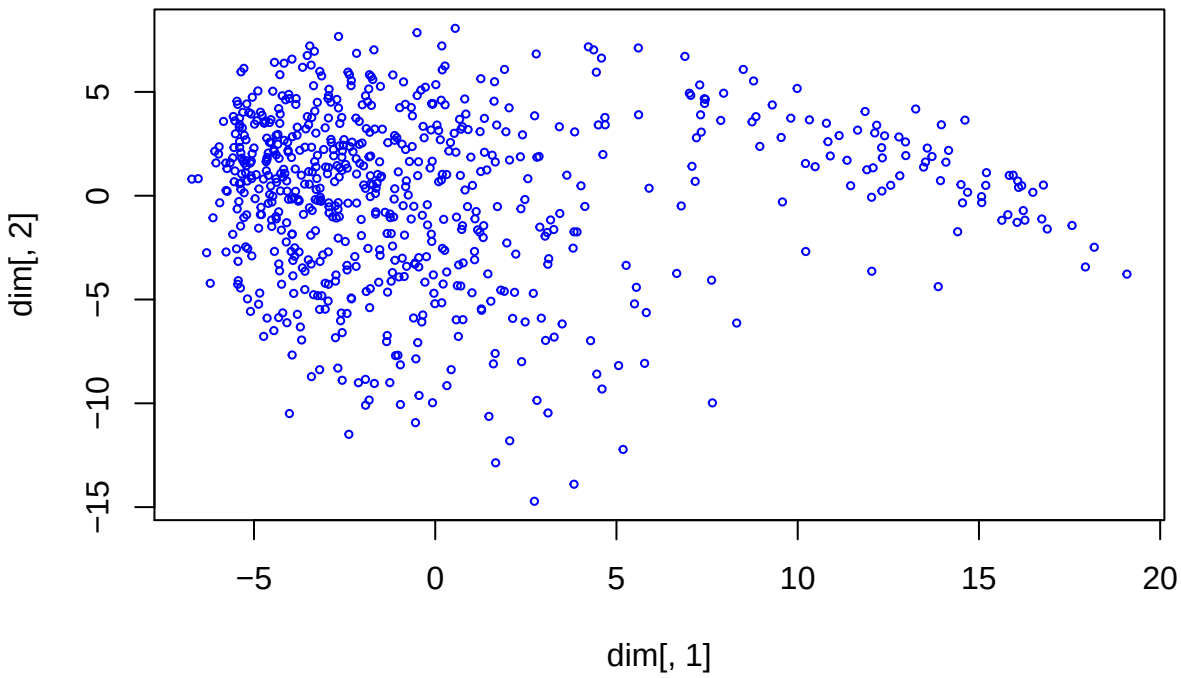
```
out<-customKmeans(data, 5, 7);
```

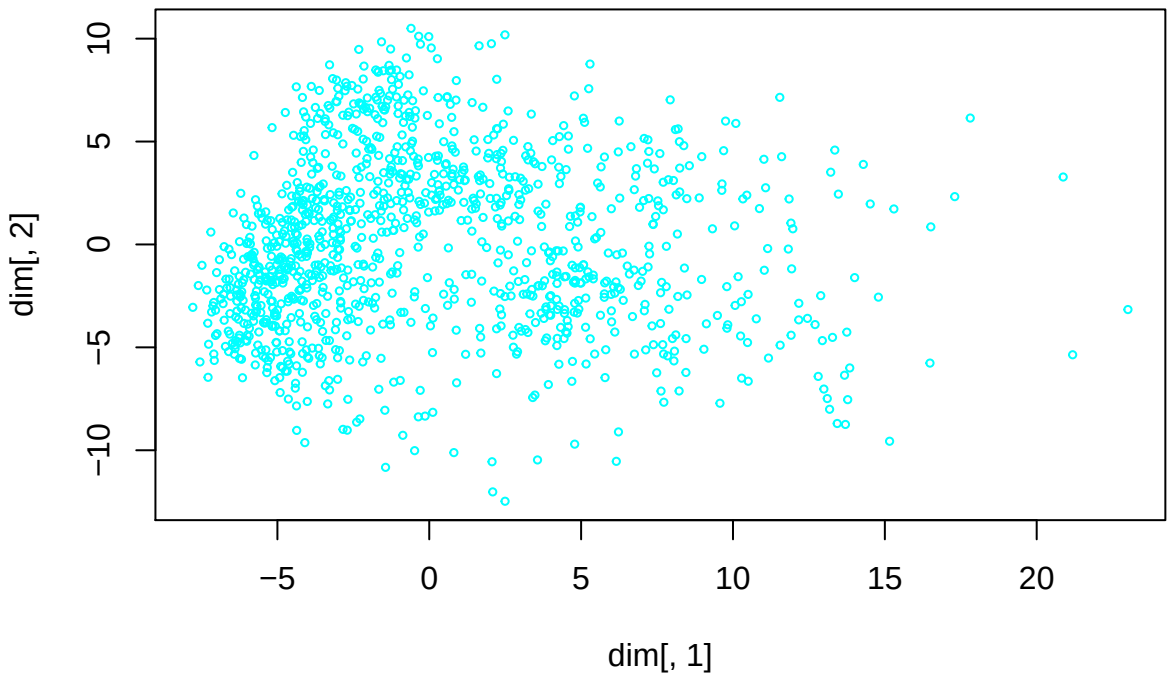
```
whole.data <- data.frame("distance"=out$distance, "cluster_result"=out$cluster, "data"=data)

for(cluster in 1:5)
{
  cluster.data <- subset(whole.data, cluster_result==cluster);

  pca <- prcomp(cluster.data[, (9:ncol(cluster.data))], scale. = T)

  dim <- pca$x

  plot(x=dim[,1], y = dim[,2], col=cluster, cex=0.5)

}
```




dim[, 2]
5
0
−5
−10
−10
−5
0
5
10
15
dim[, 1]


dim[, 2]
10
0
−10
−20
−5
0
5
10
15
20
dim[, 1]


dim[, 2]
5
0
−5
−10
−15
−5
0
5
10
15
20
dim[, 1]



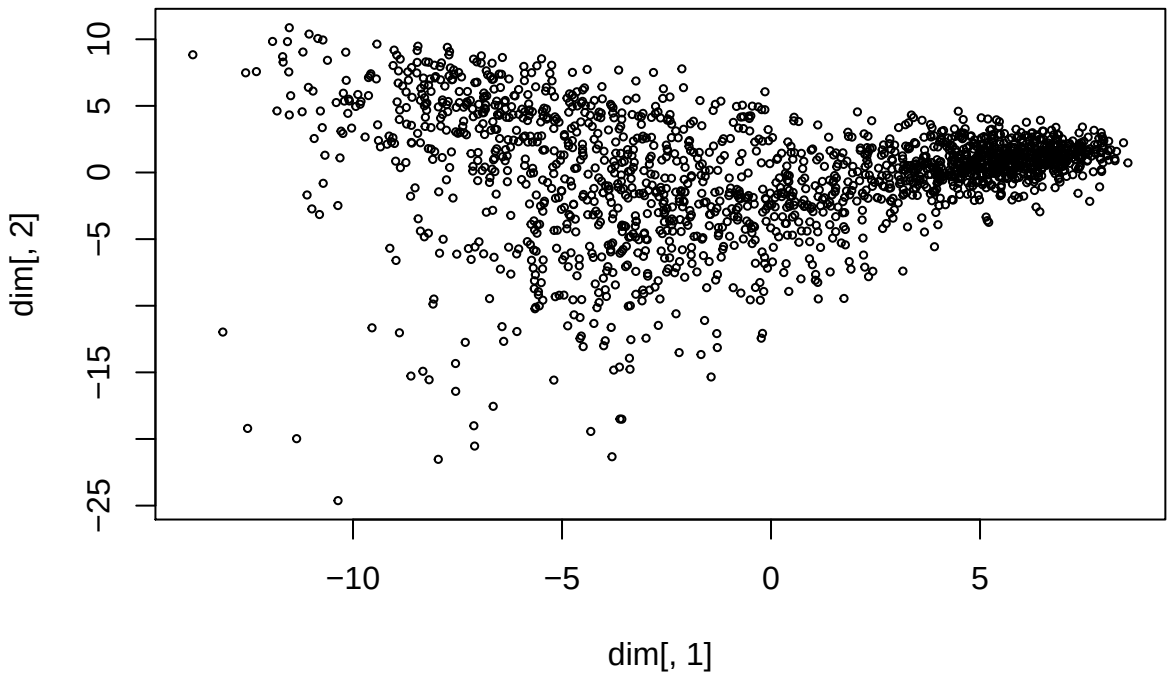
Compare with built-in k-means

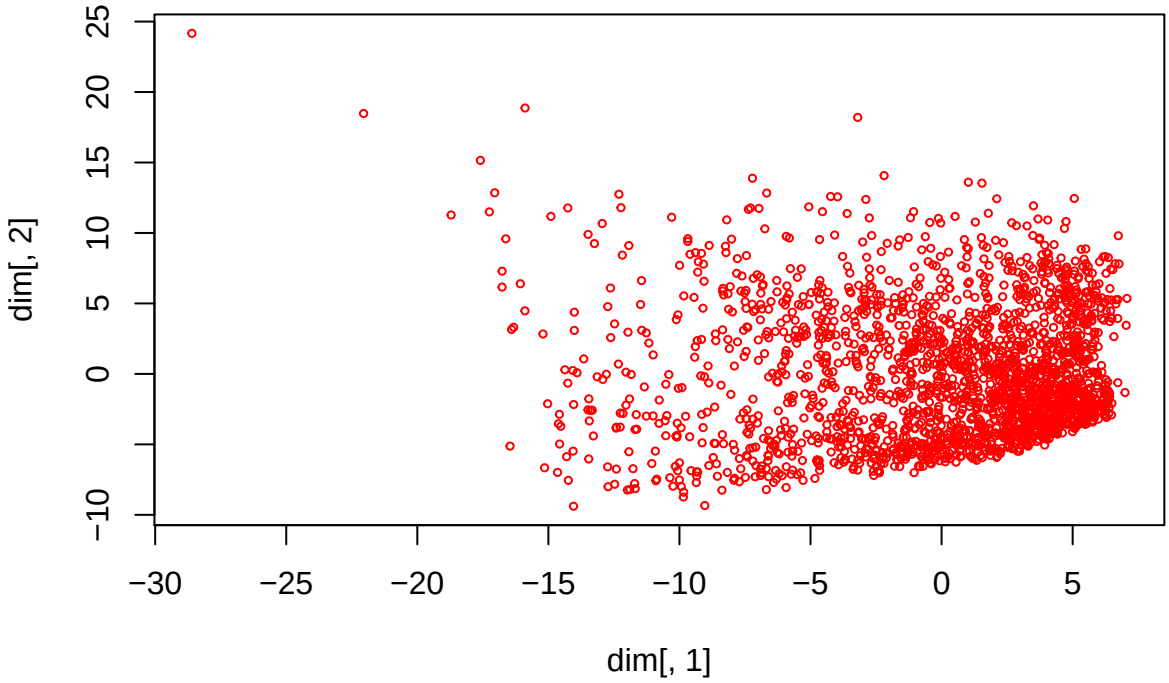
```
set.seed(1)

cl <- kmeans(data[, (1:ncol(data))], centers=5)

whole.data <- data.frame("cluster"=cl$cluster, "data"=data )


counts <- matrix(rep(0, 50), nrow=5, ncol=10)

for(i in 1:5)
{
  for(j in 0:9)
  {
    counts[i,j+1] = nrow(subset(subset(whole.data, cluster==i), data.1==j))

  }
}

counts
```

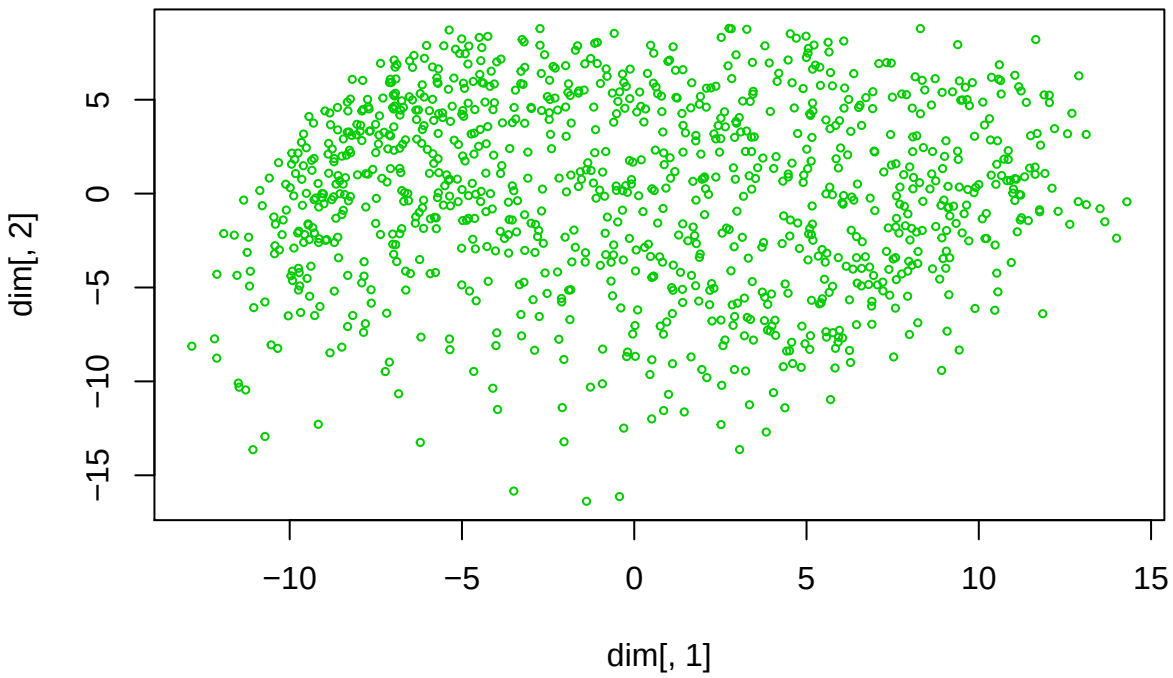
```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## [1,]  194    1  616   26  200  125  640    5   14     2
```

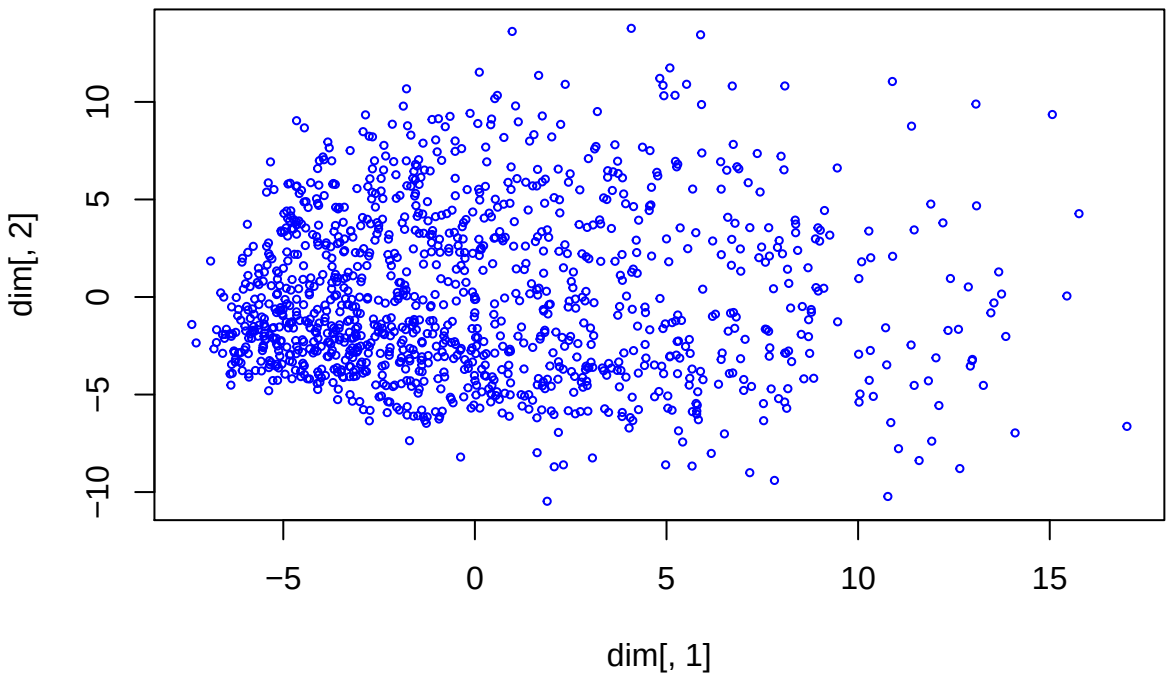
```
## [2,]  986    0   23    2    3    6   16    0    1    0
## [3,]    0 1004    7    1   43    0    3    0    1    0
## [4,]   14    0   82  618    4  390    3    0   87    0
## [5,]    0    0    3   11  402   35    2  640  439  642
```

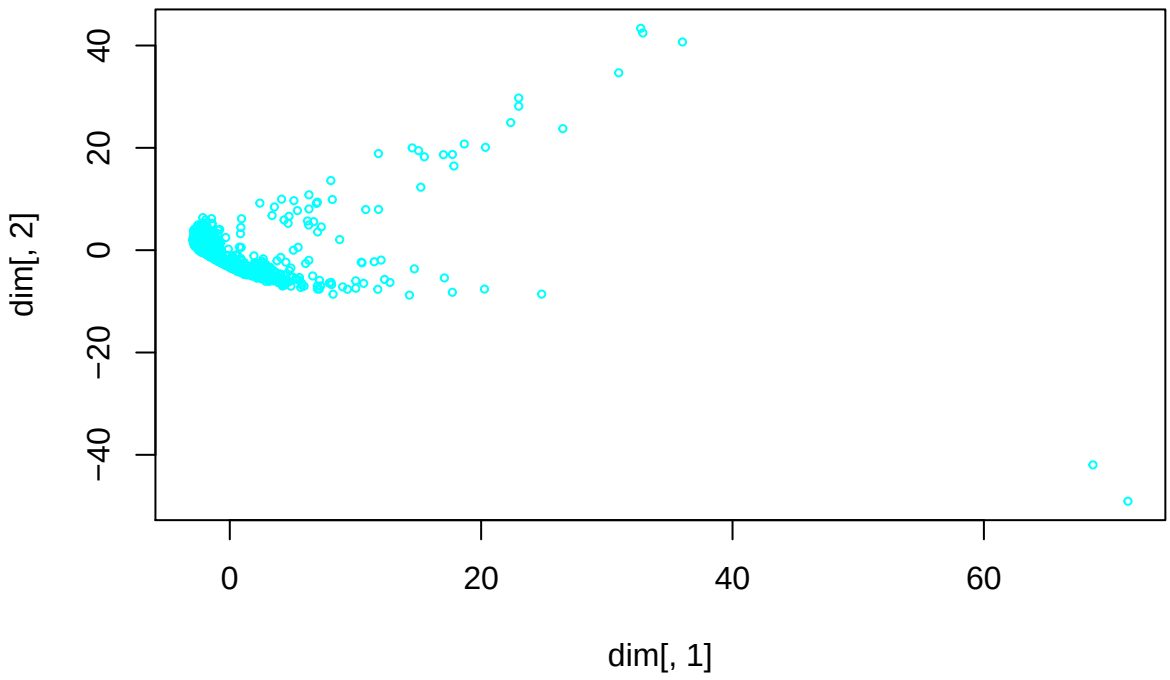
```
cl2<-kmeans(data, 5, 10);

whole.data <- data.frame("cluster_result"=cl2$cluster, "data"=data)

for(cluster in 1:5)
{
  cluster.data <- subset(whole.data, cluster_result==cluster);
  cluster.data <- cluster.data[,!apply(cluster.data, MARGIN = 2, function(x) max(x, na.rm = TRUE) == mi

  pca <- prcomp(cluster.data[, (1:ncol(cluster.data))], scale.=TRUE)

  dim <- pca$x

  plot(x=dim[,1], y = dim[,2], col=cluster, cex=0.5)

}
```




dim[, 2]
25
20
15
10
5
0
−10
−30
−25
−20
−15
−10
−5
0
5
dim[, 1]


dim[, 2]
5
0
−5
−10
−15
−10
−5
0
5
10
15
dim[, 1]


dim[, 2]
10
5
0
−5
−10
−5
0
5
10
15
dim[, 1]




```
counts <- matrix(rep(0, 50), nrow=5, ncol=10)

for(i in 1:5)
{
  for(j in 0:9)
  {
    counts[i,j+1] = nrow(subset(subset(whole.data, cluster_result==i), data.1==j))

  }
}

counts
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## [1,]  194    1  616   26  200  125  640    5   14     2
## [2,]    0    0    3   11  402   35    2  640  439   642
## [3,]  986    0   23    2    3    6   16    0    1     0
## [4,]   14    0   82  618    4  390    3    0   87     0
## [5,]    0 1004    7    1   43    0    3    0    1     0
```

Compare by count of digits in each plot

1. My implementation of kmeans:

cluster	0	1	2	3	4	5	6	7	8	9
1	592	0	128	289	17	27	299	1	43	5
2	378	0	28	3	4	15	25	2	1	2
3	63	1005	456	103	206	140	319	230	190	154
4	133	0	41	137	38	47	20	48	21	20
5	28	0	78	126	387	84	1	364	287	463

2. Built-in K-means with 1 initialization

cluster	0	1	2	3	4	5	6	7	8
1	194	1	616	26	200	125	640	5	14	2
2	986	0	23	2	3	6	16	0	1	0
3	0	1004	7	1	43	0	3	0	1	0
4	14	0	82	618	4	390	3	0	87	0
5	0	0	3	11	402	35	2	640	439	642

3. Built-in K-means with 10 initializations

cluster	0	1	2	3	4	5	6	7	8
1	194	1	616	26	200	125	640	5	14	2
2	0	0	3	11	402	35	2	640	439	642
3	986	0	23	2	3	6	16	0	1	0
4	14	0	82	618	4	390	3	0	87	0
5	0	1004	7	1	43	0	3	0	1	0

According to the table the clustering result with n different starts are identical to the clustering result with only 1 initialization.

Built-in kmeans clustering has a better concentricity in each cluster as they has less variation of digits.

This is also confirmed after comparing plots.

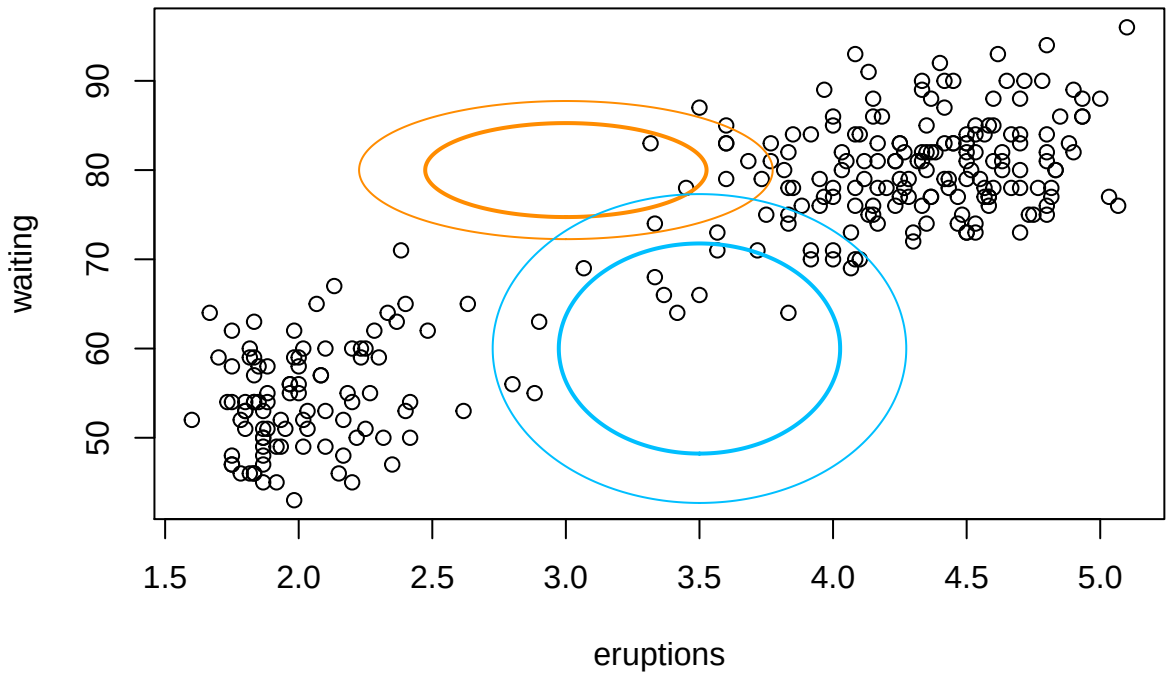
Question 2

```
rm(list=ls())

faithful = read.table("faithful.txt")

# the parameters
mu1 = c(3, 80)
mu2 = c(3.5, 60)
Sigma1 = matrix(c(0.1, 0, 0, 10), 2, 2)
Sigma2 = matrix(c(0.1, 0, 0, 50), 2, 2)
p = 0.5
```

```
# plot the current fit
library(mixtools)
```

```
## mixtools package, version 1.1.0, Released 2017-03-10
## This package is based upon work supported by the National Science Foundation under Grant No. SES-0518
```

```
plot(faithful)

addellipse <- function(mu, Sigma, ...)
{
  ellipse(mu, Sigma, alpha = .05, lwd = 1, ...)
  ellipse(mu, Sigma, alpha = .25, lwd = 2, ...)
}

addellipse(mu1, Sigma1, col = "darkorange")
addellipse(mu2, Sigma2, col = "deepskyblue")
```




```
library(mvtnorm)
```

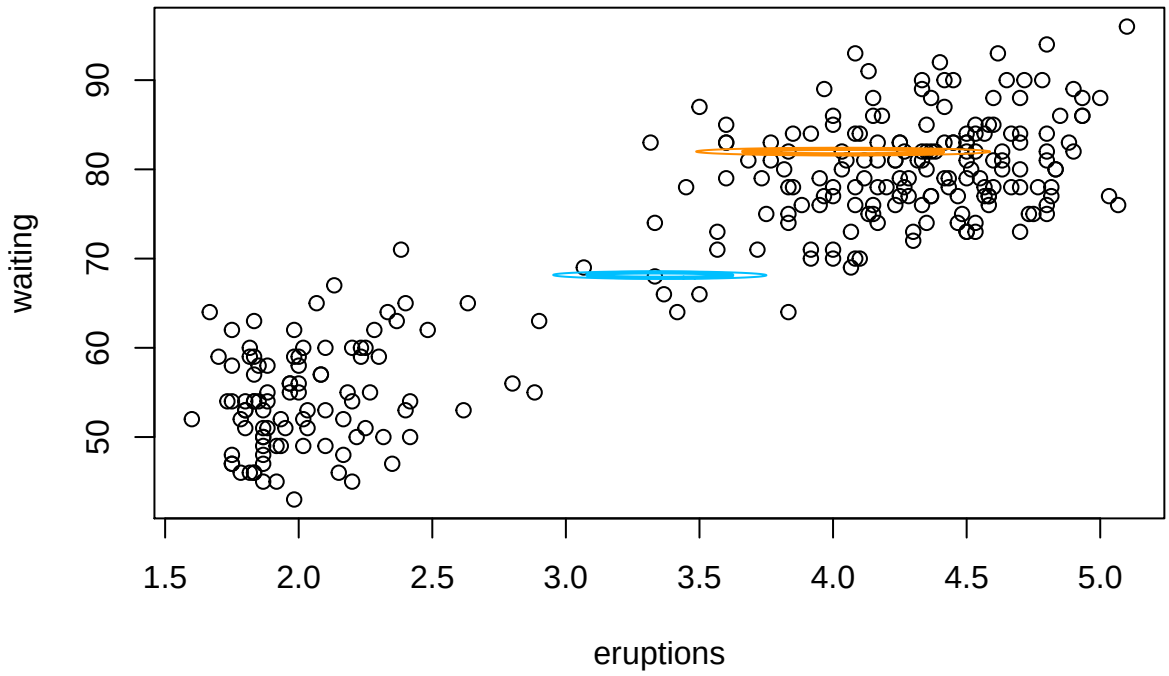
```
##
## Attaching package: 'mvtnorm'
```

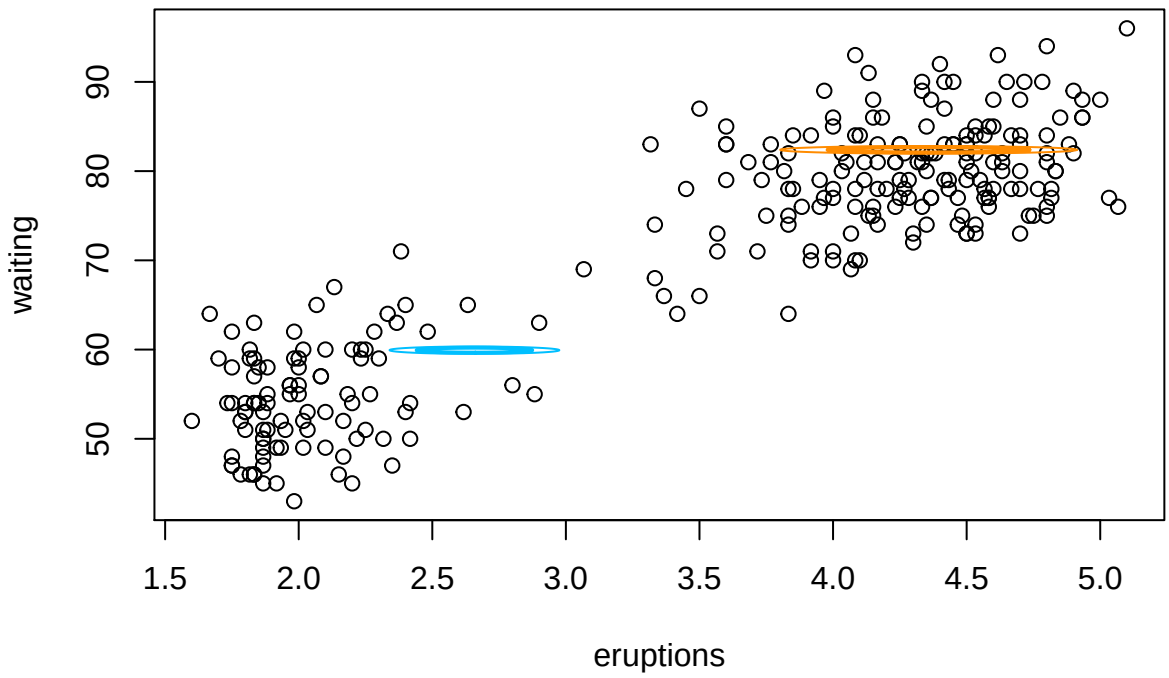
```
## The following objects are masked from 'package:mixtools':
```

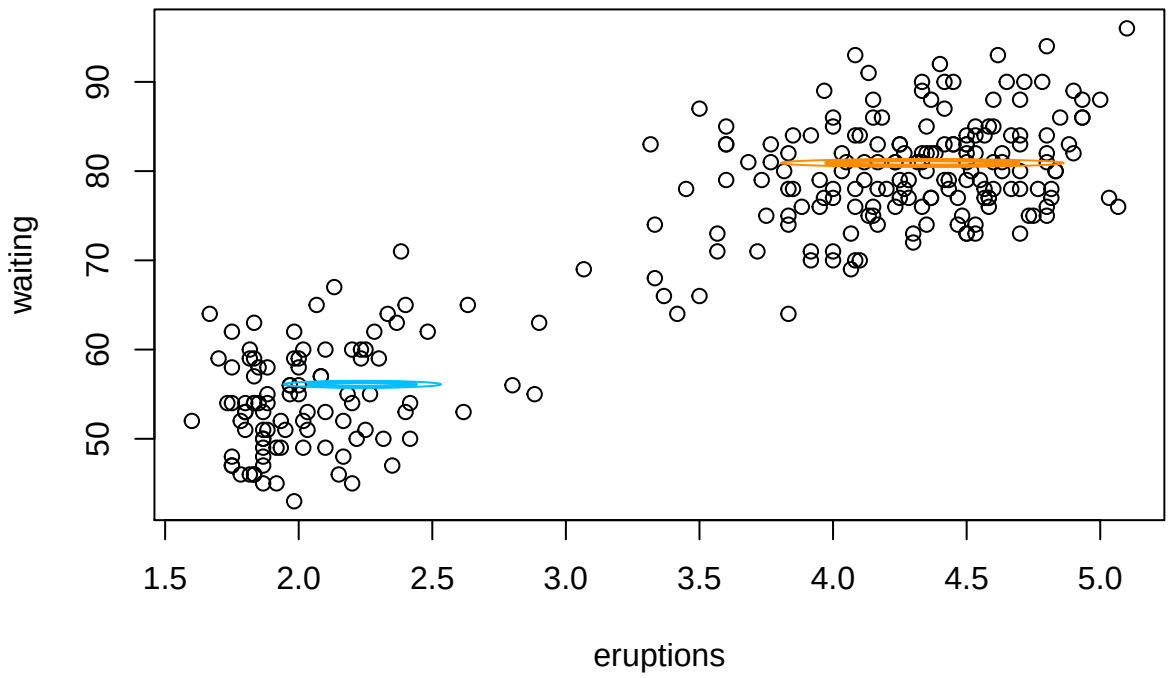
```
##
##     dmvnorm, rmvnorm
```

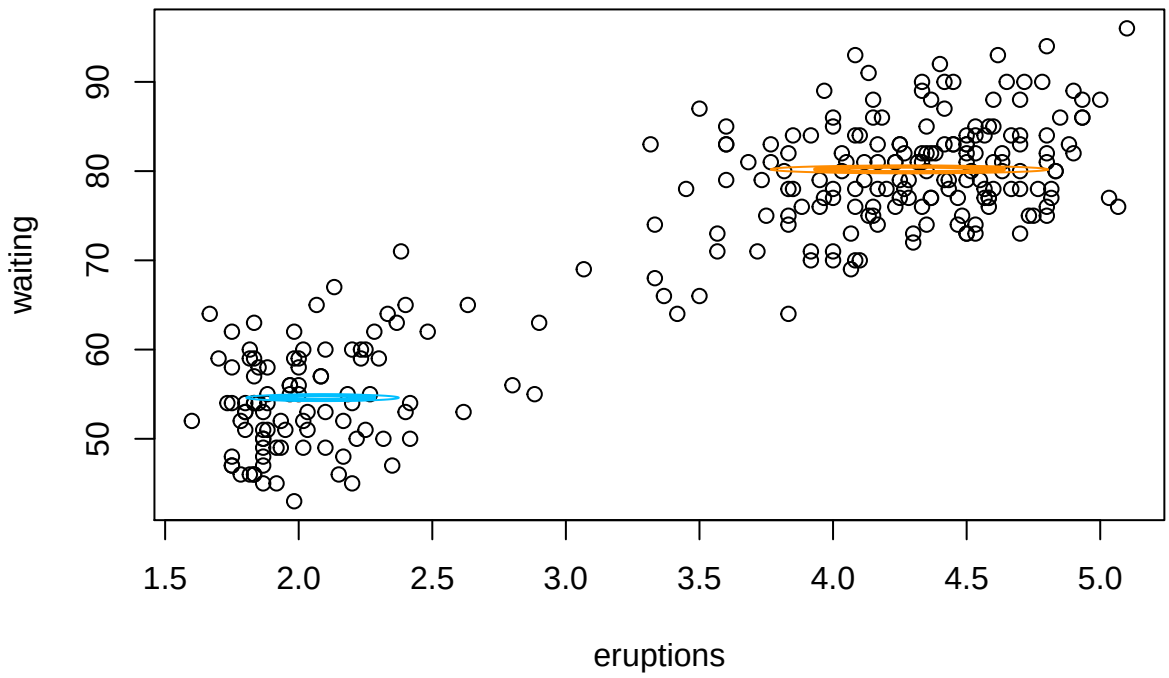
```
l = list()
l[[1]]<- list(mixing.weight=p, means = mu1, cov=Sigma1)
l[[2]]<-list(mixing.weight=p, means = mu2, cov=Sigma2)

epsilon = 10^-5

.cov <- function(n, r, dat, m, N.k)
{

  (t(r * (dat[,1:2] -m))  %*%  (( dat[,1:2]-m))) / N.k/n
}

n <- nrow(faithful)

for(i in 1:100)
{
    #E
    r <- sapply(l, function(r)
    {
      r$mixing.weight *  mvtnorm::dmvnorm(faithful[,1:2], r$means, r$cov)
    })
    r <- apply(r, 1, sum)

    rs <- sapply(l, function(e)
    {
      e$mixing.weight * mvtnorm::dmvnorm(faithful[,1:2], e$means, e$cov) / r
    })

    N.k <- apply(rs, 2, sum)


    #M
    m <- lapply(1:2, function(e)
    {
      apply(rs[,e] * data.matrix(faithful[,1:2]), 2, sum) / N.k[e]
    })

    # Compute the new covariances
    c <- lapply(1:2, function(e)
    {
      .cov(n, rs[,e], data.matrix(faithful[,1:2]), m[[e]], N.k[e])
    })

    # Compute the new mixing weights
    mi <- N.k / nrow(faithful)

    # Update the old parameters
    l <- lapply(1:2, function(e)
    {
      list(mixing.weight = mi[e], means=m[[e]], cov=(c[[e]]))
    })
```

```
    if(i <4 || i==100)
    {
      plot(faithful)
      addellipse(l[[1]]$means, l[[1]]$cov/n, col = "darkorange")
      addellipse(l[[2]]$means, l[[2]]$cov/n, col = "deepskyblue")
    }

}
```




waiting
50
60
70
80
90
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0
eruptions


waiting
50
60
70
80
90
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0
eruptions




```
print(l)
```

```
## [[1]]
## [[1]]$mixing.weight
## [1] 0.6367426
##
## [[1]]$means
## eruptions   waiting
##   4.28578  80.19092
##
## [[1]]$cov
##            eruptions    waiting
## eruptions 12.2218479 -0.1316292
## waiting   -0.1316292  8.8108081
##
##
## [[2]]
## [[2]]$mixing.weight
## [1] 0.3632574
##
## [[2]]$means
## eruptions   waiting
##  2.088999 54.606145
##
## [[2]]$cov
```

```
##             eruptions     waiting
## eruptions  3.69591628 -0.01010919
## waiting   -0.01010919  6.53906253
```

Parameters: mu1: 4.28578 80.19092 mu2: 2.088999 54.606145 Sigma1: 12.2218479 -0.1316292 -0.1316292 8.8108081 Sigma2: 3.69591628 -0.01010919 -0.01010919 6.53906253 p: 0.3632574

This algorithm converges fast, compared with regular Gradient Descent algorithm.

```
y <- 0.3632574 * rmvnorm(100, l[[1]]$means, l[[1]]$cov )+(1-0.3632574)*rmvnorm(100, l[[2]]$means, l[[2]]

y <- apply(y, 1, sum)

hist(y)
```