

HW 4.2

Run Packages and Import Data

```
library("cluster")
library("knitr")

# built in kmeans function
# function (x, centers, iter.max = 10L, nstart = 1L, algorithm = c("Hartigan-Wong",
# "Lloyd", "Forgy", "MacQueen"), trace = FALSE)

data <- read.table("iris.txt")

# remove species label (categorical RESPONSE variable, should not be used to build model)
nosp_iris <- iris[, -5]
print(nosp_iris)
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
## 1	5.1	3.5	1.4	0.2
## 2	4.9	3.0	1.4	0.2
## 3	4.7	3.2	1.3	0.2
## 4	4.6	3.1	1.5	0.2
## 5	5.0	3.6	1.4	0.2
## 6	5.4	3.9	1.7	0.4
## 7	4.6	3.4	1.4	0.3
## 8	5.0	3.4	1.5	0.2
## 9	4.4	2.9	1.4	0.2
## 10	4.9	3.1	1.5	0.1
## 11	5.4	3.7	1.5	0.2
## 12	4.8	3.4	1.6	0.2
## 13	4.8	3.0	1.4	0.1
## 14	4.3	3.0	1.1	0.1
## 15	5.8	4.0	1.2	0.2
## 16	5.7	4.4	1.5	0.4
## 17	5.4	3.9	1.3	0.4
## 18	5.1	3.5	1.4	0.3
## 19	5.7	3.8	1.7	0.3
## 20	5.1	3.8	1.5	0.3
## 21	5.4	3.4	1.7	0.2
## 22	5.1	3.7	1.5	0.4
## 23	4.6	3.6	1.0	0.2
## 24	5.1	3.3	1.7	0.5
## 25	4.8	3.4	1.9	0.2
## 26	5.0	3.0	1.6	0.2
## 27	5.0	3.4	1.6	0.4
## 28	5.2	3.5	1.5	0.2
## 29	5.2	3.4	1.4	0.2
## 30	4.7	3.2	1.6	0.2
## 31	4.8	3.1	1.6	0.2

## 32	5.4	3.4	1.5	0.4
## 33	5.2	4.1	1.5	0.1
## 34	5.5	4.2	1.4	0.2
## 35	4.9	3.1	1.5	0.2
## 36	5.0	3.2	1.2	0.2
## 37	5.5	3.5	1.3	0.2
## 38	4.9	3.6	1.4	0.1
## 39	4.4	3.0	1.3	0.2
## 40	5.1	3.4	1.5	0.2
## 41	5.0	3.5	1.3	0.3
## 42	4.5	2.3	1.3	0.3
## 43	4.4	3.2	1.3	0.2
## 44	5.0	3.5	1.6	0.6
## 45	5.1	3.8	1.9	0.4
## 46	4.8	3.0	1.4	0.3
## 47	5.1	3.8	1.6	0.2
## 48	4.6	3.2	1.4	0.2
## 49	5.3	3.7	1.5	0.2
## 50	5.0	3.3	1.4	0.2
## 51	7.0	3.2	4.7	1.4
## 52	6.4	3.2	4.5	1.5
## 53	6.9	3.1	4.9	1.5
## 54	5.5	2.3	4.0	1.3
## 55	6.5	2.8	4.6	1.5
## 56	5.7	2.8	4.5	1.3
## 57	6.3	3.3	4.7	1.6
## 58	4.9	2.4	3.3	1.0
## 59	6.6	2.9	4.6	1.3
## 60	5.2	2.7	3.9	1.4
## 61	5.0	2.0	3.5	1.0
## 62	5.9	3.0	4.2	1.5
## 63	6.0	2.2	4.0	1.0
## 64	6.1	2.9	4.7	1.4
## 65	5.6	2.9	3.6	1.3
## 66	6.7	3.1	4.4	1.4
## 67	5.6	3.0	4.5	1.5
## 68	5.8	2.7	4.1	1.0
## 69	6.2	2.2	4.5	1.5
## 70	5.6	2.5	3.9	1.1
## 71	5.9	3.2	4.8	1.8
## 72	6.1	2.8	4.0	1.3
## 73	6.3	2.5	4.9	1.5
## 74	6.1	2.8	4.7	1.2
## 75	6.4	2.9	4.3	1.3
## 76	6.6	3.0	4.4	1.4
## 77	6.8	2.8	4.8	1.4
## 78	6.7	3.0	5.0	1.7
## 79	6.0	2.9	4.5	1.5
## 80	5.7	2.6	3.5	1.0
## 81	5.5	2.4	3.8	1.1
## 82	5.5	2.4	3.7	1.0
## 83	5.8	2.7	3.9	1.2
## 84	6.0	2.7	5.1	1.6
## 85	5.4	3.0	4.5	1.5

## 86	6.0	3.4	4.5	1.6
## 87	6.7	3.1	4.7	1.5
## 88	6.3	2.3	4.4	1.3
## 89	5.6	3.0	4.1	1.3
## 90	5.5	2.5	4.0	1.3
## 91	5.5	2.6	4.4	1.2
## 92	6.1	3.0	4.6	1.4
## 93	5.8	2.6	4.0	1.2
## 94	5.0	2.3	3.3	1.0
## 95	5.6	2.7	4.2	1.3
## 96	5.7	3.0	4.2	1.2
## 97	5.7	2.9	4.2	1.3
## 98	6.2	2.9	4.3	1.3
## 99	5.1	2.5	3.0	1.1
## 100	5.7	2.8	4.1	1.3
## 101	6.3	3.3	6.0	2.5
## 102	5.8	2.7	5.1	1.9
## 103	7.1	3.0	5.9	2.1
## 104	6.3	2.9	5.6	1.8
## 105	6.5	3.0	5.8	2.2
## 106	7.6	3.0	6.6	2.1
## 107	4.9	2.5	4.5	1.7
## 108	7.3	2.9	6.3	1.8
## 109	6.7	2.5	5.8	1.8
## 110	7.2	3.6	6.1	2.5
## 111	6.5	3.2	5.1	2.0
## 112	6.4	2.7	5.3	1.9
## 113	6.8	3.0	5.5	2.1
## 114	5.7	2.5	5.0	2.0
## 115	5.8	2.8	5.1	2.4
## 116	6.4	3.2	5.3	2.3
## 117	6.5	3.0	5.5	1.8
## 118	7.7	3.8	6.7	2.2
## 119	7.7	2.6	6.9	2.3
## 120	6.0	2.2	5.0	1.5
## 121	6.9	3.2	5.7	2.3
## 122	5.6	2.8	4.9	2.0
## 123	7.7	2.8	6.7	2.0
## 124	6.3	2.7	4.9	1.8
## 125	6.7	3.3	5.7	2.1
## 126	7.2	3.2	6.0	1.8
## 127	6.2	2.8	4.8	1.8
## 128	6.1	3.0	4.9	1.8
## 129	6.4	2.8	5.6	2.1
## 130	7.2	3.0	5.8	1.6
## 131	7.4	2.8	6.1	1.9
## 132	7.9	3.8	6.4	2.0
## 133	6.4	2.8	5.6	2.2
## 134	6.3	2.8	5.1	1.5
## 135	6.1	2.6	5.6	1.4
## 136	7.7	3.0	6.1	2.3
## 137	6.3	3.4	5.6	2.4
## 138	6.4	3.1	5.5	1.8
## 139	6.0	3.0	4.8	1.8

## 140	6.9	3.1	5.4	2.1
## 141	6.7	3.1	5.6	2.4
## 142	6.9	3.1	5.1	2.3
## 143	5.8	2.7	5.1	1.9
## 144	6.8	3.2	5.9	2.3
## 145	6.7	3.3	5.7	2.5
## 146	6.7	3.0	5.2	2.3
## 147	6.3	2.5	5.0	1.9
## 148	6.5	3.0	5.2	2.0
## 149	6.2	3.4	5.4	2.3
## 150	5.9	3.0	5.1	1.8

Set Seed and Run Model

```
# kmeans fit to train
set.seed(3283) # set random seed
kmeansmodel <- kmeans(nosp_iris, centers = 3, nstart = 30, algorithm = "Lloyd")

## Warning: did not converge in 10 iterations

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# 3 centers to start to check which combination of predictors is the best (3 types of species)
# using 30 (relatively big number) for number of starts to avoid getting stuck in undesirable local opt
# using default Lloyd algorithm for kmeans
```

Find the Best Combination of Predictors by Graphing

```
# Find best combination of predictors

par(mfrow = c(2, 2)) # set plots next to each other

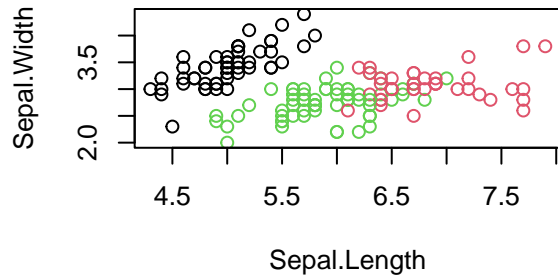
# sepal length and width
plot(nosp_iris[c("Sepal.Length", "Sepal.Width")],
     col = kmeansmodel$cluster,
     main = "Sepal Length and Sepal Width")

# petal length and width
plot(nosp_iris[c("Petal.Length", "Petal.Width")],
     col = kmeansmodel$cluster,
     main = "Petal Length and Petal Width")

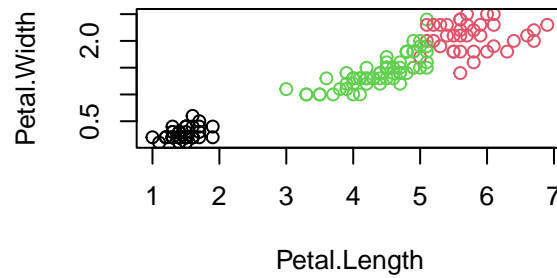
# sepal length and petal width
plot(nosp_iris[c("Sepal.Length", "Petal.Width")],
     col = kmeansmodel$cluster,
     main = "Sepal Length and Petal Width")

# petal length and sepal width
plot(nosp_iris[c("Petal.Length", "Sepal.Width")],
     col = kmeansmodel$cluster,
     main = "Petal Length and Sepal Width")
```

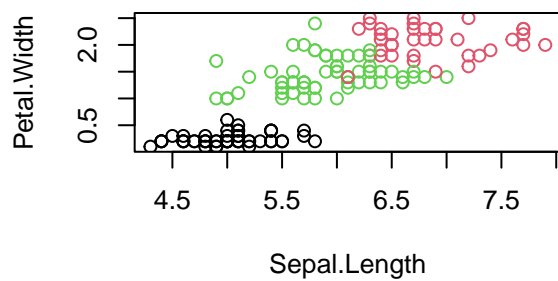
Sepal Length and Sepal Width



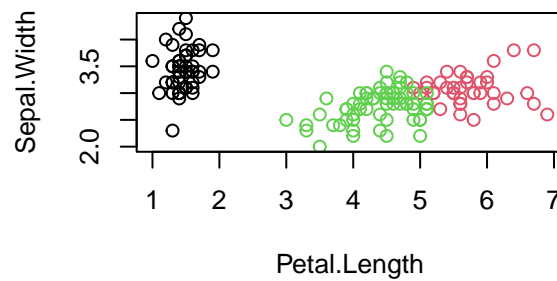
Petal Length and Petal Width



Sepal Length and Petal Width



Petal Length and Sepal Width



From just looking at it, seems like petal length and petal width has the least overlap

Check for Best k (# of Clusters) to Use Using Elbow Method

Best k value (center) to use for petal length and petal width (test out with for loop)

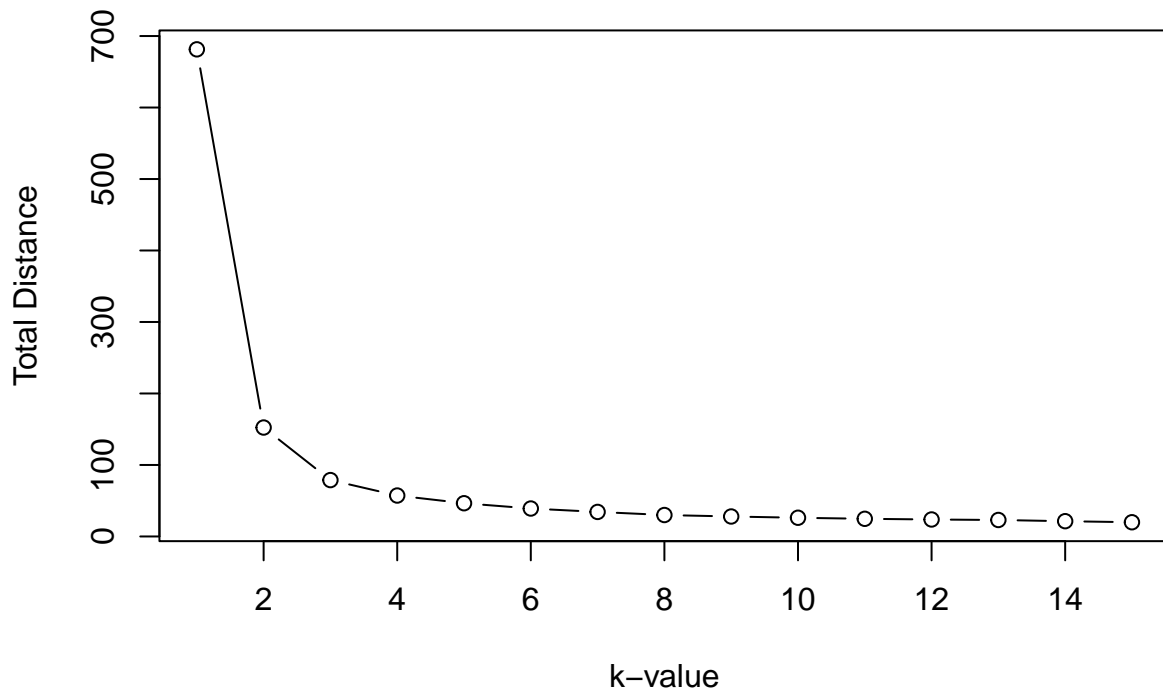
Using Elbow Method: Check graph of total distance vs k (# clusters) and wherever it stops having drastic decrease

total within distance of kmeans model is denoted with withinss

```
suppressWarnings ( {
ratios <- list()

for (k in 1:15) {
  kmeansmodel <- kmeans(nosp_iris, centers = k, nstart = 30, algorithm = "Lloyd")
  ratios <- append(ratios, kmeansmodel$tot.withinss)
}

par(mfrow=c(1,1))
plot(1:15, ratios, xlab = "k-value", ylab = "Total Distance", type="b")
})
```



```
# From the graph, seems like the best k to use is 3 (where the elbow bends)
```

Using Silhouette, Sum of Squares, Confusion Matrix for Evaluation

```
# Determine how good this model is with k = 3
```

```
# To get a numeric understanding of how good it is, will use the silhouette method
```

```
# The silhouette method measures quality of clustering by determining how well each object lies within its
```

```
# A high average silhouette width indicates good clustering.
```

```
suppressWarnings ( {  
kmeansmodel <- kmeans(nosp_iris, centers = 3, nstart = 30, algorithm = "Lloyd")  
})
```

```
s <- silhouette(kmeansmodel$cluster, dist(nosp_iris))
```

```
avg_s <- mean(s[,3]) # 3 is to index towards the silhouette values
```

```
print(paste("The average silhouette value of k = 3 is", avg_s, "and as the silhouette value > 0.5, it in"))
```

```
## [1] "The average silhouette value of k = 3 is 0.55281901235641 and as the silhouette value > 0.5, it in"
```

```
# Sum of squares (evaluation)
```

```
kmeansmodel$withinss
```

```
## [1] 23.87947 39.82097 15.15100
```

```
# Confusion matrix (evaluation)
```

```
table(data$Species, kmeansmodel$cluster)
```

```
##  
##           1  2  3  
## setosa      0  0 50  
## versicolor  2 48  0  
## virginica  36 14  0
```