

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

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

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

```
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...
```

##We need to prepare the variables for clustering

##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
```

```
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
```

```
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)
```

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

```
library(factoextra)
```

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

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

```
##Setting the number of clusters
```

```
NumCluster=4
```

```
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, just 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

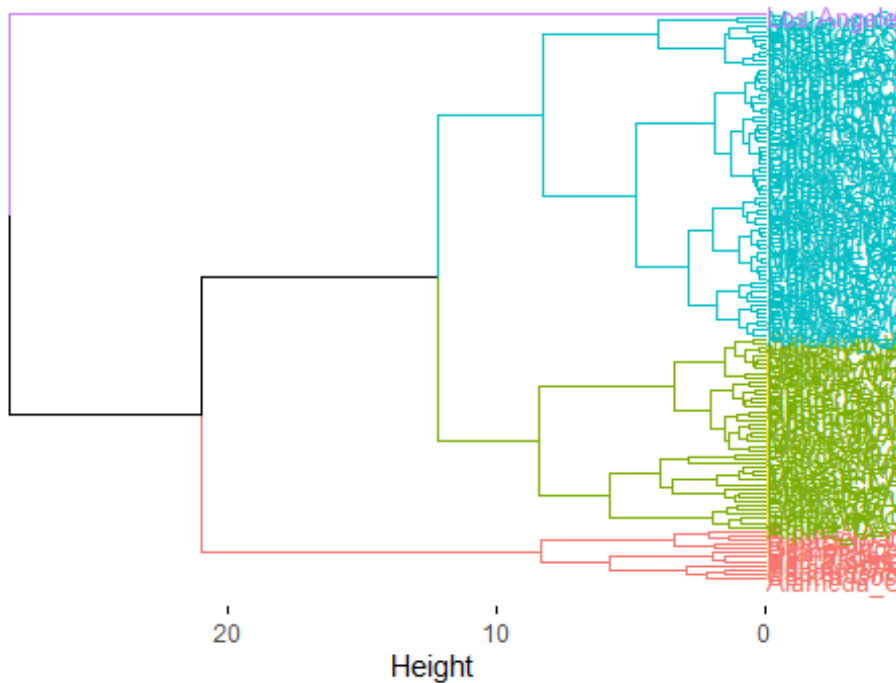
##VISUALIZING RESULTS

##A dendrogram of the cluster results

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

```

Cluster Dendrogram



```

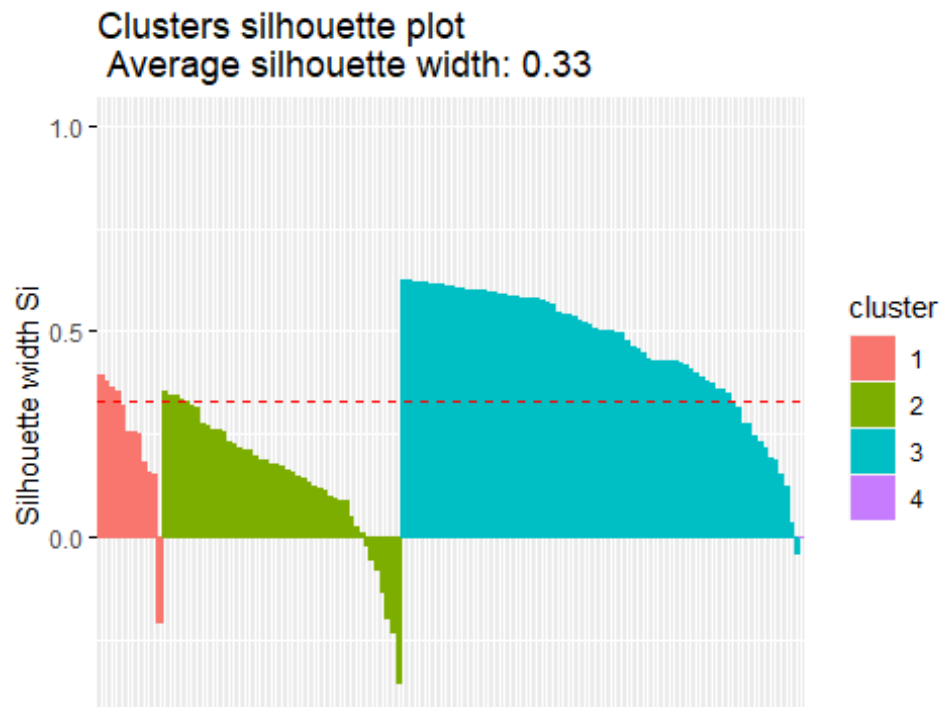
library(factoextra)

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

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 Divisive method

##Indicating required clusters

```
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"
```

We will also 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 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:

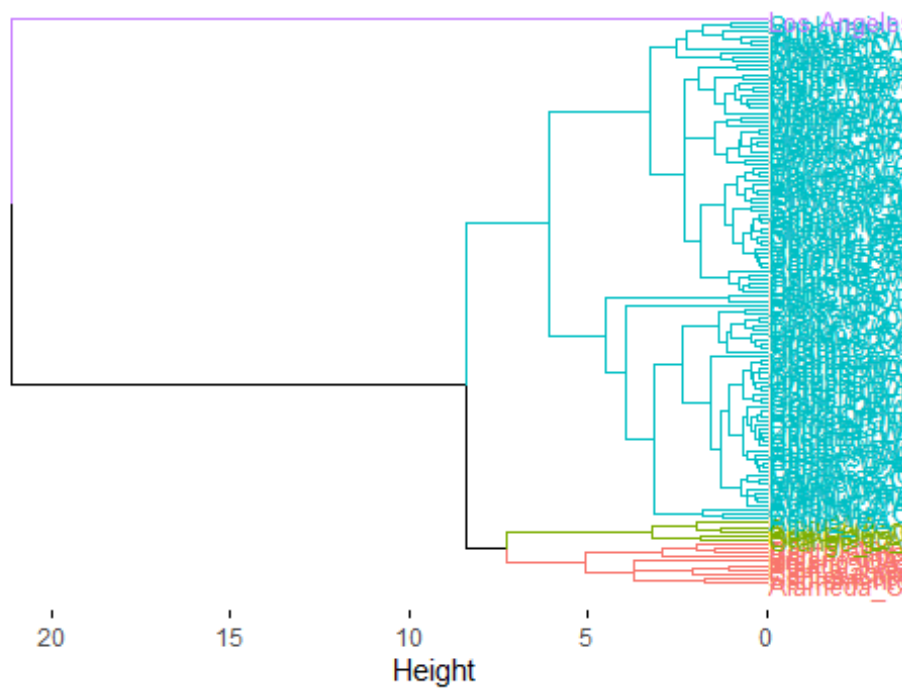
```
covid[covid$Location=="King_WA" , 'dia']
```

```
## [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)
```

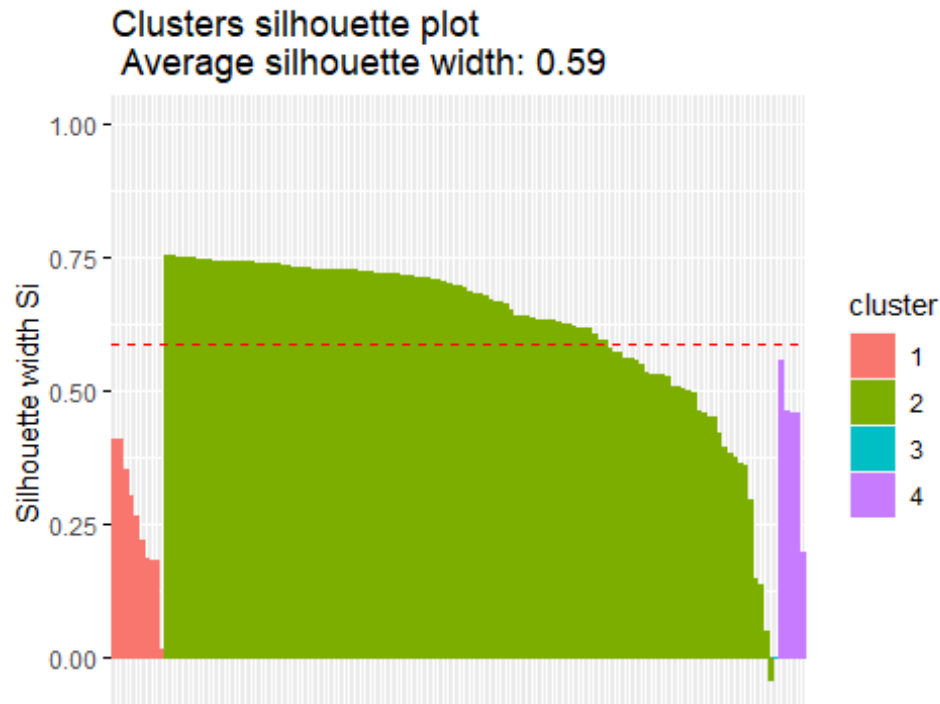
Cluster Dendrogram



##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,]

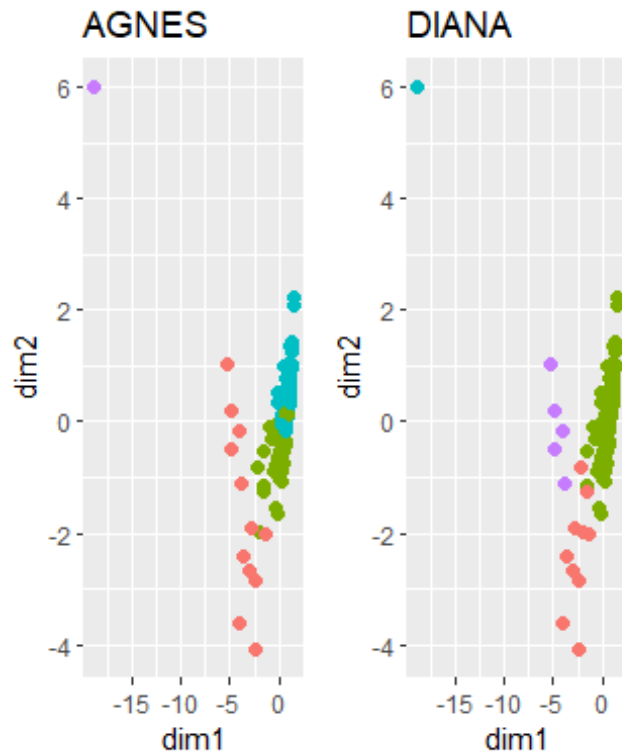
##           cluster neighbor  sil_width
## Multnomah_OR      2         1 -0.04078789
```

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

##COMPARING AGGLOMERATING AND DIVISIVE CLUSTERS


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

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

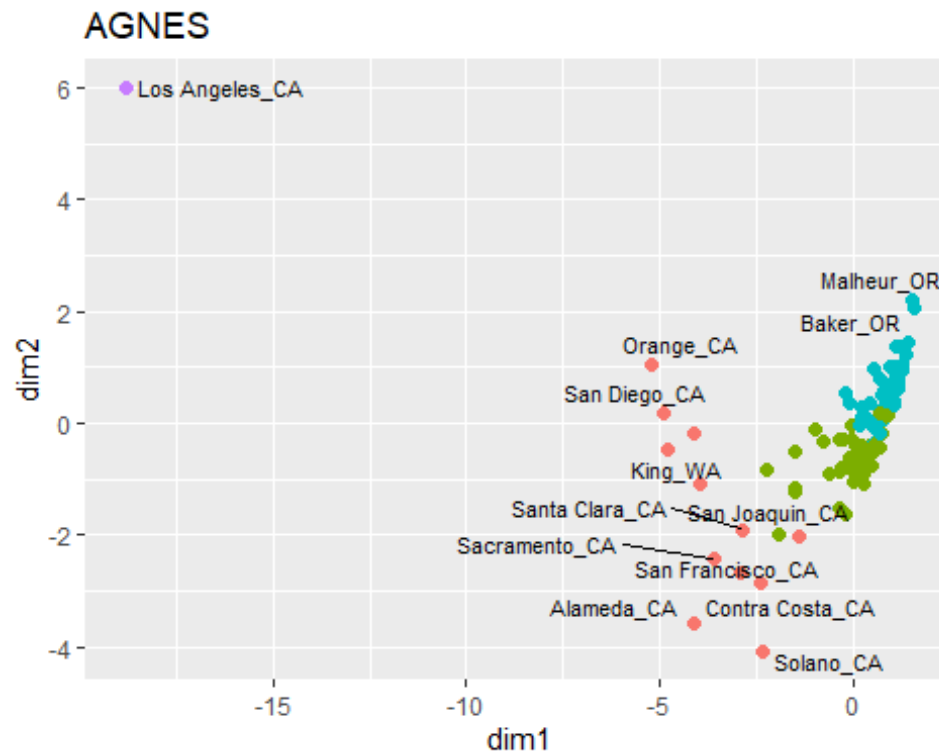


```
##From the visual plots, the results for both hierarchical clustering methods  
appear to be pretty consistent
```

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

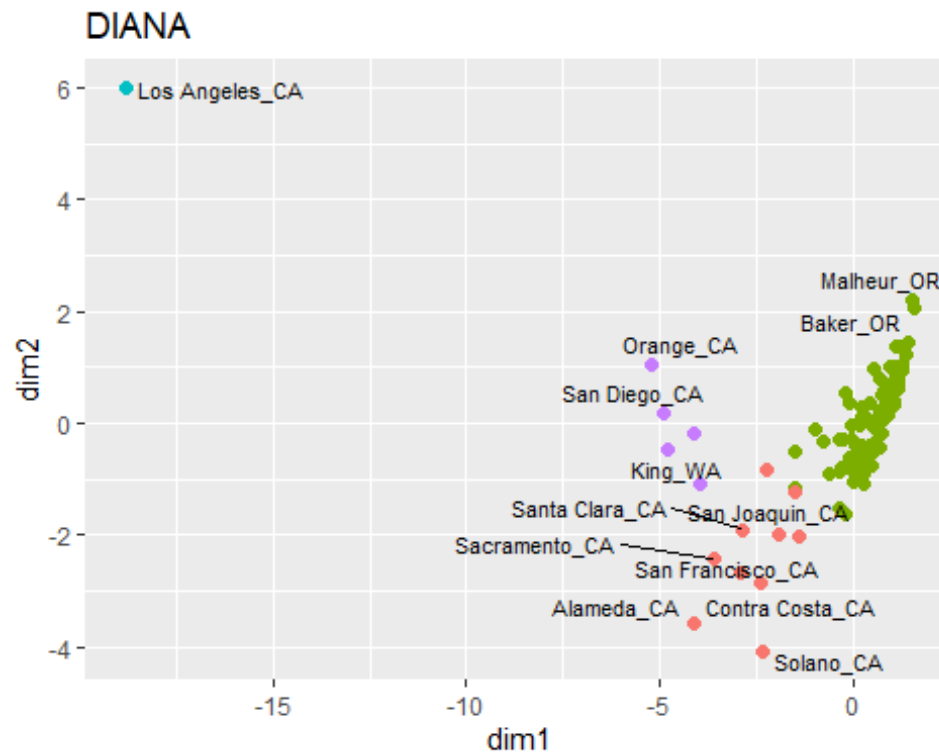
```
library(ggrepel)  
agnPlot + geom_text_repel(size=3,aes(label=Location))
```

```
## 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
```

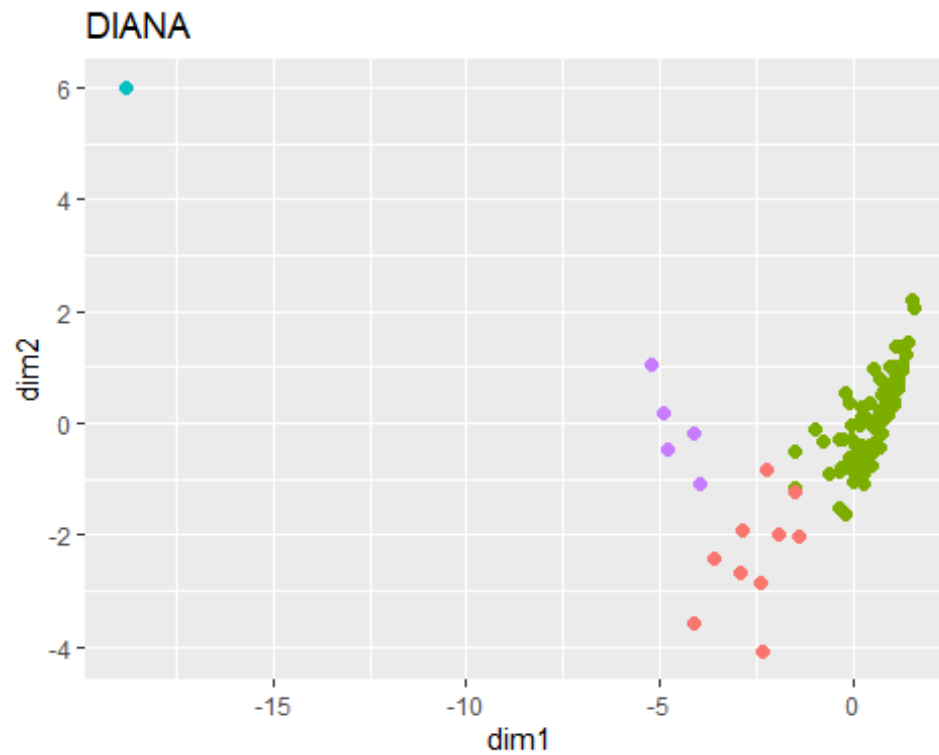


#It looks like there are too many overlaps for the large majority of names to appear. Instead, we will need to try and label anomalies from the agn and dia plots

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

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

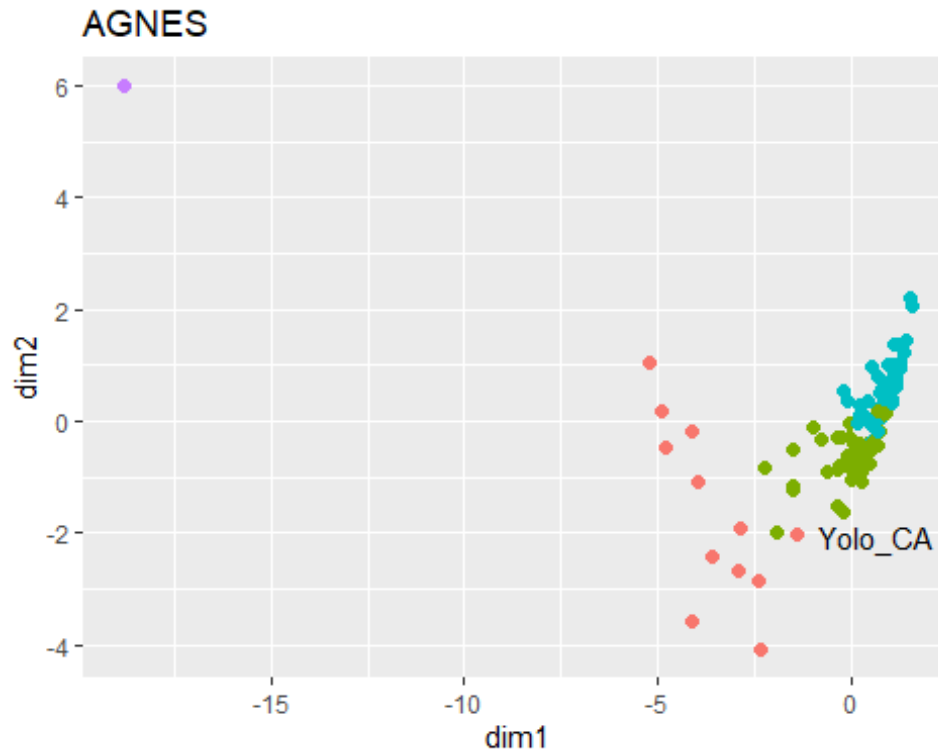
```
## Warning: ggrepel: 1 unlabeled data points (too many overlaps). Consider
## increasing max.overlaps
```



```
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.