Results Template

Clustering

Contents

Introduction

```
library(easystats)

summary(report::report(sessionInfo()))
```

The analysis was done using the R Statistical language (v4.0.2; R Core Team, 2020) on macOS Catalina 10.15.6, using the packages factoextra (v1.0.7), effectsize (v0.4.1), ggplot2 (v3.3.2), stringr (v1.4.0), forcats (v0.5.0), tidyr (v1.1.2), readr (v1.3.1), dplyr (v1.0.3), rmarkdown (v2.6.6), here (v0.1), tibble (v3.0.6), purrr (v0.3.4), parameters (v0.10.1.1), insight (v0.11.1.1), see (v0.6.1.1), performance (v0.6.1.1), cluster (v2.1.1), modelbased (v0.4.0), easystats (v0.2.0), correlation (v0.5.0), bayestestR (v0.8.0.1), report (v0.2.0), dendextend (v1.14.0) and tidyverse (v1.3.0).

Data

```
df <- read_csv("data/class_wide_1.csv")
```

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

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

Clustering

Introduction

In this task, individuals heard spoken speech tokens and freely classified them into groups. Using hierarchical clustering we aim to see what clusters or groups appear as a result of the free classification task.

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

Data Preparation

1. Rows are observations (individuals) and columns are variables
2. Any missing value in the data must be removed or estimated.
3. The data must be standardized (i.e., scaled) to make variables comparable (I am not doing this here)

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.
```

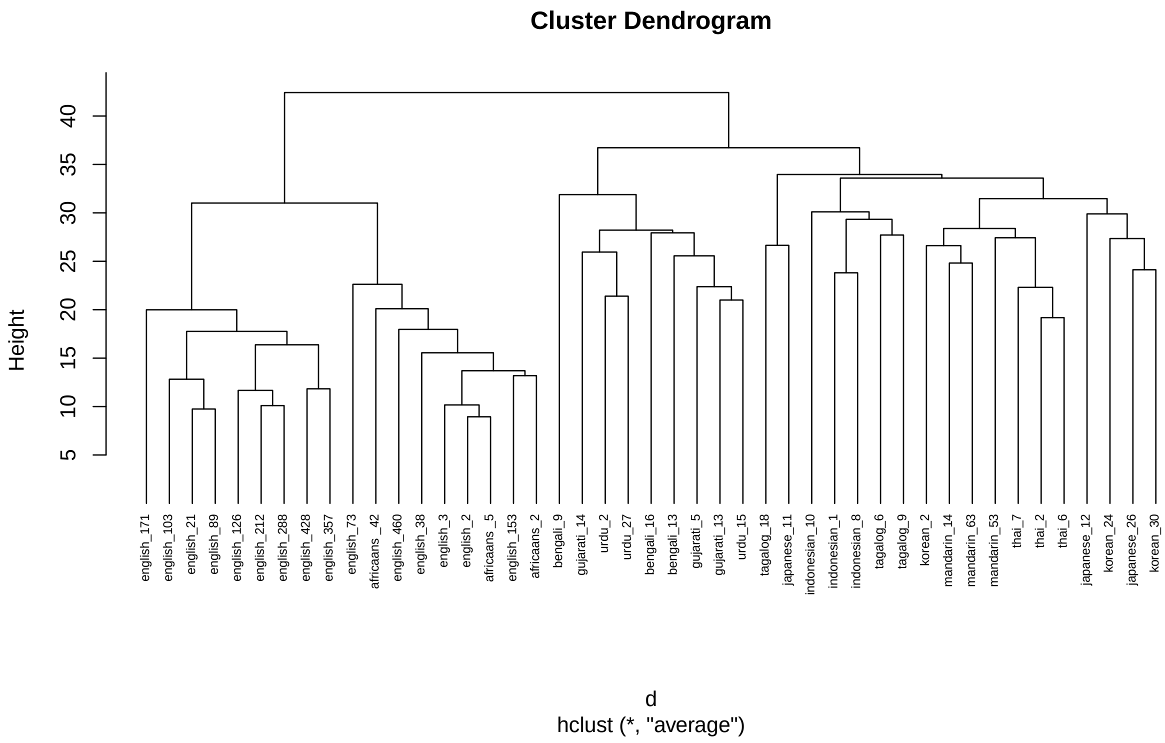
```
clust_data <- select(clust_data, -X1, -`54`) # remove extra col sub 54 has weird formatting

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
> 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
> 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
> 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
> 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
> 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
> 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
>             34 35 36 38 4 40 41 42 43 44 45 46 47 48 49  5 50 51 52 53 55 56 58 59
> bengali_9    8 10  8  1 3  1 10  1  1 12  1  5  1  5  8  1  3  7  1  8  9  1  1  5
> bengali_13   8 10 11  1 4 12  1  1  8 11  1  5  4  1  8  5  4  7  3  8  9  1  8 11
> bengali_16   8 10 11  6 3  8  8  1  8 11  1  1  2  5  7  5  4  7  3  8  9  8  1  6
> gujarati_5   6 10  8  1 2  8  7  1  8  8  3 11  2  2  8 10  3  7 11  8  9  7  3 11
> gujarati_13  8 10  2  1 2 12  1  1  8 11  1 11  6  5  8  2  4  7  1  8  9  7 10  5
> gujarati_14  6 10  9  1 4 13  2  1  8 11  6  3  4  5  8  3  3  7 15  8  8  8  6  5
>             6 78 87 90 91 96 105 110 111 115 121 123 125 132 133 135 148 151 152
> bengali_9    9  1 11  1 11  1   6  11   1   2   1   9   1   3   1   1   1   5   1
> bengali_13   7  1 11  1 11  1   6  11   7   8   6   9   1   6   2   3   6   9   1
> bengali_16   7  5 11  2  6  1   6  10   6   8   6  10  10   4   2   3   1   7   4
> gujarati_5   7  1 11  2 10  1   1  11   6   8   6   9  10   4   3   2   3   5   3
> gujarati_13 7  1 11  2 11  1   6  11   2   8   6   9  10   4   2   1   1   5   1
> gujarati_14 6  2 11  8 11  1   6  11   6   9   6   9   8   4   2   1   2   5   3
>             153 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169
> bengali_9     8   4   8   6   5   1   5   1   7   4   1   5   1   7   1   2
> bengali_13    8   4  10   6   5   2   1  14   7   6   4   5   1   4   2   4
> bengali_16    8  11   8   6   3   2   3  14   7   7   1   5   1   7   4   4
> gujarati_5    2   5   9   6   3   1   3  14   7   5   6   6   1   4   2   5
> gujarati_13   2   5   9   6   3   1   4  14   7   5   6   5   1   7   3   6
> gujarati_14   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

```
# 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)
```



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.

The height of the cut to the dendrogram controls the number of clusters obtained. It plays the same role as the k in k-means clustering. In order to identify sub-groups (i.e. clusters), we can cut the dendrogram with cutree:

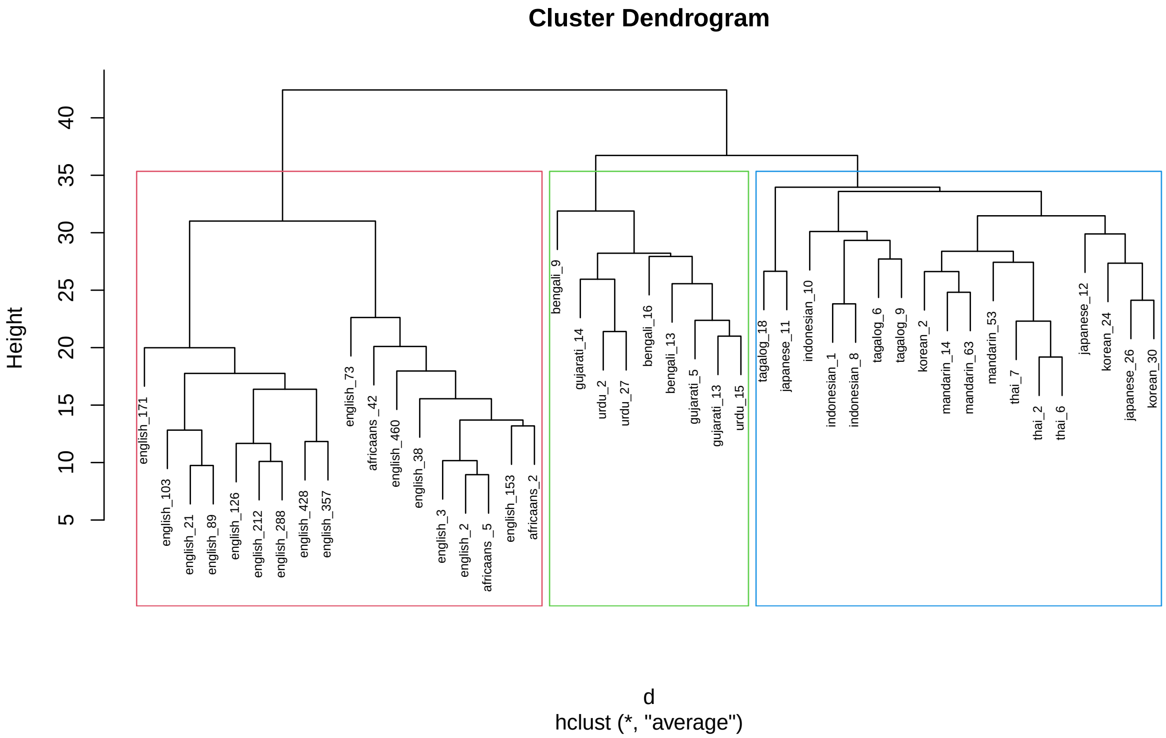
```
# Ward's method
hc5 <- hclust(d, method = "average" )

# Cut tree into 4 groups
sub_grp <- cutree(hc5, k = 3)

# Number of members in each cluster
table(sub_grp)
```

```
> sub_grp
>  1  2  3
>  9 18 18
```

```
## sub_grp
##  1  2  3  4
##  7 12 19 12
```

Visualize clusters on dendrogram

```
plot(hc5, cex = 0.6)
rect.hclust(hc5, k = 3, border = 2:5)
```

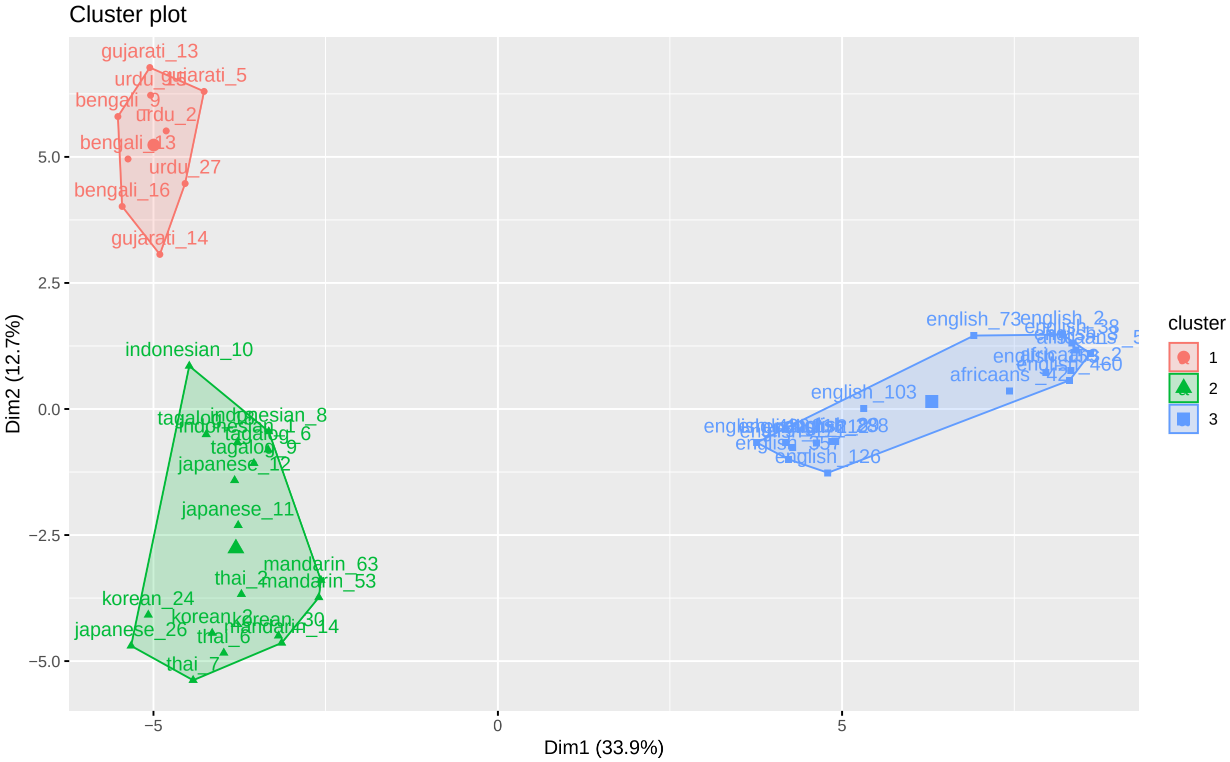


From this, we glean that 3 clusters seem to be adequate. Generally participants groups speakers into 3 clusters/groups:

- English/African into clust 1
- Indo/European into clust 2
- Asian into clust 3

```
clust_data <- clust_data %>%
  mutate(cluster = sub_grp)
```

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



Full Code

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

```
# Set up the environment (or use local alternative `source("utils/config.R")`)
source("https://raw.githubusercontent.com/RealityBending/TemplateResults/main/utils/config.R")

fast <- FALSE  # Make this false to skip the chunks
library(easystats)

summary(report::report(sessionInfo()))
df <- read_csv("data/class_wide_1.csv")
report::cite_packages(sessionInfo())
library(here)
library(tidyverse)  # data manipulation
library(cluster)    # clustering algorithms
library(factoextra) # clustering visualization
library(dendextend) # for comparing two dendrograms


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
```

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

head(clust_data)# show first couple rows

# 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)


# Ward's method
hc5 <- hclust(d, method = "average" )

# Cut tree into 4 groups
sub_grp <- cutree(hc5, k = 3)

# Number of members in each cluster
table(sub_grp)
## sub_grp
##  1  2  3  4
##  7 12 19 12

plot(hc5, cex = 0.6)
rect.hclust(hc5, k = 3, border = 2:5)


clust_data <- clust_data %>%
  mutate(cluster = sub_grp)

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

Package References

```r
report::cite_packages(sessionInfo())
```

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