Free Classification: Clustering Project

Clustering

Contents

Data

Eighty-four participants (one participant was not used due to some weird coding issue) took part a free speech classification task. The speech samples were selected from The Speech Accent Archive. The talkers included three American English regional dialects, three international English dialects, and nine nonnative accents. The nonnative accents were split into three accents from East Asia, three accents from South Asia, and three accents from Southeast Asia. The American English dialects included the New England dialect, the Southern dialect, and the Midland dialect. The international English dialects included British English, Australian English, and Africaans. The native languages of the nonnative-accented talkers were Mandarin, Korean, and Japanese from East Asia, Bengali, Gujarati, and Urdu from South Asia, and Indonesian, Tagalog, and Thai from Southeast Asia. We have data in wide format. Each row is a talker type and each col is a participant.

Clustering

Introduction

In this task, individuals heard speech tokens from a number of different speakers and freely classified them into groups. Based on previous work, I used hierarchical clustering to examine what natural clusters or groups formed as the result of free classification.

```
# For reproducibility
set.seed(666)
```

```
library(here)
library(tidyverse)  # data manipulation
library(cluster)    # clustering algorithms
library(factoextra) # clustering visualization
library(dendextend) # for comparing two dendrograms
library(fpc) # kmeans clustering
```

Data Preparation

1. I wrangled the DF so that each row corresponds to each talker and each column corresponds to each participant.
2. I removed missing data.
3. I did not standardize the data.

Read in the data

```
clust_data <- read_csv(here("data", "class_wide_1.csv")) # read in data
```

```
## Warning: Missing column names filled in: 'X1' [1]
```

```
## Parsed with column specification:
## cols(
##   .default = col_double(),
##   speaker = col_character(),
##   `54` = col_character()
## )
```

```
## See spec(...) for full column specifications.
```

```
clust_data <- select(clust_data, -X1, -`54`) # remove extra col sub 54 has weird formatting

clust_data <- as.data.frame(clust_data) # turn into df

rownames(clust_data) <- clust_data$speaker # make row names speaker

clust_data <- select(clust_data,-speaker) # remove extra col sub 54 has weird formatting

head(clust_data)# show first couple rows
```

```
##             8 7 1 10 11 12 14 15 16 17 18 19 2 20 23 25 26 27 28 29  3 30 31 32 33 34 35 36 38 4 40 4
## bengali_9   1 5 5  1 11  2  1  8  4  2  2  1 9  7  4  5  1  1  1 11  5  1  7  7  9  8 10  8  1 3  1 1
## bengali_13  6 5 5  7 14  4  2  7  4  2  6  3 9  1  4  5  4  2  3 11 12  1  8 11  9  8 10 11  1 4 12
## bengali_16  1 5 5  7  7  4  3  6  2  8  3  3 3  1  3  4  6  1  3 10  2  1  7  8  9  8 10 11  6 3  8
## gujarati_5  4 5 5  1 14  4  1  7  4  9  9  1 9  4  3  5  4  2  4  8  9  1  7  9  9  6 10  8  1 2  8
## gujarati_13 1 5 5  1 15  4  2  8  4  2  6  1 9  4  5  5  6  2  4  8  5  1  7  9  9  8 10  2  1 2 12
## gujarati_14 5 5 5  1  7  4  1  8  4  9  9  3 9  5  7  5  4  4  6  1  5  1  6  9  9  6 10  9  1 4 13
##             45 46 47 48 49  5 50 51 52 53 55 56 58 59 6 78 87 90 91 96 105 110 111 115 121 123 125 13
## bengali_9    1  5  1  5  8  1  3  7  1  8  9  1  1  5 9  1 11  1 11  1   6  11   1   2   1   9   1
## bengali_13   1  5  4  1  8  5  4  7  3  8  9  1  8 11 7  1 11  1 11  1   6  11   7   8   6   9   1
## bengali_16   1  1  2  5  7  5  4  7  3  8  9  8  1  6 7  5 11  2  6  1   6  10   6   8   6  10  10
## gujarati_5   3 11  2  2  8 10  3  7 11  8  9  7  3 11 7  1 11  2 10  1   1  11   6   8   6   9  10
## gujarati_13  1 11  6  5  8  2  4  7  1  8  9  7 10  5 7  1 11  2 11  1   6  11   2   8   6   9  10
## gujarati_14  6  3  4  5  8  3  3  7 15  8  8  8  6  5 6  2 11  8 11  1   6  11   6   9   6   9   8
##             148 151 152 153 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169
## bengali_9     1   5   1   8   4   8   6   5   1   5   1   7   4   1   5   1   7   1   2
## bengali_13    6   9   1   8   4  10   6   5   2   1  14   7   6   4   5   1   4   2   4
## bengali_16    1   7   4   8  11   8   6   3   2   3  14   7   7   1   5   1   7   4   4
## gujarati_5    3   5   3   2   5   9   6   3   1   3  14   7   5   6   6   1   4   2   5
## gujarati_13   1   5   1   2   5   9   6   3   1   4  14   7   5   6   5   1   7   3   6
## gujarati_14   2   5   3   8   5   9   6   3   8   4   5   3   7   6   7   6   7   5   1
```

Agglomerative Hierarchical Clustering

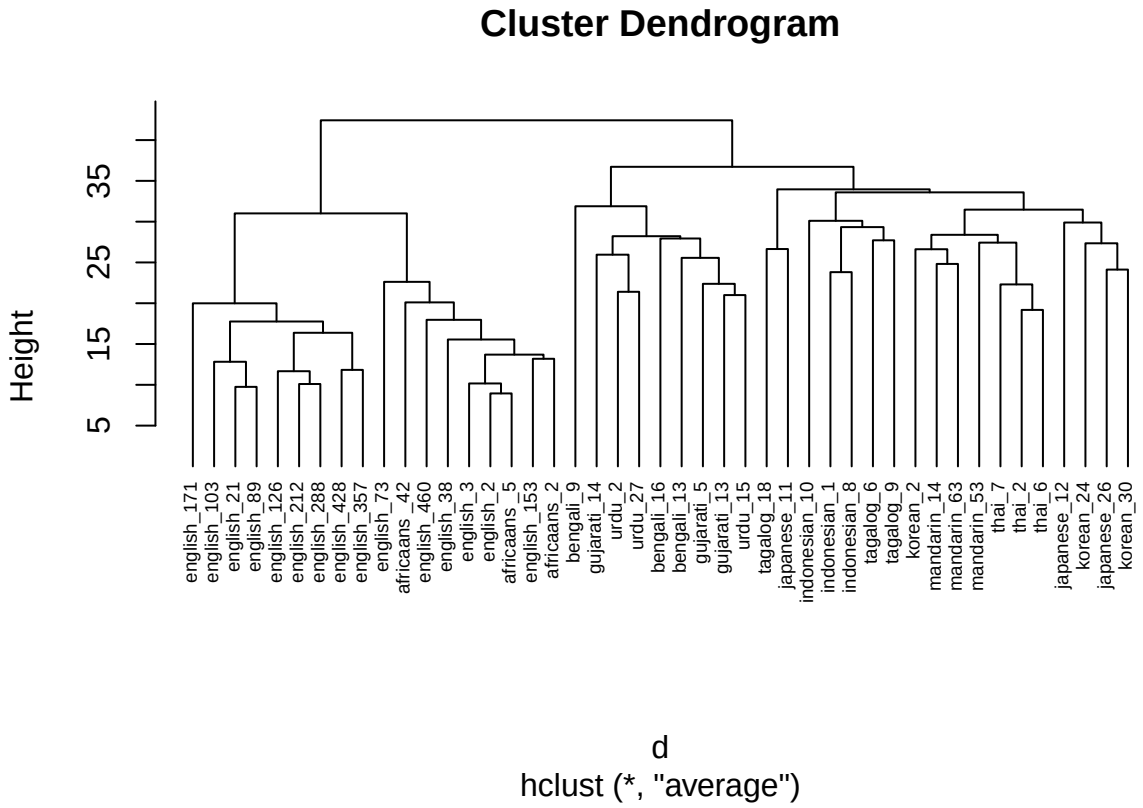
I am going to cluster the data using average link clustering. Average link clustering computes all pairwise dissimilarities between the elements, and considers the average of these dissimilarities as the distance between clusters.

1. I calculate the dissimilarity matrix using euclidean distance.
2. I compute the clustering with average link.
3. I plot the cluster solution

```
# Dissimilarity matrix
d <- dist(clust_data, method = "euclidean")

# Hierarchical clustering using Average Linkage
hc1 <- hclust(d, method = "average" )

# Plot the obtained dendrogram
plot(hc1, cex = 0.6, hang = -1)
```



How Many Clusters?

In the dendrogram displayed above, each leaf corresponds to one observation. As we move up the tree, observations that are similar to each other are combined into branches, which are themselves fused at a higher height.

The height of the fusion, provided on the vertical axis, indicates the (dis)similarity between two observations. The higher the height of the fusion, the less similar the observations are. Note that, conclusions about the

proximity of two observations can be drawn only based on the height where branches containing those two observations first are fused. We cannot use the proximity of two observations along the horizontal axis as a criteria of their similarity.

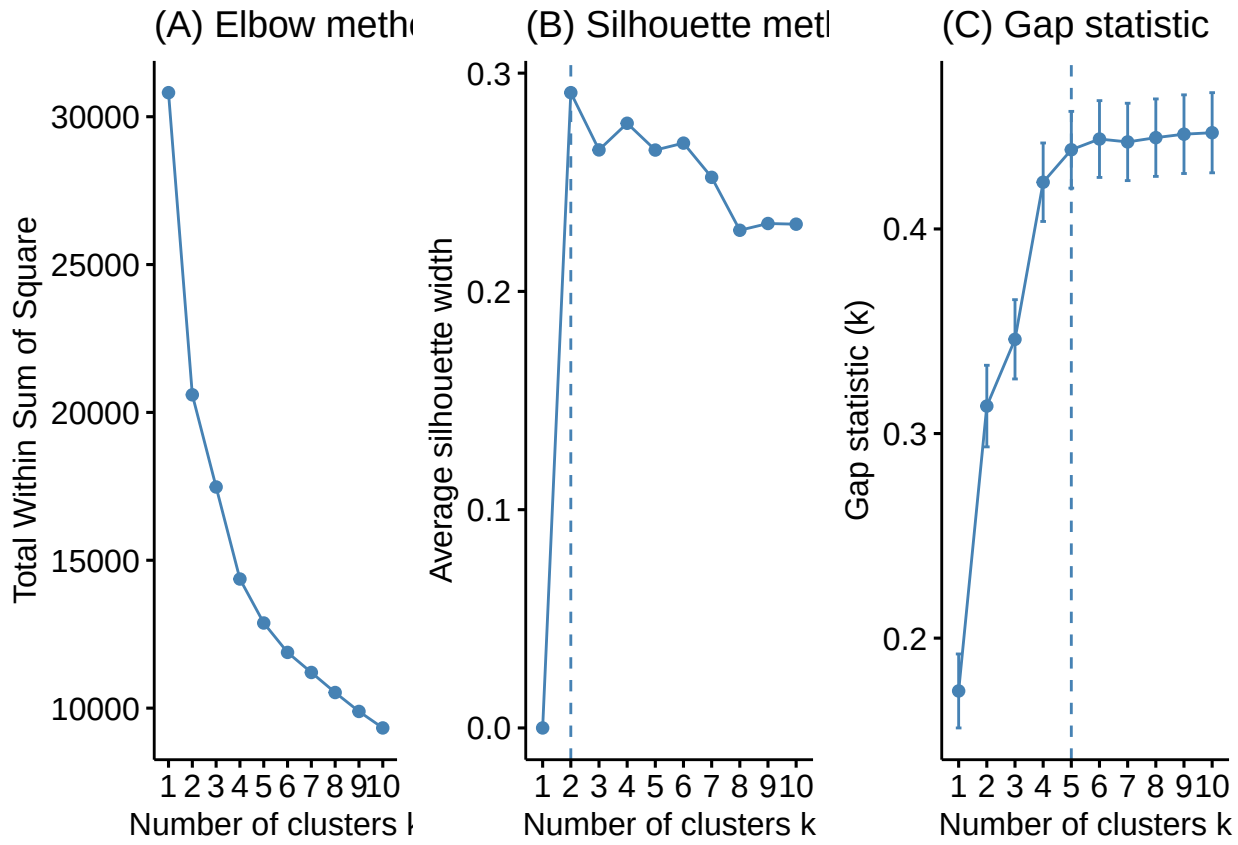
Although hierarchical clustering provides a fully connected dendrogram representing the cluster relationships, you may still need to choose the preferred number of clusters to extract. Fortunately we can execute approaches similar to k-means clustering. The following compares results provided by the elbow, silhouette, and gap statistic methods. There is no definitively clear optimal number of clusters in this case; although, the silhouette method and Elbow method suggest 2-5 clusters.

Humans cant live with this ambiguity. Let's use k-means clustering to determine the number of clusters we should use.

```
# Plot cluster results
p1 <- fviz_nbclust(clust_data, FUN = hcut, method = "wss",
                   k.max = 10) +
  ggtitle("(A) Elbow method")
p2 <- fviz_nbclust(clust_data, FUN = hcut, method = "silhouette",
                   k.max = 10) +
  ggtitle("(B) Silhouette method")
p3 <- fviz_nbclust(clust_data, FUN = hcut, method = "gap_stat",
                   k.max = 10) +
  ggtitle("(C) Gap statistic")
```

```
## Clustering k = 1,2,..., K.max (= 10): .. done
## Bootstrapping, b = 1,2,..., B (= 100)  [one "." per sample]:
## .................................................. 50
## .................................................. 100
```

```
# Display plots side by side
gridExtra::grid.arrange(p1, p2, p3, nrow = 1)
```



K-means

K-means is another type of clustering algorithm. For a more objective way to determine how many clusters there are, I am going to run k-means clustering over a range of cluster values (here 3-10 clusters). I will use the `fpc` package and the `kmeansrun` function. This function iterates over a number of clusters and chooses the best number of clusters.

```
#run kmeans over a number of ranges (3:10) here

cl <- kmeansruns(clust_data, krange = 3:10, iter.max = 1000)

# pick the best one
cl$bestk
```

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

The k-means analysis suggests 3 clusters. Let's visualize what this looks like.

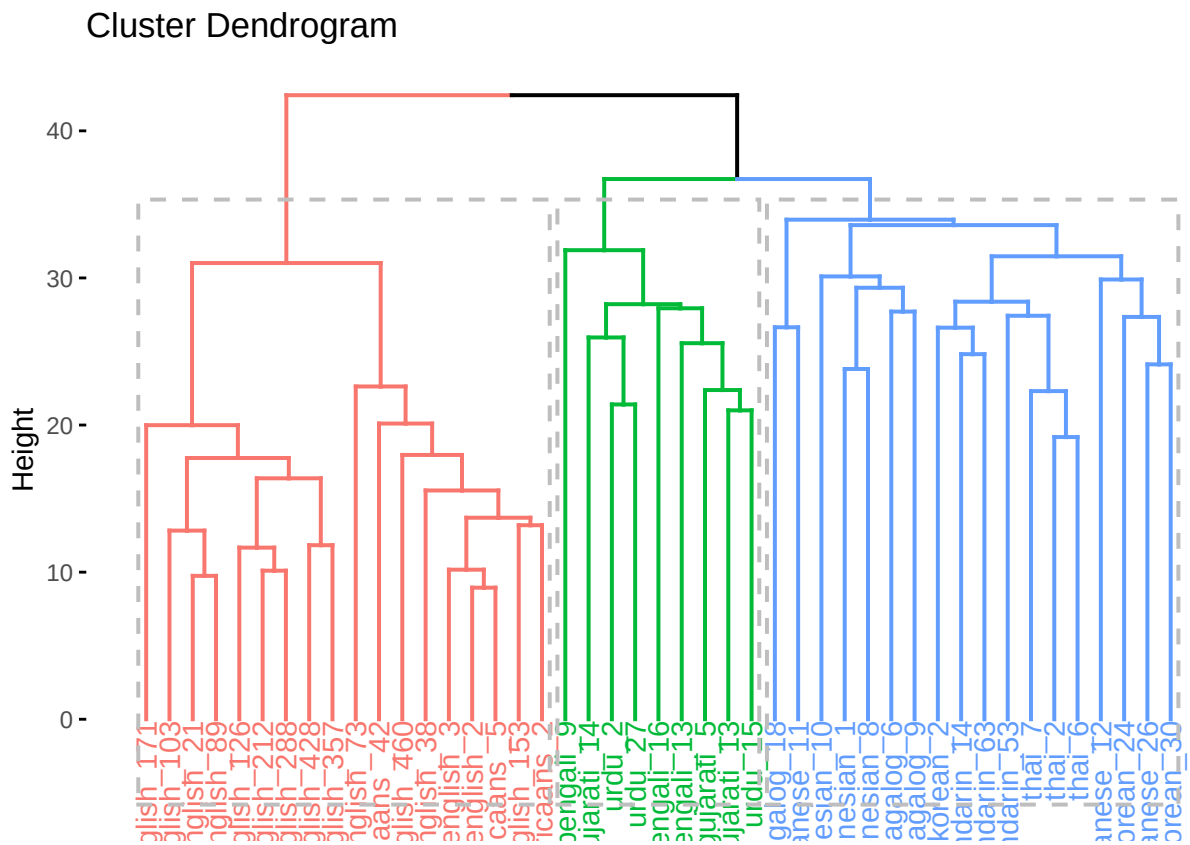
Visualize Clusters

Dendogram

Here is a dendogram cut at 3.

```
hc.cut <- hcut(clust_data, k = 3, hc_method = "average")

fviz_dend(hc.cut, show_labels = TRUE, rect = TRUE)
```




```
ggsave("dendogram.png", width=10, height=8, dpi=700)
```

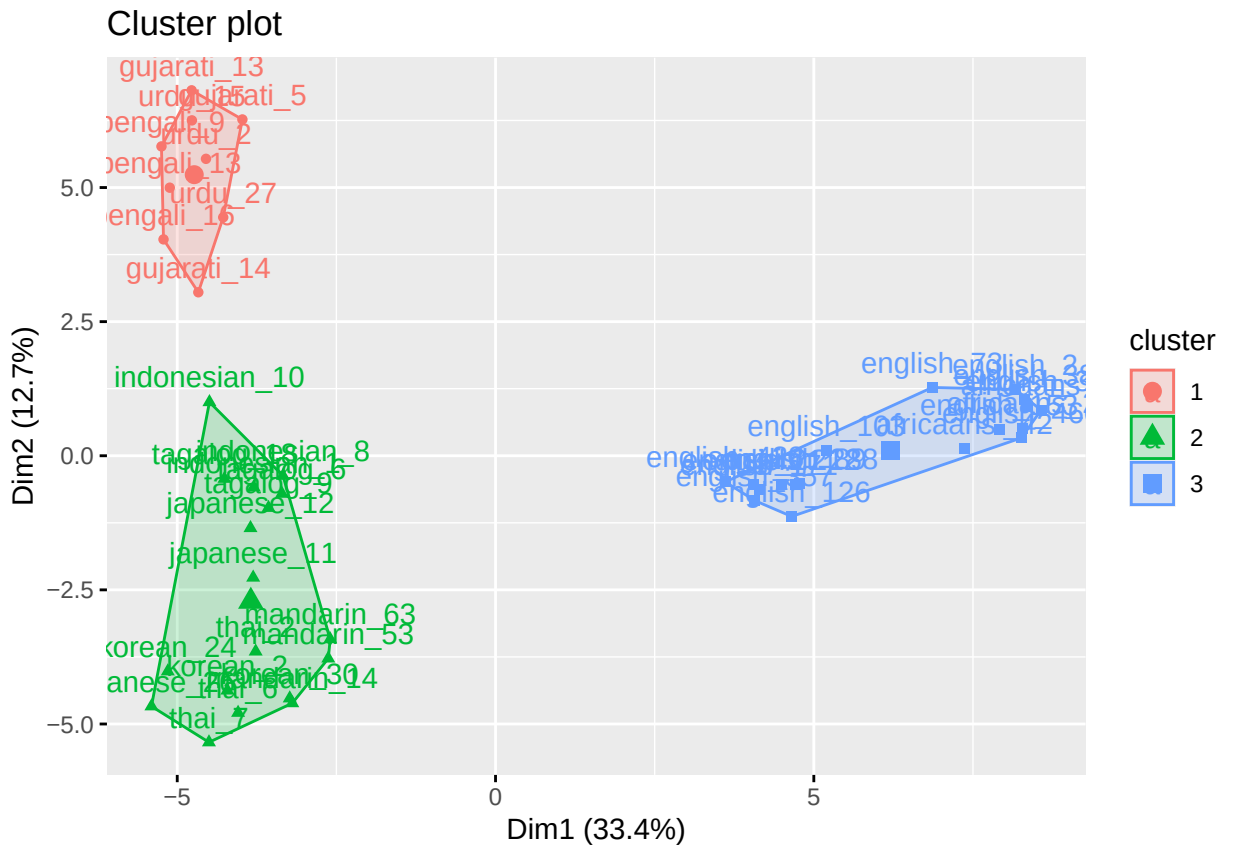
3 Clusters Let's visualize the clusters in two dimensions so it is a bit easier to read. This I saved this cluster figure as "3clust.png." I also saved the data with the cluster number of each speech token as "speech_group.csv." With this you can visualize the clusters how you want.

```
# Cut tree into 3 groups
sub_grp <- cutree(hc.cut, k = 3)

# Number of members in each cluster
sub_grp
```

```
##     bengali_9    bengali_13    bengali_16     gujarati_5    gujarati_13    gujarati_14         urdu_2
##             1             1             1             1              1              1              1
##       urdu_27  indonesian_1  indonesian_8 indonesian_10     tagalog_6     tagalog_9    tagalog_18
##             1             2             2             2              2              2              2
##        thai_6        thai_7   japanese_11   japanese_12   japanese_26      korean_2     korean_24
##             2             2             2             2              2              2              2
##   mandarin_14   mandarin_53   mandarin_63    english_21    english_89   english_103   english_428
##             2             2             2             3              3              3              3
##   english_357   english_288   english_171   english_126     english_3    english_73   english_153
##             3             3             3             3              3              3              3
##    english_38   english_460   africaans_2  africaans _5 africaans _42
##             3             3             3             3              3
```

```
fviz_cluster(list(data = clust_data, cluster = sub_grp))
```




```
ggsave("3clust.png", width=10, height=8, dpi=700)
```

Conclusion

From this, we glean that three clusters are adequate. Generally speaking, participants grouped speakers into three clusters/groups:

- Cluster 1: English/African
- Cluster 2: Indo/European
- Cluster 3: Asian

Just to summarize, I ran a hierarchical clustering analysis using the average link method to classify talkers in a free classification task. Because there was some ambuguity in terms of the correct correct number of clusters, I ran an iterative k-means analysis ranging from three clusters to ten cluster. This analysis suggested we should use three clusters.

Full Code

The full script of executive code contained in this document is reproduced here.

```
# For reproducibility
set.seed(666)
library(here)
library(tidyverse)  # data manipulation
library(cluster)    # clustering algorithms
```

```r
library(factoextra) # clustering visualization
library(dendextend) # for comparing two dendrograms
library(fpc) # kmeans clustering


clust_data <- read_csv(here("data", "class_wide_1.csv")) # read in data

clust_data <- select(clust_data, -X1, -`54`) # remove extra col sub 54 has weird formatting

clust_data <- as.data.frame(clust_data) # turn into df

rownames(clust_data) <- clust_data$speaker # make row names speaker

clust_data <- select(clust_data,-speaker) # remove extra col sub 54 has weird formatting

head(clust_data)# show first couple rows

# Dissimilarity matrix
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# Plot cluster results
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p2 <- fviz_nbclust(clust_data, FUN = hcut, method = "silhouette",
                   k.max = 10) +
  ggtitle("(B) Silhouette method")
p3 <- fviz_nbclust(clust_data, FUN = hcut, method = "gap_stat",
                   k.max = 10) +
  ggtitle("(C) Gap statistic")

# Display plots side by side
gridExtra::grid.arrange(p1, p2, p3, nrow = 1)

#run kmeans over a number of ranges (3:10) here

cl <- kmeansruns(clust_data, krange = 3:10, iter.max = 1000)

# pick the best one
cl$bestk


hc.cut <- hcut(clust_data, k = 3, hc_method = "average")

fviz_dend(hc.cut, show_labels = TRUE, rect = TRUE)
```

```r
ggsave("dendogram.png", width=10, height=8, dpi=700)

# Cut tree into 3 groups
sub_grp <- cutree(hc.cut, k = 3)

# Number of members in each cluster
sub_grp

fviz_cluster(list(data = clust_data, cluster = sub_grp))

ggsave("3clust.png", width=10, height=8, dpi=700)
```

References