Homewok5

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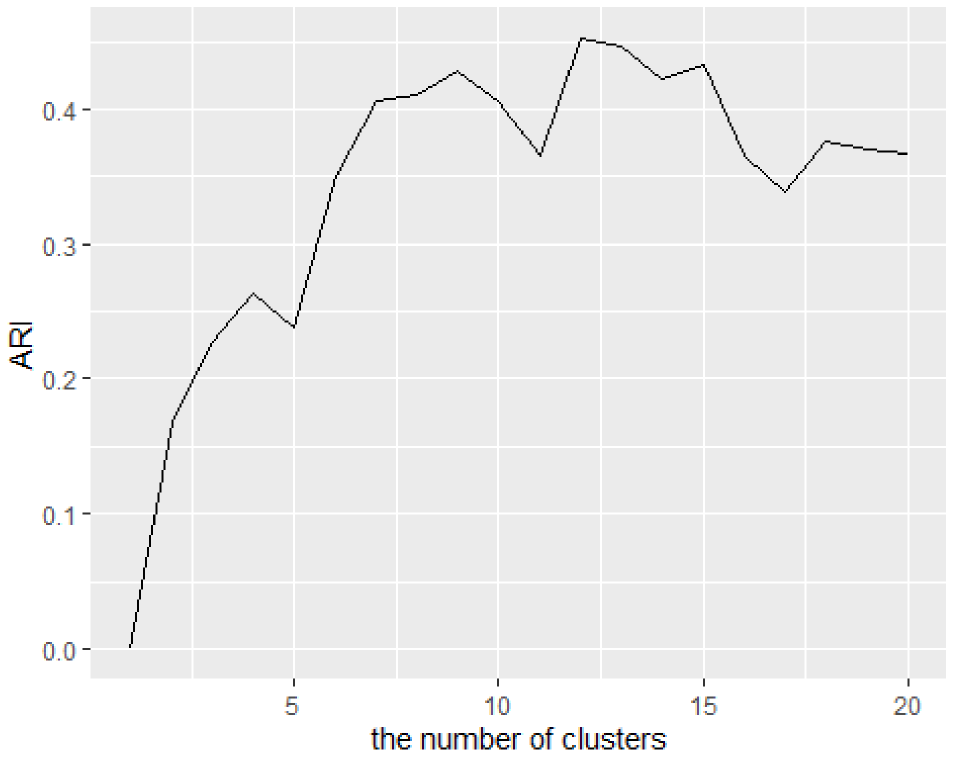
```r
library(stats)
library(ggplot2)
library(data.table)
library(kernlab)

# use data.table::fread to read the compressed CSV data file into R as a data
 table.
dt<- fread("zip.test.gz")

#To exclude the label column (that is the first column)
df<-as.matrix(dt[, -1])
```

Spectral clustering involves computing an N x N affinity/kernel matrix (quadratic time/space in N), then an eigen-decomposition (cubic time in N), which results in a matrix of eigenvectors, which are new features/column that can be clustered with a standard algorithm like kmeans. Spectral clustering is useful for detecting clusters that are non-linear/non-spherical in shape. 1.Use kernlab::specc in R to compute a spectral clustering on the first 300 rows of the zip.test data, from 1 to 20 clusters. Compute ARI of each clustering and plot y=ARI as a function of x=number of clusters using default parameters of specc. What number of clusters is the most accurate?

```r
  metrics.dt.list <- list()

  for(n.clusters in 1: 20){
    if(n.clusters == 1){
      result = data.table(n.clusters,ARI=0)
    }
    else{
      fit <- specc(df[1:300,],n.clusters)
      result <- data.table(n.clusters,ARI=pdfCluster::adj.rand.index(fit@.Dat
a, dt[1:300,][["V1"]]))

    }
    metrics.dt.list[[paste(n.clusters)]] <- result


  }
  metrics.dt <- do.call(rbind, metrics.dt.list)
```

```
 ggplot()+geom_line(aes(n.clusters, ARI),data=metrics.dt) + xlab("the number
of clusters") + ylab("ARI")
```

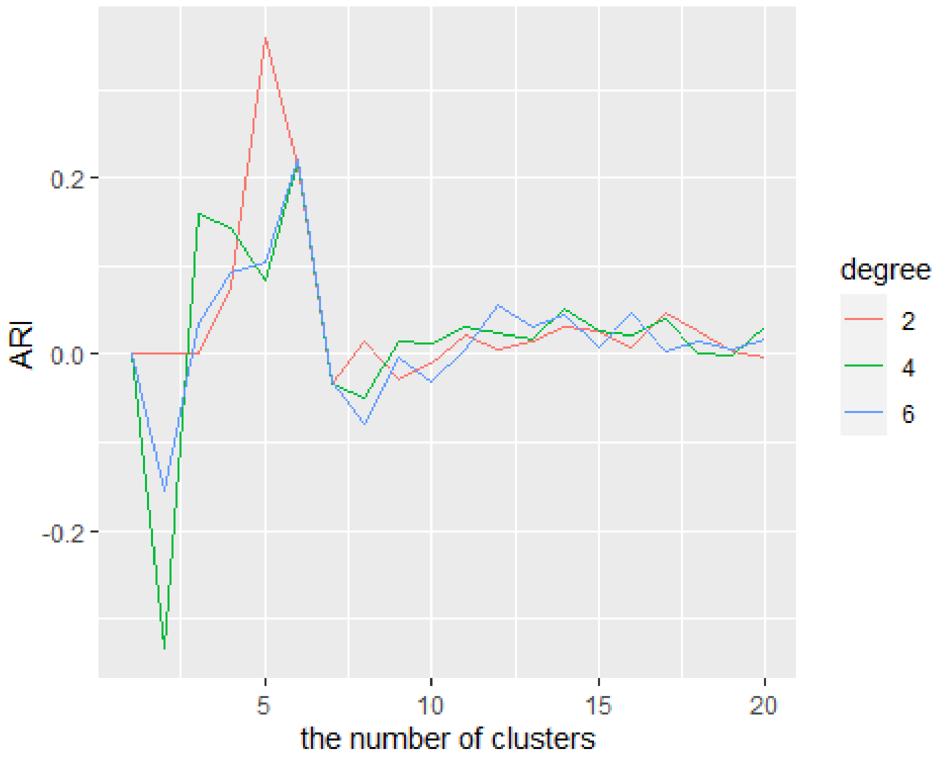


From the picture, we can find that when the cluster is 12, it is the accurate.

2.Again compute spectral clusterings but using a polynomial kernel (kernlab:polydot) instead of the default RBF kernel. Compute clusterings using three different polynomial degree values (2, 4, 6) and 1 to 20 clusters. Compute ARI of each clustering and plot y=ARI as a function of x=number of clusters, using different colors for the different polynomial degrees. What number of clusters and polynomial degree is most accurate? accurate?

```
 dt <- data.table(matrix(numeric(), 60, 3))
  index = 1
  for(n.clusters in 1: 20){
      for (degree in seq(2,6,2)) {
          if(n.clusters == 1){
            temp <- c(n.clusters,degree,0)
            dt[index,names(dt) := as.list(temp)]
          }
        else{
          fit <- specc(df[1:300,],n.clusters,polydot(degree=degree))
          ARI = pdfCluster::adj.rand.index(fit@.Data, dt[1:300,][["V1"]])
          temp <- c(n.clusters,degree,ARI)
          dt[index,names(dt) := as.list(temp)]
        }
```

```
          index = index + 1
      }


  }


# g <- ggplot()+geom_line(aes(V1, V3),data=dt) + xlab("the number of clusters
") + ylab("ARI")
#
# g + facet_grid(rows = vars(V2))
ggplot( aes(x=V1, y=V3, group=V2, color=factor(V2)),data=dt) +
  geom_line() +
  labs(x = "the number of clusters", y="ARI", color = "degree")
```



From the picture, we can find that the most accurate at

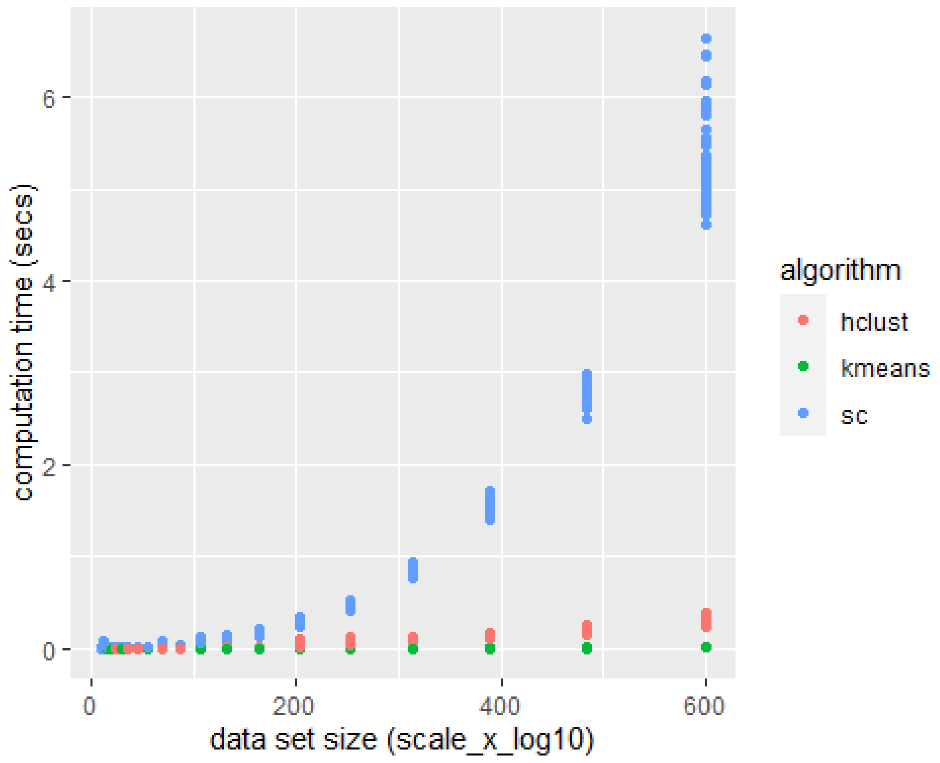
when degree = 2 and cluster = 5

when degree = 4 and cluster = 6

when degree = 6 and cluster = 6

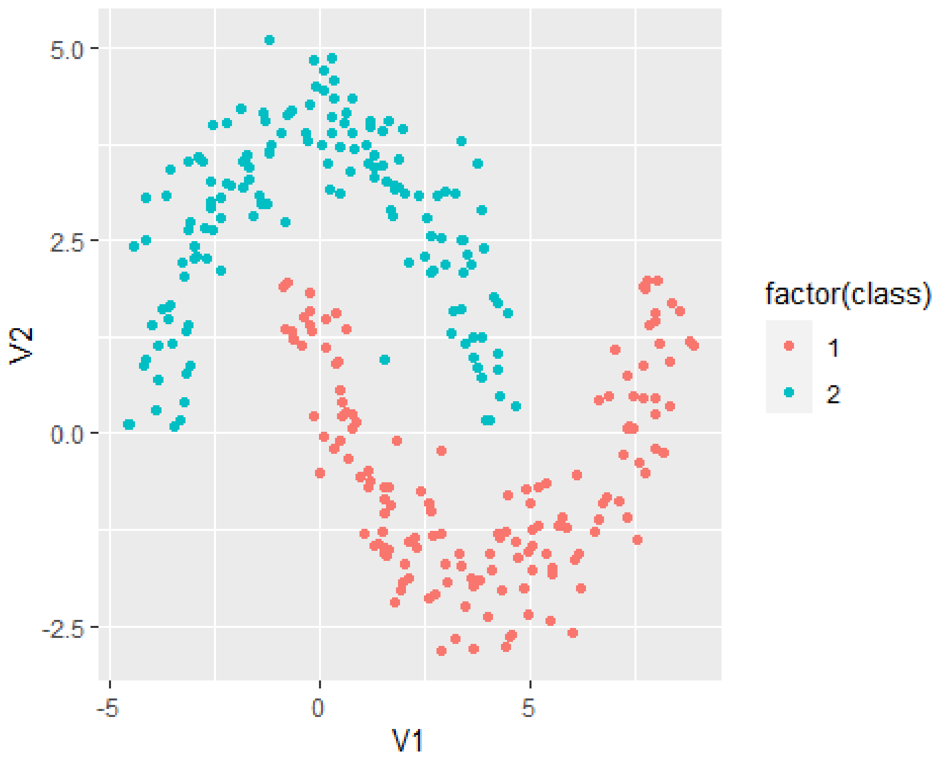
3.Use microbenchmark to compute timings of kmeans, hclust, and specc for several subset sizes N. Plot y=time in seconds versus x=subset size, with each algorithm in a different color. Use log/log scales so that different time complexity classes appear as lines with different slopes. Use a large enough range of N so that the complexity class of each algorithm is clear (kmeans linear, hclust quadratic, specc cubic).

```r
Myplot <- function(data.set){
    time.dt.list <- list()
    (log.scale.seq <- as.integer(c(10^seq(1, log10(600), l=20))))
    # seq(10, 1000, by =100)
    for (N in log.scale.seq) {
        X <- data.set[1:N,]
        timing.df <- microbenchmark::microbenchmark(hclust={
              d.mat <- stats::dist(X, method="manhattan")
              as.matrix(d.mat)
              cl.tree <- stats::hclust(d.mat, method="single")
             stats::cutree(cl.tree, k=3)
            },
            kmeans={
                  stats::kmeans(X, 3)
          },
          sc ={
                  specc(X,3)
          })
          time.dt.list[[paste(N)]] <- data.table(N, timing.df)
    }
    time.dt <- do.call(rbind, time.dt.list)
    time.dt[, data.size := N]
    time.dt[, time.seconds := time/1e9]
    time.dt[, algorithm := expr]

    g<-ggplot()+
      geom_point(aes(x=data.size,y=time.seconds,color=algorithm),data=time.dt
)+
      xlab("data set size (scale_x_log10)") + ylab("computation time (secs)")


    return(g)
}


Myplot(df[1:1000,])
```



Code a simple spectral clustering algorithm from scratch (without using any special packages like kernlab), using the descriptions in the textbooks. Compute a kernal/similarity matrix, then either the un-normalized or normalized graph Laplacian, then compute its eigenvalues/vectors, then consider the eigenvectors corresponding to the smallest eigenvalues, then run stats::kmeans. Run the algorithm on the halfcircle/moons data we saw in class, and draw the two different clusters in different colors.

```r
# spectral clustering
SPC <- function(data.matrix, K){

    #we total have two parameters in the function
    if(is.na(data.matrix) || is.na(K)){
        stop("You need to input valid parameters!!")
    }

    nodes <- dim(data.matrix)[1]

    #initialize Similarity matrix or adjacency matrix
    similarity.matrix <- matrix(NA, nrow = nodes, ncol=nodes)

    # Using Gaussian kernel (sigma = 0.09) to cluster the data
    #if two points have the small similarity value,
    #these two points will have a stronger link

    sigma <- 0.09
    for (i in 1:nodes){
      for (j in 1: nodes){
          similarity.matrix[i,j] <- exp(-sum((data.matrix[i,] - data.matrix[j
,])^2)/(2*sigma^2))
      }
    }

    #calculate the degree matrix
    #it means how many connection between
    #the first data point to the rest N-1 data points
    S_degree <- rowSums(similarity.matrix)

    #calculate Laplacian
    Laplacian <- diag(S_degree) - similarity.matrix
    normalize.Laplacian <- diag(S_degree^(-1/2)) %*%  similarity.matrix %*% d
iag(S_degree^(-1/2))

    #error = sum()
    # ev <- eigen(Laplacian)
    #
    # e <- kmeans(ev$vectors[,which.min(ev$values)], K, iter.max=50)$cluster

    ev <-eigen(normalize.Laplacian)
    ev.vector <- ev$vectors[,1:K]

    for (index in 1:nodes) {
        ev.vector[index,] <- ev.vector[i,] / sqrt(sum(ev.vector[index,]^2))
    }

    e <- kmeans(ev.vector, K, iter.max=50)$cluster

    return(e)
}




set.seed(1)
halfcircle <- function(r, center = c(0, 0), class, sign, N=150, noise=0.5) {
  angle <- runif(N, 0, pi)
  rad <- rnorm(N, r, noise)
  data.table(
    V1 = rad * cos(angle) + center[1],
    V2 = sign * rad * sin(angle) + center[2],
    class = factor(class))
}


X.dt <- rbind(
  halfcircle(4, c(0, 0), 1, 1),
  halfcircle(4, c(4, 2), 2, -1))

X.mat <- as.matrix(X.dt[, 1:2])

K <- 2
class = SPC(X.mat,K)


DF <- as.data.frame(cbind(X.mat,class))

ggplot()+
  geom_point(aes(
    V1, V2, color=factor(class)),
    data=DF)
```



I code my own function by using Gaussian kernel (sigma = 0.09) to build similarity matrix. I find something very interesting, when sigma = 0.09, the answer is most accurate.