Ciencia de datos, práctica 4

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Abstract

Contents

```
> plot_kmeans <- function (clusters, centers, xlab="", ylab="") {
    maxx <- max(clusters[[1]][,1])</pre>
    maxy <- max(clusters[[1]][,2])</pre>
    minx <- min(clusters[[1]][,1])</pre>
    miny <- min(clusters[[1]][,2])</pre>
    for (cluster in clusters){
      maxx <- max(maxx, max(cluster[,1]))</pre>
      maxy <- max(maxy, max(cluster[,2]))</pre>
      minx <- min(minx, min(cluster[,1]))</pre>
      miny <- min(miny, min(cluster[,2]))</pre>
    color_i <- 1
    colors = c("red", "blue", "pink", "yellow", "black", "brown")
    for (cluster in clusters){
      plot(cluster[,1], cluster[,2], type="p", col=colors[color_i], xlim=c(minx, maxx), y
      par(new=TRUE)
      color_i <- (color_i%(length(colors)+1))+1</pre>
    plot(centers[,1], centers[,2], type="p", col="green", xlim=c(minx, maxx), ylim=c(min
+ }
> distance <- function (point1, point2) {</pre>
    acc <- 0
    len <- length(point1)</pre>
    for (i in 1:len){
      acc <- acc + (point1[i]-point2[i])^2</pre>
    }
+
    acc^{(1/2)}
+ }
> kmeans_cluster <- function (data, centroids) {
    d_default <- distance(c(max(data), max(data)), c(min(data), min(data)))</pre>
    classification <- c()</pre>
    for (j in 1:nrow(data)){
        point <- data[j,]</pre>
        best_c \leftarrow 0
        best\_d \leftarrow d\_default
+
        for (i in 1:nrow(centroids)){
           centroid <- centroids[i,]</pre>
           d <- distance (point, centroid)</pre>
           if (d < best_d){
             best_d \leftarrow d
             best_c <- i
+
      classification <- c(classification, best_c)</pre>
    }
    classification <- as.data.frame(classification)</pre>
    rownames(classification) <- rownames(datos1)</pre>
```

```
+ classification
+ }
> kmeans_split <- function (data, cluster) {
+ clusters=cbind(cluster,data)
  cluster1=subset(clusters, clusters[,1]==1)
   cluster2=subset(clusters, clusters[,1]==2)
   cluster1=cluster1[,-1]
   cluster2=cluster2[,-1]
    list(cluster1, cluster2)
+ }
> kmeans_new_centroids <- function(split){
    centroids <- c()</pre>
+
    for (cluster in split) {
     for (colum in cluster) {
        acc <- 0
        for (element in colum){
        acc <- acc + element/length(colum)</pre>
+
+
        centroids <- c(centroids, acc)</pre>
+
    }
+
+
    t(matrix(centroids,length(split[[1]]),length(split)))
+ }
> same_centroids <- function(c1, c2){</pre>
   len <- length(c1)</pre>
    ans <- T
   for (i in 1:len){
     if (c1[i]!=c2[i]){
        ans \leftarrow F
     }
    }
    ans
> datos1 <- read.table("datos1.txt")</pre>
> datos1
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    4
2
       3
                   5
3
      1
                   2
4
      5
                   5
5
      0
                   1
6
       2
                   2
7
       4
                   5
                   1
> centroides <- matrix(c(0,1,2,2),2,2)
> centroides <- t(centroides)
> centroides
```

```
[,1] [,2]
[1,] 0 1
```

[2,] 2 2

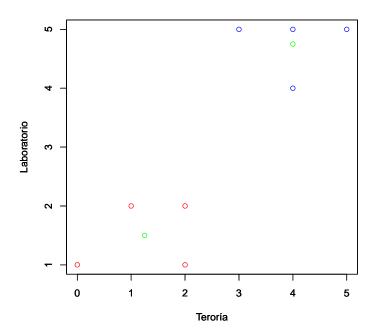
- > classkms<-kmeans(datos1,centroides,4)</pre>
- > classkms\$cluster
- 1 2 3 4 5 6 7 8
- 2 2 1 2 1 1 2 1
- > classkms\$centers

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- 1 1.25 1.50
- 2 4.00 4.75
- > classkms\$size
- [1] 4 4
- > classkms\$iter
- [1] 1
- > classkms\$ifault
- [1] 0
- > classkms\$totss
- [1] 42.75
- > classkms\$withinss
- [1] 3.75 2.75
- > classkms\$totss.withinss

NULL

- > classkms\$betweenss
- [1] 36.25
- > clusters <- cbind(classkms\$cluster,datos1)</pre>
- > cluster1 <- subset(clusters, clusters[,1]==1)</pre>
- > cluster2 <- subset(clusters, clusters[,1]==2)</pre>
- > cluster1 <- cluster1[,-1]</pre>
- > cluster2 <- cluster2[,-1]</pre>
- > clusters <- list(cluster1, cluster2)</pre>



[,1] [,2] [1,] 1.25 1.50 [2,] 4.00 4.75

