

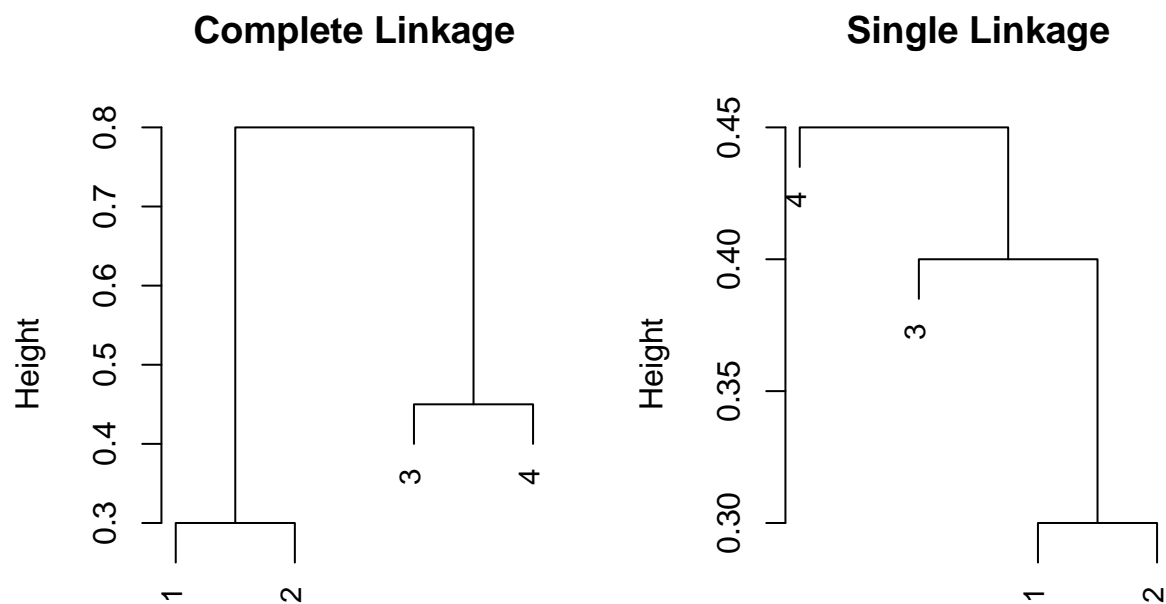
STATS 415 hw11 solution

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Question 1

(a) & (b)



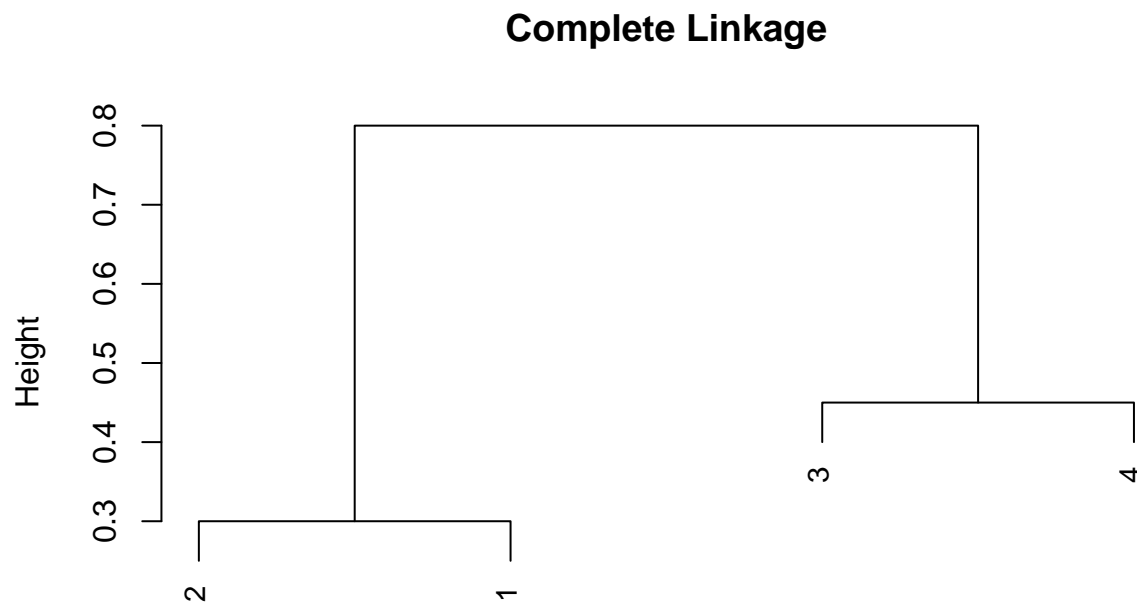
(c)

Cluster1: 1,2; Cluster2:3,4.

(d)

Cluster1:4; Cluster2:2,3,4.

(e)



Question 2

(a)

We load the package ISLR so to access the dataset USArrests and then use the `hclust()` function to perform hierarchical clustering.

```
library(ISLR)
```

```
## Warning: package 'ISLR' was built under R version 3.3.3
```

```
library(cluster)
```

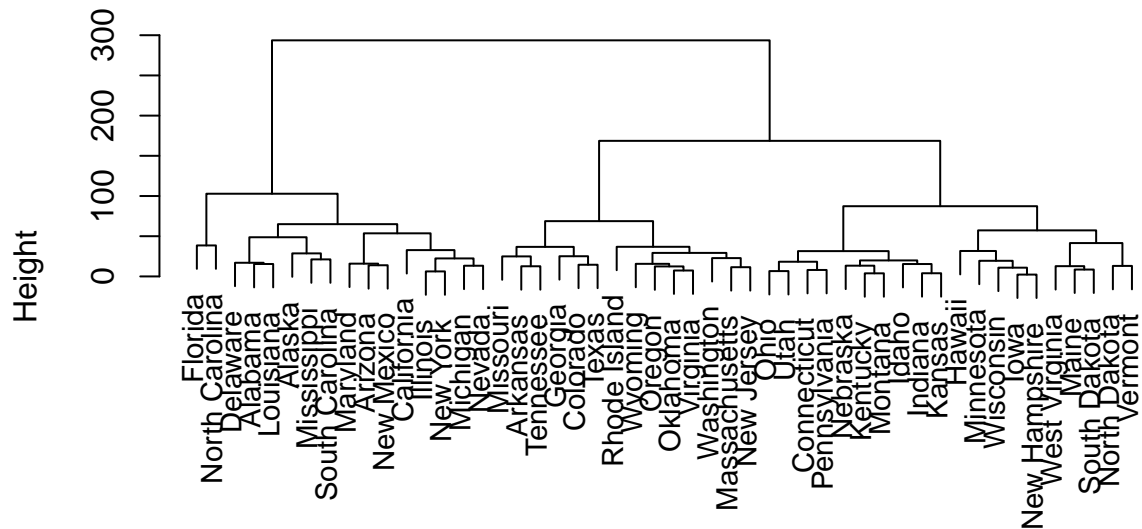
```
## Warning: package 'cluster' was built under R version 3.3.3
```

```
data("USArrests")
```

```
hc.complete=hclust(dist(USArrests),method='complete')
```

```
plot(hc.complete,main="Complete Linkage", xlab="", sub="", cex=.9)
```

Complete Linkage



(b)

```
cutree(hc.complete,3)
```

##	Alabama	Alaska	Arizona	Arkansas	California
##	1	1	1	2	1
##	Colorado	Connecticut	Delaware	Florida	Georgia
##	2	3	1	1	2
##	Hawaii	Idaho	Illinois	Indiana	Iowa
##	3	3	1	3	3
##	Kansas	Kentucky	Louisiana	Maine	Maryland
##	3	3	1	3	1
##	Massachusetts	Michigan	Minnesota	Mississippi	Missouri
##	2	1	3	1	2
##	Montana	Nebraska	Nevada	New Hampshire	New Jersey
##	3	3	1	3	2
##	New Mexico	New York	North Carolina	North Dakota	Ohio
##	1	1	1	3	3
##	Oklahoma	Oregon	Pennsylvania	Rhode Island	South Carolina
##	2	2	3	2	1
##	South Dakota	Tennessee	Texas	Utah	Vermont
##	3	2	2	3	3
##	Virginia	Washington	West Virginia	Wisconsin	Wyoming
##	2	2	3	3	2

```
names(which(cutree(hc.complete,1)==1))
```

```
## [1] "Alabama"      "Alaska"      "Arizona"     "Arkansas"
## [5] "California"   "Colorado"    "Connecticut" "Delaware"
## [9] "Florida"     "Georgia"     "Hawaii"      "Idaho"
## [13] "Illinois"    "Indiana"     "Iowa"        "Kansas"
## [17] "Kentucky"    "Louisiana"   "Maine"       "Maryland"
## [21] "Massachusetts" "Michigan"    "Minnesota"   "Mississippi"
## [25] "Missouri"    "Montana"     "Nebraska"    "Nevada"
## [29] "New Hampshire" "New Jersey"  "New Mexico"  "New York"
## [33] "North Carolina" "North Dakota" "Ohio"        "Oklahoma"
## [37] "Oregon"      "Pennsylvania" "Rhode Island" "South Carolina"
## [41] "South Dakota" "Tennessee"   "Texas"       "Utah"
## [45] "Vermont"     "Virginia"    "Washington"  "West Virginia"
## [49] "Wisconsin"   "Wyoming"
```

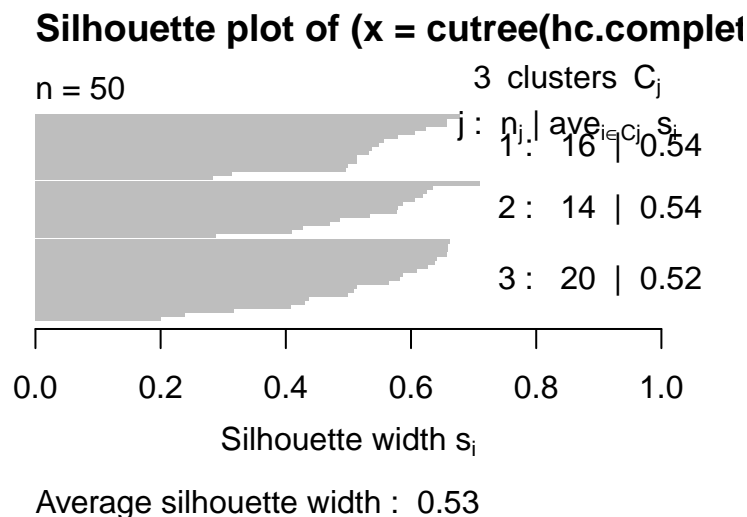
```
names(which(cutree(hc.complete,2)==2))
```

```
## [1] "Arkansas"      "Colorado"    "Connecticut" "Georgia"
## [5] "Hawaii"        "Idaho"       "Indiana"     "Iowa"
## [9] "Kansas"        "Kentucky"    "Maine"       "Massachusetts"
## [13] "Minnesota"     "Missouri"    "Montana"     "Nebraska"
## [17] "New Hampshire" "New Jersey"  "North Dakota" "Ohio"
## [21] "Oklahoma"      "Oregon"      "Pennsylvania" "Rhode Island"
## [25] "South Dakota"  "Tennessee"   "Texas"       "Utah"
## [29] "Vermont"       "Virginia"    "Washington"  "West Virginia"
## [33] "Wisconsin"     "Wyoming"
```

```
names(which(cutree(hc.complete,3)==3))
```

```
## [1] "Connecticut" "Hawaii"      "Idaho"       "Indiana"
## [5] "Iowa"        "Kansas"      "Kentucky"    "Maine"
## [9] "Minnesota"   "Montana"     "Nebraska"    "New Hampshire"
## [13] "North Dakota" "Ohio"        "Pennsylvania" "South Dakota"
## [17] "Utah"        "Vermont"     "West Virginia" "Wisconsin"
```

```
plot(silhouette(cutree(hc.complete,3),dist(USArrests)))
```

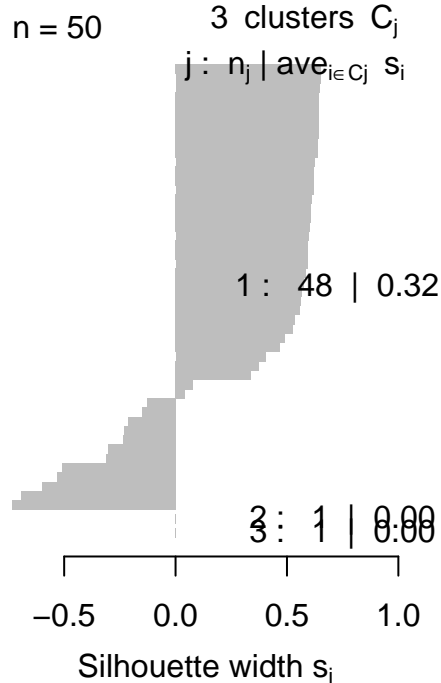


The average silhouette width is 0.53. There is no observation with negative silhouette score which indicates a good clustering result.

(c)

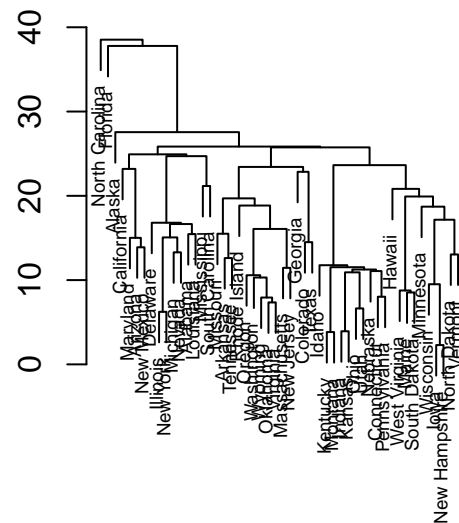
```
hc.single=hclust(dist(USArrests),method='single')
par(mfrow=c(1,2))
plot(silhouette(cutree(hc.single,3),dist(USArrests)))
plot(hc.single,main="Single Linkage", xlab="", sub="", cex=.6)
```

Silhouette plot of (x = cutr



Average silhouette width : 0.3

Single Linkage



```
names(which(cutree(hc.single,1)==1))
```

```
## [1] "Alabama"      "Alaska"      "Arizona"     "Arkansas"
## [5] "California"   "Colorado"    "Connecticut" "Delaware"
## [9] "Florida"     "Georgia"     "Hawaii"      "Idaho"
## [13] "Illinois"    "Indiana"     "Iowa"        "Kansas"
## [17] "Kentucky"    "Louisiana"   "Maine"       "Maryland"
## [21] "Massachusetts" "Michigan"    "Minnesota"   "Mississippi"
## [25] "Missouri"    "Montana"     "Nebraska"    "Nevada"
## [29] "New Hampshire" "New Jersey"  "New Mexico"  "New York"
## [33] "North Carolina" "North Dakota" "Ohio"        "Oklahoma"
## [37] "Oregon"      "Pennsylvania" "Rhode Island" "South Carolina"
## [41] "South Dakota" "Tennessee"   "Texas"       "Utah"
## [45] "Vermont"     "Virginia"    "Washington"  "West Virginia"
## [49] "Wisconsin"   "Wyoming"
```

```
names(which(cutree(hc.single,2)==2))
```

```
## [1] "North Carolina"
```

```
names(which(cutree(hc.single,3)==3))
```

```
## [1] "North Carolina"
```

There are 48 states are clustered in one group. Compared with complete linkage, single linkage tends to yield trailing clusters. The average silhouette width is 0.3 which is much poorer than complete linkage.

(d)

```
set.seed(1111)
```

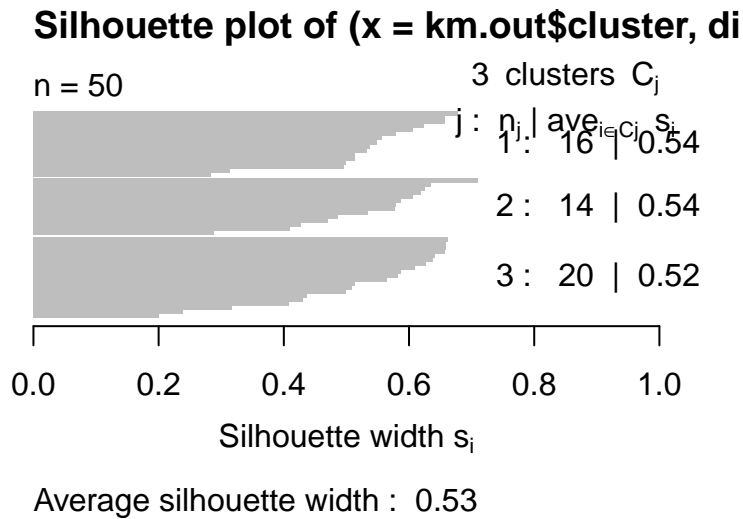
```
km.out=kmeans(USArrests,3,nstart=20)
```

```
km.out$cluster
```

##	Alabama	Alaska	Arizona	Arkansas	California
##	1	1	1	2	1
##	Colorado	Connecticut	Delaware	Florida	Georgia
##	2	3	1	1	2
##	Hawaii	Idaho	Illinois	Indiana	Iowa
##	3	3	1	3	3
##	Kansas	Kentucky	Louisiana	Maine	Maryland
##	3	3	1	3	1
##	Massachusetts	Michigan	Minnesota	Mississippi	Missouri
##	2	1	3	1	2
##	Montana	Nebraska	Nevada	New Hampshire	New Jersey
##	3	3	1	3	2
##	New Mexico	New York	North Carolina	North Dakota	Ohio
##	1	1	1	3	3
##	Oklahoma	Oregon	Pennsylvania	Rhode Island	South Carolina
##	2	2	3	2	1
##	South Dakota	Tennessee	Texas	Utah	Vermont
##	3	2	2	3	3
##	Virginia	Washington	West Virginia	Wisconsin	Wyoming
##	2	2	3	3	2

```
par(mfrow=c(1,1))
```

```
plot(silhouette(km.out$cluster,dist(USArrests)))
```

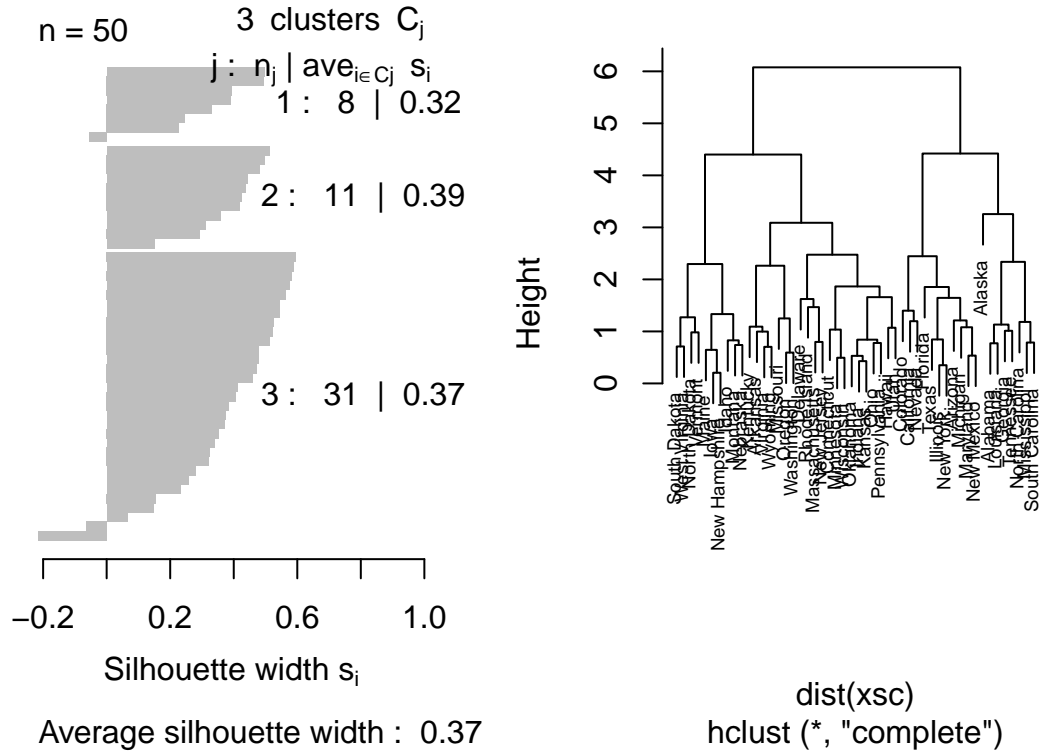


We set 20 random initial cluster assignments and report the best result. Kmeans gives us a similar clustering result as hierarchical clustering with complete linkage.

(e)

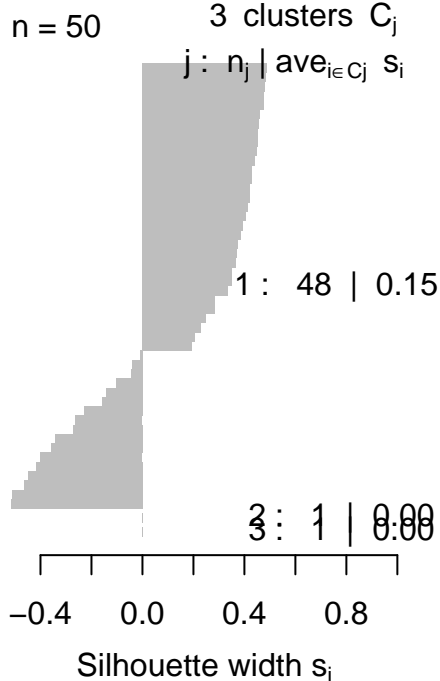
```
# hierarchical clustering
xsc=scale(USArrests)
hc.complete.sd=hclust(dist(xsc),method="complete")
hc.single.sd=hclust(dist(xsc),method='single')
par(mfrow=c(1,2))
plot(silhouette(cutree(hc.complete.sd,3),dist(xsc)))
plot(hc.complete.sd,main="Scaled Features and Complete Linkage",cex = 0.6)
```

Silhouette plot of (x = cutrScaled Features and Complete Link

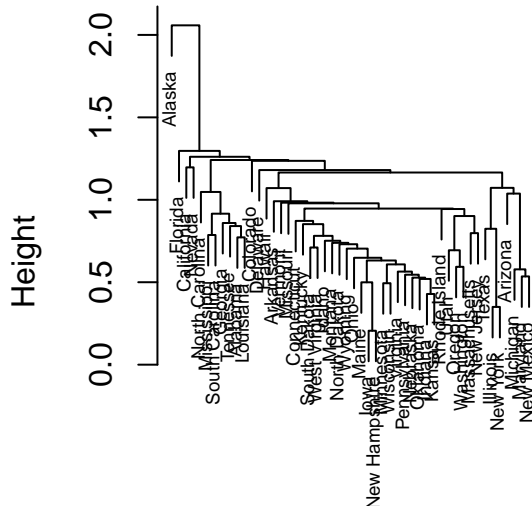


```
plot(silhouette(cutree(hc.single.sd,3),dist(xsc)))
plot(hc.single.sd,main="Scaled Features and Single Linkage", cex=.6)
```


Silhouette plot of (x = cutr Scaled Features and Single Linka



Average silhouette width : 0.15



dist(xsc)
hclust (*, "single")

```
cutree(hc.complete.sd,3)
```

##	Alabama	Alaska	Arizona	Arkansas	California
##	1	1	2	3	2
##	Colorado	Connecticut	Delaware	Florida	Georgia
##	2	3	3	2	1
##	Hawaii	Idaho	Illinois	Indiana	Iowa
##	3	3	2	3	3
##	Kansas	Kentucky	Louisiana	Maine	Maryland
##	3	3	1	3	2
##	Massachusetts	Michigan	Minnesota	Mississippi	Missouri
##	3	2	3	1	3
##	Montana	Nebraska	Nevada	New Hampshire	New Jersey
##	3	3	2	3	3
##	New Mexico	New York	North Carolina	North Dakota	Ohio
##	2	2	1	3	3
##	Oklahoma	Oregon	Pennsylvania	Rhode Island	South Carolina
##	3	3	3	3	1
##	South Dakota	Tennessee	Texas	Utah	Vermont
##	3	1	2	3	3
##	Virginia	Washington	West Virginia	Wisconsin	Wyoming
##	3	3	3	3	3

```
cutree(hc.single.sd,3)
```

##	Alabama	Alaska	Arizona	Arkansas	California
##	1	2	1	1	1

```
##      Colorado      Connecticut      Delaware      Florida      Georgia
##      1            1            1            3            1
##      Hawaii       Idaho       Illinois       Indiana       Iowa
##      1            1            1            1            1
##      Kansas       Kentucky      Louisiana      Maine       Maryland
##      1            1            1            1            1
##      Massachusetts  Michigan      Minnesota      Mississippi  Missouri
##      1            1            1            1            1
##      Montana      Nebraska      Nevada      New Hampshire  New Jersey
##      1            1            1            1            1
##      New Mexico    New York      North Carolina  North Dakota    Ohio
##      1            1            1            1            1
##      Oklahoma      Oregon      Pennsylvania      Rhode Island  South Carolina
##      1            1            1            1            1
##      South Dakota   Tennessee      Texas            Utah            Vermont
##      1            1            1            1            1
##      Virginia      Washington  West Virginia      Wisconsin      Wyoming
##      1            1            1            1            1
```

```
# kmeans
```

```
set.seed(1111)
```

```
km.out.sd=kmeans(xsc,3,nstart=20)
```

```
km.out.sd$cluster
```

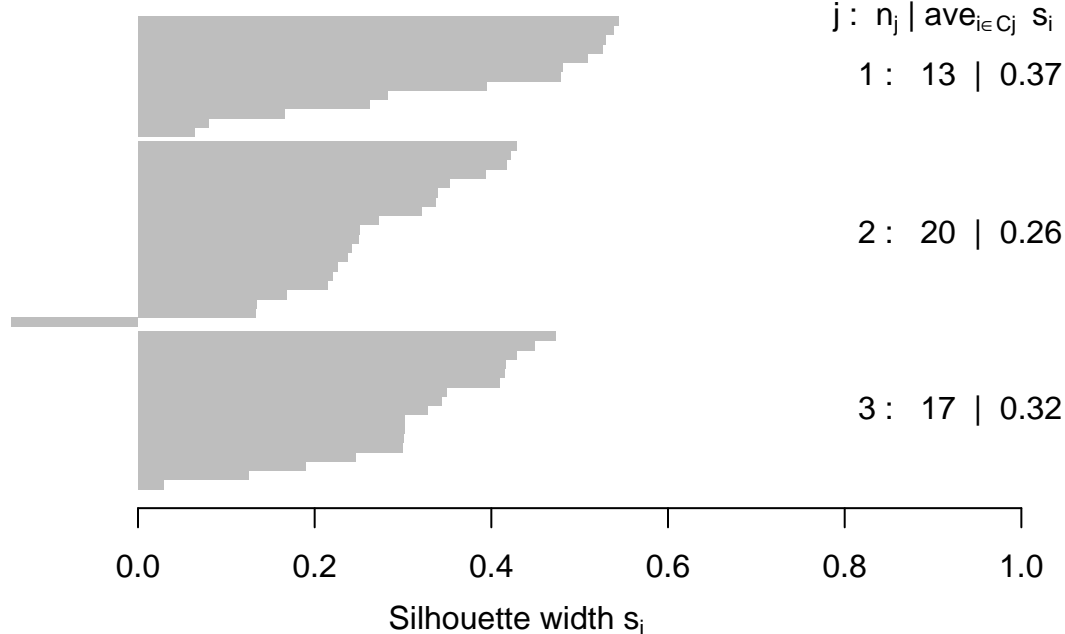
```
##      Alabama      Alaska      Arizona      Arkansas      California
##      2            2            2            3            2
##      Colorado      Connecticut      Delaware      Florida      Georgia
##      2            3            3            2            2
##      Hawaii       Idaho       Illinois       Indiana       Iowa
##      3            1            2            3            1
##      Kansas       Kentucky      Louisiana      Maine       Maryland
##      3            1            2            1            2
##      Massachusetts  Michigan      Minnesota      Mississippi  Missouri
##      3            2            1            2            2
##      Montana      Nebraska      Nevada      New Hampshire  New Jersey
##      1            1            2            1            3
##      New Mexico    New York      North Carolina  North Dakota    Ohio
##      2            2            2            1            3
##      Oklahoma      Oregon      Pennsylvania      Rhode Island  South Carolina
##      3            3            3            3            2
##      South Dakota   Tennessee      Texas            Utah            Vermont
##      1            2            2            3            1
##      Virginia      Washington  West Virginia      Wisconsin      Wyoming
##      3            3            1            1            3
```

```
par(mfrow=c(1,1))
```

```
plot(silhouette(km.out.sd$cluster,dist(xsc)))
```

Silhouette plot of (x = km.out.sd\$cluster, dist = dist(xsc))

n = 50



Average silhouette width : 0.31

The average silhouette width of scaled data are smaller in all three cases than those of unscaled data.

(f)

We use the `table()` function to compare the results

```
# compare HC
hc = cutree(hc.complete,3)
hc.sd = cutree(hc.complete.sd,3)
table(hc,hc.sd)
```

```
##      hc.sd
## hc    1  2  3
##    1  6  9  1
##    2  2  2 10
##    3  0  0 20
```

```
km = km.out$cluster
km.sd = km.out.sd$cluster
table(km,km.sd)
```

```
##      km.sd
## km    1  2  3
##    1  0 15  1
##    2  0  5  9
##    3 13  0  7
```

We see that the three clusters obtained using original variables and scaled variables are somewhat different. For hierarchical clustering, cluster 3 obtained using scaled variables mainly combines the cluster 2 and 3 obtained using original variables. Regardless of permutation of cluster number, the difference between k-means clustering results is smaller than hierarchical clustering.

Note that the variables “Murder”, “Assault” and “Rape” are the number of corresponding arrests per 100,000 while the variable “UrbanPop” is the percentage of urban population. These variables have different units but all represent a ratio. The range of them don’t differ too much. The results from unscaled data also give better clustering result. Therefore, we prefer not to scaling data.