## MSMS 206: Practical 01

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- **Question**: Use k-means clustering to divide iris dataset into 3 clusters.
- $oldsymbol{\Theta}$  After a choice of initial centroids, the k-means clustering algorithm is as follows:
- (1) calculate the distance of each data-point from each of the centroids
- (2) assign each of the data-points to its closest centroid
- (3) relocate the centroids to the average location of the data-points of similar group

And we repeat this procedure until the assignments don't change after the centroid locations were recomputed.

```
df <- iris[, -5]
```

```
dim(df)
## [1] 150 4
```

```
m <- dim(df)[1] # number of data-points
n <- dim(df)[2] # dimension of data-points
k <- 3 # number of clusters</pre>
```

```
X <- as.matrix(df)</pre>
```

Now we initialize the centroids as 3 randomly chosen data-points.

```
random_index <- sample(m, k)
centroid <- X[random_index, ]</pre>
```

We now deploy our k-means clustering algorithm.

```
cluster <- c()
repeat{
  dist_mat <- matrix(0, nrow = m, ncol = k)</pre>
```

```
for (i in 1:k) {
    d <- apply(X, 1, FUN = function(x) return(x - centroid[i, ]))

    d <- matrix(d, nrow = m, ncol = n, byrow = TRUE)

    dist_mat[,i] <- sqrt(diag( d %*% t(d) ) )
}

cluster <- apply(dist_mat, 1, FUN = function(x) return(which(x == min(x))[1]))

new_centroid <- matrix(data = 0, nrow = k, ncol = n)

for (i in 1:k) {
    new_centroid[i, ] <- mean(X[which(cluster == i), ])
}

if(any(centroid - new_centroid != 0)){
    centroid <- new_centroid
} else{
    break
}</pre>
```

## extstyle ext

In *iris* dataset, frequency distribution of 3 species was :

```
table(iris[,5])

##

## setosa versicolor virginica
## 50 50 50
```

Our k-means algorithm categorizes the iris dataset with the frequency distribution as follows:

```
table(cluster)

## cluster

## 1 2 3
## 58 38 54
```