

For this analysis, we will be clustering observations based on COVID-19 deaths, as well as similar health and demographic characteristics. We will be doing both agglomerative hierarchical clustering, which determines the number of clusters from individual groups, as well as divisive clustering, which determines the number of clusters after starting from one large cluster that contains all observations. I will also compare the results of both types of clustering visually. The unit of analysis here is the county.

```
link='https://github.com/Public-Policy-  
COVID/students_merge/raw/main/Merged_data.csv'
```

```
myfile=url(link)
```

```
##Reading in data
```

```
covid=read.csv(file=myfile)
```

```
##Reset row names to R format
```

```
row.names(covid)=NULL
```

```
str(covid,width = 50,strict.width='cut')
```

```
## 'data.frame':  133 obs. of  19 variables:  
## $ Number_of_beds      : num  3667 0 52 553 25 ..  
## $ Number_of_hospitals : num   22 0 1 6 1 1 10 1..  
## $ Location            : chr   "Alameda_CA" "Al"..  
## $ Urban_Rural_Code    : chr   "Large central m"..  
## $ Deaths_COVID       : int   573 0 31 101 12 1..  
## $ Deaths_total       : int  10908 0 415 2313 ..  
## $ never               : num   0.019 0.025 0.045..  
## $ rarely              : num   0.008 0.085 0.013..  
## $ sometimes          : num   0.055 0.088 0.099..  
## $ frequently         : num   0.123 0.19 0.188 ..  
## $ always              : num   0.795 0.612 0.655..  
## $ mask_score          : num    3.67 3.28 3.4 3.3..  
## $ total_population    : num  1671329 1129 3975..  
## $ white_total_pct     : num    49.3 67.9 89.7 85..  
## $ black_total_pct     : num    11.03 0.35 2.68 1..  
## $ aian_total_pct      : num    1.06 25.69 2.33 2..  
## $ asian_total_pct     : num    32.33 1.59 1.67 5..  
## $ nhopi_total_pct     : num    0.94 0 0.29 0.29 ..  
## $ multiracial_total_pct: num    5.35 4.43 3.38 4...
```

```
##VARIABLE PREPARATION##
```

```
##First, we want to include the variable for COVID deaths in the cluster  
analysis, but it is currently a string variable. We will need to change to  
numeric
```

```
as.numeric('Deaths_COVID')
```

```
## Warning: NAs introduced by coercion
```

```
## [1] NA
```

##Now, we will choose the variables to cluster around COVID deaths. We will include total population, mask score, the number of hospital beds, the total percent of the population that is white, and the total percent of the population that is black. Although we only have total deaths and not deaths per 100K, clustering around total population should help control for variation due to population.

```
dfClus=covid[c('Number_of_beds','mask_score','Deaths_COVID','Deaths_total','Number_of_hospitals','black_total_pct','white_total_pct')]
```

```
summary(dfClus)
```

```
## Number_of_beds      mask_score    Deaths_COVID    Deaths_total
## Min.   :    0.0    Min.   :2.470    Min.   :  0    Min.   :  0
## 1st Qu.:   25.0    1st Qu.:3.301    1st Qu.:  0    1st Qu.:  0
## Median :   131.0    Median :3.464    Median :  22    Median :   637
## Mean   :   885.4    Mean   :3.428    Mean   :  206    Mean   :  2896
## 3rd Qu.:   553.0    3rd Qu.:3.591    3rd Qu.: 128    3rd Qu.: 2537
## Max.   :26672.0    Max.   :3.822    Max.   :8034    Max.   :75463
## Number_of_hospitals black_total_pct white_total_pct
## Min.   :  0        Min.   : 0.000    Min.   :49.28
## 1st Qu.:  1        1st Qu.: 0.770    1st Qu.:82.16
## Median :  2        Median : 1.260    Median :88.64
## Mean   :  5        Mean   : 2.318    Mean   :85.50
## 3rd Qu.:  4        3rd Qu.: 2.620    3rd Qu.:91.84
## Max.   :112        Max.   :14.770    Max.   :96.13
```

##Rescale the units into a new variable

```
dfClus=scale(dfClus)
```

```
summary(dfClus)
```

```
## Number_of_beds      mask_score    Deaths_COVID    Deaths_total
## Min.   :-0.3334    Min.   :-4.2726    Min.   :-0.2704    Min.   :-0.37704
## 1st Qu.: -0.3240    1st Qu.: -0.5659    1st Qu.: -0.2704    1st Qu.: -0.37704
## Median : -0.2841    Median :  0.1612    Median : -0.2415    Median : -0.29411
## Mean   :  0.0000    Mean   :  0.0000    Mean   :  0.0000    Mean   :  0.00000
## 3rd Qu.: -0.1252    3rd Qu.:  0.7277    3rd Qu.: -0.1024    3rd Qu.: -0.04674
## Max.   :  9.7118    Max.   :  1.7581    Max.   :10.2736    Max.   :  9.44771
## Number_of_hospitals black_total_pct white_total_pct
## Min.   :-0.44686    Min.   :-0.8976    Min.   :-3.8920
## 1st Qu.: -0.35749    1st Qu.: -0.5994    1st Qu.: -0.3585
## Median : -0.26812    Median : -0.4097    Median :  0.3379
## Mean   :  0.00000    Mean   :  0.0000    Mean   :  0.0000
## 3rd Qu.: -0.08937    3rd Qu.:  0.1169    3rd Qu.:  0.6818
## Max.   :  9.56284    Max.   :  4.8214    Max.   :  1.1428
```

##We will set Location as the row names, which will allow us to look at cluster results for each county.

```
row.names(dfClus)=covid$Location
head(dfClus)
```

```
##           Number_of_beds mask_score Deaths_COVID Deaths_total
## Alameda_CA      1.0476322  1.0666781    0.4816583    1.04310240
## Alpine_CA      -0.3334445 -0.6640201   -0.2703586   -0.37704284
## Amador_CA      -0.3138601 -0.1465949   -0.2296736   -0.32301275
## Butte_CA       -0.1251719 -0.2090427   -0.1378042   -0.07590643
## Calaveras_CA   -0.3240289 -0.6104934   -0.2546096   -0.32691854
## Colusa_CA      -0.3153666  0.1790262   -0.2546096   -0.36194046
##           Number_of_hospitals black_total_pct white_total_pct
## Alameda_CA      1.51932965      3.3732540    -3.89196747
## Alpine_CA      -0.44686166     -0.7620594    -1.88666366
## Amador_CA      -0.35748933      0.1401204     0.44640953
## Butte_CA       0.08937233     -0.1618969     0.01654805
## Calaveras_CA   -0.35748933     -0.4794022     0.58611451
## Colusa_CA      -0.35748933     -0.3903458     0.60223432
```

```
set.seed(999) ##This is for replicability of results
```

##Determine the sitance method and compute distance matrix

```
library(cluster)
dfClus_D=cluster::daisy(x=dfClus)
```

##HIERARCHIZING AGGLOMERATIVE##

##First, set the number of clusters

```
NumCluster=4
```

##Next, apply the function:

```
library(factoextra)
```

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

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

```
res.agnes= hcut(dfClus_D,
               k = NumCluster,isdiss=T,
               hc_func='agnes',
               hc_method = "ward.D2")
```

```

##Cluster
covid$agn=as.factor(res.agnes$cluster)

##Let's check the first cluster for reference

covid[covid$agn==1,'Location']

## [1] "Alameda_CA"          "Contra Costa_CA"      "Orange_CA"
## [4] "Riverside_CA"         "Sacramento_CA"       "San Bernardino_CA"
## [7] "San Diego_CA"        "San Francisco_CA"    "San Mateo_CA"
## [10] "Santa Clara_CA"      "Solano_CA"           "King_WA"

##Let's check the results through a table

table(covid$agn)

##
##  1  2  3  4
## 12 45 75  1

##The results indicate that Cluster 4 has only one observation. Let's check
which county it is.

covid[covid$agn==4,'Location']

## [1] "Los Angeles_CA"

##Los Angeles County appears to be the sole observation.

##Let's check King County's cluster

covid[covid$Location=="King_WA",'agn']

## [1] 1
## Levels: 1 2 3 4

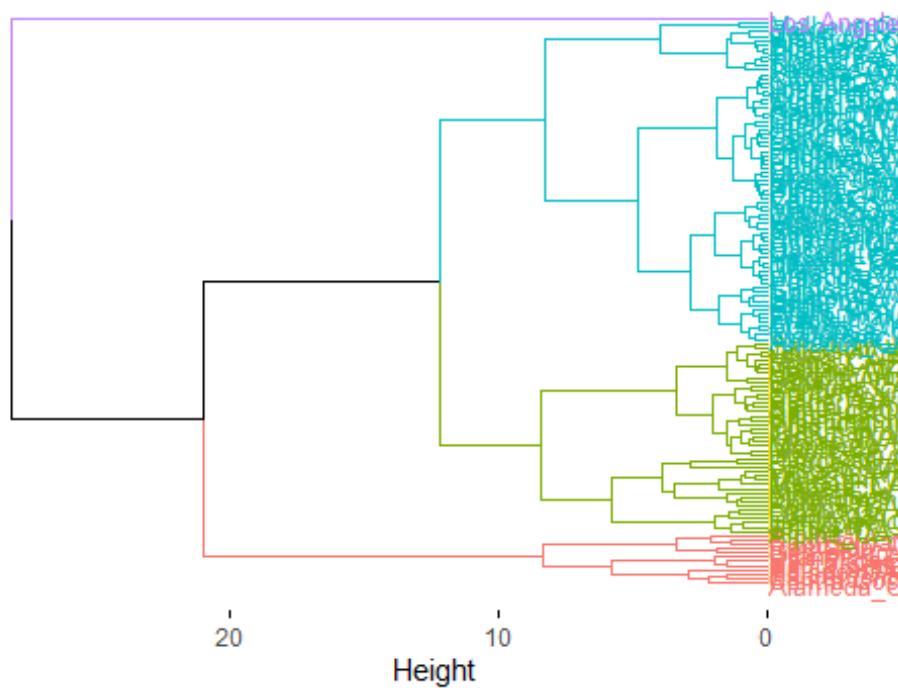
##VISUALIZING AGGLOMERATIVE RESULTS

##We will produce a dendrogram of the cluster results

fviz_dend(res.agnes,k=NumCluster, cex = 0.7, horiz = T)

```

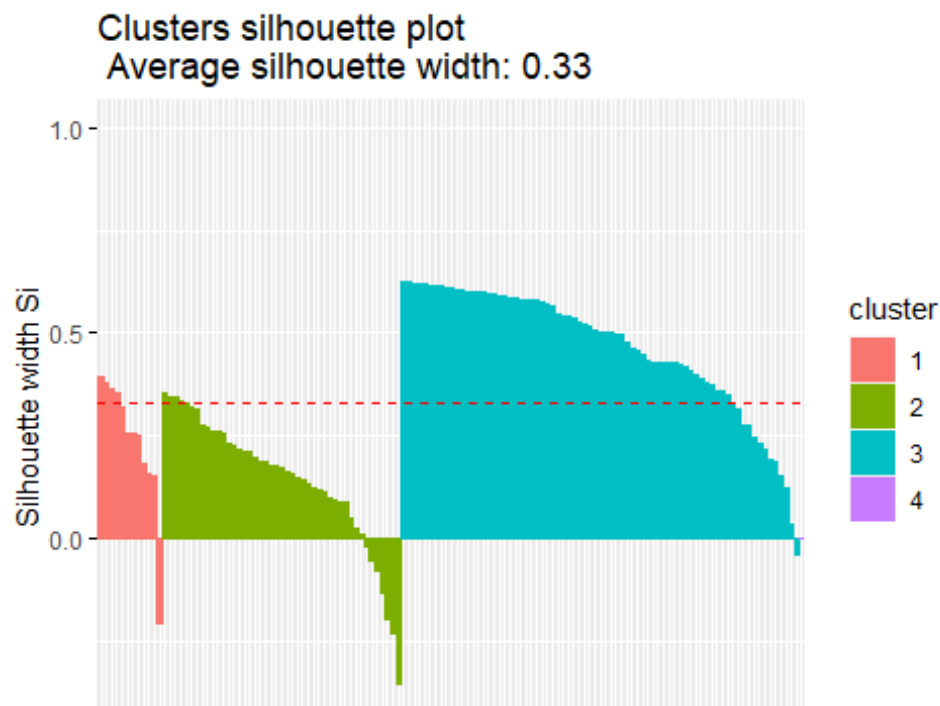
Cluster Dendrogram



##Let's visualize our cluster results with a silhouette plot

```
library(factoextra)
fviz_silhouette(res.agnes)
```

```
##  cluster size ave.sil.width
## 1         1   12         0.24
## 2         2   45         0.14
## 3         3   75         0.47
## 4         4    1         0.00
```



##It appears that clusters 1,2, and 3 each have negative silhouettes, which means these are poorly clustered

#Saving individual silhouettes

```
agnEval=data.frame(res.agnes$silinfo$widths)
head(agnEval)
```

```
##           cluster neighbor sil_width
## Alameda_CA         1         2 0.3919787
## King_WA             1         2 0.3804824
## Sacramento_CA       1         2 0.3653891
## San Bernardino_CA   1         2 0.3530916
## San Diego_CA        1         2 0.3198629
## Riverside_CA        1         2 0.2560581
```

##Let's check the observations with negative silhouettes

```
agnEval[agnEval$sil_width<0,]

##           cluster neighbor  sil_width
## San Mateo_CA         1         2 -0.20528803
## Lassen_CA            2         3 -0.01850048
## San Joaquin_CA       2         1 -0.05384687
## Jefferson_WA         2         3 -0.07849399
## Del Norte_CA         2         3 -0.13087586
## San Juan_WA          2         3 -0.19746628
```

```
## Ferry_WA          2          3 -0.23240216
## Okanogan_WA       2          3 -0.35433693
## San Benito_CA     3          2 -0.04121742
```

##In total, there are nine observations that are poorly clustered: One in cluster 1, Seven in Cluster 2, and One in Cluster 3

##HIERARCHIZING METHOD##

##Apply the function

```
library(factoextra)
```

```
res.diana= hcut(dfClus_D, k = NumCluster,
                hc_func='diana',
                hc_method = "ward.D")
```

##Clustering

```
covid$dia=as.factor(res.diana$cluster)
```

##Querying the data frame

```
covid[covid$dia==1, 'Location']
```

```
## [1] "Alameda_CA"      "Contra Costa_CA"  "Fresno_CA"
"Sacramento_CA"
## [5] "San Francisco_CA" "San Joaquin_CA"   "San Mateo_CA"     "Santa
Clara_CA"
## [9] "Solano_CA"       "Pierce_WA"
```

##Check the results by each cluster:

```
table(covid$dia)
```

```
##
##  1  2  3  4
## 10 117  1  5
```

#The results indicate that Cluster 2 has the Large majority of observations. Let's check that one

```
covid[covid$dia==2, 'Location']
```

```
## [1] "Alpine_CA"      "Amador_CA"       "Butte_CA"
## [4] "Calaveras_CA"   "Colusa_CA"       "Del Norte_CA"
## [7] "El Dorado_CA"   "Glenn_CA"        "Humboldt_CA"
## [10] "Imperial_CA"    "Inyo_CA"         "Kern_CA"
## [13] "Kings_CA"       "Lake_CA"         "Lassen_CA"
## [16] "Madera_CA"      "Marin_CA"        "Mariposa_CA"
```

```
## [19] "Mendocino_CA"      "Merced_CA"         "Modoc_CA"
## [22] "Mono_CA"           "Monterey_CA"       "Napa_CA"
## [25] "Nevada_CA"         "Placer_CA"         "Plumas_CA"
## [28] "San Benito_CA"     "San Luis Obispo_CA" "Santa Barbara_CA"
## [31] "Santa Cruz_CA"     "Shasta_CA"         "Sierra_CA"
## [34] "Siskiyou_CA"       "Sonoma_CA"         "Stanislaus_CA"
## [37] "Sutter_CA"         "Tehama_CA"         "Trinity_CA"
## [40] "Tulare_CA"        "Tuolumne_CA"       "Ventura_CA"
## [43] "Yolo_CA"           "Yuba_CA"           "Baker_OR"
## [46] "Benton_OR"         "Clackamas_OR"      "Clatsop_OR"
## [49] "Columbia_OR"       "Coos_OR"           "Crook_OR"
## [52] "Curry_OR"         "Deschutes_OR"      "Douglas_OR"
## [55] "Gilliam_OR"        "Grant_OR"          "Harney_OR"
## [58] "Hood River_OR"     "Jackson_OR"        "Jefferson_OR"
## [61] "Josephine_OR"     "Klamath_OR"        "Lake_OR"
## [64] "Lane_OR"           "Lincoln_OR"        "Linn_OR"
## [67] "Malheur_OR"        "Marion_OR"         "Morrow_OR"
## [70] "Multnomah_OR"      "Polk_OR"           "Sherman_OR"
## [73] "Tillamook_OR"      "Umatilla_OR"       "Union_OR"
## [76] "Wallowa_OR"        "Wasco_OR"          "Washington_OR"
## [79] "Wheeler_OR"        "Yamhill_OR"        "Adams_WA"
## [82] "Asotin_WA"         "Benton_WA"         "Chelan_WA"
## [85] "Clallam_WA"        "Clark_WA"          "Columbia_WA"
## [88] "Cowlitz_WA"        "Douglas_WA"        "Ferry_WA"
## [91] "Franklin_WA"       "Garfield_WA"       "Grant_WA"
## [94] "Grays Harbor_WA"   "Island_WA"         "Jefferson_WA"
## [97] "Kitsap_WA"         "Kittitas_WA"       "Klickitat_WA"
## [100] "Lewis_WA"          "Lincoln_WA"        "Mason_WA"
## [103] "Okanogan_WA"       "Pacific_WA"        "Pend Oreille_WA"
## [106] "San Juan_WA"       "Skagit_WA"         "Skamania_WA"
## [109] "Snohomish_WA"     "Spokane_WA"        "Stevens_WA"
## [112] "Thurston_WA"       "Wahkiakum_WA"      "Walla Walla_WA"
## [115] "Whatcom_WA"        "Whitman_WA"        "Yakima_WA"
```

##Let's check King County:

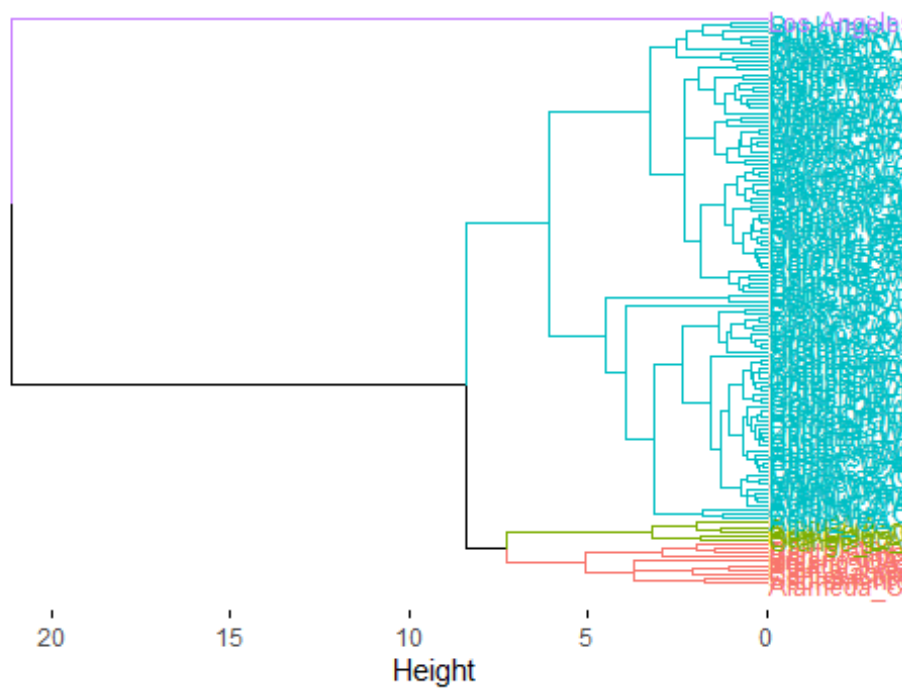
```
covid[covid$Location=="King_WA" , 'dia']
```

```
## [1] 4
## Levels: 1 2 3 4
```

##Now, to evaluate results, we will produce a cluster dendrogram

```
fviz_dend(res.diana,k=NumCluster, cex = 0.7, horiz = T)
```


Cluster Dendrogram

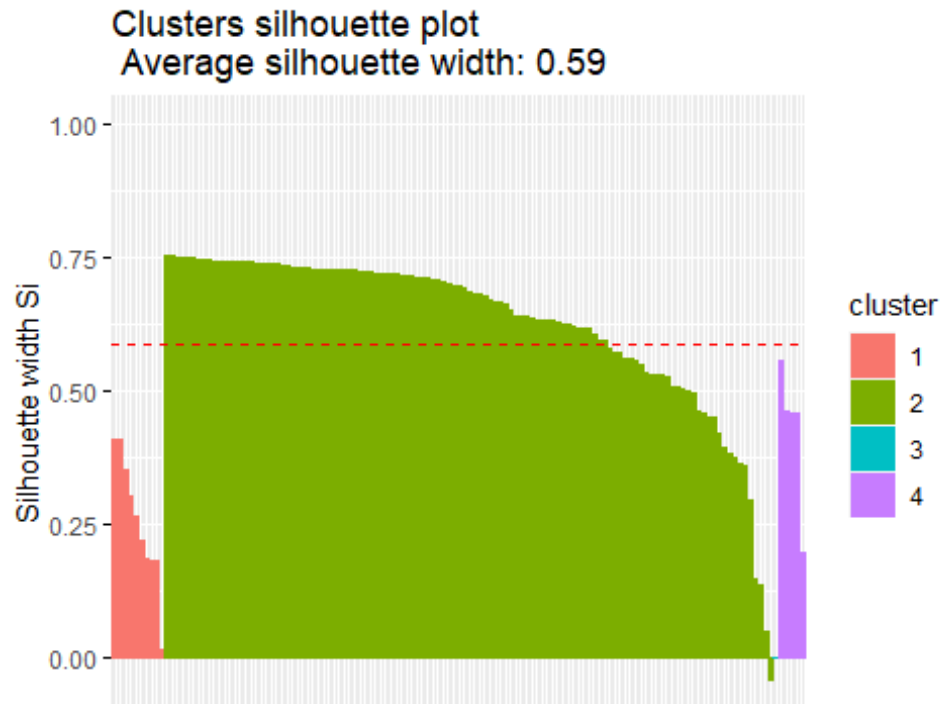


##To visualize results, we will produce silhouettes

##Report average silhouettes

```
library(factoextra)
fviz_silhouette(res.diana)
```

```
## cluster size ave.sil.width
## 1      1    10      0.25
## 2      2   117      0.63
## 3      3     1      0.00
## 4      4     5      0.43
```



#Cluster 2 has a negative silhouette, meaning it is poorly clustered.

##Next we will save silhouettes

```
diaEval=data.frame(res.diana$silinfo$widths)
head(diaEval)
```

```
##           cluster neighbor sil_width
## San Joaquin_CA      1         4 0.4104780
## Contra Costa_CA     1         4 0.4078738
## Solano_CA           1         4 0.3537789
## San Francisco_CA    1         4 0.3027197
## Alameda_CA          1         4 0.2676310
## Sacramento_CA       1         4 0.2209684
```

##Let's check the poorly clustered silhouette in Cluster 2

```
diaEval[diaEval$sil_width<0,]

##           cluster neighbor  sil_width
## Multnomah_OR      2         1 -0.04078789
```

##It Looks Like Multnomah County is the poorly clustered result

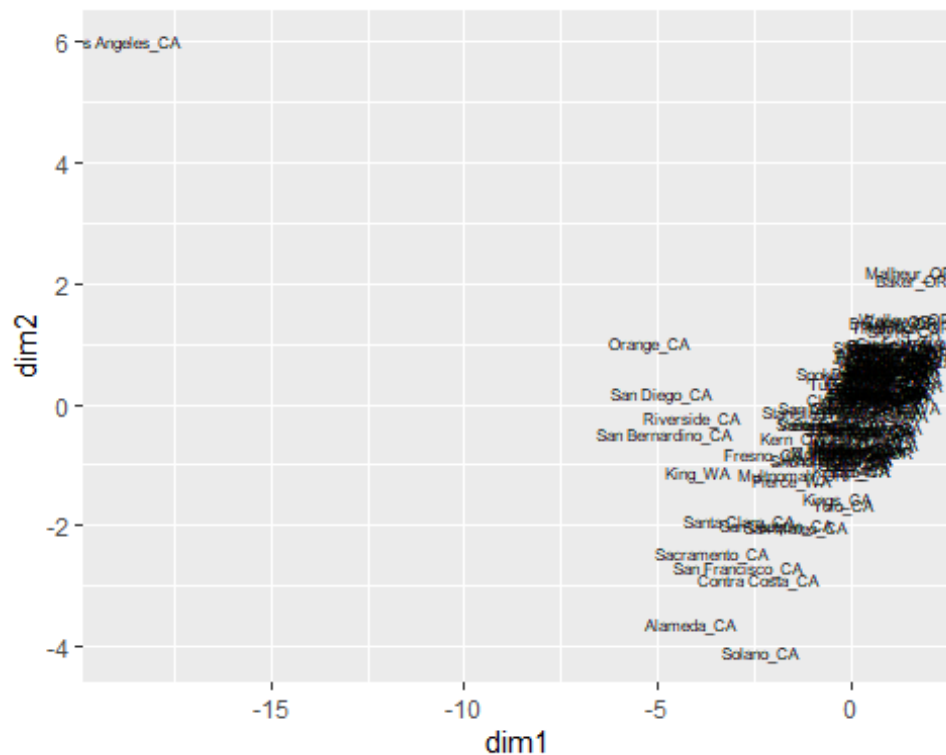
##COMPARING AGGLOMERATIVE AND DIVISIVE CLUSTERS

```
projectedData = cmdscale(dfClus_D, k=2)
#
# save coordinates to original data frame
```

```
covid$dim1 = projectedData[,1]
covid$dim2 = projectedData[,2]
```

```
##Map the clusters
```

```
base= ggplot(data=covid,
             aes(x=dim1, y=dim2,
                 label=Location))
base + geom_text(size=2)
```



```
##Plot the Agglomerating Results
```

```
agnPlot=base + labs(title = "AGNES") + geom_point(size=2,
                                                    aes(color=agn),
                                                    show.legend = F)
```

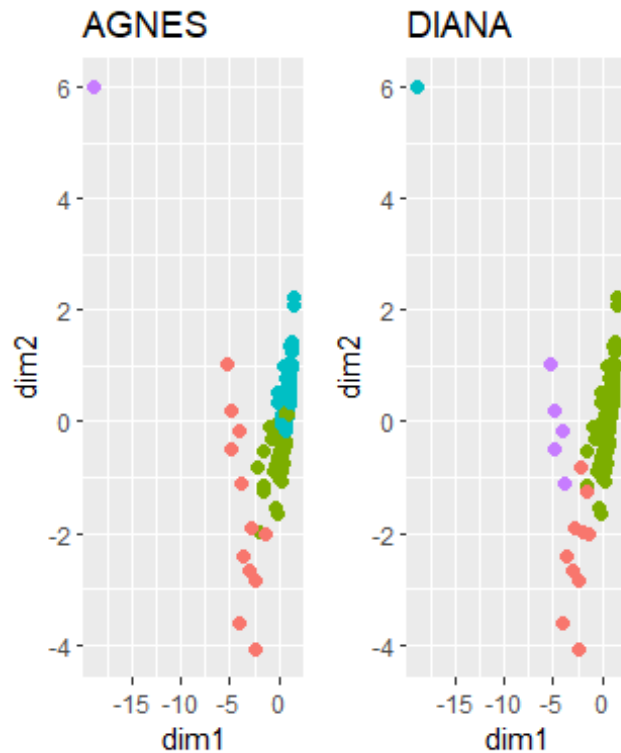
```
##Plot the Divisive Results
```

```
diaPlot=base + labs(title = "DIANA") + geom_point(size=2,
```

```
aes(color=dia),  
show.legend = F)
```

```
##Let's Look at the visual results
```

```
library(ggpubr)  
ggarrange(agnPlot, diaPlot, ncol = 3)
```

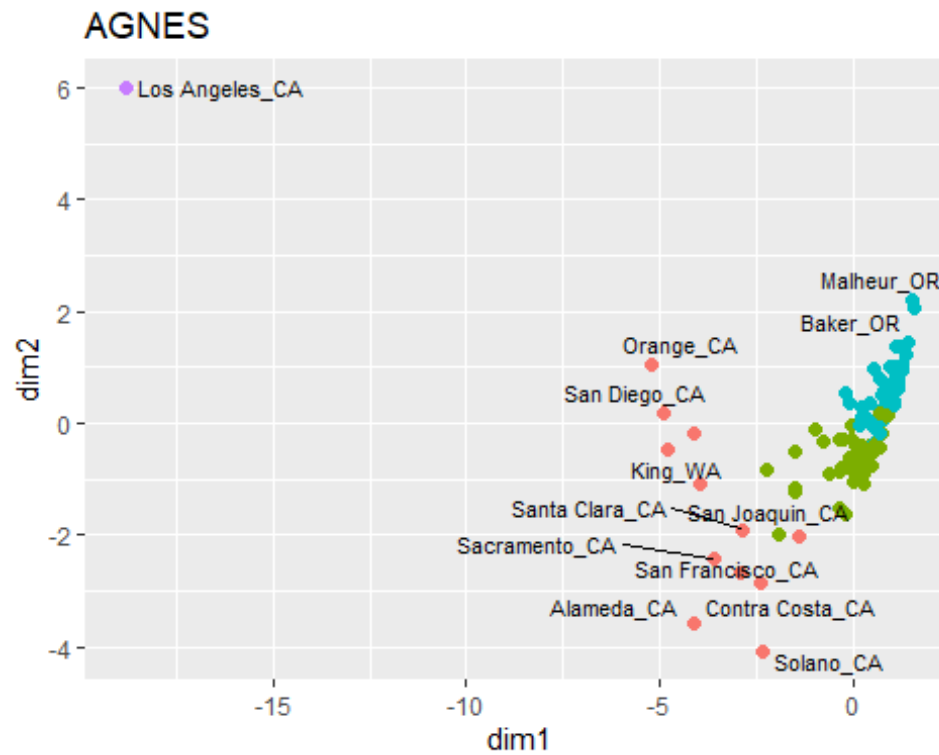


```
##From the visual plots, the results for both hierarchical clustering methods  
appear to be pretty consistent
```

```
##We can label the two hierarchical clustering plots
```

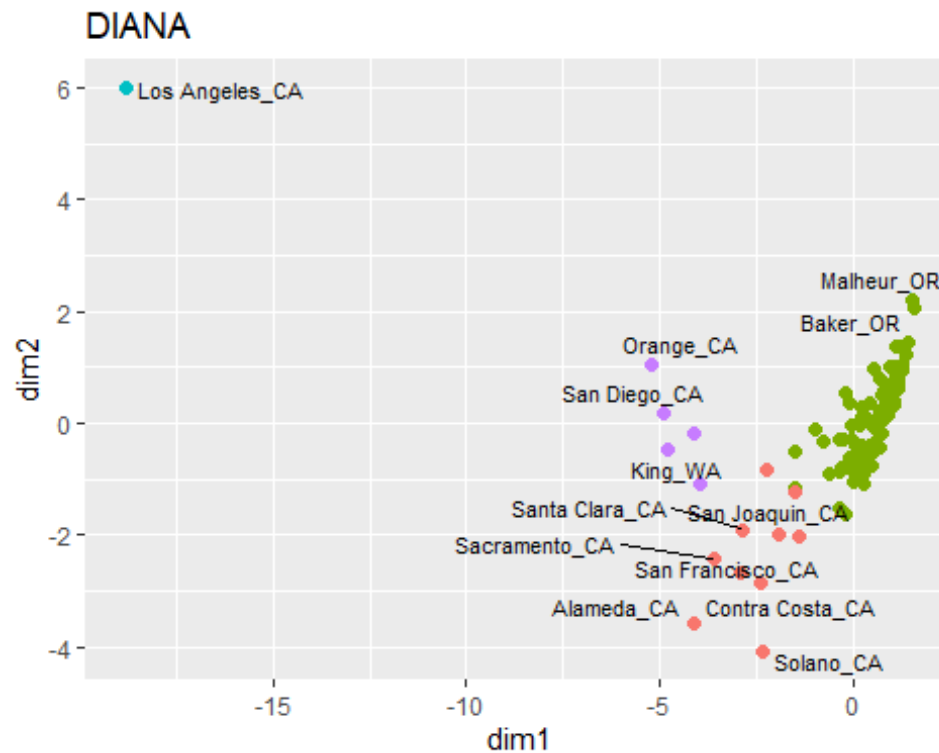
```
library(ggrepel)  
agnPlot + geom_text_repel(size=3,aes(label=Location))
```

```
## Warning: ggrepel: 120 unlabeled data points (too many overlaps). Consider  
## increasing max.overlaps
```



```
diaPlot + geom_text_repel(size=3,aes(label=Location))
```

```
## Warning: ggrepel: 120 unlabeled data points (too many overlaps). Consider  
## increasing max.overlaps
```

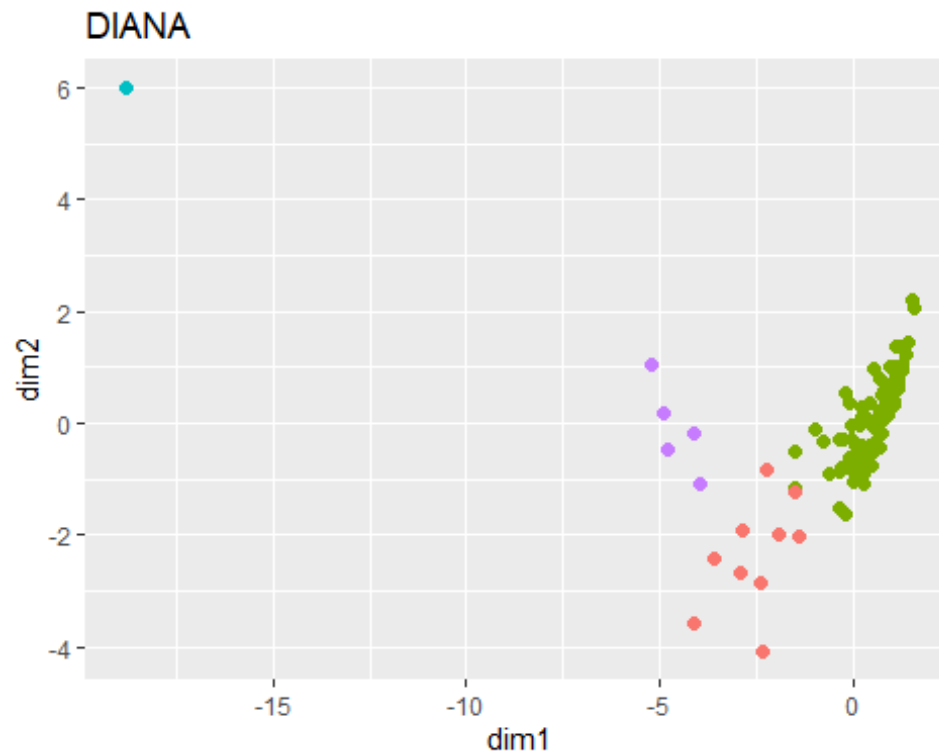


#It looks like there are too many overlaps for the large majority of names to appear. Instead, we will need to try and label anomalies from the agn and dia plots

```
LABEL=ifelse(diaEval$sil_width<0, covid$Location,"")
```

```
diaPlot + geom_text_repel(aes(label=LABEL))
```

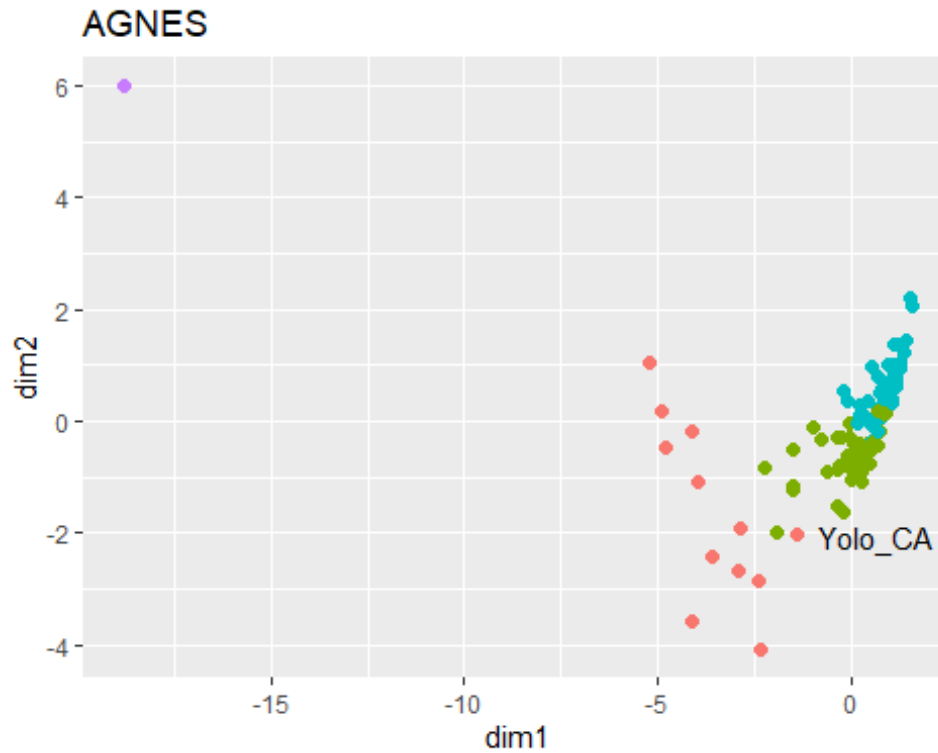
```
## Warning: ggrepel: 1 unlabeled data points (too many overlaps). Consider
## increasing max.overlaps
```



```
LABEL=ifelse(agnEval$sil_width<0, covid$Location,"")
```

```
agnPlot + geom_text_repel(aes(label=LABEL))
```

```
## Warning: ggrepel: 8 unlabeled data points (too many overlaps). Consider  
## increasing max.overlaps
```



Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.