## MKTG-352 Asssignment 2

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#### Part 1

### Step 0

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

### Step 1

## #

SaveM\_T\_max <int>

```
Smartwatch <- read.csv("SmartwatchData.csv", stringsAsFactors = FALSE)</pre>
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 = na.rm = TRUE)
    Innov_mean = mean(Innov, na.rm = TRUE), Innov_min = min(Innov, na.rm = TRUE), Innov_max = n
    ConstCom_mean = mean(ConstCom, na.rm = TRUE), ConstCom_min = min(ConstCom, na.rm = TRUE),
    SaveM_T_mean = mean(SaveM_T, na.rm = TRUE), SaveM_T_min = min(SaveM_T, na.rm = TRUE), SaveM_T_min = min(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>
         35.5
                                       213.
## 1
                     24
                                                   100
                                                              390
                                                                         4.10
## # i 7 more variables: Innov_max <int>, ConstCom_mean <dbl>, ConstCom_min <int>,
       ConstCom_max <int>, SaveM_T_mean <dbl>, SaveM_T_min <int>,
```

### Step 2

### Step 3

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

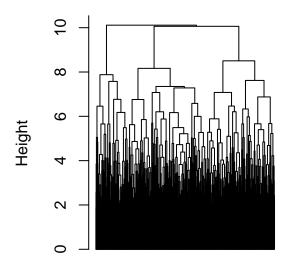
### Step 4

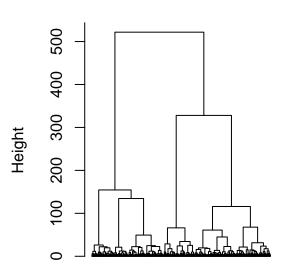
```
hc_complete <- hclust(dissimilarity, method = "complete")
hc_ward <- hclust(dissimilarity, method = "ward.D")

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 = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = FALSE, hang = -1, main = "Dendrogram - ward.D", xlab = "", sub = plot(hc_ward, labels = blot(hc_ward, labels = blot(
```

### **Dendrogram - complete**

### Dendrogram - ward.D





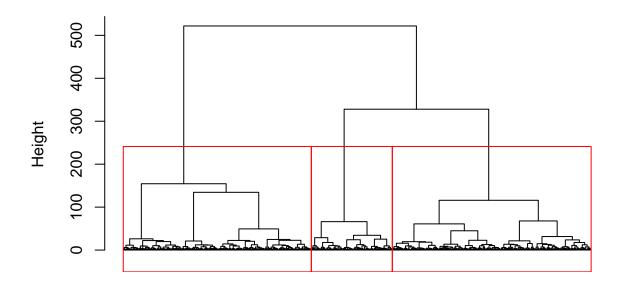
```
par(mfrow = c(1,1))
```

### Step 5

```
ks <- 2:10
avg_sil <- function(hc, d, k) {</pre>
  cl <- cutree(hc, k = k)</pre>
  sil <- cluster::silhouette(cl, d)</pre>
  mean(sil[, 3])
}
sil_complete <- sapply(ks, function(k) avg_sil(hc_complete, dissimilarity, k))</pre>
sil_ward
              <- sapply(ks, function(k) avg_sil(hc_ward,</pre>
                                                                 dissimilarity, k))
best_k_complete <- ks[which.max(sil_complete)]</pre>
                 <- ks[which.max(sil_ward)]</pre>
best_k_ward
best_method <- if (max(sil_complete) >= max(sil_ward)) "complete" else "ward.D"
             <- if (best_method == "complete") best_k_complete else best_k_ward</pre>
best_k
          <- if (best_method == "complete") hc_complete else hc_ward</pre>
hc final
```

```
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

Step 6

```
final_clusters <- cutree(hc_final, k = best_k)
Smartwatch$Cluster <- factor(final_clusters)
head(Smartwatch$Cluster)</pre>
```

```
## [1] 1 2 2 2 2 1
## Levels: 1 2 3
```

### Step 7

```
cluster_counts <- table(Smartwatch$Cluster)</pre>
cluster_counts
##
##
     1
         2
             3
## 425 173 402
Step 8
cluster_summary <- Smartwatch %>%
  group_by(Cluster) %>%
  summarise(across(where(is.numeric), ~ mean(.x, na.rm = TRUE)), .groups = "drop")
cluster_summary
## # A tibble: 3 x 39
##
     Cluster Observations Innov ConstCom CreatCom TimelyInf SaveM_T SaveM_L TaskMgm
##
     <fct>
                    <dbl> <dbl>
                                    <dbl>
                                             <dbl>
                                                        <dbl>
                                                                <dbl>
                                                                        <dbl>
                                                                                 <dbl>
## 1 1
                     511.
                           3.69
                                     4.09
                                              4.19
                                                         3.67
                                                                 3.45
                                                                         3.00
                                                                                  3.27
## 2 2
                     484.
                           4.17
                                     5.46
                                              2.27
                                                         5.64
                                                                 2.03
                                                                          3.77
                                                                                  5.06
                     496. 4.50
                                     4.99
                                              5.20
                                                         4.36
                                                                                  4.79
## 3 3
                                                                 4.07
                                                                         5.10
## # i 30 more variables: DeviceSt <dbl>, Photo <dbl>, Wellness <dbl>,
## #
       Athlete <dbl>, Style <dbl>, Price <dbl>, iPhone <dbl>, CompBuy <dbl>,
## #
       Health <dbl>, Finc <dbl>, Sales <dbl>, Advt <dbl>, Edu <dbl>, Cons <dbl>,
```

#### Step 9

## #

## #

## #

```
write.csv(cluster_summary, "Segment_summary.csv", row.names = FALSE)
```

Snap <dbl>, YouTube <dbl>, Pod\_radio <dbl>, TV <dbl>, NewsP <dbl>,

AmznP <dbl>, Age <dbl>, Female <dbl>, Degree <dbl>, Income <dbl>

Eng <dbl>, Tech <dbl>, Retail <dbl>, SMB <dbl>, FB\_Insta <dbl>, Twit <dbl>,