

hw2_4.2.R

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2020-05-25

```
#HW2 Question 4.2
# Clear environment
rm(list = ls())
data <- read.table("iris.txt", header = TRUE)

set.seed(1)
#type_num<-length(levels(data[,5]))

##### MODEL 1: USE 4 PREDICTORS#####
#creat a vector to store cluster number
cluster_num<-rep(0,5)

scdata <- data # initialize value/size of sdata
for (i in 1:4) {scdata[,i] <- (data[,i]-min(data[,i]))/(max(data[,i])-min(data[,i])) }

#x: numeric matrix, numeric data frame or a numeric vector
#centers: Possible values are the number of clusters (k) or a set of initial (distinct) cluster centers
#iter.max: The maximum number of iterations allowed. Default value is 10.
#nstart: The number of random starting partitions when centers is a number. Trying nstart > 1 is often

csum<- rep(0,10)
result <- frame()

for (cluster_num in 2:11 ){
  # first use all four predictors to feed the kmeans function
  nmodel<-kmeans(scddata[,1:4], cluster_num, iter.max = 10, nstart = 20)
  #print(cluster_num)

  for (i in 1:nrow(scddata)) {

    #calculate the total distance between cluster center and each data point
    csum[(cluster_num-1)] = csum[(cluster_num-1)] + dist(rbind(scddata[i,1:4],nmodel$centers[nmodel$cluster
  ])
  cat("4 predictors results:")
  print(table(nmodel$cluster, data$Species))
}
```

```

## 4 predictors results:
##      setosa versicolor virginica
## 1      50          0          0
## 2       0          50         50
## 4 predictors results:
##      setosa versicolor virginica
## 1       0          47         14
## 2      50          0          0
## 3       0           3         36
## 4 predictors results:
##      setosa versicolor virginica
## 1      50          0          0
## 2       0          0         29
## 3       0         23         19
## 4       0         27          2
## 4 predictors results:
##      setosa versicolor virginica
## 1       0         23         19
## 2       0         27          2
## 3      28          0          0
## 4       0          0         29
## 5      22          0          0
## 4 predictors results:
##      setosa versicolor virginica
## 1       0         23         17
## 2      28          0          0
## 3      22          0          0
## 4       0          0         19
## 5       0          0         12
## 6       0         27          2
## 4 predictors results:
##      setosa versicolor virginica
## 1       0          0         18
## 2      28          0          0
## 3       0           3         19
## 4      22          0          0
## 5       0         25          1
## 6       0         22          1
## 7       0          0         11
## 4 predictors results:
##      setosa versicolor virginica
## 1      22          0          0
## 2       0          0         18
## 3       0         13          0
## 4       0           4         20
## 5       0          0         11
## 6       0         12          1
## 7      28          0          0
## 8       0         21          0
## 4 predictors results:
##      setosa versicolor virginica
## 1       0          2         19
## 2       0          0         16
## 3      21          0          0

```

```

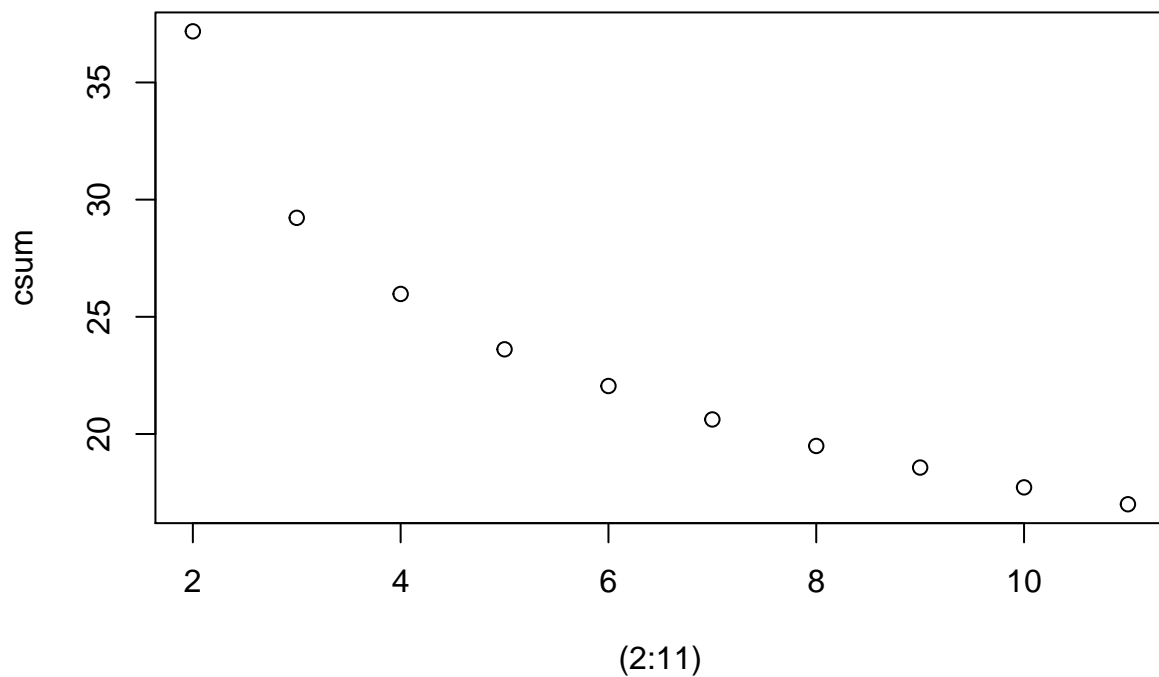
## 4      0      12      1
## 5     17       0      0
## 6     12       0      0
## 7      0       0     11
## 8      0      14      1
## 9      0      22      2
## 4 predictors results:
##      setosa versicolor virginica
## 1      21         0         0
## 2      12         0         0
## 3       0         4        17
## 4       0         0        20
## 5       0         0         3
## 6       0         0         9
## 7       0        12         1
## 8       0        21         0
## 9       0        13         0
## 10      17         0         0
## 4 predictors results:
##      setosa versicolor virginica
## 1      17         0         0
## 2      21         0         0
## 3       0         4         4
## 4       0         1        17
## 5       0         0         3
## 6       0        16         1
## 7       0        18         1
## 8      12         0         0
## 9       0         0        15
## 10      0         0         9
## 11      0        11         0

```

```

# Compare the model results with raw data result
plot((2:11),csum)

```



MODEL 2: Use Petal Length and Petal Width only, repeat the same testing

```
csum<- rep(0,10)
result <- frame()

for (cluster_num in 2:11 ){

  nmodel<-kmeans(scdata[,3:4], cluster_num, iter.max = 10, nstart = 20)
  print(cluster_num)
  for (i in 1:nrow(scdata)) {

    csum[(cluster_num-1)] = csum[(cluster_num-1)] + dist(rbind(scdata[i,3:4],nmodel$centers[nmodel$clus
  ])
  }
  cat("Petal Length and Petal Width as predictors only results:")
  print(table(nmodel$cluster, data$Species))
}
```

```
## [1] 2
## Petal Length and Petal Width as predictors only results:
##      setosa versicolor virginica
##  1      0      50      50
##  2     50       0       0
## [1] 3
## Petal Length and Petal Width as predictors only results:
##      setosa versicolor virginica
##  1     50       0       0
```

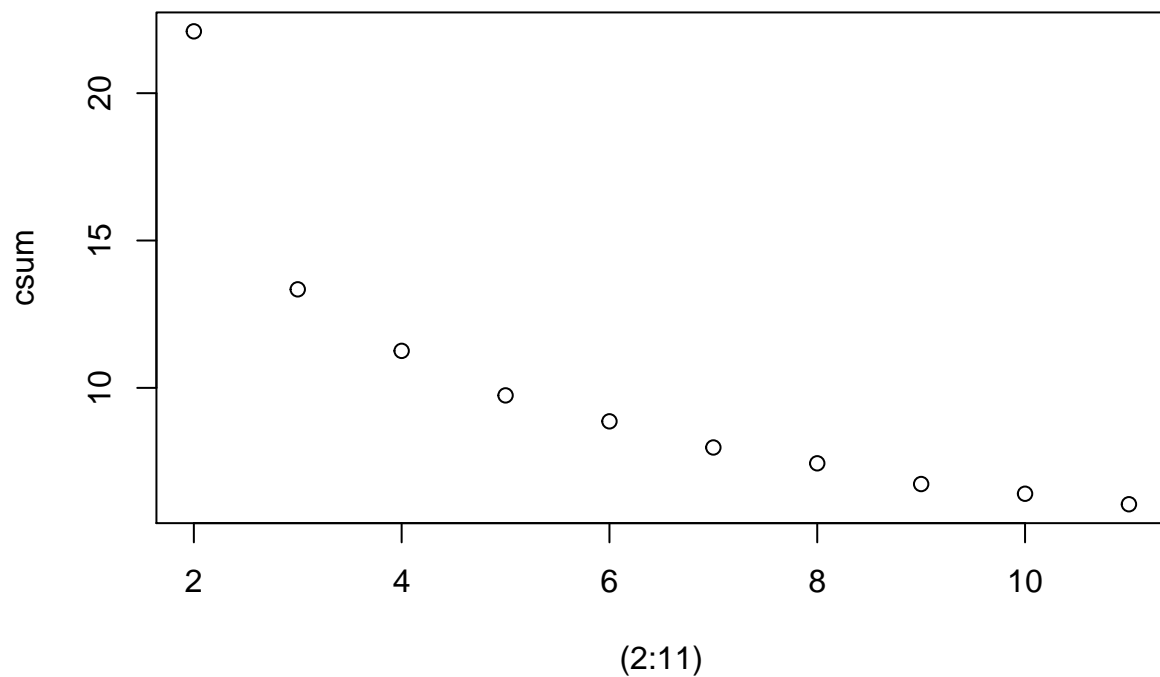
```

##      2      0      48      4
##      3      0       2     46
## [1] 4
## Petal Length and Petal Width as predictors only results:
##      setosa versicolor virginica
##      1      0      0      27
##      2      0     42      0
##      3      0      8     23
##      4     50      0      0
## [1] 5
## Petal Length and Petal Width as predictors only results:
##      setosa versicolor virginica
##      1      0      0     25
##      2      0     25      4
##      3      0     23      0
##      4     50      0      0
##      5      0      2     21
## [1] 6
## Petal Length and Petal Width as predictors only results:
##      setosa versicolor virginica
##      1      0     23      0
##      2      0     24      4
##      3      0      3     18
##      4      0      0     20
##      5     50      0      0
##      6      0      0      8
## [1] 7
## Petal Length and Petal Width as predictors only results:
##      setosa versicolor virginica
##      1     50      0      0
##      2      0     16      4
##      3      0     22      0
##      4      0      0      8
##      5      0     10      0
##      6      0      0     20
##      7      0      2     18
## [1] 8
## Petal Length and Petal Width as predictors only results:
##      setosa versicolor virginica
##      1      0      0      8
##      2     50      0      0
##      3      0      2     13
##      4      0     22      0
##      5      0      0     20
##      6      0     10      0
##      7      0      0      5
##      8      0     16      4
## [1] 9
## Petal Length and Petal Width as predictors only results:
##      setosa versicolor virginica
##      1      0     22      0
##      2      0      0      5
##      3      0      2     13
##      4      0     10      0

```

```
##      5      0      16      4
##      6     16      0      0
##      7      0      0     20
##      8      0      0      8
##      9     34      0      0
## [1] 10
## Petal Length and Petal Width as predictors only results:
##      setosa versicolor virginica
##      1     16          0          0
##      2      0          0          8
##      3      0         22          0
##      4      0          2         13
##      5      0          0          5
##      6     34          0          0
##      7      0         16          4
##      8      0          0         12
##      9      0         10          0
##     10      0          0          8
## [1] 11
## Petal Length and Petal Width as predictors only results:
##      setosa versicolor virginica
##      1     16          0          0
##      2      0          0          5
##      3      0          0          7
##      4      0          0          5
##      5      0         10          0
##      6     34          0          0
##      7      0          0          8
##      8      0          0          8
##      9      0         22          0
##     10      0          2         13
##     11      0         16          4
```

```
plot((2:11),csum)
```



MODEL 3: Use Sepal.Length, Sepal.Width and Petal.Length as predictors, repeat the

```
csum<- rep(0,10)
result <- frame()

for (cluster_num in 2:11 ){

  nmodel<-kmeans(scdata[,1:3], cluster_num, iter.max = 10, nstart = 20)
  print(cluster_num)
  for (i in 1:nrow(scdata)) {

    csum[(cluster_num-1)] = csum[(cluster_num-1)] + dist(rbind(scdata[i,1:3],nmodel$centers[nmodel$clus
  ])
  }
  cat("SepalLength,Sepal Width and PetalLength as predictors results:")
  print(table(nmodel$cluster, data$Species))
}
```

```
## [1] 2
## SepalLength,Sepal Width and PetalLength as predictors results:
##      setosa versicolor virginica
##  1      50           1           0
##  2       0          49          50
## [1] 3
## SepalLength,Sepal Width and PetalLength as predictors results:
##      setosa versicolor virginica
##  1      50           0           0
```

```

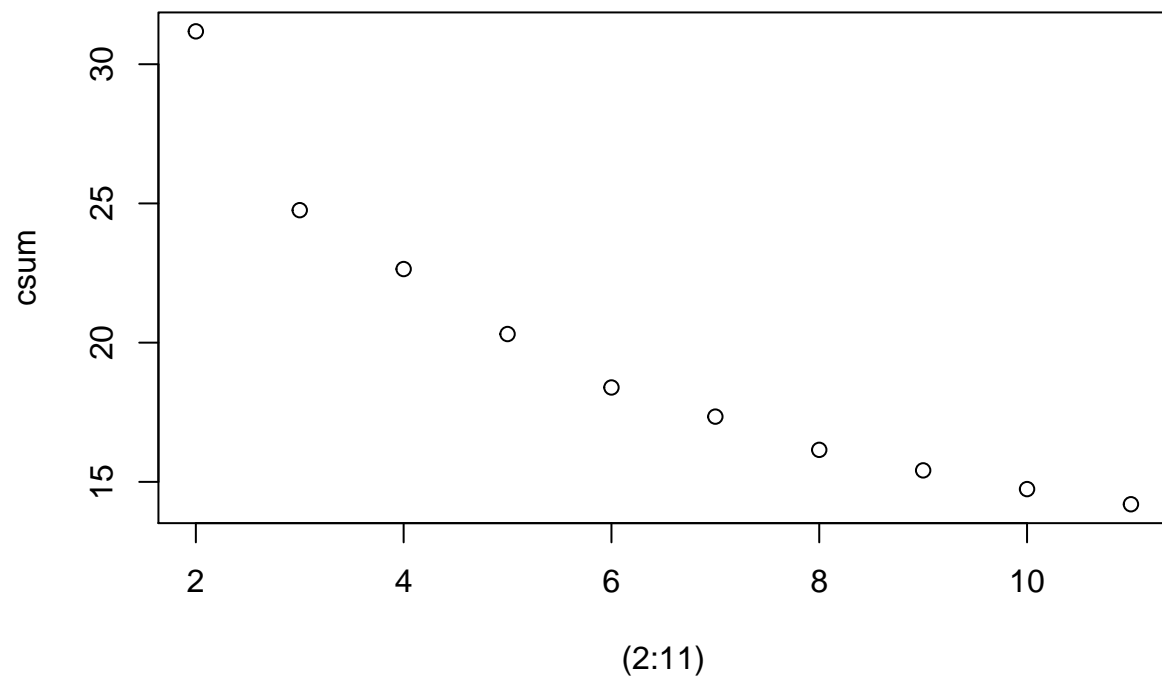
##      2      0      10      35
##      3      0      40      15
## [1] 4
## SepalLength,Sepal Width and PetalLength as predictors results:
##      setosa versicolor virginica
##      1      0      0      14
##      2      0      21      30
##      3      0      29      6
##      4     50      0      0
## [1] 5
## SepalLength,Sepal Width and PetalLength as predictors results:
##      setosa versicolor virginica
##      1      0      0      14
##      2      0      29      6
##      3      0      21      30
##      4     22      0      0
##      5     28      0      0
## [1] 6
## SepalLength,Sepal Width and PetalLength as predictors results:
##      setosa versicolor virginica
##      1     24      0      0
##      2      0      0     12
##      3     26      0      0
##      4      0     19      2
##      5      0     21     13
##      6      0     10     23
## [1] 7
## SepalLength,Sepal Width and PetalLength as predictors results:
##      setosa versicolor virginica
##      1     28      0      0
##      2      0     14      1
##      3      0     21      5
##      4      0      0     12
##      5      0      5     13
##      6      0     10     19
##      7     22      0      0
## [1] 8
## SepalLength,Sepal Width and PetalLength as predictors results:
##      setosa versicolor virginica
##      1      0      0     12
##      2     12      0      0
##      3      0     21      5
##      4     22      0      0
##      5     16      0      0
##      6      0      5     13
##      7      0     10     19
##      8      0     14      1
## [1] 9
## SepalLength,Sepal Width and PetalLength as predictors results:
##      setosa versicolor virginica
##      1      0     12      3
##      2     12      0      0
##      3     16      0      0
##      4      0      0     12

```



```
##      5      0      20      5
##      6      0      14      1
##      7      0       4     13
##      8      0       0     16
##      9     22       0      0
## [1] 10
## SepalLength, Sepal Width and PetalLength as predictors results:
##      setosa versicolor virginica
##      1      0      0      19
##      2      0      0       3
##      3      0      4      11
##      4     26      0       0
##      5      0     20       5
##      6      0      0       9
##      7      0     12       2
##      8      7      0       0
##      9     17      0       0
##     10      0     14       1
## [1] 11
## SepalLength, Sepal Width and PetalLength as predictors results:
##      setosa versicolor virginica
##      1     20      0       0
##      2     16      0       0
##      3      0      0       3
##      4      0      4     13
##      5      0     15       1
##      6      0      0       9
##      7      4      0       0
##      8     10      0       0
##      9      0      5     19
##     10      0     14       4
##     11      0     12       1
```

```
plot((2:11), csum)
```



CONCLUSION

cat("\n Conclusion: From the results from 3 models with different predictors we can conclude: \n 1. From

##

Conclusion: From the results from 3 models with different predictors we can conclude:

1. From the plot K VS Total Distance, The best K value is 3.

2. The best model is the one using Petal Length and Petal Width.