

MKTG-352 Asssignment 2

MinJae Jo

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###Step 1

```
suppressPackageStartupMessages({  
  library(dplyr)  
  library(cluster)  
})
```

###Step 1

```
Smartwatch <- read.csv("SmartwatchData.csv", stringsAsFactors = FALSE)  
  
summary_stats <- Smartwatch %>%  
  summarise(  
    Age_mean = mean(Age, na.rm = TRUE), Age_min = min(Age, na.rm = TRUE), Age_max = max(Age, na.rm = TRUE),  
    Price_mean = mean(Price, na.rm = TRUE), Price_min = min(Price, na.rm = TRUE), Price_max = max(Price, na.rm = TRUE),  
    Innov_mean = mean(Innov, na.rm = TRUE), Innov_min = min(Innov, na.rm = TRUE), Innov_max = max(Innov, na.rm = TRUE),  
    ConstCom_mean = mean(ConstCom, na.rm = TRUE), ConstCom_min = min(ConstCom, na.rm = TRUE), ConstCom_max = max(ConstCom, na.rm = TRUE),  
    SaveM_T_mean = mean(SaveM_T, na.rm = TRUE), SaveM_T_min = min(SaveM_T, na.rm = TRUE), SaveM_T_max = max(SaveM_T, na.rm = TRUE)  
  )  
  
summary_stats
```

```
## # A tibble: 1 x 15  
##   Age_mean Age_min Age_max Price_mean Price_min Price_max Innov_mean Innov_min  
##   <dbl>   <int>   <int>     <dbl>     <int>     <int>     <dbl>     <int>  
## 1    35.5     24     47      213.      100      390      4.10      1  
## # i 7 more variables: Innov_max <int>, ConstCom_mean <dbl>, ConstCom_min <int>,  
## #   ConstCom_max <int>, SaveM_T_mean <dbl>, SaveM_T_min <int>,  
## #   SaveM_T_max <int>
```

###Step 2

```
seg_vars <- c("Innov", "ConstCom", "CreatCom", "TimelyInf", "SaveM_T", "SaveM_L",  
             "TaskMgm", "DeviceSt", "Photo", "Wellness", "Athlete", "Style", "Price")
```

```
SegmentationData <- Smartwatch %>%
  select(1, all_of(seg_vars)) %>%
  rename(Observations = 1)

SegmentationDataScaled <- SegmentationData
SegmentationDataScaled[, -1] <- scale(SegmentationDataScaled[, -1])
```

Step 3

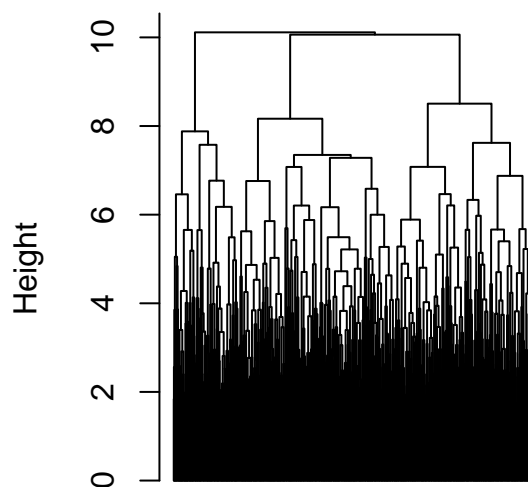
```
dissimilarity <- dist(SegmentationDataScaled[, -1], method = "euclidean")
```

Step 4

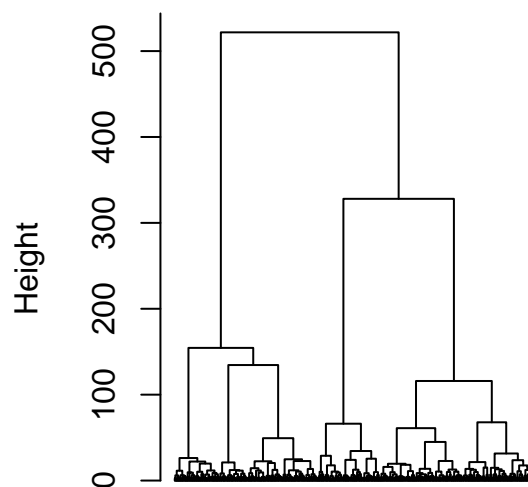
```
hc_complete <- hclust(dissimilarity, method = "complete")
hc_ward <- hclust(dissimilarity, method = "ward.D")

par(mfrow = c(1,2))
plot(hc_complete, labels = FALSE, hang = -1, main = "Dendrogram - complete", xlab = "", sub = "")
plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = "")
```

Dendrogram – complete



Dendrogram – ward.D



```
par(mfrow = c(1,1))
```

Step 5

```
ks <- 2:10

avg_sil <- function(hc, d, k) {
  cl <- cutree(hc, k = k)
  sil <- cluster::silhouette(cl, d)
  mean(sil[, 3])
}

sil_complete <- sapply(ks, function(k) avg_sil(hc_complete, dissimilarity, k))
sil_ward <- sapply(ks, function(k) avg_sil(hc_ward, dissimilarity, k))

best_k_complete <- ks[which.max(sil_complete)]
best_k_ward <- ks[which.max(sil_ward)]

best_method <- if (max(sil_complete) >= max(sil_ward)) "complete" else "ward.D"
best_k <- if (best_method == "complete") best_k_complete else best_k_ward
hc_final <- if (best_method == "complete") hc_complete else hc_ward

plot(hc_final, labels = FALSE, hang = -1,
     main = paste("Final dendrogram -", best_method, "(k =", best_k, ")"),
     xlab = "", sub = "")
rect.hclust(hc_final, k = best_k, border = "red")
```

Final dendrogram – ward.D (k = 3)



```
best_method; best_k
```

```
## [1] "ward.D"
```

```
## [1] 3
```