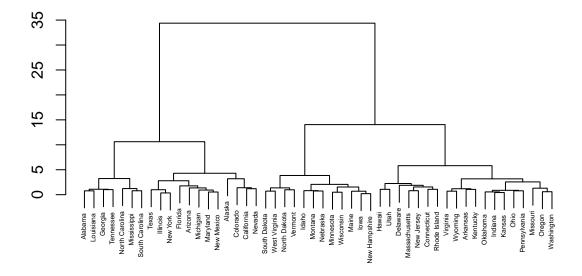
Hierarchical Clustering

USArrests dataset

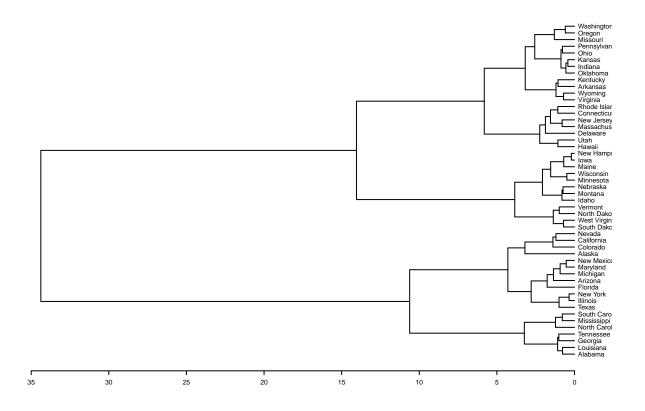
```
# husarrests.r
df0 <- USArrests
str(df0)
## 'data.frame':
                   50 obs. of 4 variables:
## $ Murder : num 13.2 10 8.1 8.8 9 7.9 3.3 5.9 15.4 17.4 ...
## $ Assault : int 236 263 294 190 276 204 110 238 335 211 ...
## $ UrbanPop: int 58 48 80 50 91 78 77 72 80 60 ...
           : num 21.2 44.5 31 19.5 40.6 38.7 11.1 15.8 31.9 25.8 ...
## $ Rape
head(df0)
             Murder Assault UrbanPop Rape
##
## Alabama
              13.2
                        236
                               58 21.2
              10.0
                        263
                                48 44.5
## Alaska
              8.1
## Arizona
                        294
                                80 31.0
## Arkansas
                8.8 190
                                50 19.5
                9.0
                        276
                                91 40.6
## California
## Colorado
                7.9
                        204
                                 78 38.7
# scale dataframe
df <- scale(df0)</pre>
head(df)
##
                 Murder
                          Assault
                                   UrbanPop
                                                    Rape
## Alabama
             1.24256408 0.7828393 -0.5209066 -0.003416473
## Alaska 0.50786248 1.1068225 -1.2117642 2.484202941
## Arizona
             0.07163341 1.4788032 0.9989801 1.042878388
## Arkansas
             0.23234938 0.2308680 -1.0735927 -0.184916602
## California 0.27826823 1.2628144 1.7589234 2.067820292
## Colorado 0.02571456 0.3988593 0.8608085 1.864967207
# find distances
distance = dist(df)
head(distance)
```

```
length(distance)
## [1] 1225
# distance in a matrix display
distmat = as.matrix(distance)
dim(distmat)
## [1] 50 50
distmat[1:7,1:7]
                       Alaska Arizona Arkansas California Colorado Connecticut
              Alabama
## Alabama 0.000000 2.703754 2.293520 1.289810 3.263110 2.651067
                                                                     3.215297
## Alaska
            2.703754 0.000000 2.700643 2.826039 3.012541 2.326519
                                                                      4.739912
## Arizona
            2.293520 2.700643 0.000000 2.717758 1.310484 1.365031
                                                                     3.262858
## Arkansas 1.289810 2.826039 2.717758 0.000000 3.763641 2.831051
                                                                     2.607639
## California 3.263110 3.012541 1.310484 3.763641 0.000000 1.287619 4.066390
## Colorado 2.651067 2.326519 1.365031 2.831051 1.287619 0.000000
                                                                      3.327992
## Connecticut 3.215297 4.739912 3.262858 2.607639 4.066390 3.327992
                                                                     0.000000
# Hierarchical clustering - Ward
h1 = hclust(distance, method ='ward.D')
str(h1)
## List of 7
             : int [1:49, 1:2] -15 -13 -14 -23 -20 -36 -37 -19 -46 -41 ...
## $ merge
## $ height
              : num [1:49] 0.206 0.35 0.429 0.494 0.535 ...
              : int [1:50] 1 18 10 42 33 24 40 43 13 32 ...
## $ order
## $ labels
              : chr [1:50] "Alabama" "Alaska" "Arizona" "Arkansas" ...
## $ method
               : chr "ward.D"
## $ call : language hclust(d = distance, method = "ward.D")
## $ dist.method: chr "euclidean"
## - attr(*, "class")= chr "hclust"
# Dendrogram - Ward
plot(h1,cex=0.4,xlab="",sub="",ylab="")
```

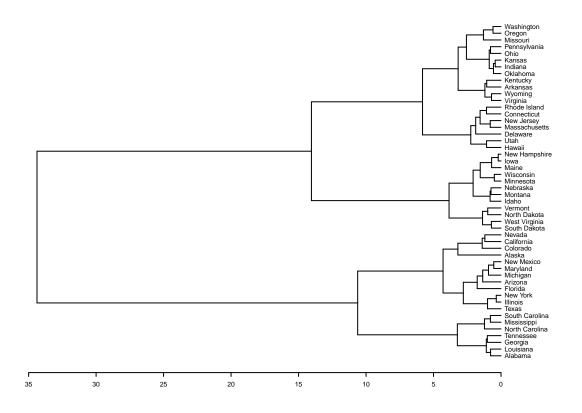
Cluster Dendrogram



```
#
par(cex=0.4)
plot(as.dendrogram(h1),horiz=T)
```



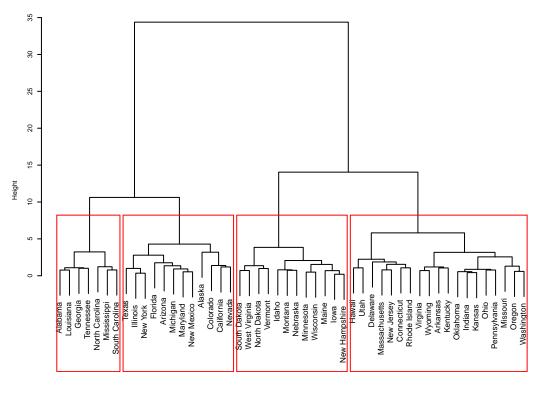
```
#
par(cex=0.4, mar=c(5, 8, 4, 8))
plot(as.dendrogram(h1),horiz=T)
```



```
#
# CUT the dendrograms to 4 clusters
#
cut1 = cutree(h1, k=4)
head(cut1)
##
      Alabama
                  Alaska
                             Arizona
                                       Arkansas California
                                                             Colorado
##
            1
                       2
                                   2
                                              3
                                                                     2
#
# dataframe with cluster numbers
df1 = data.frame(df,cluster = cut1)
head(df1)
##
                  Murder
                           Assault
                                     UrbanPop
                                                       Rape cluster
## Alabama
              1.24256408 0.7828393 -0.5209066 -0.003416473
## Alaska
              0.50786248 1.1068225 -1.2117642 2.484202941
                                                                   2
## Arizona
              0.07163341 1.4788032 0.9989801 1.042878388
                                                                   2
              0.23234938 \ 0.2308680 \ -1.0735927 \ -0.184916602
                                                                  3
## Arkansas
## California 0.27826823 1.2628144 1.7589234 2.067820292
                                                                   2
## Colorado
              0.02571456 0.3988593 0.8608085 1.864967207
                                                                   2
#
# number of members per cluster
#
table(cut1)
```

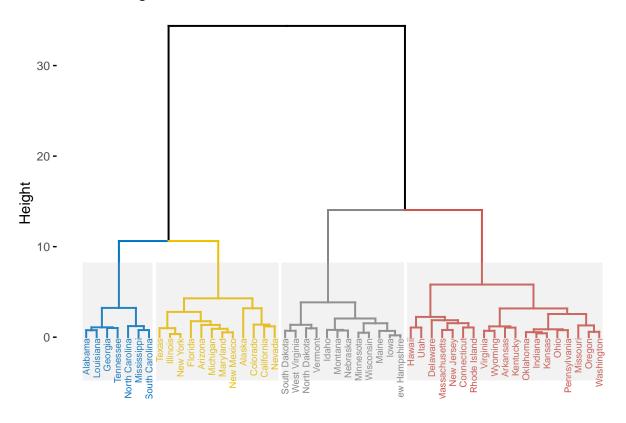
```
## cut1
## 1 2 3 4
  7 12 19 12
# members of cluster 1 (use rownames of original dataframe)
rownames(df)[1:5]
## [1] "Alabama"
                    "Alaska"
                                 "Arizona"
                                              "Arkansas"
                                                           "California"
rownames(df)[cut1 == 1]
## [1] "Alabama"
                        "Georgia"
                                                          "Mississippi"
## [5] "North Carolina" "South Carolina" "Tennessee"
# dendrogram with cut - Ward linkage
plot(h1, cex=1.2)
rect.hclust(h1,k=4,border="red")
# library factoextra
library(factoextra)
```

Cluster Dendrogram

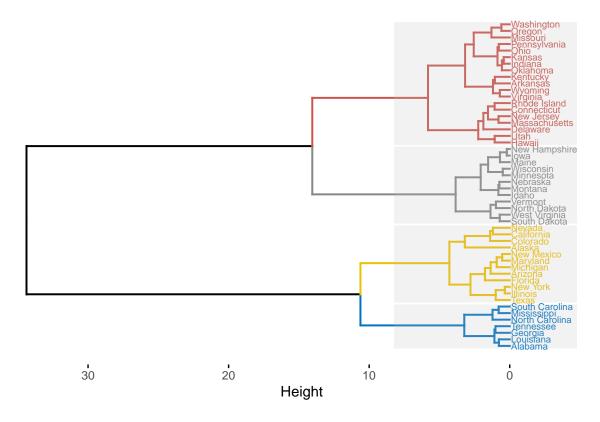


distance hclust (*, "ward.D")

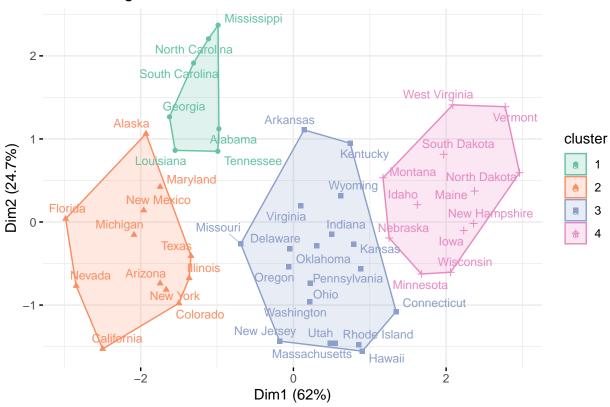
Ward linkage



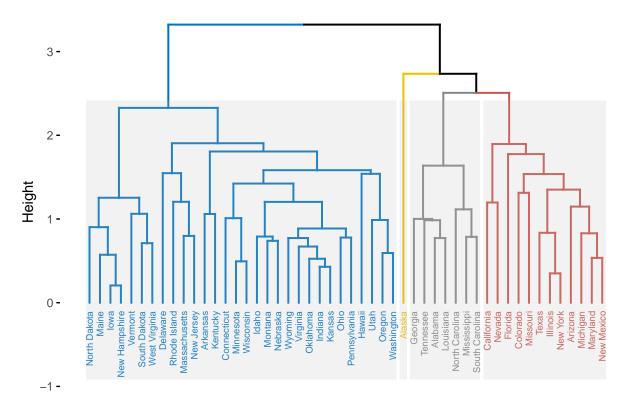
Ward linkage



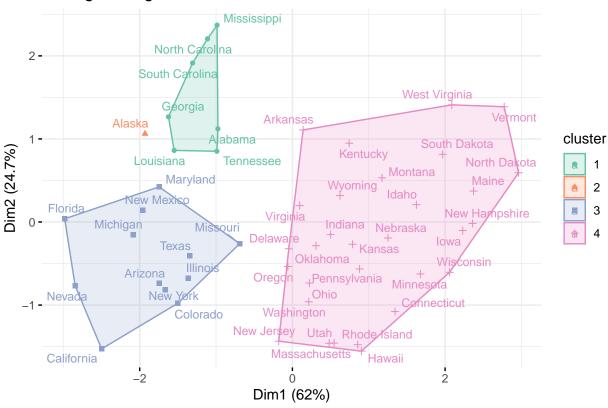
Ward linkage



average linkage



average linkage



```
# COPHENETIC distances
c1 = cophenetic(h1)
#
# display them as a matrix
#
c1mat = as.matrix(c1)
c1mat[1:6,1:6]
```

```
##
               Alabama
                          Alaska
                                   Arizona Arkansas California Colorado
## Alabama
               0.00000 10.619899 10.619899 34.37957
                                                     10.619899 10.619899
## Alaska
              10.61990 0.000000 4.292862 34.37957
                                                      3.194472 3.194472
## Arizona
              10.61990 4.292862 0.000000 34.37957
                                                      4.292862
                                                                4.292862
## Arkansas
              34.37957 34.379570 34.379570 0.00000
                                                     34.379570 34.379570
## California 10.61990
                        3.194472
                                  4.292862 34.37957
                                                      0.000000
                                                                1.392043
              10.61990
                        3.194472
                                 4.292862 34.37957
                                                      1.392043
                                                                0.000000
## Colorado
```

```
#
# compare with Euclidean distances
#
distmat[1:6,1:6]
```

```
## Alabama Alaska Arizona Arkansas California Colorado

## Alabama 0.000000 2.703754 2.293520 1.289810 3.263110 2.651067

## Alaska 2.703754 0.000000 2.700643 2.826039 3.012541 2.326519

## Arizona 2.293520 2.700643 0.000000 2.717758 1.310484 1.365031
```

```
## Arkansas 1.289810 2.826039 2.717758 0.000000 3.763641 2.831051
## California 3.263110 3.012541 1.310484 3.763641 0.000000 1.287619
## Colorado 2.651067 2.326519 1.365031 2.831051 1.287619 0.000000

##
## CPCC = correlation (euclidean distances, cophenetic distances)
##
cor(distance,c1)

## [1] 0.6844016

##
# Hierarchical clustering - average
#
c2 = cophenetic(h2)
cor(distance,c2)

## [1] 0.7180382

##
# average linkage distances are closer to euclidean distances
# than ward linkage distances
# than ward linkage distances
```