

# Cluster Analysis I

Mike Strube

October 24, 2018

## 1 Preliminaries

*In this section, the RStudio workspace and console panes are cleared of old output, variables, and other miscellaneous debris. Packages are loaded and any required data files are retrieved.*

```
options(replace.assign = TRUE, width = 65, digits = 4, scipen = 4, fig.width = 4,
        fig.height = 4)
# Clear the workspace and console.
rm(list = ls(all = TRUE))
cat("\f")
```

```
# Turn off showing of significance asterisks.
options(show.signif.stars = F)
# Set the contrast option; important for ANOVAs.
options(contrasts = c("contr.sum", "contr.poly"))
how_long <- Sys.time()
set.seed(123)
library(knitr)
```

```
library(psych)
library(ggplot2)

##
## Attaching package: 'ggplot2'
## The following objects are masked from 'package:psych':
##
##   %+%, alpha

library(MASS)
library(sciplot)
library(ggplot2)
library(vegan)

## Warning: package 'vegan' was built under R version 3.5.1
## Loading required package: permute
## Warning: package 'permute' was built under R version 3.5.1
## Loading required package: lattice
## This is vegan 2.5-2

library(smacof)
```

```
## Warning: package 'smacof' was built under R version 3.5.1
## Loading required package: plotrix
##
## Attaching package: 'plotrix'
## The following object is masked from 'package:psych':
##
##     rescale
##
## Attaching package: 'smacof'
## The following object is masked from 'package:base':
##
##     transform

library(ape)
library(ade4)

## Warning: package 'ade4' was built under R version 3.5.1

library(scatterplot3d)
library(cluster)
library(factoextra)

## Warning: package 'factoextra' was built under R version 3.5.1
## Welcome! Related Books: 'Practical Guide To Cluster Analysis in R' at https://goo.gl/13EFCZ

library(ggdendro)

## Warning: package 'ggdendro' was built under R version 3.5.1
```

## 2 Simple Case

*Let's begin with a very simple problem: 5 cases that are arranged in two-dimensional space for which Euclidean distance is easily visualized. To emphasize the distances a bit we can use squared Euclidean distance.*

```
Data <- matrix(c(2, 3, 4, 6, 7, 2, 2, 5, 4, 6), nrow = 5, ncol = 2,
               byrow = FALSE)
row.names(Data) <- c("Object 1", "Object 2", "Object 3", "Object 4",
                    "Object 5")
```

Data

```
##           [,1] [,2]
## Object 1      2      2
## Object 2      3      2
## Object 3      4      5
## Object 4      6      4
## Object 5      7      6
```

```
Data_Dist <- (dist(Data, method = "euclidean"))^2
```

Data\_Dist

```
##           Object 1 Object 2 Object 3 Object 4
## Object 2           1
## Object 3          13          10
## Object 4          20          13           5
## Object 5          41          32          10           5
```

## 2.1 Single Linkage

*The dissimilarity between two clusters (A and B) is the minimum of all possible distances between the cases in Cluster A and the cases in Cluster B.*

```
hc_1 <- hclust(Data_Dist, method = "single")
```

```
hc_1$merge
```

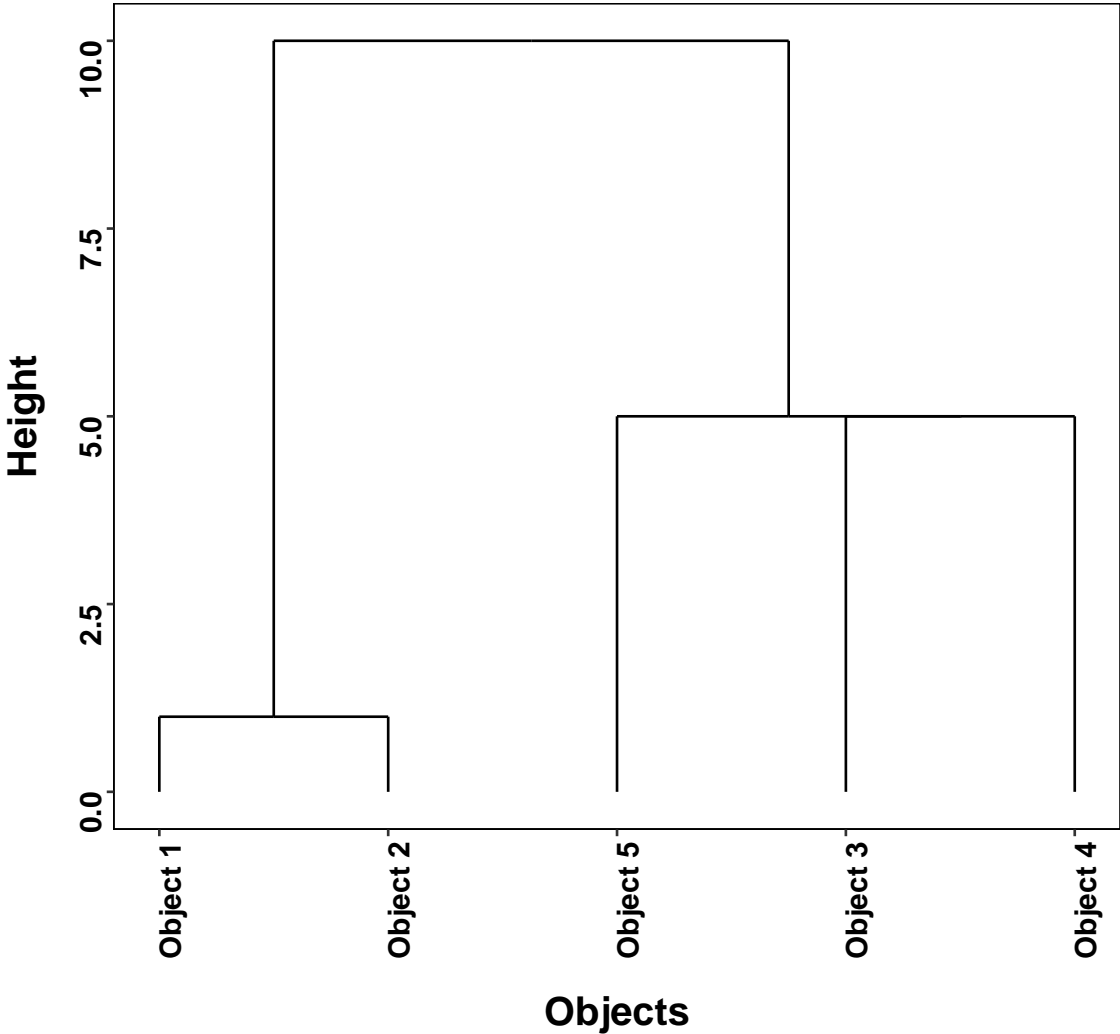
```
##      [,1] [,2]
## [1,]   -1  -2
## [2,]   -3  -4
## [3,]   -5   2
## [4,]    1   3
```

```
hc_1$height
```

```
## [1]  1  5  5 10
```

```
ggdendrogram(hc_1, theme_dendro = FALSE, size = 4) + xlab("Objects") +
  ylab("Height") + theme(text = element_text(size = 14, family = "sans",
  color = "black", face = "bold"), axis.text.y = element_text(colour = "black",
  size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
  size = 12, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
  0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
  15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
  axis.line.y = element_blank(), plot.title = element_text(size = 16,
  face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
  panel.background = element_rect(fill = "white", linetype = 1,
  color = "black"), panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
  plot.background = element_rect(fill = "white"), plot.margin = unit(c(1,
  1, 1, 1), "cm"), legend.position = "bottom", legend.title = element_blank()) +
  ggtitle("Cluster Dendrogram: Single Linkage")
```

Cluster Dendrogram: Single Linkage



## 2.2 Complete Linkage

*The dissimilarity between two clusters (A and B) is the maximum of all possible distances between the cases in Cluster A and the cases in Cluster B.*

```
hc_2 <- hclust(Data_Dist, method = "complete")
hc_2$merge
```

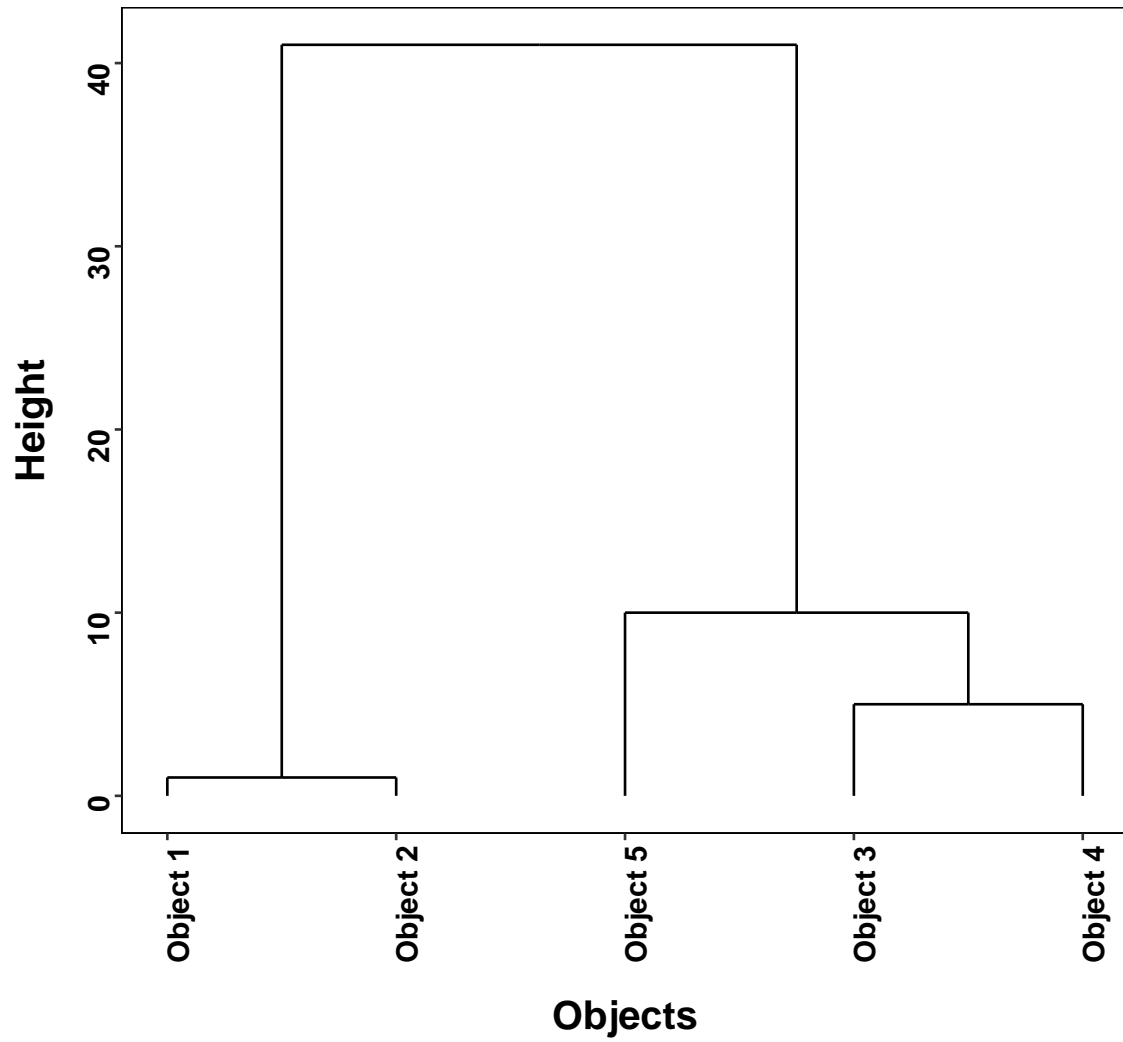
```
##      [,1] [,2]
## [1,]   -1  -2
## [2,]   -3  -4
## [3,]   -5   2
## [4,]    1   3
```

```
hc_2$height
```

```
## [1]  1  5 10 41
```

```
ggdendrogram(hc_2, theme_dendro = FALSE) + xlab("Objects") + ylab("Height") +
  theme(text = element_text(size = 14, family = "sans", color = "black",
    face = "bold"), axis.text.y = element_text(colour = "black",
    size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
    size = 12, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
    0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
    15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
    axis.line.y = element_blank(), plot.title = element_text(size = 16,
    face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
    panel.background = element_rect(fill = "white", linetype = 1,
    color = "black"), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), plot.background = element_rect(fill = "white"),
    plot.margin = unit(c(1, 1, 1, 1), "cm"), legend.position = "bottom",
    legend.title = element_blank()) + ggtitle("Cluster Dendrogram: Complete Linkage")
```

**Cluster Dendrogram: Complete Linkage**



## 2.3 Average Linkage

*The dissimilarity between two clusters (A and B) is the average of all possible distances between the cases in Cluster A and the cases in Cluster B.*

```
hc_3 <- hclust(Data_Dist, method = "average")
hc_3$merge
```

```
##      [,1] [,2]
## [1,]   -1  -2
## [2,]   -3  -4
## [3,]   -5   2
## [4,]    1   3
```

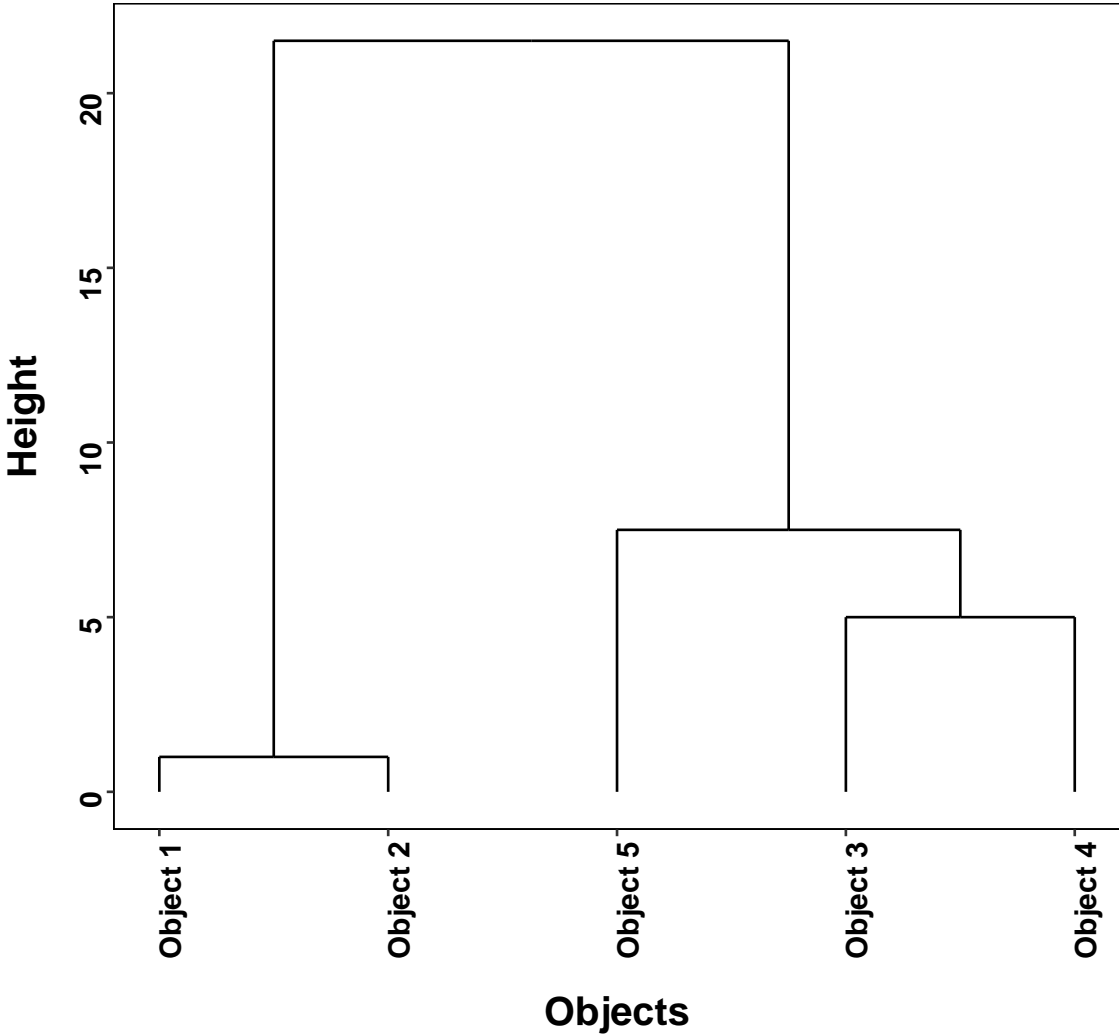
```
hc_3$height
```

```
## [1]  1.0  5.0  7.5 21.5
```

```
ggdendrogram(hc_3, theme_dendro = FALSE) + xlab("Objects") + ylab("Height") +
  theme(text = element_text(size = 14, family = "sans", color = "black",
    face = "bold"), axis.text.y = element_text(colour = "black",
    size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
    size = 12, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
    0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
    15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
    axis.line.y = element_blank(), plot.title = element_text(size = 16,
    face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
    panel.background = element_rect(fill = "white", linetype = 1,
    color = "black"), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), plot.background = element_rect(fill = "white"),
    plot.margin = unit(c(1, 1, 1, 1), "cm"), legend.position = "bottom",
    legend.title = element_blank()) + ggtitle("Cluster Dendrogram: Average Linkage")
```



**Cluster Dendrogram: Average Linkage**



## 2.4 Centroid Method

*The dissimilarity between two clusters (A and B) is the distance between the centroid for the cases in Cluster A and the centroid for the cases in Cluster B.*

```
hc_4 <- hclust(Data_Dist, method = "centroid")
hc_4$merge
```

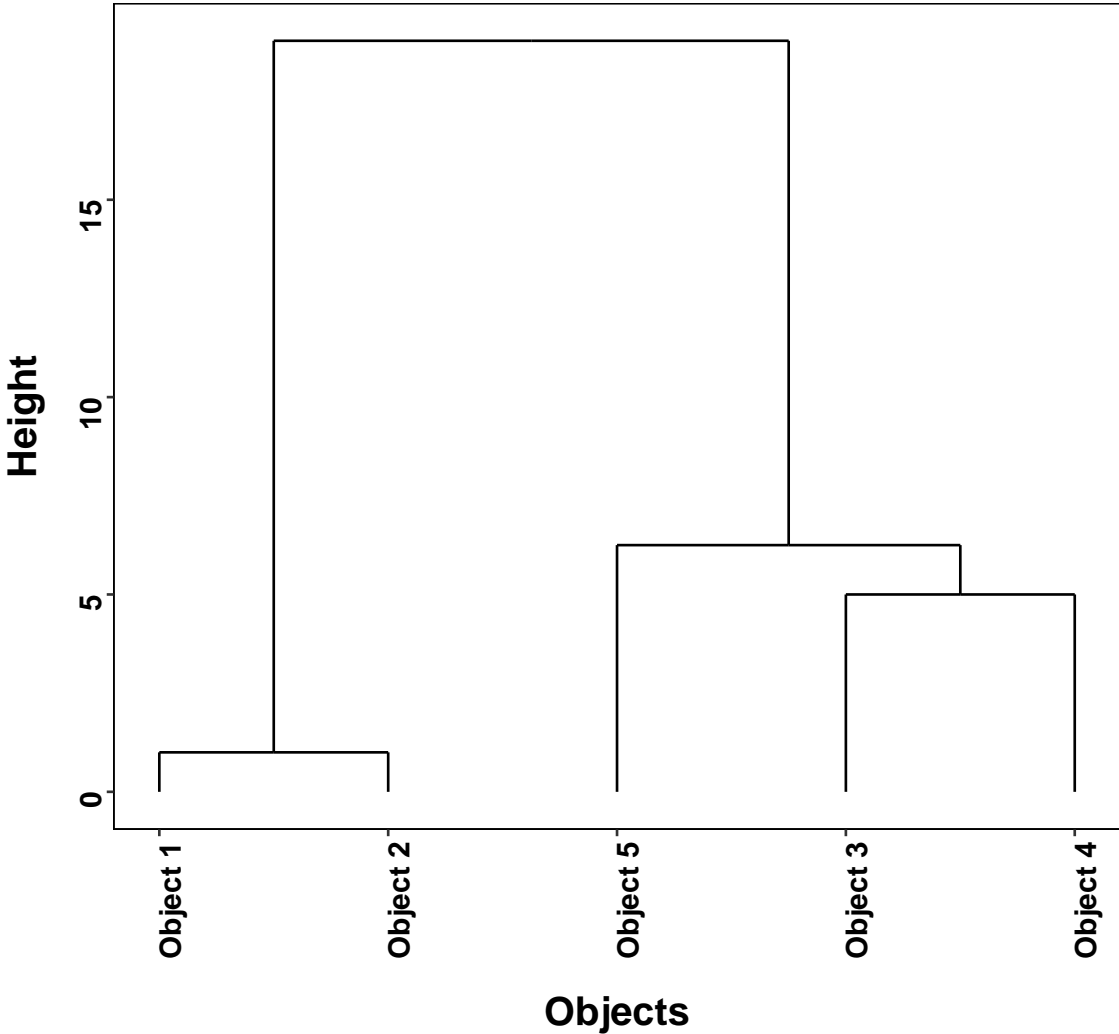
```
##      [,1] [,2]
## [1,]   -1  -2
## [2,]   -3  -4
## [3,]   -5   2
## [4,]    1   3
```

```
hc_4$height
```

```
## [1]  1.00  5.00  6.25 19.03
```

```
ggdendrogram(hc_4, theme_dendro = FALSE) + xlab("Objects") + ylab("Height") +
  theme(text = element_text(size = 14, family = "sans", color = "black",
    face = "bold"), axis.text.y = element_text(colour = "black",
    size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
    size = 12, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
    0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
    15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
    axis.line.y = element_blank(), plot.title = element_text(size = 16,
    face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
    panel.background = element_rect(fill = "white", linetype = 1,
    color = "black"), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), plot.background = element_rect(fill = "white"),
    plot.margin = unit(c(1, 1, 1, 1), "cm"), legend.position = "bottom",
    legend.title = element_blank()) + ggtitle("Cluster Dendrogram: Centroid Method")
```

**Cluster Dendrogram: Centroid Method**



## 2.5 Ward's Method

*The dissimilarity between two clusters (A and B) is the loss of information from joining the clusters, measured by the increase in error sum of squares.*

*The sum of squares for a cluster is the sum of squared deviations of each case from the centroid for the cluster. The error sum of squares is the total of these for all clusters. The two clusters among all possible combinations that have the minimum increase in error sum of squares are joined.*

*Two versions are available. The Ward D method should be chosen if squared Euclidean distances are used. the Ward D2 method will produce the traditional Ward solution starting from Euclidean distances.*

```
hc_5 <- hclust(Data_Dist, method = "ward.D")
hc_5$merge
```

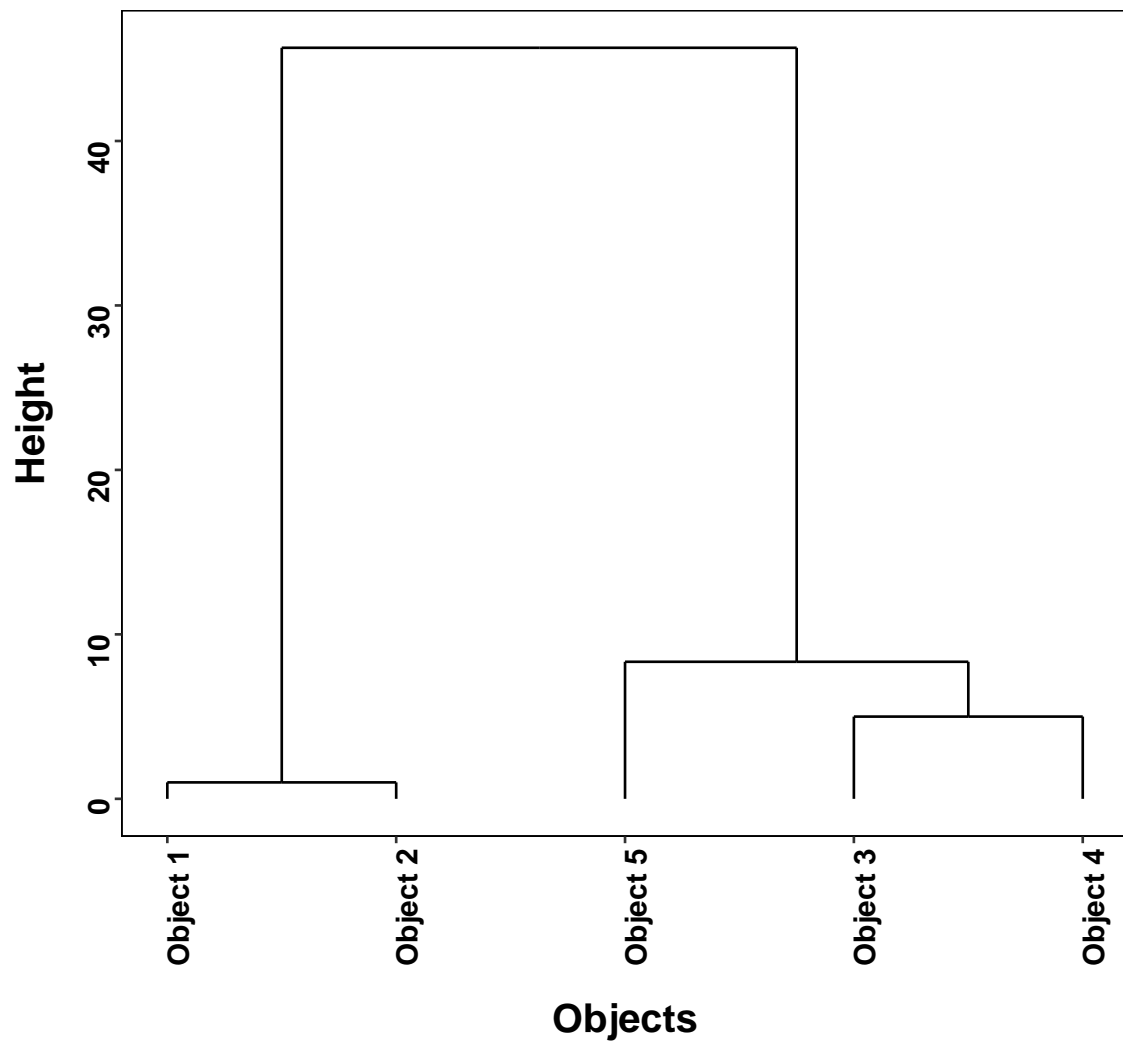
```
##      [,1] [,2]
## [1,]   -1  -2
## [2,]   -3  -4
## [3,]   -5   2
## [4,]    1   3
```

```
hc_5$height
```

```
## [1]  1.000  5.000  8.333 45.667
```

```
ggdendrogram(hc_5, theme_dendro = FALSE) + xlab("Objects") + ylab("Height") +
  theme(text = element_text(size = 14, family = "sans", color = "black",
    face = "bold"), axis.text.y = element_text(colour = "black",
    size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
    size = 12, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
    0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
    15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
    axis.line.y = element_blank(), plot.title = element_text(size = 16,
    face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
    panel.background = element_rect(fill = "white", linetype = 1,
    color = "black"), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), plot.background = element_rect(fill = "white"),
    plot.margin = unit(c(1, 1, 1, 1), "cm"), legend.position = "bottom",
    legend.title = element_blank()) + ggtitle("Cluster Dendrogram: Ward's Method (D)")
```

## Cluster Dendrogram: Ward's Method (D)



```
Data_Dist <- (dist(Data, method = "euclidean"))
hc_5 <- hclust(Data_Dist, method = "ward.D2")
hc_5$merge

##      [,1] [,2]
## [1,]  -1  -2
## [2,]  -3  -4
## [3,]  -5   2
## [4,]   1   3

hc_5$height

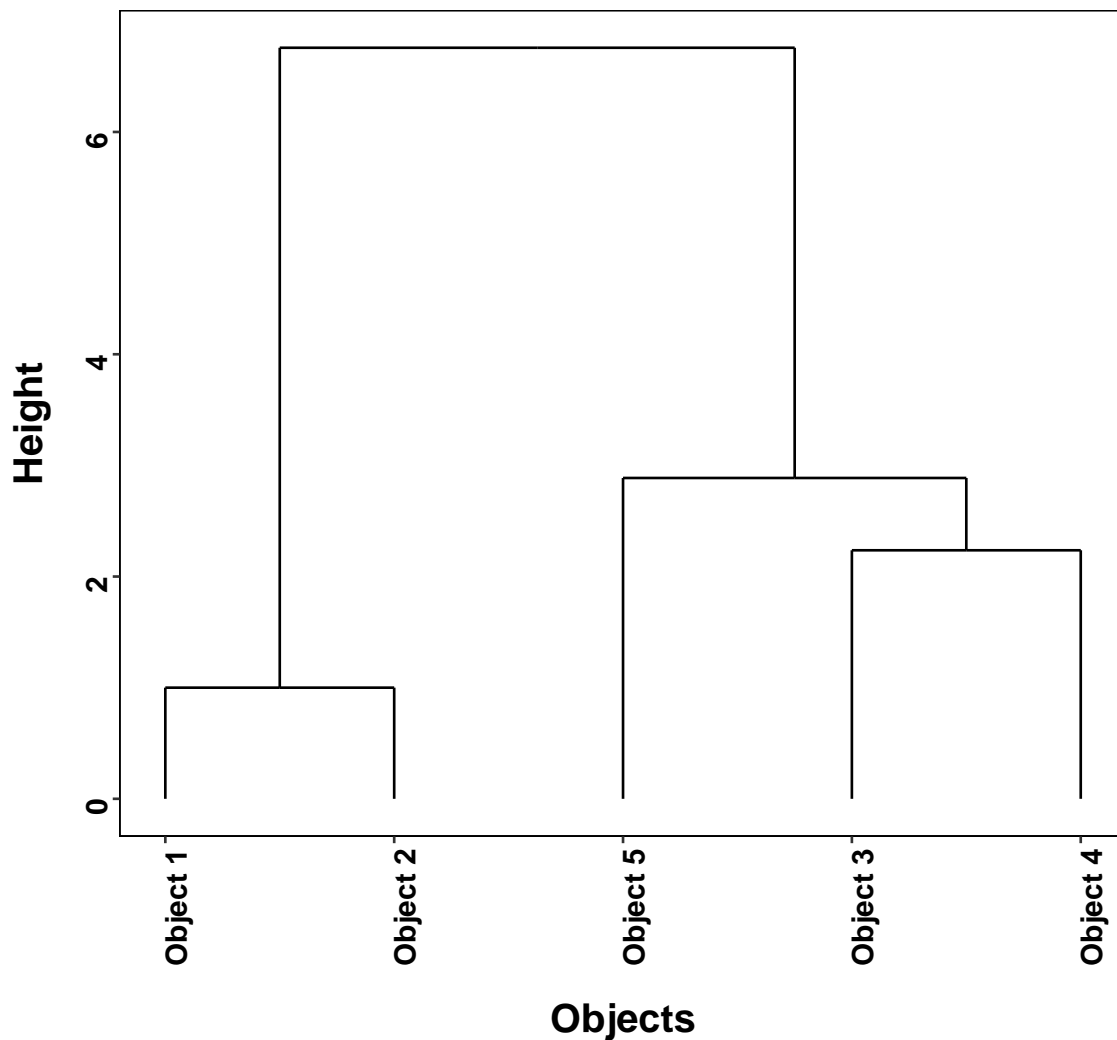
## [1] 1.000 2.236 2.887 6.758
```

```

ggdendrogram(hc_5, theme_dendro = FALSE) + xlab("Objects") + ylab("Height") +
  theme(text = element_text(size = 14, family = "sans", color = "black",
    face = "bold"), axis.text.y = element_text(colour = "black",
    size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
    size = 12, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
    0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
    15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
    axis.line.y = element_blank(), plot.title = element_text(size = 16,
    face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
    panel.background = element_rect(fill = "white", linetype = 1,
    color = "black"), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), plot.background = element_rect(fill = "white"),
    plot.margin = unit(c(1, 1, 1, 1), "cm"), legend.position = "bottom",
    legend.title = element_blank()) + ggtitle("Cluster Dendrogram: Ward's Method (D2)")

```

## Cluster Dendrogram: Ward's Method (D2)



### 3 Iris Data

*An important question is how well the different clustering methods can recover a group structure when it is known in advance. That can lend insight into the ability of the methods to identify any group structure when that structure is not known in advance.*

*A classic test data set was introduced by R. A. Fisher (1936): three species of iris, varying in their petal length, petal width, sepal length, and sepal width.*

```
# Get the drug use data from the working directory.
setwd("C:\\Courses\\Psychology 516\\PowerPoint\\2018")
Iris <- read.table("iris.csv", sep = ",", header = TRUE)
Iris <- as.data.frame(Iris)

Iris$Species[Iris$Species == "1"] <- "Setosa"
Iris$Species[Iris$Species == "2"] <- "Versicolor"
Iris$Species[Iris$Species == "3"] <- "Virginica"

Iris
```

##	Sepal_Length	Sepal_Width	Petal_Length	Petal_Width	Species
## 1	50	33	14	2	Setosa
## 2	64	28	56	22	Virginica
## 3	65	28	46	15	Versicolor
## 4	67	31	56	24	Virginica
## 5	63	28	51	15	Virginica
## 6	46	34	14	3	Setosa
## 7	69	31	51	23	Virginica
## 8	62	22	45	15	Versicolor
## 9	59	32	48	18	Versicolor
## 10	46	36	10	2	Setosa
## 11	61	30	46	14	Versicolor
## 12	60	27	51	16	Versicolor
## 13	65	30	52	20	Virginica
## 14	56	25	39	11	Versicolor
## 15	65	30	55	18	Virginica
## 16	58	27	51	19	Virginica
## 17	68	32	59	23	Virginica
## 18	51	33	17	5	Setosa
## 19	57	28	45	13	Versicolor
## 20	62	34	54	23	Virginica
## 21	77	38	67	22	Virginica
## 22	63	33	47	16	Versicolor
## 23	67	33	57	25	Virginica
## 24	76	30	66	21	Virginica
## 25	49	25	45	17	Virginica
## 26	55	35	13	2	Setosa
## 27	67	30	52	23	Virginica
## 28	70	32	47	14	Versicolor
## 29	64	32	45	15	Versicolor
## 30	61	28	40	13	Versicolor
## 31	48	31	16	2	Setosa
## 32	59	30	51	18	Virginica
## 33	55	24	38	11	Versicolor
## 34	63	25	50	19	Virginica

## 35	64	32	53	23	Virginica
## 36	52	34	14	2	Setosa
## 37	49	36	14	1	Setosa
## 38	54	30	45	15	Versicolor
## 39	79	38	64	20	Virginica
## 40	44	32	13	2	Setosa
## 41	67	33	57	21	Virginica
## 42	50	35	16	6	Setosa
## 43	58	26	40	12	Versicolor
## 44	44	30	13	2	Setosa
## 45	77	28	67	20	Virginica
## 46	63	27	49	18	Virginica
## 47	47	32	16	2	Setosa
## 48	55	26	44	12	Versicolor
## 49	50	23	33	10	Versicolor
## 50	72	32	60	18	Virginica
## 51	48	30	14	3	Setosa
## 52	51	38	16	2	Setosa
## 53	61	30	49	18	Virginica
## 54	48	34	19	2	Setosa
## 55	50	30	16	2	Setosa
## 56	50	32	12	2	Setosa
## 57	61	26	56	14	Virginica
## 58	64	28	56	21	Virginica
## 59	43	30	11	1	Setosa
## 60	58	40	12	2	Setosa
## 61	51	38	19	4	Setosa
## 62	67	31	44	14	Versicolor
## 63	62	28	48	18	Virginica
## 64	49	30	14	2	Setosa
## 65	51	35	14	2	Setosa
## 66	56	30	45	15	Versicolor
## 67	58	27	41	10	Versicolor
## 68	50	34	16	4	Setosa
## 69	46	32	14	2	Setosa
## 70	60	29	45	15	Versicolor
## 71	57	26	35	10	Versicolor
## 72	57	44	15	4	Setosa
## 73	50	36	14	2	Setosa
## 74	77	30	61	23	Virginica
## 75	63	34	56	24	Virginica
## 76	58	27	51	19	Virginica
## 77	57	29	42	13	Versicolor
## 78	72	30	58	16	Virginica
## 79	54	34	15	4	Setosa
## 80	52	41	15	1	Setosa
## 81	71	30	59	21	Virginica
## 82	64	31	55	18	Virginica
## 83	60	30	48	18	Virginica
## 84	63	29	56	18	Virginica
## 85	49	24	33	10	Versicolor
## 86	56	27	42	13	Versicolor
## 87	57	30	42	12	Versicolor
## 88	55	42	14	2	Setosa



## 89	49	31	15	2	Setosa
## 90	77	26	69	23	Virginica
## 91	60	22	50	15	Virginica
## 92	54	39	17	4	Setosa
## 93	66	29	46	13	Versicolor
## 94	52	27	39	14	Versicolor
## 95	60	34	45	16	Versicolor
## 96	50	34	15	2	Setosa
## 97	44	29	14	2	Setosa
## 98	50	20	35	10	Versicolor
## 99	55	24	37	10	Versicolor
## 100	58	27	39	12	Versicolor
## 101	47	32	13	2	Setosa
## 102	46	31	15	2	Setosa
## 103	69	32	57	23	Virginica
## 104	62	29	43	13	Versicolor
## 105	74	28	61	19	Virginica
## 106	59	30	42	15	Versicolor
## 107	51	34	15	2	Setosa
## 108	50	35	13	3	Setosa
## 109	56	28	49	20	Virginica
## 110	60	22	40	10	Versicolor
## 111	73	29	63	18	Virginica
## 112	67	25	58	18	Virginica
## 113	49	31	15	1	Setosa
## 114	67	31	47	15	Versicolor
## 115	63	23	44	13	Versicolor
## 116	54	37	15	2	Setosa
## 117	56	30	41	13	Versicolor
## 118	63	25	49	15	Versicolor
## 119	61	28	47	12	Versicolor
## 120	64	29	43	13	Versicolor
## 121	51	25	30	11	Versicolor
## 122	57	28	41	13	Versicolor
## 123	65	30	58	22	Virginica
## 124	69	31	54	21	Virginica
## 125	54	39	13	4	Setosa
## 126	51	35	14	3	Setosa
## 127	72	36	61	25	Virginica
## 128	65	32	51	20	Virginica
## 129	61	29	47	14	Versicolor
## 130	56	29	36	13	Versicolor
## 131	69	31	49	15	Versicolor
## 132	64	27	53	19	Virginica
## 133	68	30	55	21	Virginica
## 134	55	25	40	13	Versicolor
## 135	48	34	16	2	Setosa
## 136	48	30	14	1	Setosa
## 137	45	23	13	3	Setosa
## 138	57	25	50	20	Virginica
## 139	57	38	17	3	Setosa
## 140	51	38	15	3	Setosa
## 141	55	23	40	13	Versicolor
## 142	66	30	44	14	Versicolor

## 143	68	28	48	14	Versicolor
## 144	54	34	17	2	Setosa
## 145	51	37	15	4	Setosa
## 146	52	35	15	2	Setosa
## 147	58	28	51	24	Virginica
## 148	67	30	50	17	Versicolor
## 149	63	33	60	25	Virginica
## 150	53	37	15	2	Setosa

### 3.1 Descriptives and ANOVA

*The basic features of the data can be seen in descriptive information and analyses of variance. A principal component analysis also provides a convenient way to capture and display most of the important variation in the data.*

```
describeBy(Iris[, c(1:4)], group = Iris$Species, digits = 2)

##
## Descriptive statistics by group
## group: Setosa
##
##      vars  n  mean   sd median trimmed  mad min max
## Sepal_Length  1 50 50.06 3.52    50   50.02 2.97  43  58
## Sepal_Width   2 50 34.28 3.79    34   34.15 3.71  23  44
## Petal_Length  3 50 14.62 1.74    15   14.60 1.48  10  19
## Petal_Width   4 50  2.46 1.05     2    2.38 0.00   1   6
##
##      range skew kurtosis  se
## Sepal_Length  15 0.11   -0.45 0.50
## Sepal_Width   21 0.04    0.60 0.54
## Petal_Length   9 0.10    0.65 0.25
## Petal_Width    5 1.18    1.26 0.15
## -----
## group: Versicolor
##
##      vars  n  mean   sd median trimmed  mad min max
## Sepal_Length  1 50 59.36 5.16   59.0   59.38 5.19  49  70
## Sepal_Width   2 50 27.70 3.14   28.0   27.80 2.97  20  34
## Petal_Length  3 50 42.60 4.70   43.5   42.92 5.19  30  51
## Petal_Width   4 50 13.26 1.98   13.0   13.25 2.22  10  18
##
##      range skew kurtosis  se
## Sepal_Length  21 0.10   -0.69 0.73
## Sepal_Width   14 -0.34   -0.55 0.44
## Petal_Length  21 -0.57   -0.19 0.66
## Petal_Width    8 -0.03   -0.59 0.28
## -----
## group: Virginica
##
##      vars  n  mean   sd median trimmed  mad min max
## Sepal_Length  1 50 65.88 6.36   65.0   65.72 5.93  49  79
## Sepal_Width   2 50 29.74 3.22   30.0   29.62 2.97  22  38
## Petal_Length  3 50 55.52 5.52   55.5   55.10 6.67  45  69
## Petal_Width   4 50 20.26 2.75   20.0   20.32 2.97  14  25
##
##      range skew kurtosis  se
## Sepal_Length  30 0.11   -0.20 0.90
## Sepal_Width   16 0.34    0.38 0.46
## Petal_Length  24 0.52   -0.37 0.78
## Petal_Width   11 -0.12   -0.75 0.39
##
## # Check if the species are different in their sepal and petal
## # measurements.
anova(aov(Iris$Sepal_Length ~ as.factor(Species), data = Iris))

## Analysis of Variance Table
##
## Response: Iris$Sepal_Length
##
##      Df Sum Sq Mean Sq F value Pr(>F)
## as.factor(Species)  2   6321    3161    119 <2e-16
## Residuals         147   3896     27
```

```

anova(aov(Iris$Sepal_Width ~ as.factor(Species), data = Iris))

## Analysis of Variance Table
##
## Response: Iris$Sepal_Width
##           Df Sum Sq Mean Sq F value Pr(>F)
## as.factor(Species)  2   1134     567   49.2 <2e-16
## Residuals        147   1696      12

anova(aov(Iris$Petal_Length ~ as.factor(Species), data = Iris))

## Analysis of Variance Table
##
## Response: Iris$Petal_Length
##           Df Sum Sq Mean Sq F value Pr(>F)
## as.factor(Species)  2  43710   21855   1180 <2e-16
## Residuals        147   2722      19

anova(aov(Iris$Petal_Width ~ as.factor(Species), data = Iris))

## Analysis of Variance Table
##
## Response: Iris$Petal_Width
##           Df Sum Sq Mean Sq F value Pr(>F)
## as.factor(Species)  2   8041    4021    960 <2e-16
## Residuals        147    616       4

# Use PCA to show potential clustering along two dimensions.
PCA <- principal(Iris[, 1:4], nfactors = 2, rotate = "varimax", scores = TRUE)
PCA

## Principal Components Analysis
## Call: principal(r = Iris[, 1:4], nfactors = 2, rotate = "varimax",
##               scores = TRUE)
## Standardized loadings (pattern matrix) based upon correlation matrix
##           RC1    RC2    h2    u2 com
## Sepal_Length  0.96  0.05  0.92  0.0774 1.0
## Sepal_Width  -0.14  0.98  0.99  0.0091 1.0
## Petal_Length  0.94 -0.30  0.98  0.0163 1.2
## Petal_Width   0.93 -0.26  0.94  0.0647 1.2
##
##           RC1    RC2
## SS loadings      2.70 1.13
## Proportion Var    0.68 0.28
## Cumulative Var    0.68 0.96
## Proportion Explained 0.71 0.29
## Cumulative Proportion 0.71 1.00
##
## Mean item complexity = 1.1
## Test of the hypothesis that 2 components are sufficient.
##
## The root mean square of the residuals (RMSR) is 0.03
## with the empirical chi square 1.72 with prob < NA
##
## Fit based upon off diagonal values = 1

Iris <- cbind(Iris, PCA$scores)

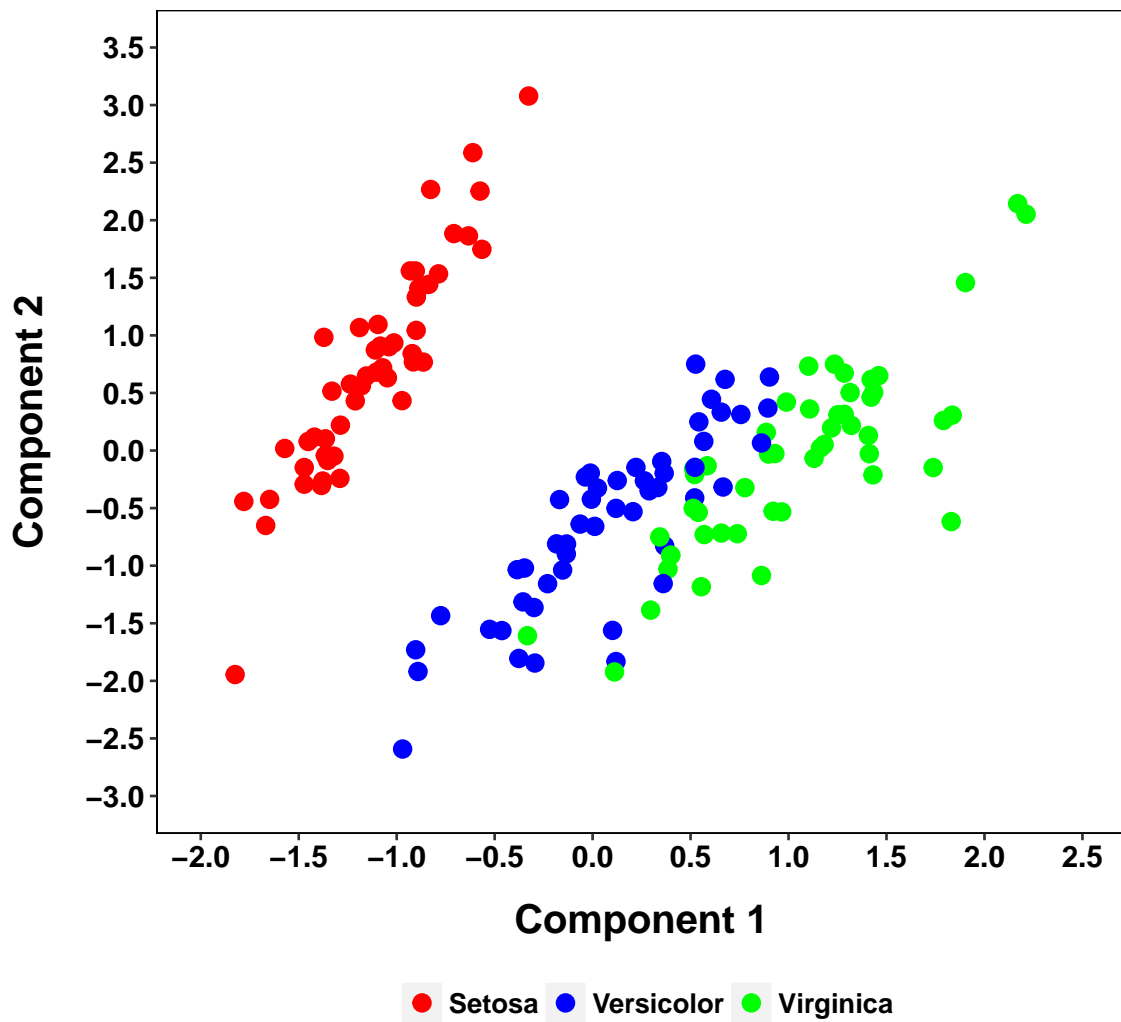
```

```

ggplot(Iris, aes(x = RC1, y = RC2, color = factor(Species))) + geom_point(shape = 19,
  size = 3) + scale_color_manual(values = c("red", "blue", "green")) +
  scale_y_continuous(breaks = c(seq(-3, 3.5, 0.5))) + scale_x_continuous(breaks = c(seq(-2,
  2.5, 0.5))) + coord_cartesian(xlim = c(-2, 2.5), ylim = c(-3,
  3.5)) + xlab("Component 1") + ylab("Component 2") + theme(text = element_text(size = 14,
  family = "sans", color = "black", face = "bold"), axis.text.y = element_text(colour = "black",
  size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
  size = 12, face = "bold", angle = 0), axis.title.x = element_text(margin = margin(15,
  0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
  15, 0, 0), size = 16), axis.line.x = element_blank(), axis.line.y = element_blank(),
  plot.title = element_text(size = 16, face = "bold", margin = margin(0,
  0, 20, 0), hjust = 0.5), panel.background = element_rect(fill = "white",
  linetype = 1, color = "black"), panel.grid.major = element_blank(),
  panel.grid.minor = element_blank(), plot.background = element_rect(fill = "white"),
  plot.margin = unit(c(1, 1, 1, 1), "cm"), legend.position = "bottom",
  legend.title = element_blank()) + ggtitle("Component Plot by Species")

```

Component Plot by Species



## 3.2 Distance Calculation

```
# Use Euclidean distance for subsequent clustering.
Iris_Dist <- dist(Iris[, 1:4], method = "euclidean")
```

## 3.3 Clustering Methods

*Each of the clustering methods can be applied to the iris data. Given the known structure of the data, the ability to recover the three species will help identify clustering methods that may be particularly useful.*

### 3.3.1 Single Linkage

```
hc_1 <- hclust(Iris_Dist, method = "single")

clustnumber <- cutree(hc_1, k = 3)
Iris_Class <- as.data.frame(cbind(clustnumber, Iris$Species))
names(Iris_Class) <- c("Cluster", "Species")
table(Iris_Class$Species)
```

```
##
##      Setosa Versicolor  Virginica
##      50         50         50
```

```
table(Iris_Class$Cluster)
```

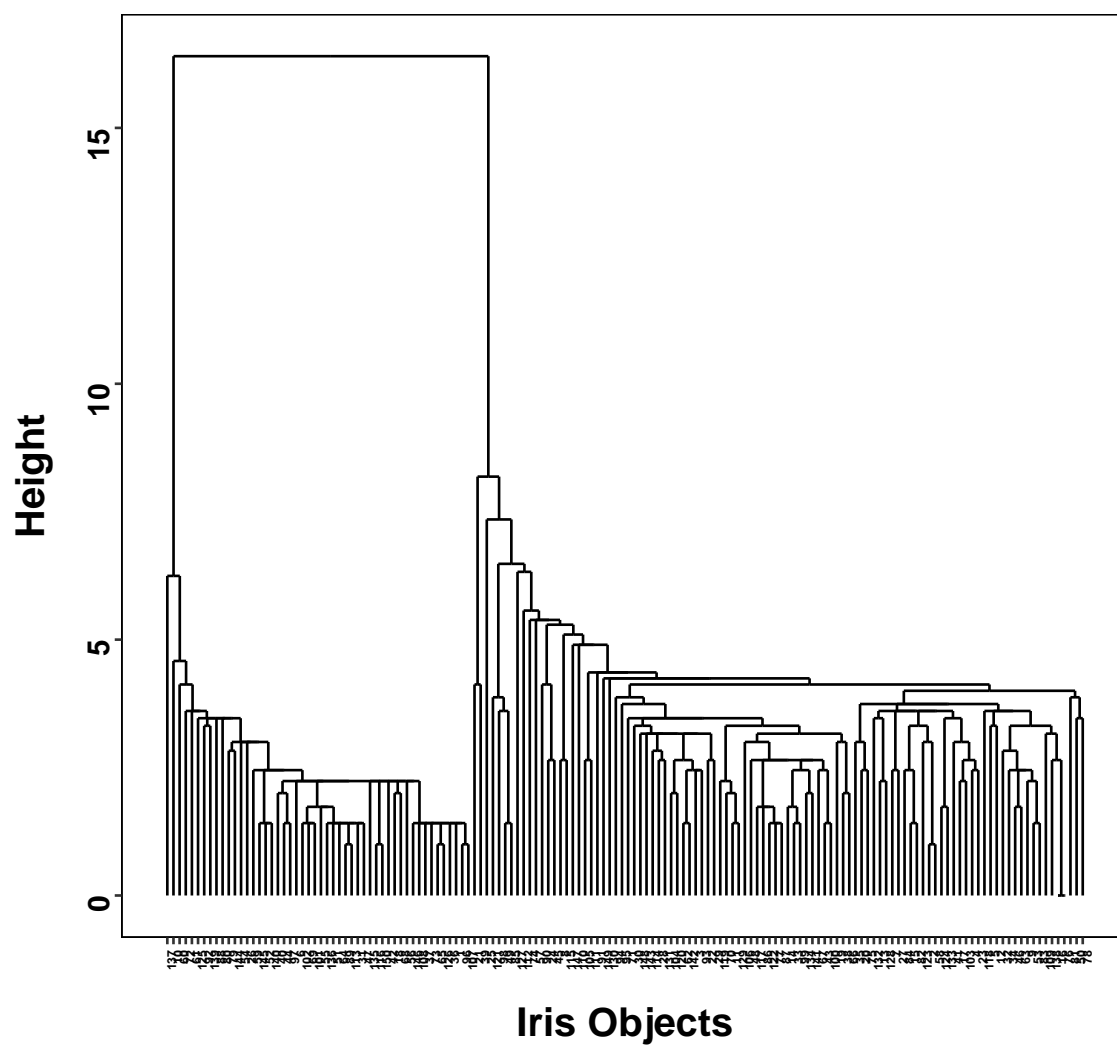
```
##
##    1  2  3
## 50 98  2
```

```
table(Iris_Class$Species, Iris_Class$Cluster)
```

```
##
##           1  2  3
## Setosa      50  0  0
## Versicolor  0 50  0
## Virginica   0 48  2
```

```
ggdendrogram(hc_1, theme_dendro = FALSE) + xlab("Iris Objects") +
  ylab("Height") + theme(text = element_text(size = 14, family = "sans",
  color = "black", face = "bold"), axis.text.y = element_text(colour = "black",
  size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
  size = 5, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
  0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
  15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
  axis.line.y = element_blank(), plot.title = element_text(size = 16,
  face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
  panel.background = element_rect(fill = "white", linetype = 1,
  color = "black"), panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
  plot.background = element_rect(fill = "white"), plot.margin = unit(c(1,
  1, 1, 1), "cm"), legend.position = "bottom", legend.title = element_blank()) +
  ggtitle("Iris Cluster Dendrogram: Single Linkage")
```

## Iris Cluster Dendrogram: Single Linkage





### 3.3.2 Complete Lingage

```
hc_2 <- hclust(Iris_Dist, method = "complete")

clustnumber <- cutree(hc_2, k = 3)
Iris_Class <- as.data.frame(cbind(clustnumber, Iris$Species))
names(Iris_Class) <- c("Cluster", "Species")
table(Iris_Class$Species)
```

```
##
##      Setosa Versicolor  Virginica
##      50          50          50
```

```
table(Iris_Class$Cluster)
```

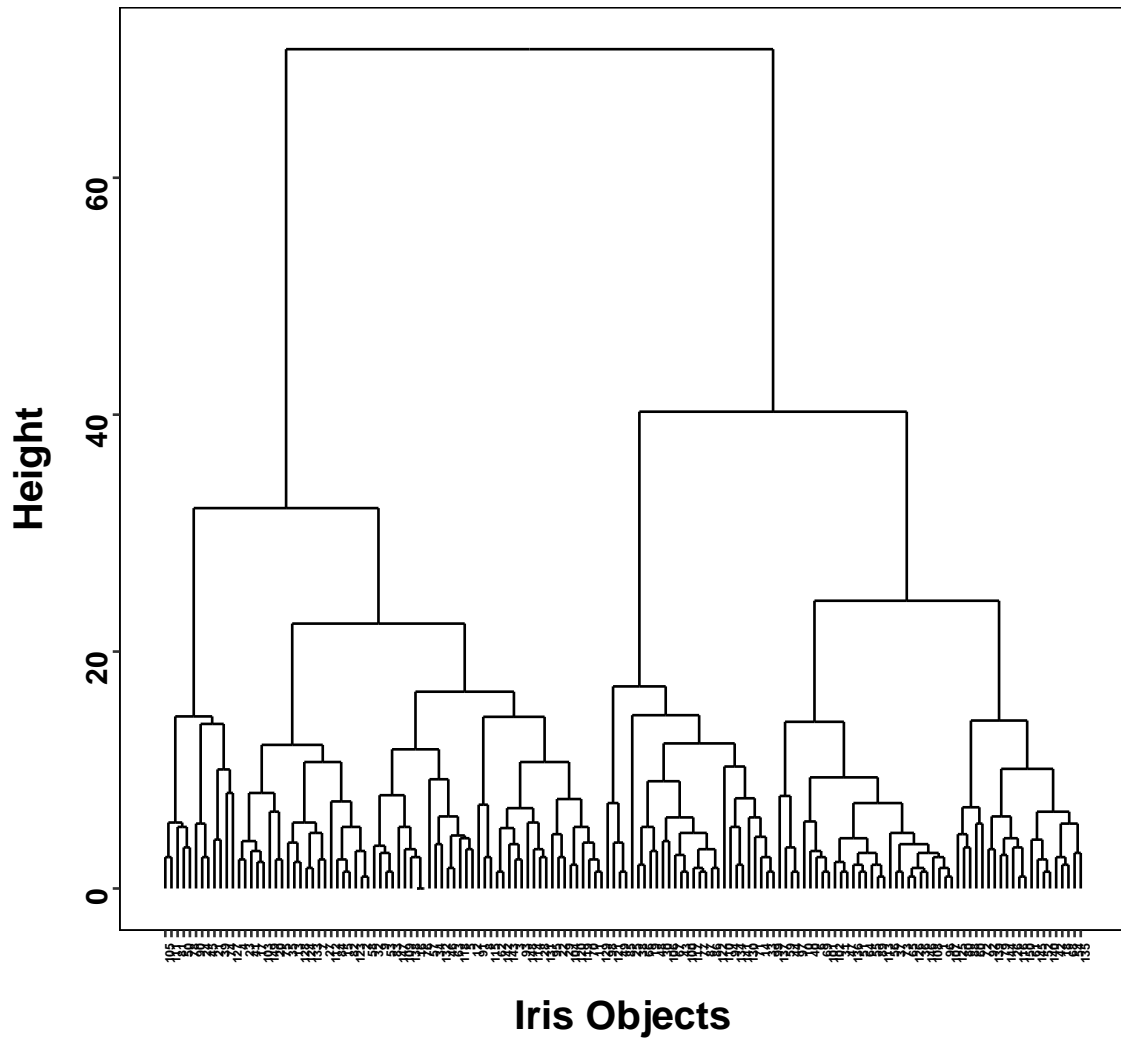
```
##
##    1  2  3
## 50 72 28
```

```
table(Iris_Class$Species, Iris_Class$Cluster)
```

```
##
##           1  2  3
## Setosa      50  0  0
## Versicolor  0 23 27
## Virginica   0 49  1
```

```
ggdendrogram(hc_2, theme_dendro = FALSE) + xlab("Iris Objects") +
  ylab("Height") + theme(text = element_text(size = 14, family = "sans",
  color = "black", face = "bold"), axis.text.y = element_text(colour = "black",
  size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
  size = 5, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
  0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
  15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
  axis.line.y = element_blank(), plot.title = element_text(size = 16,
  face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
  panel.background = element_rect(fill = "white", linetype = 1,
  color = "black"), panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
  plot.background = element_rect(fill = "white"), plot.margin = unit(c(1,
  1, 1, 1), "cm"), legend.position = "bottom", legend.title = element_blank()) +
  ggtitle("Iris Cluster Dendrogram: Complete Linkage")
```

## Iris Cluster Dendrogram: Complete Linkage



### 3.3.3 Average Linkage

```
hc_3 <- hclust(Iris_Dist, method = "average")

clustnumber <- cutree(hc_3, k = 3)
Iris_Class <- as.data.frame(cbind(clustnumber, Iris$Species))
names(Iris_Class) <- c("Cluster", "Species")
table(Iris_Class$Species)

##
##      Setosa Versicolor  Virginica
##      50         50         50

table(Iris_Class$Cluster)

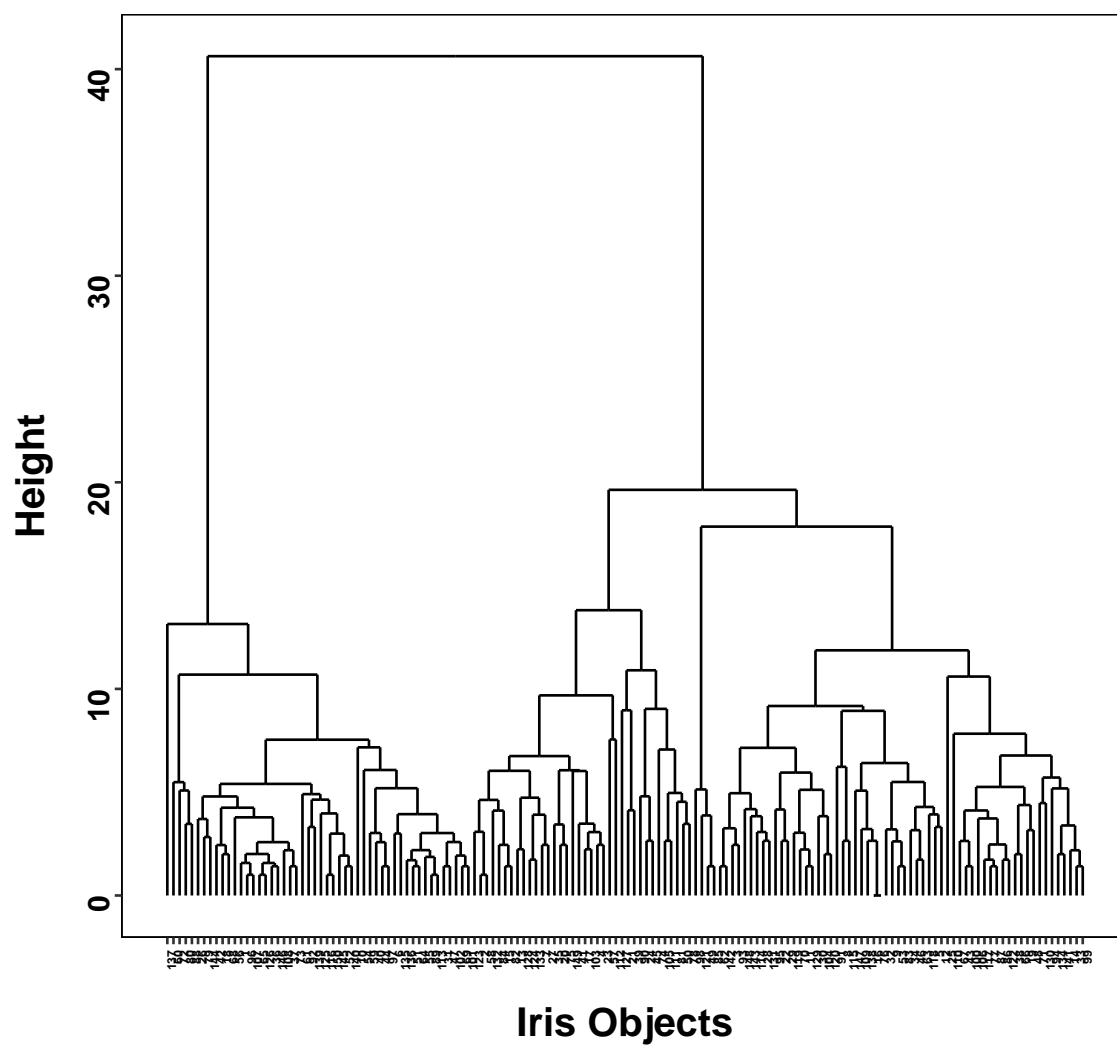
##
##    1  2  3
## 50 36 64

table(Iris_Class$Species, Iris_Class$Cluster)

##
##           1  2  3
## Setosa      50  0  0
## Versicolor  0  0 50
## Virginica   0 36 14
```

```
ggdendrogram(hc_3, theme_dendro = FALSE) + xlab("Iris Objects") +
  ylab("Height") + theme(text = element_text(size = 14, family = "sans",
  color = "black", face = "bold"), axis.text.y = element_text(colour = "black",
  size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
  size = 5, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
  0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
  15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
  axis.line.y = element_blank(), plot.title = element_text(size = 16,
  face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
  panel.background = element_rect(fill = "white", linetype = 1,
  color = "black"), panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
  plot.background = element_rect(fill = "white"), plot.margin = unit(c(1,
  1, 1, 1), "cm"), legend.position = "bottom", legend.title = element_blank()) +
  ggtitle("Iris Cluster Dendrogram: Average Linkage")
```

**Iris Cluster Dendrogram: Average Linkage**



### 3.3.4 Centroid Method

```
hc_4 <- hclust(Iris_Dist, method = "centroid")

clustnumber <- cutree(hc_4, k = 3)
Iris_Class <- as.data.frame(cbind(clustnumber, Iris$Species))
names(Iris_Class) <- c("Cluster", "Species")
table(Iris_Class$Species)
```

```
##
##      Setosa Versicolor  Virginica
##      50          50          50
```

```
table(Iris_Class$Cluster)
```

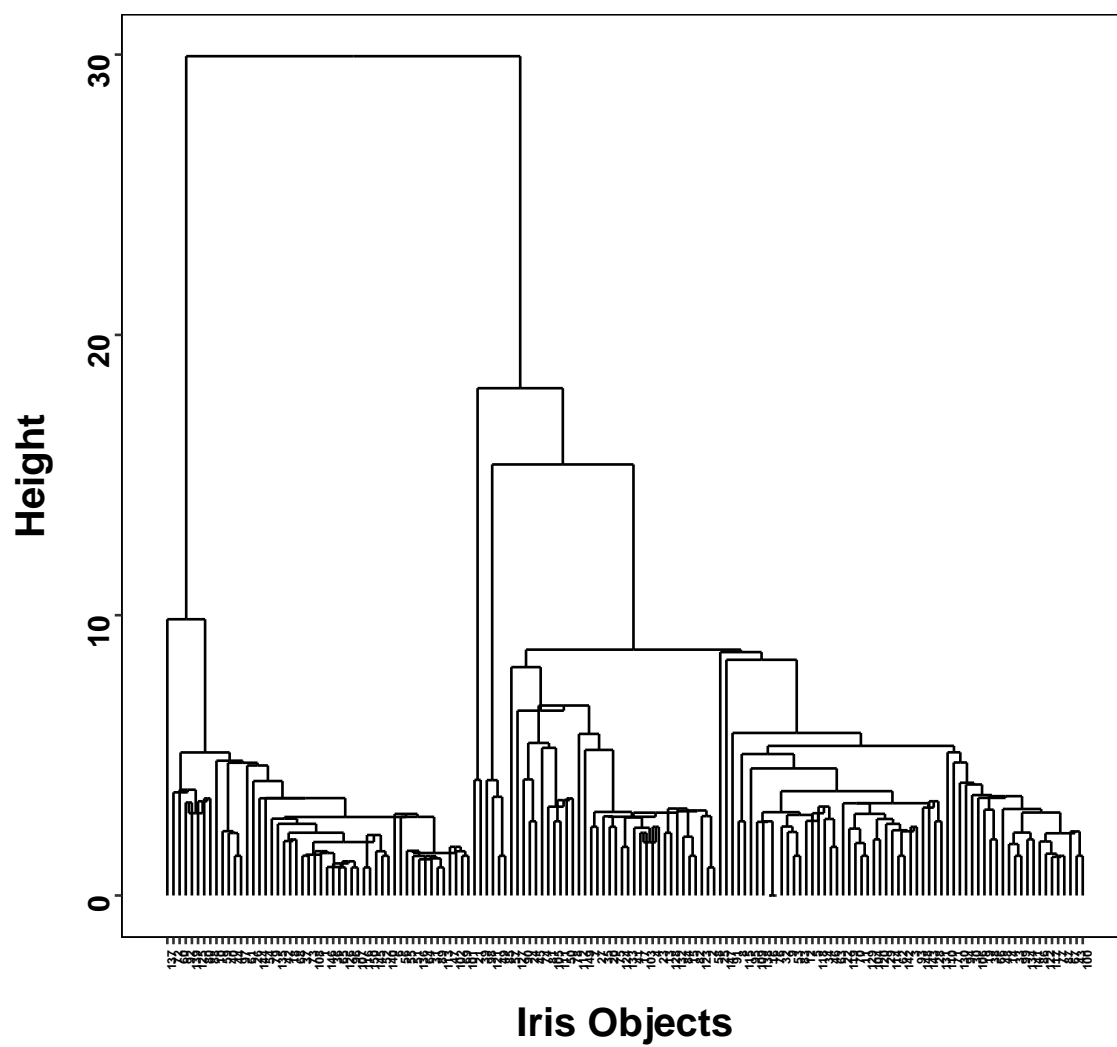
```
##
##   1  2  3
## 50 98  2
```

```
table(Iris_Class$Species, Iris_Class$Cluster)
```

```
##
##           1  2  3
## Setosa      50  0  0
## Versicolor  0 50  0
## Virginica   0 48  2
```

```
ggdendrogram(hc_4, theme_dendro = FALSE) + xlab("Iris Objects") +
  ylab("Height") + theme(text = element_text(size = 14, family = "sans",
  color = "black", face = "bold"), axis.text.y = element_text(colour = "black",
  size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
  size = 5, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
  0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
  15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
  axis.line.y = element_blank(), plot.title = element_text(size = 16,
  face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
  panel.background = element_rect(fill = "white", linetype = 1,
  color = "black"), panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
  plot.background = element_rect(fill = "white"), plot.margin = unit(c(1,
  1, 1, 1), "cm"), legend.position = "bottom", legend.title = element_blank()) +
  ggtitle("Iris Cluster Dendrogram: Centroid Method")
```

## Iris Cluster Dendrogram: Centroid Method



### 3.3.5 Ward's Method (D2)

```
hc_5 <- hclust(Iris_Dist, method = "ward.D2")

clustnumber <- cutree(hc_5, k = 3)
Iris_Class <- as.data.frame(cbind(clustnumber, Iris$Species))
names(Iris_Class) <- c("Cluster", "Species")
table(Iris_Class$Species)
```

```
##
##      Setosa Versicolor  Virginica
##      50          50          50
```

```
table(Iris_Class$Cluster)
```

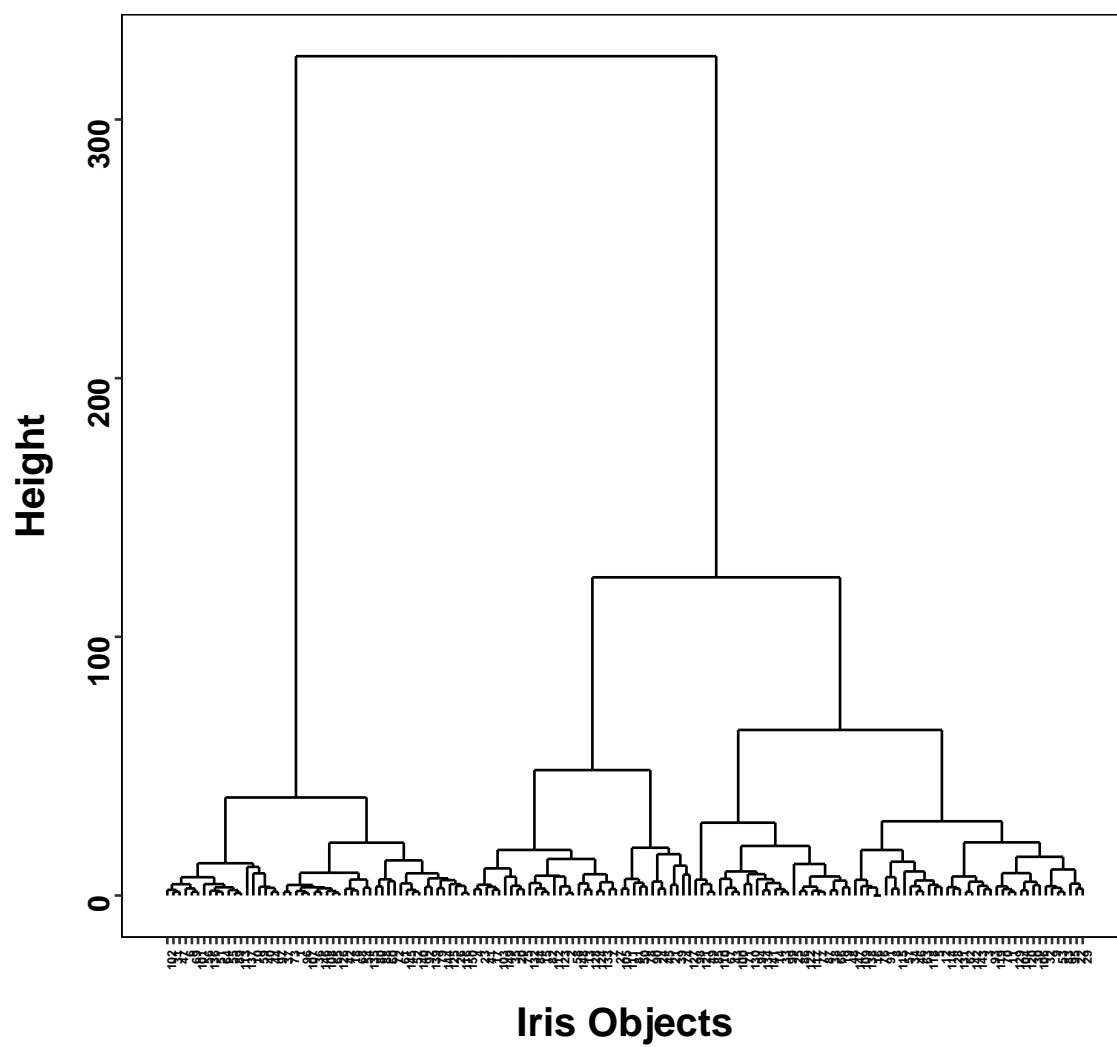
```
##
##    1  2  3
## 50 36 64
```

```
table(Iris_Class$Species, Iris_Class$Cluster)
```

```
##
##           1  2  3
## Setosa      50  0  0
## Versicolor  0  1 49
## Virginica   0 35 15
```

```
ggdendrogram(hc_5, theme_dendro = FALSE) + xlab("Iris Objects") +
  ylab("Height") + theme(text = element_text(size = 14, family = "sans",
  color = "black", face = "bold"), axis.text.y = element_text(colour = "black",
  size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
  size = 5, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
  0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
  15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
  axis.line.y = element_blank(), plot.title = element_text(size = 16,
  face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
  panel.background = element_rect(fill = "white", linetype = 1,
  color = "black"), panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
  plot.background = element_rect(fill = "white"), plot.margin = unit(c(1,
  1, 1, 1), "cm"), legend.position = "bottom", legend.title = element_blank()) +
  ggtitle("Iris Cluster Dendrogram: Ward's Method (D2)")
```

**Iris Cluster Dendrogram: Ward's Method (D2)**





### 3.3.6 Ward's Method (D)

```
Iris_Dist <- dist(Iris[, 1:4], method = "euclidean")^2

hc_5 <- hclust(Iris_Dist, method = "ward.D")

clustnumber <- cutree(hc_5, k = 3)
Iris_Class <- as.data.frame(cbind(clustnumber, Iris$Species))
names(Iris_Class) <- c("Cluster", "Species")
table(Iris_Class$Species)
```

```
##
##      Setosa Versicolor  Virginica
##      50         50         50
```

```
table(Iris_Class$Cluster)
```

```
##
##   1  2  3
## 50 36 64
```

```
table(Iris_Class$Species, Iris_Class$Cluster)
```

```
##
##           1  2  3
## Setosa      50  0  0
## Versicolor  0  1 49
## Virginica   0 35 15
```

```
ggdendrogram(hc_5, theme_dendro = FALSE) + xlab("Iris Objects") +
  ylab("Height") + theme(text = element_text(size = 14, family = "sans",
  color = "black", face = "bold"), axis.text.y = element_text(colour = "black",
  size = 12, face = "bold"), axis.text.x = element_text(colour = "black",
  size = 5, face = "bold", angle = 90), axis.title.x = element_text(margin = margin(15,
  0, 0, 0), size = 16), axis.title.y = element_text(margin = margin(0,
  15, 0, 0), size = 16, angle = 90), axis.line.x = element_blank(),
  axis.line.y = element_blank(), plot.title = element_text(size = 16,
  face = "bold", margin = margin(0, 0, 20, 0), hjust = 0.5),
  panel.background = element_rect(fill = "white", linetype = 1,
  color = "black"), panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
  plot.background = element_rect(fill = "white"), plot.margin = unit(c(1,
  1, 1, 1), "cm"), legend.position = "bottom", legend.title = element_blank()) +
  ggtitle("Iris Cluster Dendrogram: Ward's Method (D)")
```

**Iris Cluster Dendrogram: Ward's Method (D)**

