

Sanitation

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```
library(factoextra)
```

```
## Loading required package: ggplot2
```

```
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

```
library(dendextend)
```

```
##
## -----
## Welcome to dendextend version 1.16.0
## Type citation('dendextend') for how to cite the package.
##
## Type browseVignettes(package = 'dendextend') for the package vignette.
## The github page is: https://github.com/talgalili/dendextend/
##
## Suggestions and bug-reports can be submitted at: https://github.com/talgalili/dendextend/issues
## You may ask questions at stackoverflow, use the r and dendextend tags:
## https://stackoverflow.com/questions/tagged/dendextend
##
## To suppress this message use: suppressPackageStartupMessages(library(dendextend))
## -----
```

```
##
## Attaching package: 'dendextend'
```

```
## The following object is masked from 'package:stats':
##
## cutree
```

```
library(cluster)
```

```
## Warning: package 'cluster' was built under R version 4.2.2
```

```
library(tidyverse)
```

```
## — Attaching packages
```

```
## _____
```

```
## tidyverse 1.3.2 —
```

```
## ✓ tibble 3.1.8    ✓ dplyr 1.0.10
```

```
## ✓ tidyr 1.2.1     ✓ stringr 1.4.1
```

```
## ✓ readr 2.1.3     ✓ forcats 0.5.2
```

```
## ✓ purrr 0.3.4
```

```
## — Conflicts ————— tidyverse_conflicts() —
```

```
## ✗ dplyr::filter() masks stats::filter()
```

```
## ✗ dplyr::lag()   masks stats::lag()
```

```
library(knitr)
```

```
WithoutSanitation<-
```

```
read.csv("C:/Users/jenru/OneDrive/Documents/safe-sanitation-without-2019.csv", header = TRUE, sep = ",", stringsAsFactors = FALSE)
```

```
WithoutSanitation = type.convert(WithoutSanitation, as.is = TRUE)
```

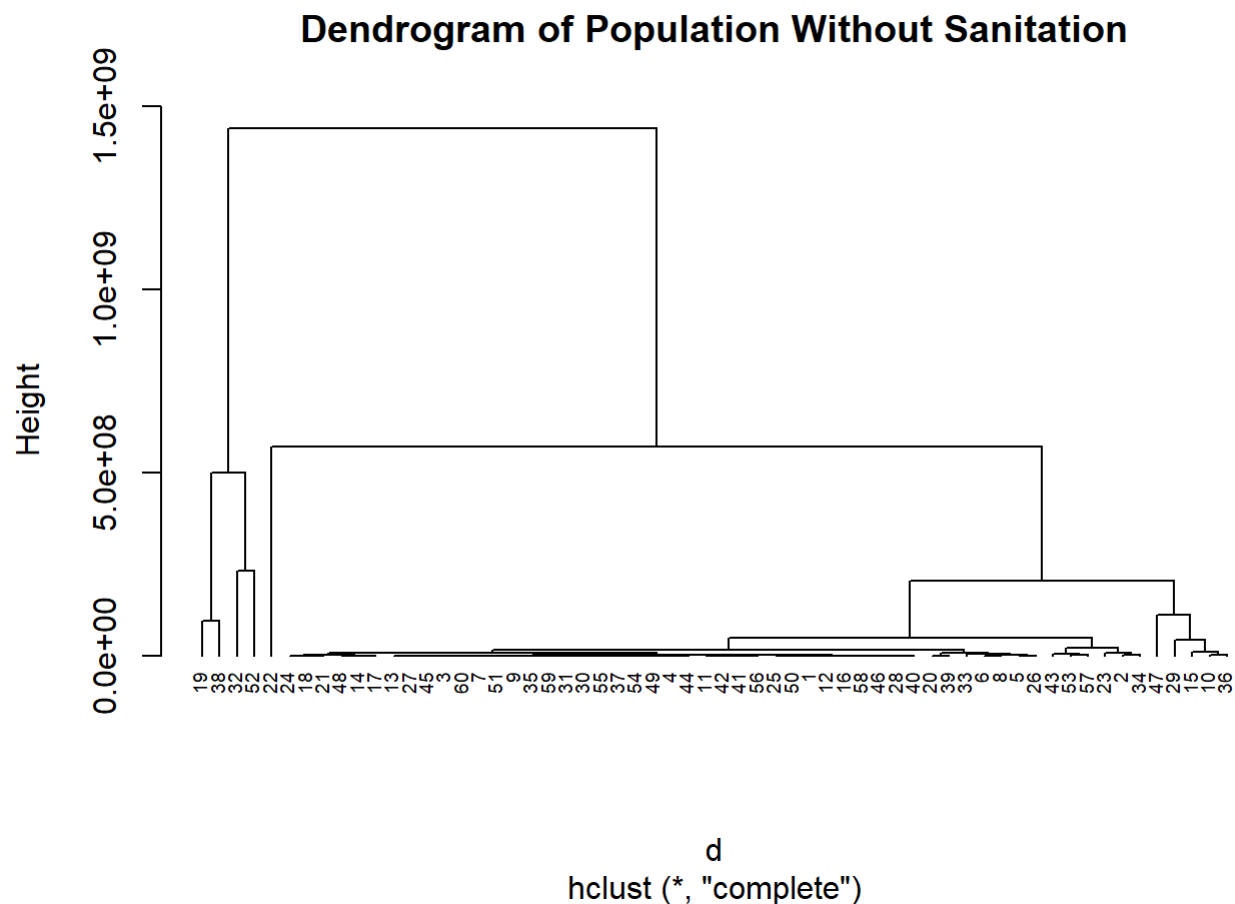
```
df<- WithoutSanitation
```

```
d<-dist(df,method="euclidean")
```

```
## Warning in dist(df, method = "euclidean"): NAs introduced by coercion
```

```
hc1<-hclust(d, method="complete")
```

```
plot(hc1, cex=0.6, hang=-1, main="Dendrogram of Population Without Sanitation")
```



```
hc_single<-agnes(df, method = "single")
hc_complete<- agnes(df, method = "complete")
hc_average<- agnes(df, method = "average")

print(hc_single$ac)
```

```
## [1] 0.949882
```

```
print(hc_complete$ac)
```

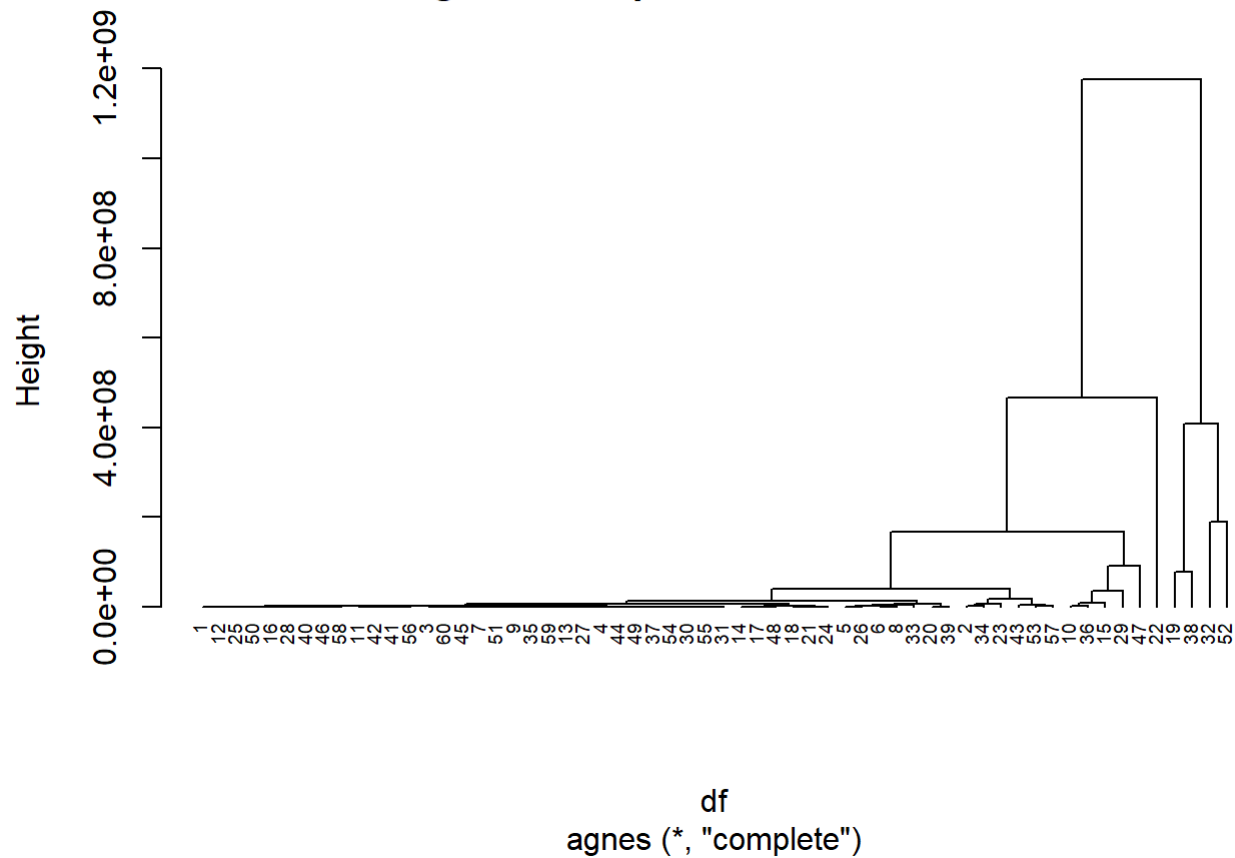
```
## [1] 0.9834165
```

```
print(hc_average$ac)
```

```
## [1] 0.9795099
```

```
pltree(hc_complete, cex = 0.6, hang=-1, main="Dendrogram of Population Without Sanitation")
```

Dendrogram of Population Without Sanitation



```
df<-WithoutSanitation
numericaldata = data.frame(WithoutSanitation[,1:3])
```

```
df2<-WithoutSanitation
```

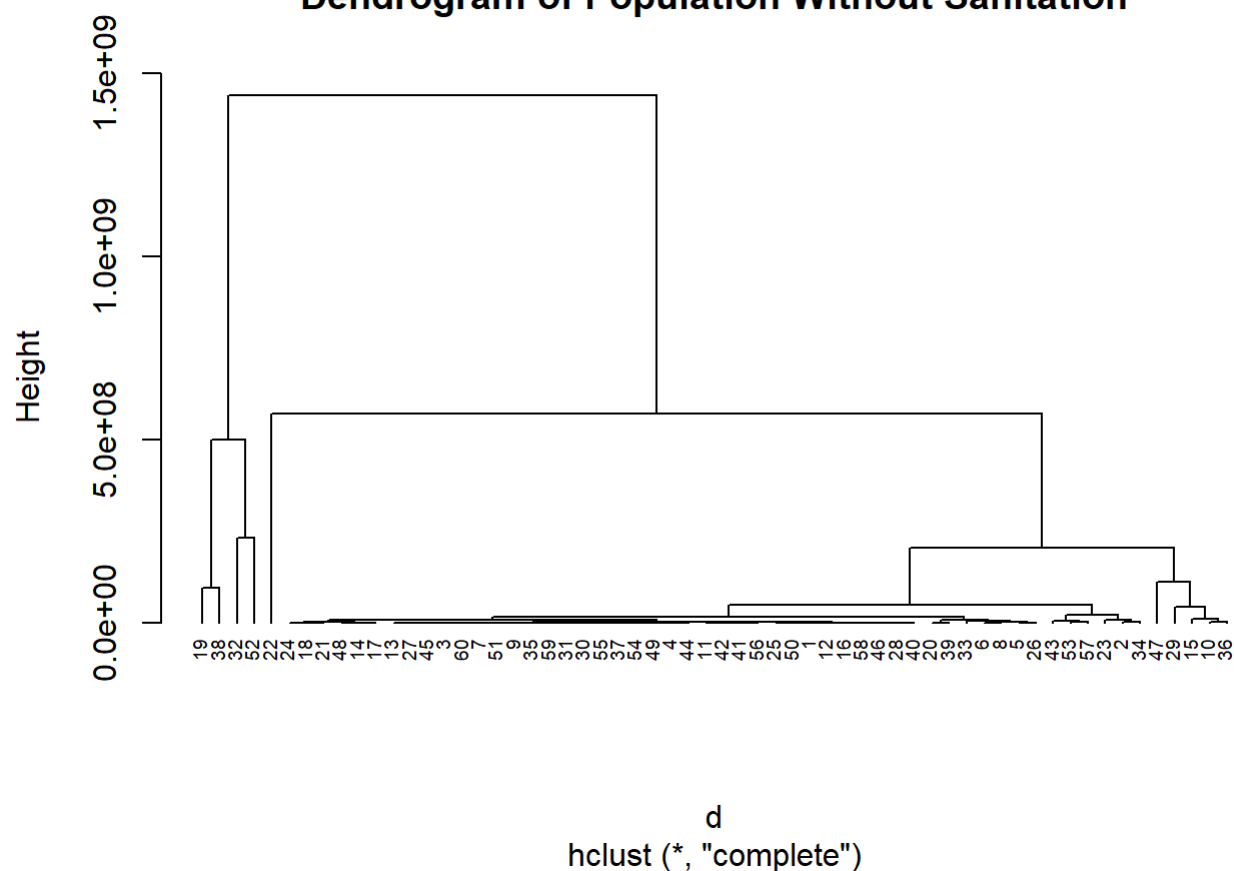
```
d<-dist(df,method="euclidean")
```

```
## Warning in dist(df, method = "euclidean"): NAs introduced by coercion
```

```
hc1<-hclust(d, method="complete")
```

```
plot(hc1, cex=0.6, hang=-1, main="Dendrogram of Population Without Sanitation")
```

Dendrogram of Population Without Sanitation



```
df2<- WithoutSanitation
```

```
hc_single<-agnes(df2, method = "single")
```

```
hc_average<- agnes(df2, method = "average")
```

```
hc_complete <- agnes(df2, method = "complete")
```

```
print(hc_single$ac)
```

```
## [1] 0.949882
```

```
print(hc_complete$ac)
```

```
## [1] 0.9834165
```

```
print(hc_average$ac)
```

```
## [1] 0.9795099
```

```
pltree(hc_complete, cex = 0.6, hang=-1, main="Dendrogram of Population without Sanitation")
```

Dendrogram of Population without Sanitation

