

# Homework 5 solution

```
# hw5sol.r
#
# Question 1
#
library(cluster)
d1 = read.csv("universities.csv")
str(d1)

## 'data.frame':    25 obs. of  7 variables:
## $ University: Factor w/ 25 levels "Brown","CalTech",...: 9 15 25 17 11 7 2 6 1 10 ...
## $ SAT       : num  14 13.8 13.8 13.6 13.8 ...
## $ Top10     : int  91 91 95 90 94 90 100 89 89 75 ...
## $ Accept    : int  14 14 19 20 30 30 25 23 22 44 ...
## $ SFRatio   : int  11 8 11 12 10 12 6 10 13 7 ...
## $ Expenses  : num  39.5 30.2 43.5 36.5 34.9 ...
## $ Grad      : int  97 95 96 93 91 95 81 95 94 87 ...

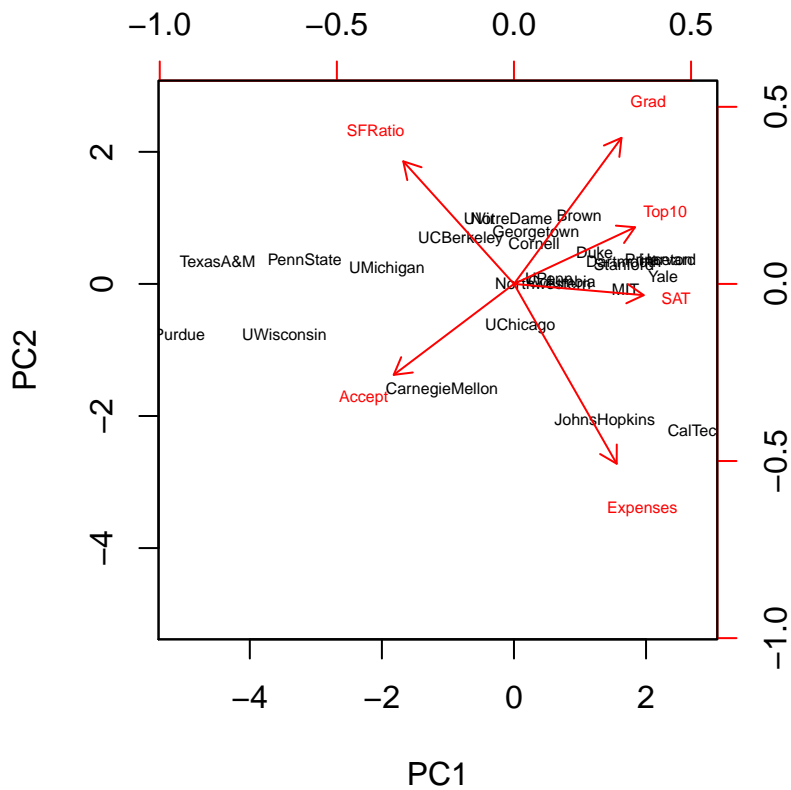
head(d1)

##   University SAT Top10 Accept SFRatio Expenses Grad
## 1   Harvard 14.00   91    14      11   39.525   97
## 2 Princeton 13.75   91    14       8   30.220   95
## 3    Yale   13.75   95    19      11   43.514   96
## 4  Stanford 13.60   90    20      12   36.450   93
## 5     MIT   13.80   94    30      10   34.870   91
## 6     Duke  13.15   90    30      12   31.585   95

#
# move the university name to the rownames
#
rownames(d1) = d1[,1]
d1$University = NULL
head(d1)

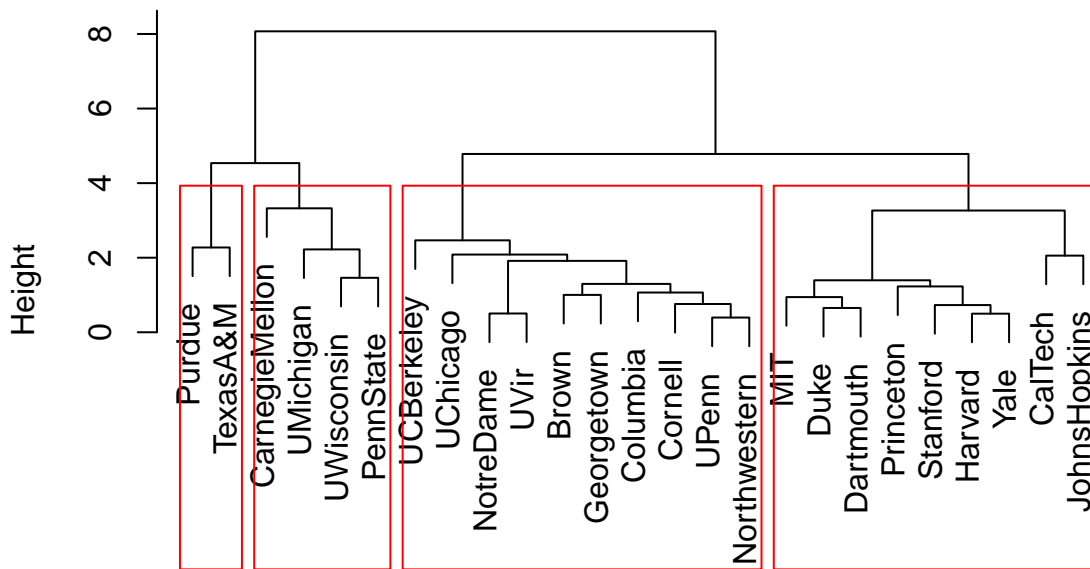
##           SAT Top10 Accept SFRatio Expenses Grad
## Harvard   14.00   91    14      11   39.525   97
## Princeton 13.75   91    14       8   30.220   95
## Yale      13.75   95    19      11   43.514   96
## Stanford  13.60   90    20      12   36.450   93
## MIT       13.80   94    30      10   34.870   91
## Duke      13.15   90    30      12   31.585   95

#
# scaling the data
#
m1=prcomp(d1, scale=T)
#
# mirror image
#
m1$rotation = -m1$rotation
m1$x = -m1$x
biplot(m1,scale=0,cex=0.5)
```



```
#
# Clusters
# Expensive schools: John Hopkins, CalTech
# Private schools are in the Top10 and High SAT range:
# Princeton, Harvard, Stanford, Yale, Duke, Darmouth
# Schools with low PC1: Texas AM, PennState, UM, UW, Purdue
# Schools with high PC2: Brown, UV, Georgetown, NotreDame, Cornell
# Average school (center of biplot): Northwestern, UPenn
#
# b) HClustering - complete
d2 = scale(d1)
distances = dist(d2)
hc1 = hclust(distances,method='complete')
plot(hc1,sub='',xlab='',main = '')
title('Complete linkage')
rect.hclust(hc1,k=4)
```

## Complete linkage



```
clusters1 = cutree(hc1,k=4)
clusters1
```

```
##      Harvard      Princeton      Yale      Stanford      MIT
##      1            1            1            1            1
##      Duke      CalTech      Dartmouth      Brown      JohnsHopkins
##      1            1            1            2            1
##      UChicago      UPenn      Cornell      Northwestern      Columbia
##      2            2            2            2            2
##      NotreDame      UVir      Georgetown      CarnegieMellon      UMichigan
##      2            2            2            3            3
##      UCBerkeley      UWisconsin      PennState      Purdue      TexasA&M
##      2            3            3            4            4
```

```
# clusters are ordered as in d2 or d1
```

```
#
```

```
# dataframe with cluster assignments
```

```
#
```

```
d22 = d1
```

```
d22$Complete = clusters1
```

```
head(d22)
```

```
##      SAT Top10 Accept SFRatio Expenses Grad Complete
## Harvard  14.00   91    14      11   39.525   97      1
## Princeton 13.75   91    14      8    30.220   95      1
## Yale     13.75   95    19     11   43.514   96      1
## Stanford 13.60   90    20     12   36.450   93      1
## MIT      13.80   94    30     10   34.870   91      1
## Duke     13.15   90    30     12   31.585   95      1
```

```
#
```

```
# HClustering - single
```

```
#
```

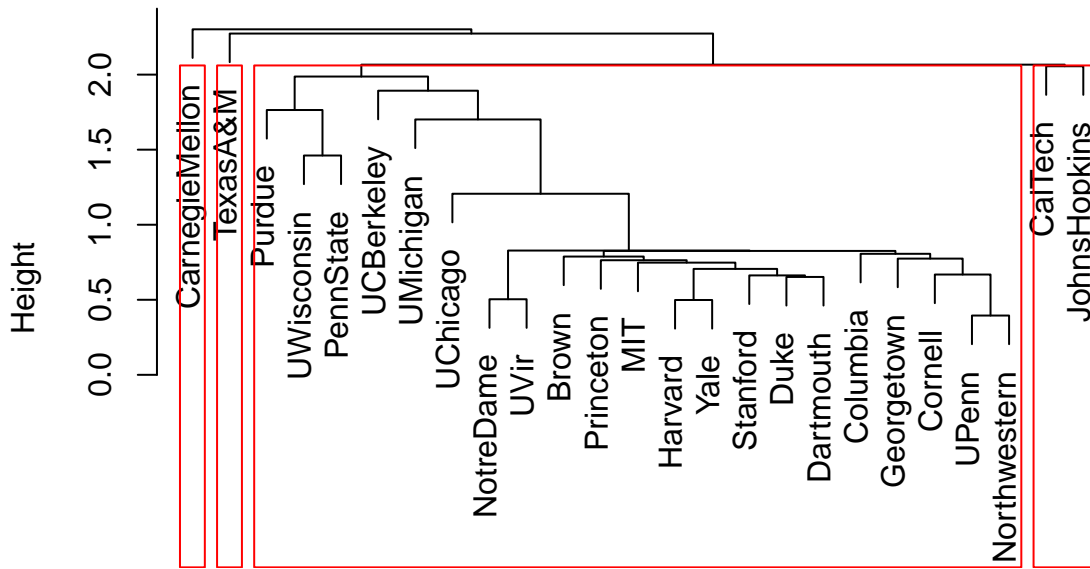
```
hc2 = hclust(distances,method='single')
```

```
plot(hc2,sub='',xlab='',main = '')
```

```
title('Single linkage')
```

```
rect.hclust(hc2,k=4)
```

## Single linkage



```
clusters2 = cutree(hc2,k=4)
#
# dataframe with cluster assignments
#
d23 = d1
d23$Single = clusters2
#
# compare clusters
#
d3 = merge(d22,d23)
d3
```

##	SAT	Top10	Accept	SFRatio	Expenses	Grad	Complete	Single
## 1	10.05	28	90	19	9.066	69	4	1
## 2	10.75	49	67	25	8.704	67	4	4
## 3	10.81	38	54	18	10.185	80	3	1
## 4	10.85	40	69	15	11.857	71	3	1
## 5	11.80	65	68	16	15.470	85	3	1
## 6	12.25	77	44	14	13.349	92	2	1
## 7	12.40	95	40	17	15.140	78	2	1
## 8	12.55	74	24	12	20.126	92	2	1
## 9	12.55	81	42	13	15.122	94	2	1
## 10	12.60	62	59	9	25.026	72	3	3
## 11	12.60	85	39	11	28.052	89	2	1
## 12	12.80	83	33	13	21.864	90	2	1
## 13	12.85	80	36	11	27.553	90	2	1
## 14	12.90	75	50	13	38.380	87	2	1
## 15	13.05	75	44	7	58.691	87	1	2
## 16	13.10	76	24	12	31.510	88	2	1
## 17	13.10	89	22	13	22.704	94	2	1
## 18	13.15	90	30	12	31.585	95	1	1
## 19	13.40	89	23	10	32.162	95	1	1
## 20	13.60	90	20	12	36.450	93	1	1
## 21	13.75	91	14	8	30.220	95	1	1
## 22	13.75	95	19	11	43.514	96	1	1
## 23	13.80	94	30	10	34.870	91	1	1

```
## 24 14.00    91    14    11  39.525  97      1    1
## 25 14.15   100    25     6  63.575  81      1    2

#
# c) K-means
#
set.seed(2)
k=4
kmeans = kmeans(d2,centers=k,nstart = 20)
assignments = kmeans$cluster
clusplot(d2,assignments,lines=0,color=T,shade=T,labels=k,cex=0.6,main='K-means Universities')
#
# K-means clusters separate Universities well
#
# find out which universities assigned to each cluster
#
d4 = d1
d4$kmeans = assignments
d4[order(d4$kmeans),]
```

```
##          SAT Top10 Accept SFRatio Expenses Grad kmeans
## UChicago    12.90    75    50     13   38.380   87     1
## UPenn       12.85    80    36     11   27.553   90     1
## Cornell     12.80    83    33     13   21.864   90     1
## Northwestern 12.60    85    39     11   28.052   89     1
## NotreDame   12.55    81    42     13   15.122   94     1
## UVir        12.25    77    44     14   13.349   92     1
## Georgetown  12.55    74    24     12   20.126   92     1
## CarnegieMellon 12.60    62    59     9   25.026   72     1
## UMichigan    11.80    65    68    16   15.470   85     1
## UCBerkeley   12.40    95    40     17   15.140   78     1
## CalTech     14.15   100    25     6   63.575   81     2
## JohnsHopkins 13.05    75    44     7   58.691   87     2
## Harvard     14.00    91    14     11   39.525   97     3
## Princeton   13.75    91    14     8   30.220   95     3
## Yale        13.75    95    19     11   43.514   96     3
## Stanford    13.60    90    20     12   36.450   93     3
## MIT         13.80    94    30     10   34.870   91     3
## Duke        13.15    90    30     12   31.585   95     3
## Dartmouth   13.40    89    23     10   32.162   95     3
## Brown       13.10    89    22     13   22.704   94     3
## Columbia    13.10    76    24     12   31.510   88     3
## UWisconsin   10.85    40    69     15   11.857   71     4
## PennState   10.81    38    54     18   10.185   80     4
## Purdue      10.05    28    90     19    9.066   69     4
## TexasA&M    10.75    49    67     25    8.704   67     4
```

```
#
# Question 2
#
library(cluster)
d1 = read.csv("brands.csv")
str(d1)
```

```
## 'data.frame':   43 obs. of  10 variables:
## $ Brand      : Factor w/ 43 levels "ACCheerios","AllBran",...: 1 6 7 10 17 19 21 23 25 29 ...
## $ Manuf      : Factor w/ 3 levels "G","K","Q": 1 1 1 1 1 1 1 1 1 1 ...
## $ Calories   : int   110 110 110 110 110 110 110 110 100 130 ...
```

```
## $ Protein : int 2 6 1 1 1 3 2 2 2 3 ...
## $ Fat      : int 2 2 1 1 1 1 1 1 1 2 ...
## $ Sodium   : int 180 290 180 180 280 250 260 180 220 170 ...
## $ Fiber    : num 1.5 2 0 0 0 1.5 0 0 2 1.5 ...
## $ Chydrates: num 10.5 17 12 12 15 11.5 21 12 15 13.5 ...
## $ Sugar    : int 10 1 13 13 9 10 3 12 6 10 ...
## $ Potassium: int 70 105 55 65 45 90 40 55 90 120 ...
```

```
rownames(d1) = d1[,1]
d1$Brand = NULL
head(d1)
```

```
##           Manuf Calories Protein Fat Sodium Fiber Chydrates Sugar
## ACCheerios      G      110       2  2    180   1.5      10.5    10
## Cheerios        G      110       6  2    290   2.0      17.0     1
## CocoaPuffs      G      110       1  1    180   0.0      12.0    13
## CountChocula    G      110       1  1    180   0.0      12.0    13
## GoldenGrahams   G      110       1  1    280   0.0      15.0     9
## HoneyNutCheerios G      110       3  1    250   1.5      11.5    10
```

```
##           Potassium
## ACCheerios        70
## Cheerios          105
## CocoaPuffs        55
## CountChocula      65
## GoldenGrahams     45
## HoneyNutCheerios  90
```

```
#
# dataframe with numeric columns only
#
d2 = d1
manuf = d2[,1]
table(manuf)
```

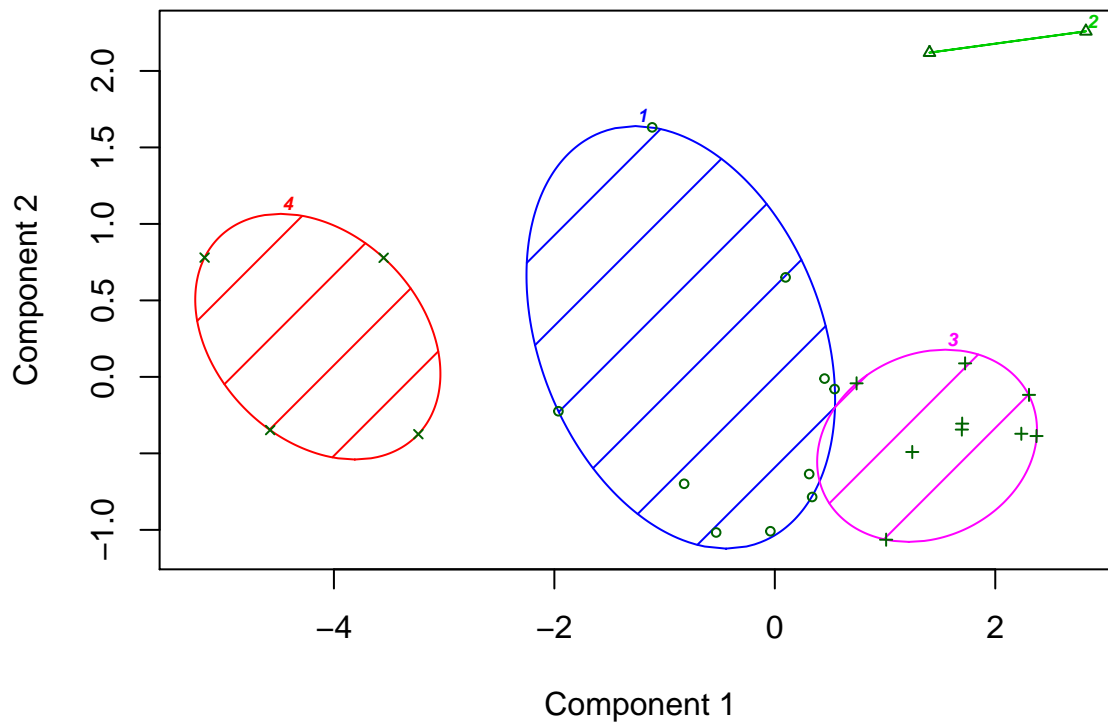
```
## manuf
##  G  K  Q
## 17 20  6
```

```
# d2$Brand = NULL
d2$Manuf = NULL
head(d2)
```

```
##           Calories Protein Fat Sodium Fiber Chydrates Sugar Potassium
## ACCheerios      110       2  2    180   1.5      10.5    10       70
## Cheerios        110       6  2    290   2.0      17.0     1      105
## CocoaPuffs      110       1  1    180   0.0      12.0    13       55
## CountChocula    110       1  1    180   0.0      12.0    13       65
## GoldenGrahams   110       1  1    280   0.0      15.0     9       45
## HoneyNutCheerios 110       3  1    250   1.5      11.5    10       90
```

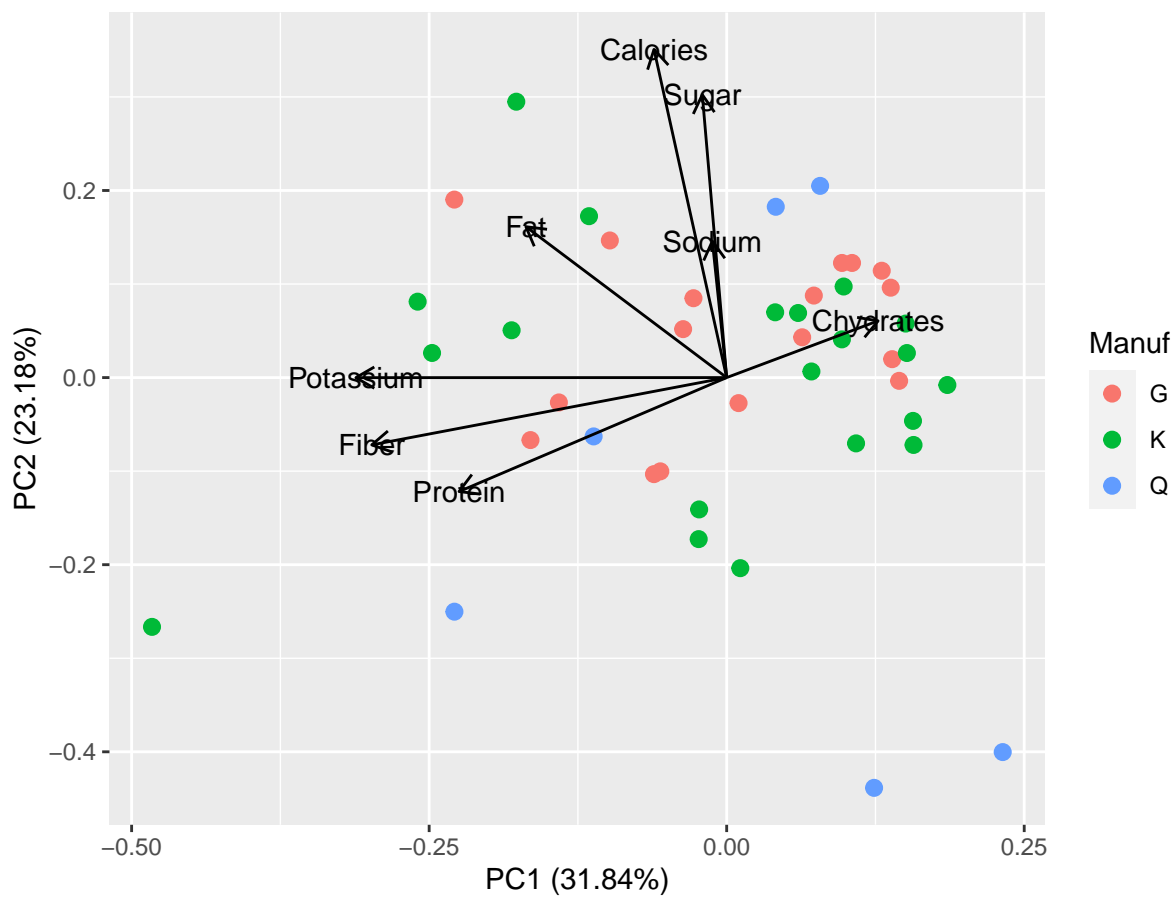
```
#
# a) principal components
#
m2 = prcomp(d2, scale=T)
#
# plot
library(ggfortify) # autoplot()
```

## K-means Universities



These two components explain 89.98 % of the point variability.

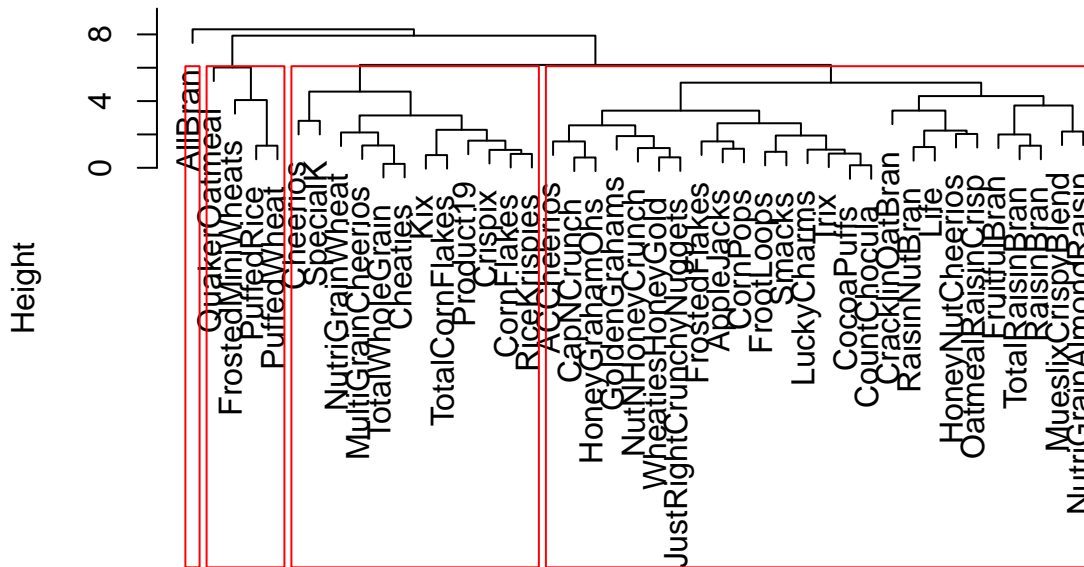
```
#  
autoplot(m2,data=d1,colour = 'Manuf',loadings = TRUE,loadings.label = TRUE,size=2.5,  
         loadings.colour = 'black',loadings.label.colour='black')
```



```
#
# Most G and K brands have lots of Carbohydrates.
# it is not clear that some brands are associated with more nutritional elements
#
# b) Complete and single linkage
#
# distances - scaled data
#
d3 = scale(d2)
d = dist(d3)
#
# complete linkage
#
hcomplete = hclust(d,method="complete")
plot(hcomplete,main='Complete linkage')
rect.hclust(hcomplete,k=4)
```



## Complete linkage



d  
hclust (\*, "complete")

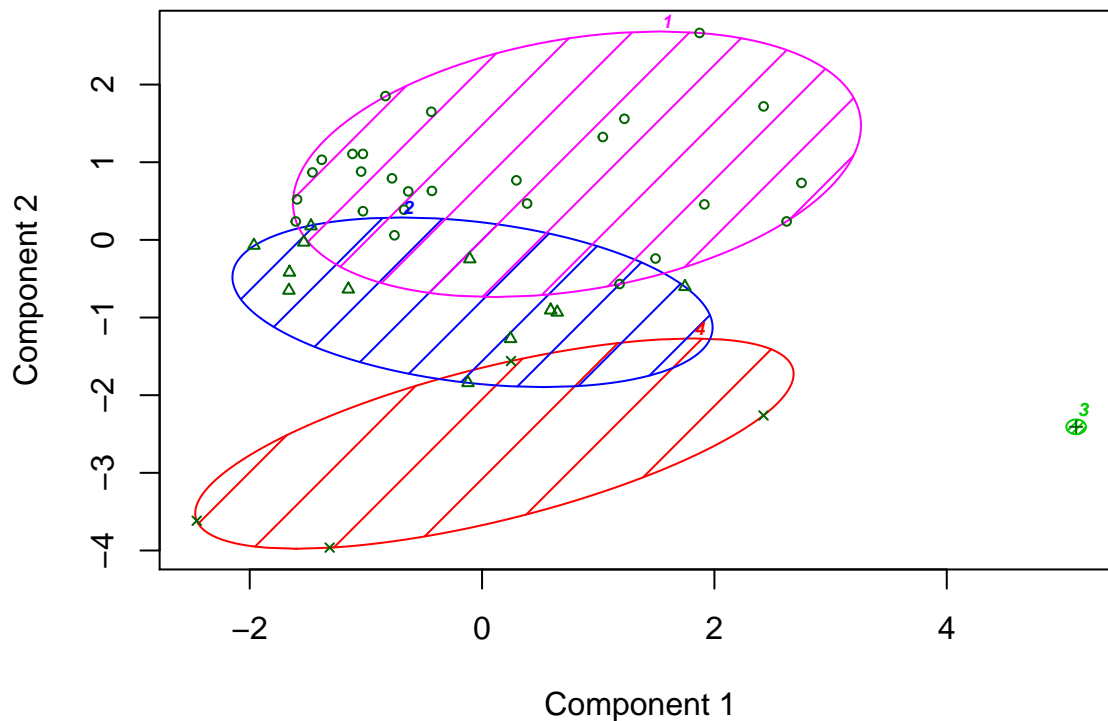
```
#
# add cluster assignment column
#
assignment = cutree(hcomplete,4)
dcomplete = data.frame(d1,assignment)
dcomplete = dcomplete[order(-assignment),]
dcomplete[,c(1,2,10)]
```

##	Manuf	Calories	assignment
## FrostedMiniWheats	K	100	4
## PuffedRice	Q	50	4
## PuffedWheat	Q	50	4
## QuakerOatmeal	Q	100	4
## AllBran	K	70	3
## Cheerios	G	110	2
## Kix	G	110	2
## MultiGrainCheerios	G	100	2
## TotalCornFlakes	G	110	2
## TotalWholeGrain	G	100	2
## Cheaties	G	100	2
## CornFlakes	K	100	2
## Crispix	K	110	2
## NutriGrainWheat	K	90	2
## Product19	K	100	2
## RiceKrispies	K	110	2
## SpecialK	K	110	2
## ACheerios	G	110	1
## CocoaPuffs	G	110	1
## CountChocula	G	110	1

## GoldenGrahams	G	110	1
## HoneyNutCheerios	G	110	1
## LuckyCharms	G	110	1
## OatmealRaisinCrisp	G	130	1
## RaisinNutBran	G	100	1
## TotalRaisinBran	G	140	1
## Trix	G	110	1
## WheatiesHoneyGold	G	110	1
## AppleJacks	K	110	1
## CornPops	K	110	1
## CracklinOatBran	K	110	1
## FrootLoops	K	110	1
## FrostedFlakes	K	110	1
## FruitfulBran	K	120	1
## JustRightCrunchyNuggets	K	110	1
## MueslixCrispyBlend	K	160	1
## NutNHoneyCrunch	K	120	1
## NutriGrainAlmondRaisin	K	140	1
## RaisinBran	K	120	1
## Smacks	K	110	1
## CapNCrunch	Q	120	1
## HoneyGrahamOhs	Q	120	1
## Life	Q	100	1

```
#
clusplot(d2,assignment,lines=0,color=T,shade=T,labels=4,cex=0.6,main='Complete linkage')
```

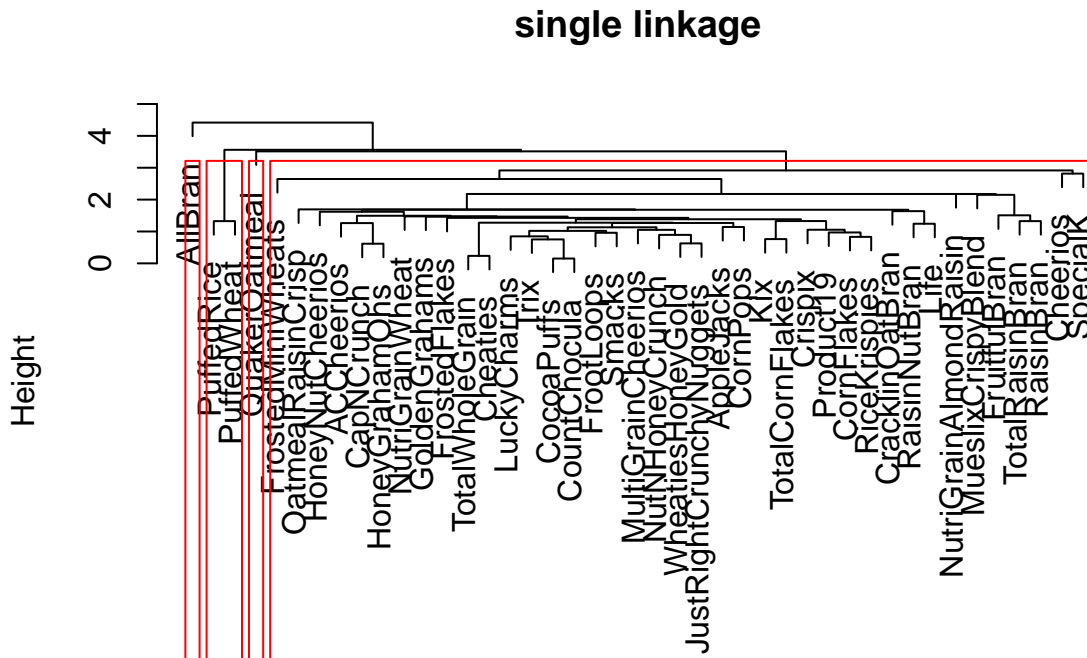
### Complete linkage



These two components explain 55.03 % of the point variability.

```
#
# single linkage
#
```

```
hsingle = hclust(d,method="single")
plot(hsingle,main='single linkage')
rect.hclust(hsingle,k=4)
```



d  
hclust (\*, "single")

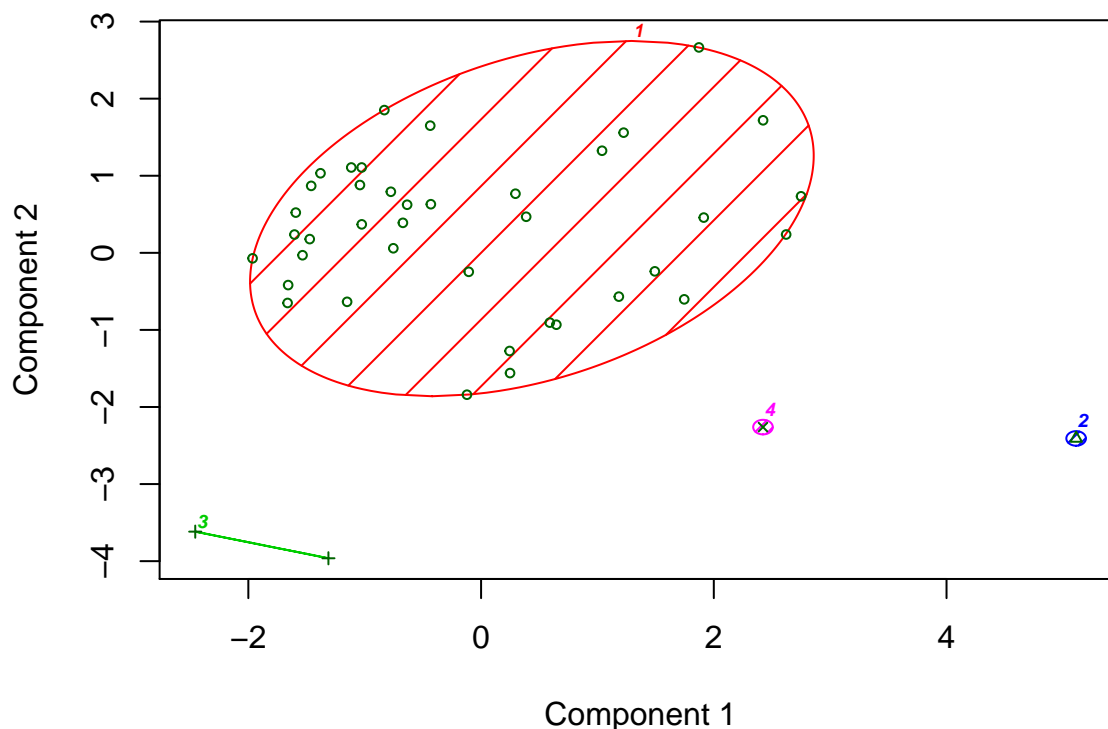
```
#
# add cluster assignment column
#
assignment2 = cutree(hsingle,4)
dsingle = data.frame(d1,assignment2)
dsingle = dsingle[order(-assignment2),]
dsingle[,c(1,2,10)]
```

##	Manuf	Calories	assignment2
## QuakerOatmeal	Q	100	4
## PuffedRice	Q	50	3
## PuffedWheat	Q	50	3
## AllBran	K	70	2
## ACheerios	G	110	1
## Cheerios	G	110	1
## CocoaPuffs	G	110	1
## CountChocula	G	110	1
## GoldenGrahams	G	110	1
## HoneyNutCheerios	G	110	1
## Kix	G	110	1
## LuckyCharms	G	110	1
## MultiGrainCheerios	G	100	1
## OatmealRaisinCrisp	G	130	1
## RaisinNutBran	G	100	1
## TotalCornFlakes	G	110	1

## TotalRaisinBran	G	140	1
## TotalWholeGrain	G	100	1
## Trix	G	110	1
## Cheaties	G	100	1
## WheatiesHoneyGold	G	110	1
## AppleJacks	K	110	1
## CornFlakes	K	100	1
## CornPops	K	110	1
## CracklinOatBran	K	110	1
## Crispix	K	110	1
## FrootLoops	K	110	1
## FrostedFlakes	K	110	1
## FrostedMiniWheats	K	100	1
## FruitfulBran	K	120	1
## JustRightCrunchyNuggets	K	110	1
## MueslixCrispyBlend	K	160	1
## NutNHoneyCrunch	K	120	1
## NutriGrainAlmondRaisin	K	140	1
## NutriGrainWheat	K	90	1
## Product19	K	100	1
## RaisinBran	K	120	1
## RiceKrispies	K	110	1
## Smacks	K	110	1
## SpecialK	K	110	1
## CapNCrunch	Q	120	1
## HoneyGrahamOhs	Q	120	1
## Life	Q	100	1

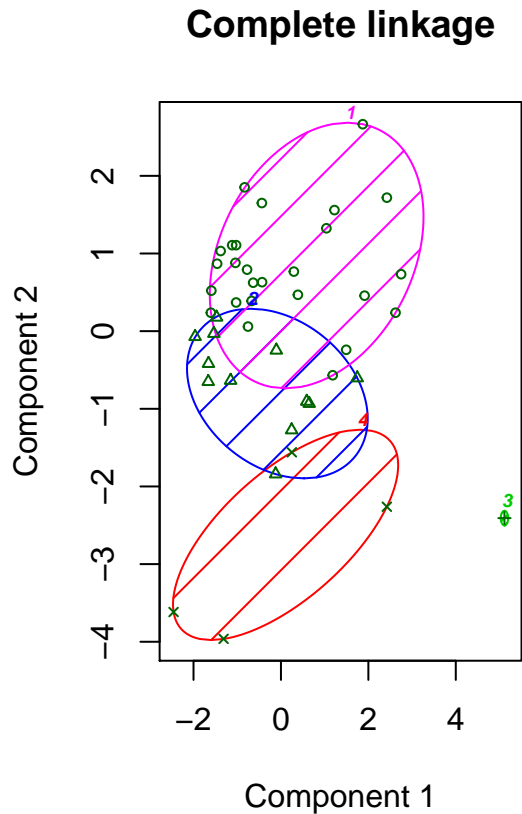
```
#
clusplot(d2,assignment2,lines=0,color=T,shade=T,labels=4,cex=0.6,main='single linkage')
```

### single linkage

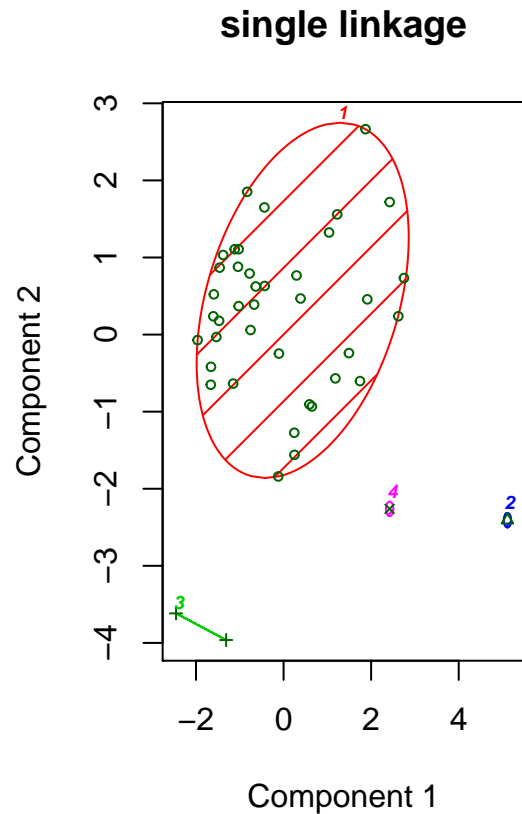


These two components explain 55.03 % of the point variability.

```
#
# compare plots
#
par(mfrow=c(1,2))
clusplot(d2,assignment,lines=0,color=T,shade=T,labels=4,cex=0.6,main='Complete linkage')
clusplot(d2,assignment2,lines=0,color=T,shade=T,labels=4,cex=0.6,main='single linkage')
```



These two components explain



These two components explain

```
par(mfrow=c(1,1))
#
# two largest clusters in complete linkage
# appear as a single big cluster in single linkage
#
# while brands 41-43 and 26 appear in a cluster using complete linkage
# only 41-42 appear in a cluster using single linkage, leaving 26 in the largest cluster
#
# cluster with only one brand contains
d1[c(18),]
```

```
##           Manuf Calories Protein Fat Sodium Fiber Chydrates Sugar Potassium
## AllBran      K          70         4    1   260     9          7     5       320
```

```
#
# cluster with four brands (single) that are split into two clusters (complete)
d1[c(26,41:43),]
```

```
##           Manuf Calories Protein Fat Sodium Fiber Chydrates Sugar
## FrostedMiniWheats K      100      3  0     0   3.0       14    7
## PuffedRice        Q       50      1  0     0   0.0       13    0
## PuffedWheat       Q       50      2  0     0   1.0       10    0
## QuakerOatmeal     Q      100      5  2     0   2.7        1    1
```

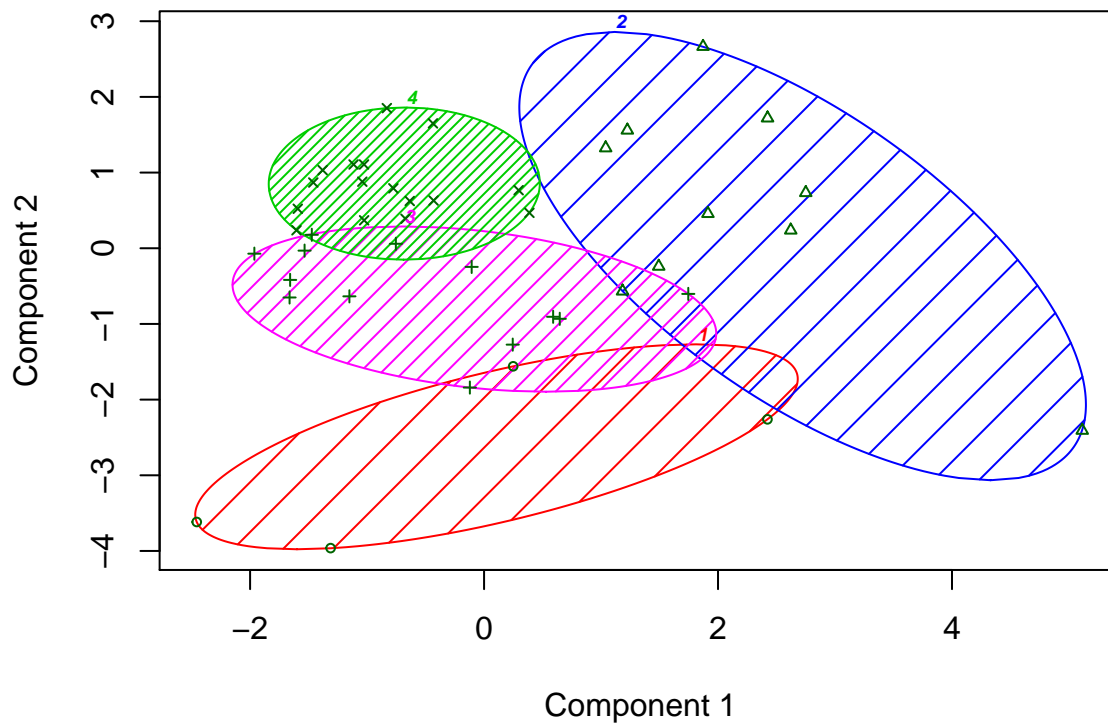
```
## Potassium
## FrostedMiniWheats 100
## PuffedRice 15
## PuffedWheat 50
## QuakerOatmeal 110
```

```
#
# c) kmeans
#
kmodel = kmeans(d3,4,nstart=20)
assignment3 = kmodel$cluster
dkmeans = data.frame(d1,assignment3)
dkmeans = dkmeans[order(-assignment3),]
dkmeans[,c(1,2,10)]
```

```
## Manuf Calories assignment3
## ACheerios G 110 4
## CocoaPuffs G 110 4
## CountChocula G 110 4
## GoldenGrahams G 110 4
## HoneyNutCheerios G 110 4
## LuckyCharms G 110 4
## Trix G 110 4
## WheatiesHoneyGold G 110 4
## AppleJacks K 110 4
## CornPops K 110 4
## FrootLoops K 110 4
## FrostedFlakes K 110 4
## NutNHoneyCrunch K 120 4
## Smacks K 110 4
## CapNCrunch Q 120 4
## HoneyGrahamOhs Q 120 4
## Cheerios G 110 3
## Kix G 110 3
## MultiGrainCheerios G 100 3
## TotalCornFlakes G 110 3
## TotalWholeGrain G 100 3
## Cheaties G 100 3
## CornFlakes K 100 3
## Crispix K 110 3
## JustRightCrunchyNuggets K 110 3
## NutriGrainWheat K 90 3
## Product19 K 100 3
## RiceKrispies K 110 3
## SpecialK K 110 3
## OatmealRaisinCrisp G 130 2
## RaisinNutBran G 100 2
## TotalRaisinBran G 140 2
## AllBran K 70 2
## CracklinOatBran K 110 2
## FruitfulBran K 120 2
## MueslixCrispyBlend K 160 2
## NutriGrainAlmondRaisin K 140 2
## RaisinBran K 120 2
## Life Q 100 2
## FrostedMiniWheats K 100 1
## PuffedRice Q 50 1
```

```
## PuffedWheat          Q      50      1
## QuakerOatmeal        Q     100     1
# dkmeans
clusplot(d2,assignment3,lines=0,color=T,shade=T,labels=4,cex=0.6,main='K-means Cereals')
```

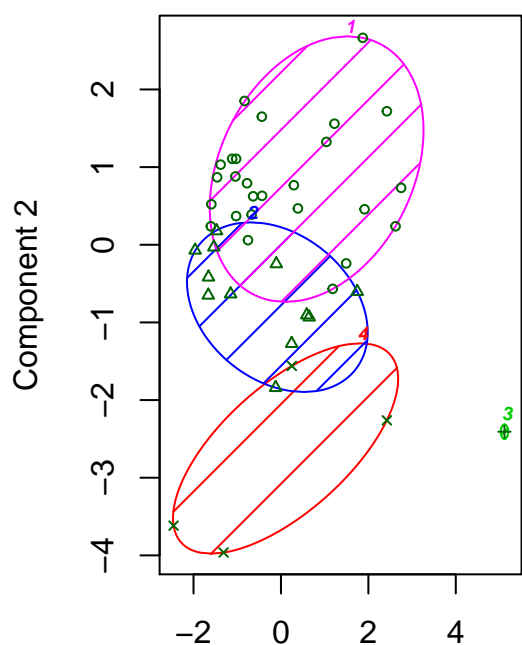
## K-means Cereals



These two components explain 55.03 % of the point variability.

```
#
# compare k-means with Complete linkage
#
par(mfrow=c(1,2))
clusplot(d2,assignment,lines=0,color=T,shade=T,labels=4,cex=0.6,main='Complete linkage')
clusplot(d2,assignment3,lines=0,color=T,shade=T,labels=4,cex=0.6,main='K-means Cereals')
```

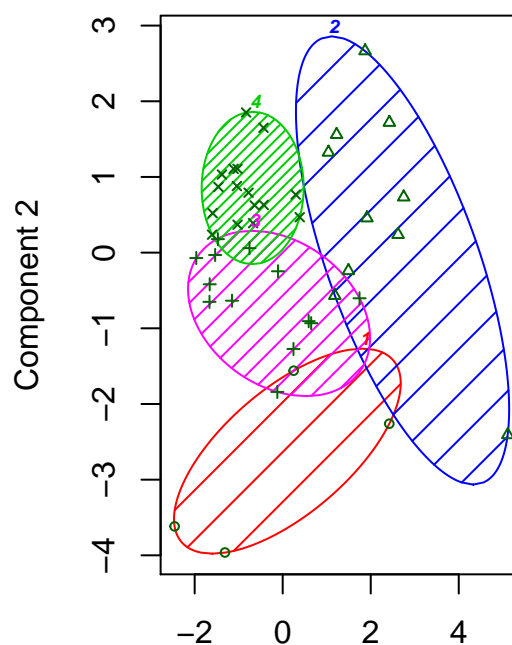
## Complete linkage



Component 1

These two components explain

## K-means Cereals



Component 1

These two components explain

```
par(mfrow=c(1,1))
#
# Two clusters seem to be the same in both Complete linkage and k-means
#
# k-means seems to perform better since overall the clusters have less overlap
# than those from Complete linkage
#
```