HUDM6122 Homework_04

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0.1 Ex 4.1

Consider 51 objects O1, . , O51 assumed to be arranged along a straight line with the jth object being located at a point with coordinate j. Define the similarity sij between object i and object j as… and then apply classical multidimensional scaling to the resulting dissimilarity matrix. Explain the shape of the derived two-dimensional solution.

MY SOLUTION:
First, I define the function of dissimilarities δ_{ij} as follows, where the input paramter X is a n*1 matrix that contains all the coordination of 51 objects.

```
> D_dis <- function(X) {
+   n <- dim(X)[1] # to have the length of any input n*1 matrix
+   S <- matrix(0, n, n) # to make a n*n empty matrix
+   D <- matrix(0, n, n) # to make a n*n empty matrix
+   # to make the similarity matrix by conditions
+   for (i in c(1:n)) {
+     for (j in c(1:n)){
+       if (i == j){S[i,j] <- 9}
+       else if (abs(i-j) >= 1 & abs(i-j) <= 3){S[i,j] <- 8}
+       else if (abs(i-j) >= 4 & abs(i-j) <= 6){S[i,j] <- 7}
+       else if (abs(i-j) >= 7 & abs(i-j) <= 9){S[i,j] <- 6}
+       else if (abs(i-j) >= 10 & abs(i-j) <= 12){S[i,j] <- 5}
+       else if (abs(i-j) >= 13 & abs(i-j) <= 15){S[i,j] <- 4}
+       else if (abs(i-j) >= 16 & abs(i-j) <= 18){S[i,j] <- 3}
+       else if (abs(i-j) >= 19 & abs(i-j) <= 21){S[i,j] <- 2}
+       else if (abs(i-j) >= 22 & abs(i-j) <= 24){S[i,j] <- 1}
+       else if (abs(i-j) >= 25){S[i,j] <- 0}
+     }
+   } # similarity matrix finished!
+   # using the elements in the Similarity matrix to generate Dissimilarities Matrix
+   for (i in c(1:n)) {
+     for (j in c(1:n)) {
+       D[i,j] <- sqrt(S[i,i] + S[j,j] - 2*S[i,j])
+     }
+   } # dissimilarity matrix finished!
+   return(D)
+ }
```

Next, I randomly generate a n*1 matrix with 51 integers by using `sample()` function. And plug this vector to the dissimilarity function above.

```
> obs_ <- function(n) {
+   number_vec <- c(1:n)
+   # change the number array to matrix
+   return(matrix(number_vec,n,1))
+ }
```

The functions above looks good. I try to generate 51 observations and plug them into the dissimilarity matrix function to get the required D matrix.

```
> # generate 51 observations
> observations <- obs_(51)
> # plug the n*1 matrix into the dissimilarity martix function
> D <- D_dis(observations)
> # select a part of the dissimilarity matrix
> D[1:5,1:5]
         [,1]     [,2]     [,3]     [,4]     [,5]
[1,] 0.000000 1.414214 1.414214 1.414214 2.000000
[2,] 1.414214 0.000000 1.414214 1.414214 1.414214
[3,] 1.414214 1.414214 0.000000 1.414214 1.414214
[4,] 1.414214 1.414214 1.414214 0.000000 1.414214
[5,] 2.000000 1.414214 1.414214 1.414214 0.000000
```

This dissimilarity matrix looks good. Then I run the classical multidimensional scaling to this resulting matrix. Note, this is a non-Euclidean case. Some of the eigenvalue may be negative.

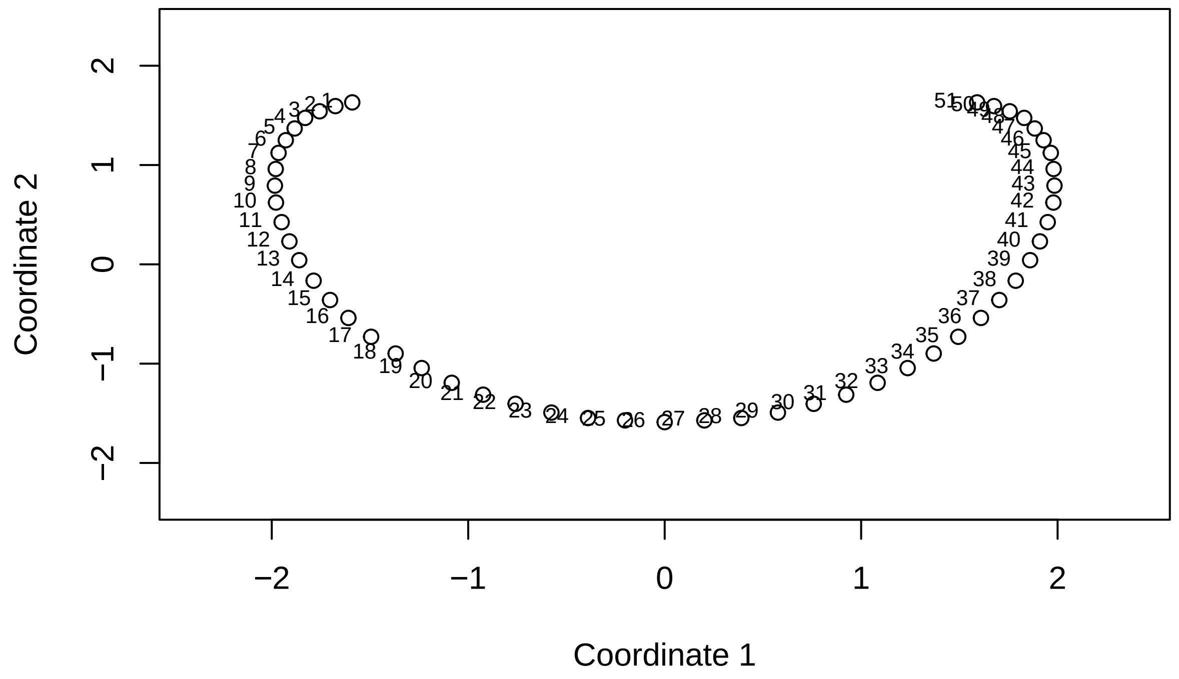
```
> d_mds <- cmdscale(D, k=50, eig = T)
> lam <- d_mds$eig
> # d_mds$points
> cumsum(abs(lam))/sum(abs(lam))
 [1] 0.4428488 0.6744323 0.7382541 0.7657231 0.7924526 0.8183668 0.8430174
 [8] 0.8615740 0.8736449 0.8845189 0.8953701 0.9048445 0.9116561 0.9167756
[15] 0.9217895 0.9267112 0.9314246 0.9355091 0.9389073 0.9422424 0.9455372
[22] 0.9486160 0.9513996 0.9540916 0.9565647 0.9589956 0.9611009 0.9630147
[29] 0.9646832 0.9663473 0.9677584 0.9691622 0.9704291 0.9714991 0.9725150
[36] 0.9734831 0.9744191 0.9753283 0.9762204 0.9771018 0.9775266 0.9778771
[43] 0.9778771 0.9782091 0.9785814 0.9796588 0.9808172 0.9831840 0.9856796
[50] 0.9927144 1.0000000
> cumsum(abs(lam^2))/sum(abs(lam^2))
 [1] 0.7608520 0.9689196 0.9847222 0.9876495 0.9904214 0.9930267 0.9953842
 [8] 0.9967201 0.9972854 0.9977441 0.9982010 0.9985492 0.9987292 0.9988309
[15] 0.9989284 0.9990224 0.9991086 0.9991733 0.9992181 0.9992613 0.9993034
[22] 0.9993402 0.9993702 0.9993983 0.9994221 0.9994450 0.9994622 0.9994764
[29] 0.9994872 0.9994979 0.9995057 0.9995133 0.9995195 0.9995240 0.9995280
[36] 0.9995316 0.9995350 0.9995382 0.9995413 0.9995443 0.9995450 0.9995455
[43] 0.9995455 0.9995459 0.9995465 0.9995510 0.9995562 0.9995779 0.9996021
[50] 0.9997941 1.0000000
```

These values suggest that the first two coordinates will give an adequate representation of the simulated dissimilarity distances. Then, I make the scatter plot using the first two scores.

```
> lim <- range(d_mds$points[,1] * (-1)) * 1.2
>
```

```
> plot(d_mds$points[,1]*(-1), d_mds$points[,2]*(-1),
+      xlab = "Coordinate 1", ylab = "Coordinate 2",
+      xlim = lim, ylim = lim)
```

```
> lim <- range(d_mds$points[,1]) * 1.2
> plot(d_mds$points[,1], d_mds$points[,2],
+      xlab = "Coordinate 1", ylab = "Coordinate 2",
+      xlim = lim, ylim = lim)
> text(d_mds$points[,1], d_mds$points[,2], labels = c(1:51), pos=2,cex = 0.7)
```



This two-dimensional plot has the symmetrical shape, which is reasonable since the mid-point,i.e., the 26th point, has the same dissimilarity with both the points on its left and right. Therefore, if we project all point on y-axis, it actually represent the dissimilarity degree between the each point and the 26th point.

0.2 Ex. 4.2

Write an R function to calculate the chi-squared distance matrices for both rows and columns in a two-dimensional contingency table.

MY SOLUTION Based on the definition of chi-squared distance matrices, I write the function as follows:

```
> chi_squared_dist_matrices <- function(tbl){
+   # Calculate row sums and column sums
+   row_sums <- apply(tbl, 1, sum)
+   col_sums <- apply(tbl, 2, sum)
+   # Calculate total count and expected counts
+   total_count <- sum(tbl)
+
+   # to have the dim of the input matrix
+   c <- ncol(tbl)
+   r <- nrow(tbl)
+   # make a empty matrix to load all elements
+   col_d_matrix <- matrix(0,c,c)
+
+   # using loop to write the each ij entries into this matrix
+   for (i in c(1:c)) {
+     for (j in c(1:c)) {
+       d_ij <- 0
+       for (k in c(1:r)) {
+         p_k_dot <- row_sums[k]/total_count
+         p_k_i <- tbl[k,i]/col_sums[i]
+         p_k_j <- tbl[k,j]/col_sums[j]
+         d_ij <- d_ij + (1/p_k_dot)*(p_k_i-p_k_j)^2
+       }
+       col_d_matrix[i,j] <- d_ij
+     }
+   }
+   # make a empty matrix to load all elements
+   row_d_matrix <- matrix(0,r,r)
+
+   # using loop to write the each ij entries into this matrix
+   for (i in c(1:r)) {
+     for (j in c(1:r)) {
+       d_ij <- 0
+       for (k in c(1:r)) {
+         p_dot_k <- col_sums[k]/total_count
+         p_i_k <- tbl[i,k]/row_sums[i]
+         p_j_k <- tbl[j,k]/row_sums[j]
+         d_ij <- d_ij + (1/p_dot_k)*(p_i_k-p_j_k)^2
+       }
+       row_d_matrix[i,j] <- d_ij
+     }
+   }
+   return(list(col_d_matrix, row_d_matrix))
+ }
```

This function return a list that contains both columns distance matrix and rows distance matrix. By using the index, like [[1]]or [[2]], to extract the columns or rows distance matrix, respectively. Next, I created a two-dimensional contigency table to test this function.

```
> # Create a contingency table
> tbl <- table(c("A", "A", "B", "B"), c("X", "Y", "X", "Z"))
> tbl

    X Y Z
  A 1 1 0
  B 1 0 1
> # plug this simulated table into the function above
> dist_m <-chi_squared_dist_matrices(tbl)
> # the columns distance matrix is
> dist_m[[1]]
     [,1] [,2] [,3]
[1,]    0    1    1
[2,]    1    0    4
[3,]    1    4    0
> # the row distance matrix is
> dist_m[[2]]
     [,1] [,2]
[1,]    0    1
[2,]    1    0
```