

Lab 9

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```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.3    v purrr   0.3.4
## v tibble  3.0.4    v dplyr   1.0.2
## v tidyr   1.1.2    v stringr 1.4.0
## v readr   1.4.0    v forcats 0.5.0
```

```
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
```

```
seeds <- read.table(
  "https://archive.ics.uci.edu/ml/machine-learning-databases/00236/seeds_dataset.txt"
)
colnames(seeds) <- c("area",
  "perimeter",
  "compactness",
  "length_of_kernel",
  "width_of_kernel",
  "asy_coeff",
  "length_of_kernel_groove",
  "Class")
summary(seeds)
```

```
##      area      perimeter      compactness      length_of_kernel
## Min.   :10.59  Min.   :12.41  Min.   :0.8081  Min.   :4.899
## 1st Qu.:12.27  1st Qu.:13.45  1st Qu.:0.8569  1st Qu.:5.262
## Median :14.36  Median :14.32  Median :0.8734  Median :5.524
## Mean   :14.85  Mean   :14.56  Mean   :0.8710  Mean   :5.629
## 3rd Qu.:17.30  3rd Qu.:15.71  3rd Qu.:0.8878  3rd Qu.:5.980
## Max.   :21.18  Max.   :17.25  Max.   :0.9183  Max.   :6.675
## width_of_kernel  asy_coeff      length_of_kernel_groove      Class
## Min.   :2.630  Min.   :0.7651  Min.   :4.519      Min.   :1
## 1st Qu.:2.944  1st Qu.:2.5615  1st Qu.:5.045      1st Qu.:1
## Median :3.237  Median :3.5990  Median :5.223      Median :2
## Mean   :3.259  Mean   :3.7002  Mean   :5.408      Mean   :2
## 3rd Qu.:3.562  3rd Qu.:4.7687  3rd Qu.:5.877      3rd Qu.:3
## Max.   :4.033  Max.   :8.4560  Max.   :6.550      Max.   :3
```

```
cor(dplyr::select(seeds, -Class))
```

```
##               area  perimeter compactness length_of_kernel
## area           1.0000000  0.9943409   0.6082884    0.9499854
## perimeter      0.9943409  1.0000000   0.5292436    0.9724223
## compactness    0.6082884  0.5292436   1.0000000    0.3679151
## length_of_kernel 0.9499854  0.9724223   0.3679151    1.0000000
## width_of_kernel 0.9707706  0.9448294   0.7616345    0.8604149
## asy_coeff      -0.2295723 -0.2173404  -0.3314709   -0.1715624
## length_of_kernel_groove 0.8636927  0.8907839   0.2268248    0.9328061
##               width_of_kernel  asy_coeff length_of_kernel_groove
## area           0.9707706 -0.22957233    0.86369275
## perimeter      0.9448294 -0.21734037    0.89078390
## compactness    0.7616345 -0.33147087    0.22682482
## length_of_kernel 0.8604149 -0.17156243    0.93280609
## width_of_kernel 1.0000000 -0.25803655    0.74913147
## asy_coeff      -0.2580365  1.00000000   -0.01107902
## length_of_kernel_groove 0.7491315 -0.01107902    1.00000000
```

```
dim(seeds)
```

```
## [1] 210 8
```

```
x <- seeds %>%
  dplyr::select(-Class) %>%
  scale()

set.seed(1)

seeds_train_index <- seeds %>%
  mutate(ind = 1:nrow(seeds)) %>%
  group_by(Class) %>%
  mutate(n = n()) %>%
  sample_frac(size = .75, weight = n) %>%
  ungroup() %>%
  pull(ind)

library(nnet)
class_labels <- pull(seeds, Class) %>%
  class.ind()

seeds_train <- x[seeds_train_index, ]
train_class <- class_labels[seeds_train_index,]
seeds_test <- x[-seeds_train_index, ]
test_class <- class_labels[-seeds_train_index,]

nn_seeds <- nnet(
  x = seeds_train,
  y = train_class,
  size = 4,
  decay = 0,
```

```
softmax = TRUE,  
maxit=500  
)
```

```
## # weights: 47  
## initial value 179.079752  
## iter 10 value 10.357187  
## iter 20 value 0.304073  
## iter 30 value 0.002143  
## iter 40 value 0.000138  
## iter 40 value 0.000061  
## iter 40 value 0.000061  
## final value 0.000061  
## converged
```

```
nn_pred <- predict(nn_seeds, seeds_test,  
                  type="class")  
  
tab_seeds <- table(slice(  
  seeds,  
  -seeds_train_index) %>% pull(Class),  
  nn_pred)  
  
1-sum(diag(tab_seeds))/sum(tab_seeds)
```

```
## [1] 0.1111111
```

```
library(nnet)
library(MASS)
```

```
##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##      select
```

```
train_Boston <- sample(
  1:nrow(Boston),
  nrow(Boston)/2
)

x <- scale(Boston)

Boston_train <- x[train_Boston, ]
train_medv <- x[train_Boston, "medv"]
Boston_test <- x[-train_Boston, ]
test_medv <- x[-train_Boston, "medv"]

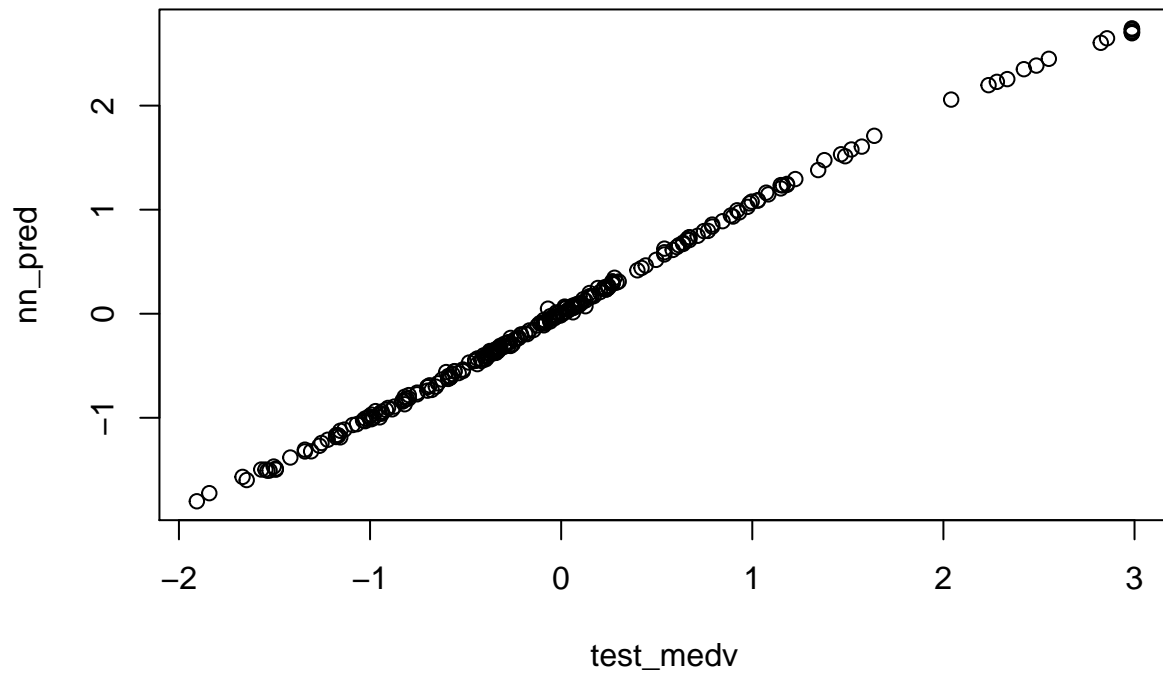
nn_Boston <- nnet(
  Boston_train,
  train_medv,
  size=10,
  decay=1,
  softmax=FALSE,
  maxit=1000,
  linout=TRUE
)
```

```
## # weights: 161
## initial value 469.211580
## iter 10 value 39.116735
## iter 20 value 22.164051
## iter 30 value 17.626264
## iter 40 value 14.619830
## iter 50 value 12.655570
## iter 60 value 11.292161
## iter 70 value 10.583592
## iter 80 value 10.254760
## iter 90 value 10.097962
## iter 100 value 10.015590
## iter 110 value 9.948224
## iter 120 value 9.917840
## iter 130 value 9.905889
## iter 140 value 9.901823
## iter 150 value 9.900874
## iter 160 value 9.900509
## iter 170 value 9.900410
## iter 180 value 9.900337
```

```
## iter 190 value 9.900141
## iter 200 value 9.900086
## iter 210 value 9.900065
## final value 9.900062
## converged
```

```
nn_pred <- predict(
  nn_Boston,
  Boston_test,
  type="raw"
)
```

```
plot(test_medv, nn_pred)
```



```
mean((test_medv - nn_pred)^2)
```

```
## [1] 0.003687532
```

```

library(e1071)
library(cluster)
set.seed(1)

data("iris")

Species <- pull(iris, Species)

xy <- dplyr::select(iris, -Species) %>%
  scale() %>%
  data.frame() %>%
  mutate(Species = Species) # scale predictors

iris_train_index <- iris %>%
  mutate(ind = 1:nrow(iris)) %>%
  group_by(Species) %>%
  mutate(n = n()) %>%
  sample_frac(size = .8, weight = n) %>%
  ungroup() %>%
  pull(ind)

iris_train <- slice(xy, iris_train_index)
iris_test <- slice(xy, -iris_train_index)
class_labels <- pull(xy, Species) %>%
  class.ind()

iris_nnet1 <- tune.nnet(
  Species~.,
  data = iris_train,
  size = 1:30,
  tunecontrol = tune.control(sampling = "cross", cross=5)
)

head(summary(iris_nnet1))

## $best.parameters
##   size
## 2     2
##
## $best.performance
## [1] 0.03333333
##
## $method
## [1] "nnet"
##
## $nparcomb
## [1] 30
##
## $train.ind
## $train.ind$`(0.881,24.8]`
## [1] 40 83 90 35 111 112 120 78 22 70 28 37 61 46 67 71 116 44 49
## [20] 117 56 89 50 7 20 100 80 99 16 2 118 65 79 101 41 77 107 13
## [39] 109 114 82 19 17 57 11 31 115 74 95 55 45 52 68 119 9 97 81

```

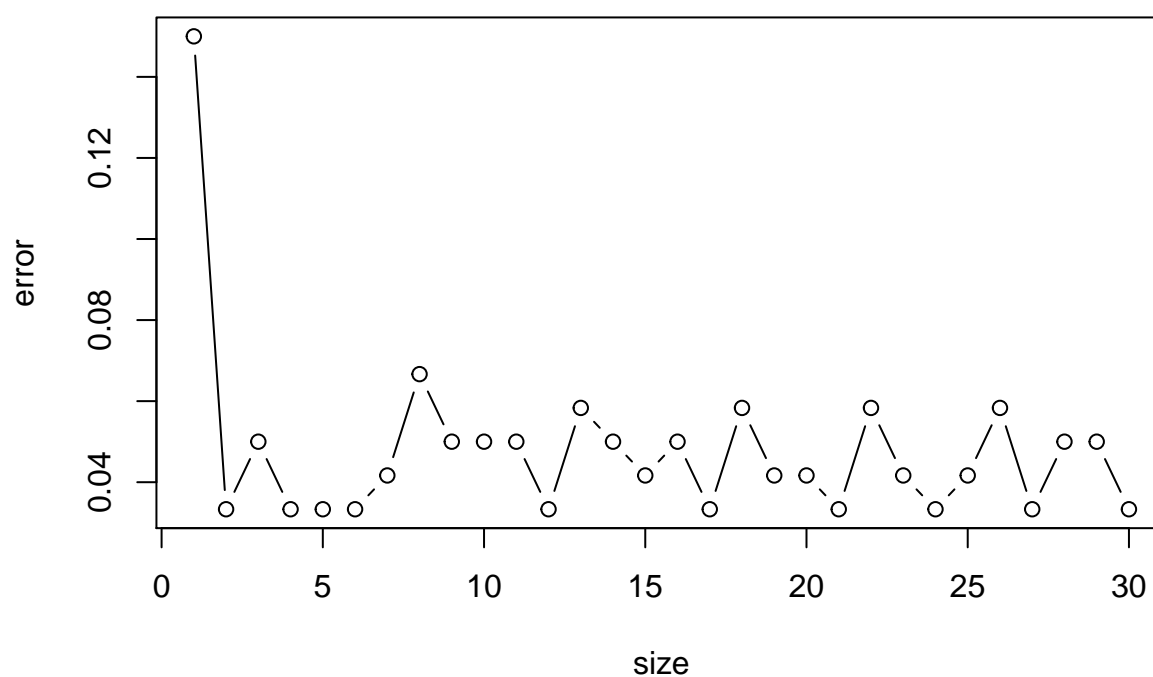
```

## [58] 113 108 85 32 87 94 12 30 14 62 6 72 64 38 102 91 3 104 69
## [77] 54 5 88 33 84 47 8 4 98 18 27 36 63 110 25 21 66 73 23
## [96] 75
##
## $train.ind$(24.8,48.6)
## [1] 106 96 103 60 51 93 34 10 1 43 59 26 15 58 29 24 42 48 76
## [20] 39 105 53 92 86 20 100 80 99 16 2 118 65 79 101 41 77 107 13
## [39] 109 114 82 19 17 57 11 31 115 74 95 55 45 52 68 119 9 97 81
## [58] 113 108 85 32 87 94 12 30 14 62 6 72 64 38 102 91 3 104 69
## [77] 54 5 88 33 84 47 8 4 98 18 27 36 63 110 25 21 66 73 23
## [96] 75
##
## $train.ind$(48.6,72.4)
## [1] 106 96 103 60 51 93 34 10 1 43 59 26 15 58 29 24 42 48 76
## [20] 39 105 53 92 86 40 83 90 35 111 112 120 78 22 70 28 37 61 46
## [39] 67 71 116 44 49 117 56 89 50 7 95 55 45 52 68 119 9 97 81
## [58] 113 108 85 32 87 94 12 30 14 62 6 72 64 38 102 91 3 104 69
## [77] 54 5 88 33 84 47 8 4 98 18 27 36 63 110 25 21 66 73 23
## [96] 75
##
## $train.ind$(72.4,96.2)
## [1] 106 96 103 60 51 93 34 10 1 43 59 26 15 58 29 24 42 48 76
## [20] 39 105 53 92 86 40 83 90 35 111 112 120 78 22 70 28 37 61 46
## [39] 67 71 116 44 49 117 56 89 50 7 20 100 80 99 16 2 118 65 79
## [58] 101 41 77 107 13 109 114 82 19 17 57 11 31 115 74 91 3 104 69
## [77] 54 5 88 33 84 47 8 4 98 18 27 36 63 110 25 21 66 73 23
## [96] 75
##
## $train.ind$(96.2,120)
## [1] 106 96 103 60 51 93 34 10 1 43 59 26 15 58 29 24 42 48 76
## [20] 39 105 53 92 86 40 83 90 35 111 112 120 78 22 70 28 37 61 46
## [39] 67 71 116 44 49 117 56 89 50 7 20 100 80 99 16 2 118 65 79
## [58] 101 41 77 107 13 109 114 82 19 17 57 11 31 115 74 95 55 45 52
## [77] 68 119 9 97 81 113 108 85 32 87 94 12 30 14 62 6 72 64 38
## [96] 102
##
##
## $sampling
## [1] "5-fold cross validation"

```

```
plot(iris_nnet1)
```

Performance of `nnet`



```
library(nnet)
nn_iris <- nnet(
  x = dplyr::select(iris_train, -Species),
  y = class_labels[iris_train_index, ],
  size = iris_nnet1$best.parameters[1,1],
  decay = 0,
  softmax = TRUE
)
```

```
## # weights: 19
## initial value 139.787195
## iter 10 value 51.659855
## iter 20 value 12.382653
## iter 30 value 2.538123
## iter 40 value 0.820028
## iter 50 value 0.000596
## iter 60 value 0.000139
## final value 0.000086
## converged
```

```
nn_pred <- predict(
  nn_iris,
  dplyr::select(iris_test, -Species),
  type="class"
)
```



```
tab <- table(pull(iris_test, Species),
  nn_pred
)
```

```
tab
```

```
##           nn_pred
##           setosa versicolor virginica
## setosa         10          0          0
## versicolor      0          10          0
## virginica       0           2          8
```

```
1- sum(diag(tab))/sum(tab)
```

```
## [1] 0.06666667
```

```
set.seed(1)
```

```
iris_nnet2 <- tune.nnet(
  Species~.,
  data = iris_train,
  size = 1:20,
  decay = 0:3,
  tunecontrol = tune.control(sampling = "cross", cross=5)
)
```

```
head(summary(iris_nnet2))
```

```
## $best.parameters
##   size decay
## 11    11    0
##
## $best.performance
## [1] 0.01666667
##
## $method
## [1] "nnet"
##
## $nparcomb
## [1] 80
##
## $train.ind
## $train.ind$(0.881,24.8] '
## [1] 99 44 102 33 84 35 70 105 42 38 20 28 86 95 90 40 83 25 113
## [20] 119 111 88 6 24 32 114 2 45 18 22 65 13 81 94 48 63 23 46
## [39] 92 77 29 66 67 56 101 80 62 93 69 108 31 116 17 9 57 60 19
## [58] 26 30 72 53 110 10 118 11 27 75 15 50 103 91 16 47 12 104 112
## [77] 8 49 3 98 64 55 71 96 36 4 115 5 52 41 61 120 78 58 107
## [96] 76
##
## $train.ind$(24.8,48.6] '
## [1] 113 112 107 104 112 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1
```

```

## [1] 68 39 1 34 87 43 14 82 59 51 97 85 21 106 54 74 7 73 79
## [20] 109 37 89 100 117 32 114 2 45 18 22 65 13 81 94 48 63 23 46
## [39] 92 77 29 66 67 56 101 80 62 93 69 108 31 116 17 9 57 60 19
## [58] 26 30 72 53 110 10 118 11 27 75 15 50 103 91 16 47 12 104 112
## [77] 8 49 3 98 64 55 71 96 36 4 115 5 52 41 61 120 78 58 107
## [96] 76
##
## $train.ind$(48.6,72.4)
## [1] 68 39 1 34 87 43 14 82 59 51 97 85 21 106 54 74 7 73 79
## [20] 109 37 89 100 117 99 44 102 33 84 35 70 105 42 38 20 28 86 95
## [39] 90 40 83 25 113 119 111 88 6 24 69 108 31 116 17 9 57 60 19
## [58] 26 30 72 53 110 10 118 11 27 75 15 50 103 91 16 47 12 104 112
## [77] 8 49 3 98 64 55 71 96 36 4 115 5 52 41 61 120 78 58 107
## [96] 76
##
## $train.ind$(72.4,96.2)
## [1] 68 39 1 34 87 43 14 82 59 51 97 85 21 106 54 74 7 73 79
## [20] 109 37 89 100 117 99 44 102 33 84 35 70 105 42 38 20 28 86 95
## [39] 90 40 83 25 113 119 111 88 6 24 32 114 2 45 18 22 65 13 81
## [58] 94 48 63 23 46 92 77 29 66 67 56 101 80 62 93 47 12 104 112
## [77] 8 49 3 98 64 55 71 96 36 4 115 5 52 41 61 120 78 58 107
## [96] 76
##
## $train.ind$(96.2,120)
## [1] 68 39 1 34 87 43 14 82 59 51 97 85 21 106 54 74 7 73 79
## [20] 109 37 89 100 117 99 44 102 33 84 35 70 105 42 38 20 28 86 95
## [39] 90 40 83 25 113 119 111 88 6 24 32 114 2 45 18 22 65 13 81
## [58] 94 48 63 23 46 92 77 29 66 67 56 101 80 62 93 69 108 31 116
## [77] 17 9 57 60 19 26 30 72 53 110 10 118 11 27 75 15 50 103 91
## [96] 16
##
##
## $sampling
## [1] "5-fold cross validation"

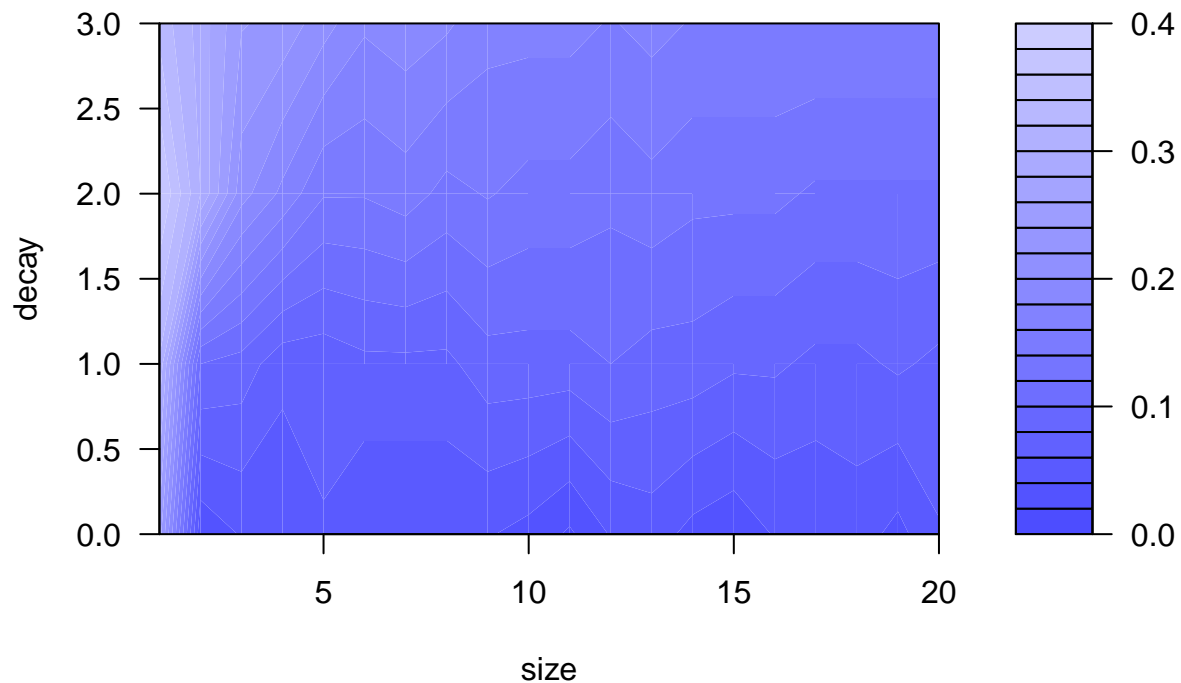
```

```

plot(iris_nnet2)

```

Performance of `nnet`



```
nn_iris_d_s <- nnet(  
  x = dplyr::select(iris_train, -Species),  
  y = class_labels[iris_train_index, ],  
  size = iris_nnet2$best.parameters[1,1],  
  decay = iris_nnet2$best.parameters[1,2],  
  softmax = TRUE  
)
```

```
## # weights:  91  
## initial  value 164.446139  
## iter  10 value 15.814895  
## iter  20 value 1.891497  
## iter  30 value 0.102615  
## final   value 0.000056  
## converged
```

```
# Compute test error  
nn_pred <- predict(  
  nn_iris_d_s,  
  dplyr::select(iris_test, -Species),  
  type="class"  
)  
  
tab <- table(pull(iris_test, Species),  
  nn_pred
```

```

)

tab

##          nn_pred
##          setosa versicolor virginica
##  setosa         10          0          0
##  versicolor      0          10          0
##  virginica       0           2           8

1- sum(diag(tab))/sum(tab)

## [1] 0.06666667

```

```
library(cluster)
library(factoextra) # PCA
```

```
## Warning: package 'factoextra' was built under R version 4.0.4
```

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

```
library(pgmm) # coffee data
data("coffee")
set.seed(1)
x <- dplyr::select(coffee, - Variety, - Country)
x_scaled <- scale(x)
kmeans_coffee <- kmeans(x_scaled, 2)
kmeans_coffee$tot.withinss
```

```
## [1] 330.8912
```

```
kmeans_coffee <- kmeans(x_scaled, 3)
kmeans_coffee$tot.withinss
```

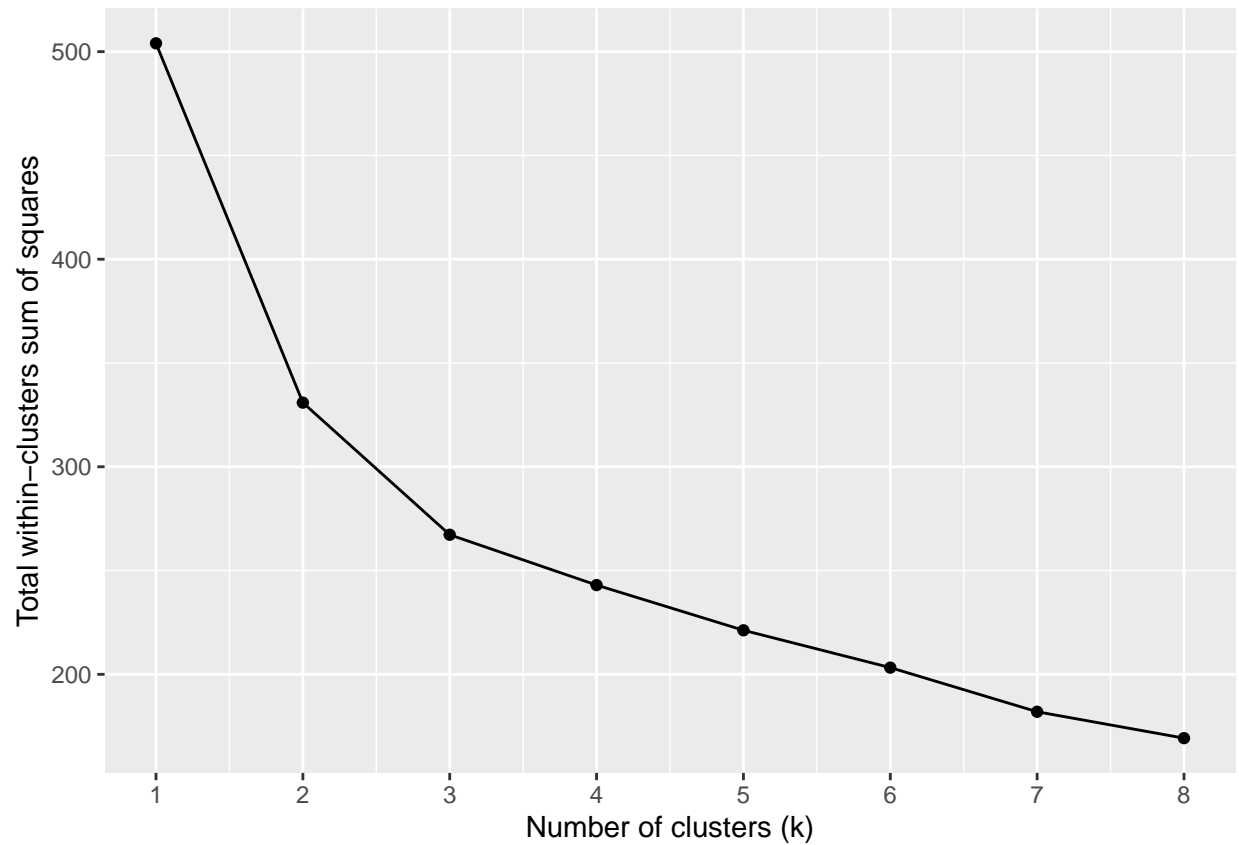
```
## [1] 267.2453
```

```
# Let's select K using elbow method
withclusterss <- function(K,x){
  kmeans(x, K)$tot.withinss
}
```

```
K <- 1:8
```

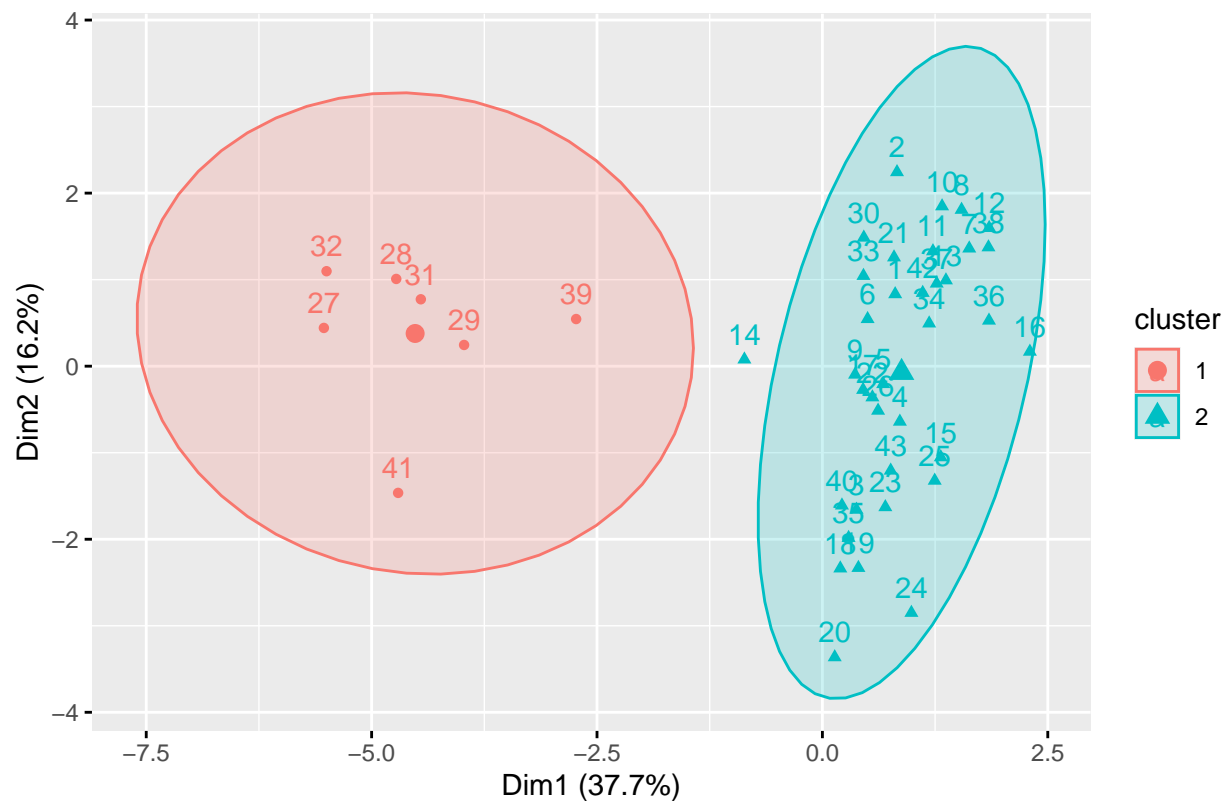
```
wcss <- lapply(as.list(K), function(k){
  withclusterss(k, x_scaled)
}) %>% unlist()
```

```
ggplot(tibble(K = K, wcss = wcss), aes(x = K, y = wcss)) +
  geom_point() +
  geom_line() +
  xlab("Number of clusters (k)") +
  ylab("Total within-clusters sum of squares") +
  scale_x_continuous(breaks=c(seq(1,K[length(K)])))
```



```
kmeans_coffee <- kmeans(x_scaled, 2)
fvPCA <- fviz_cluster(kmeans_coffee,
                      x_scaled,
                      ellipse.type = "norm",
                      main = "Plot the results of k-means clustering after PCA")
fvPCA
```

Plot the results of k-means clustering after PCA



```
library(cluster)
library(factoextra) # PCA
library(pgmm) # coffee data
data("coffee")
set.seed(1)
x <- dplyr::select(coffee, - Variety, - Country)
x_scaled <- scale(x)
kmeans_coffee <- kmeans(x_scaled, 2)
kmeans_coffee$tot.withinss
```

```
## [1] 330.8912
```

```
kmeans_coffee <- kmeans(x_scaled, 3)
kmeans_coffee$tot.withinss
```

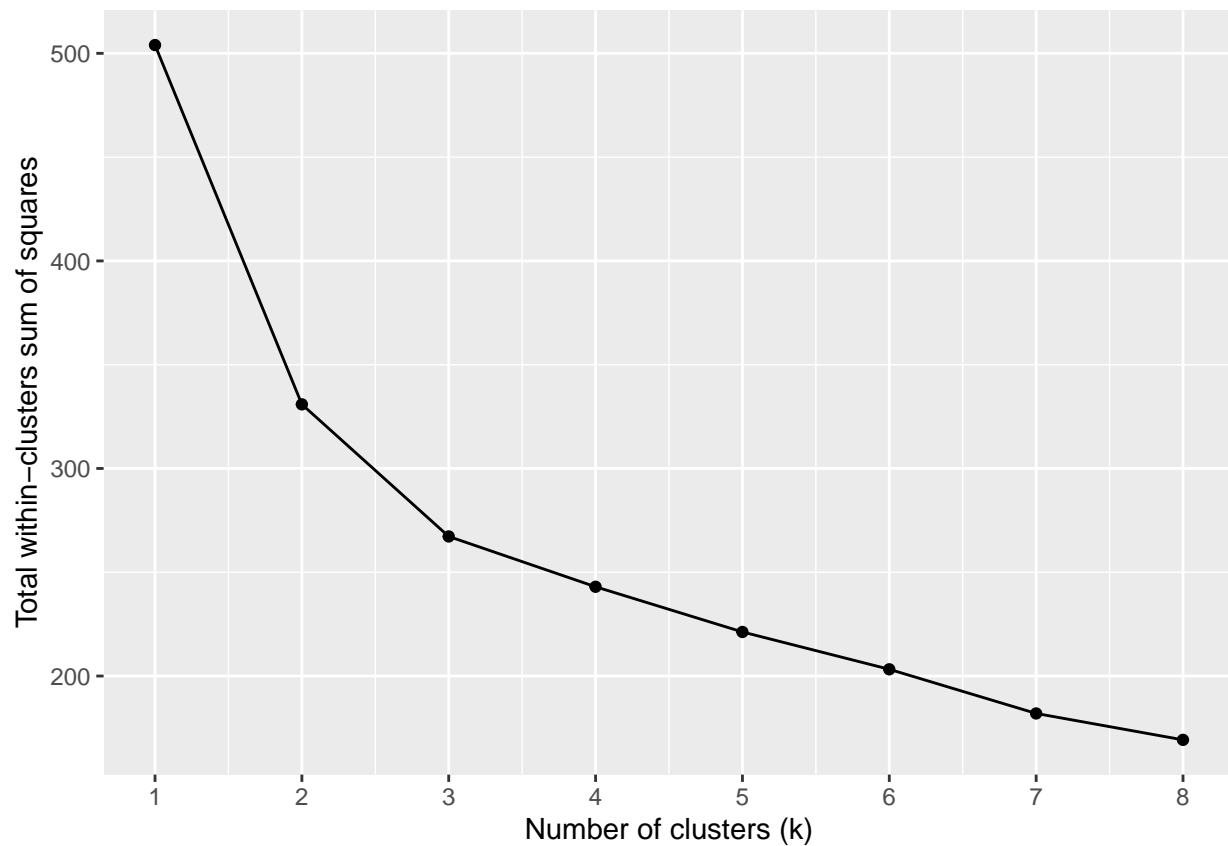
```
## [1] 267.2453
```

```
# Let's select K using elbow method
withclusterss <- function(K,x){
  kmeans(x, K)$tot.withinss
}
```

```
K <- 1:8
```

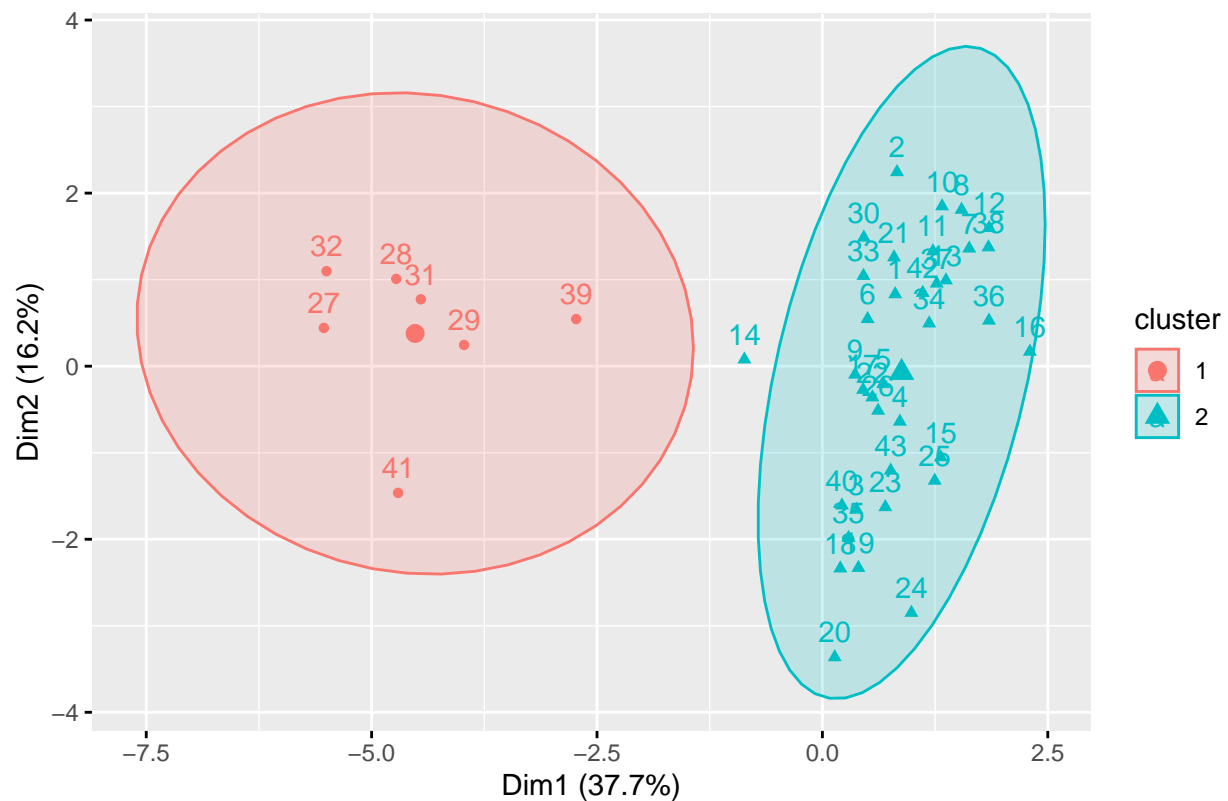
```
wcss <- lapply(as.list(K), function(k){
  withclusterss(k, x_scaled)
}) %>% unlist()

ggplot(tibble(K = K, wcss = wcss), aes(x = K, y = wcss)) +
  geom_point() +
  geom_line() +
  xlab("Number of clusters (k)") +
  ylab("Total within-clusters sum of squares") +
  scale_x_continuous(breaks=c(seq(1,K[length(K)])))
```



```
kmeans_coffee <- kmeans(x_scaled, 2)
fvPCA <- fviz_cluster(kmeans_coffee,
  x_scaled,
  ellipse.type = "norm",
  main = "Plot the results of k-means clustering after PCA")
fvPCA
```


Plot the results of k-means clustering after PCA



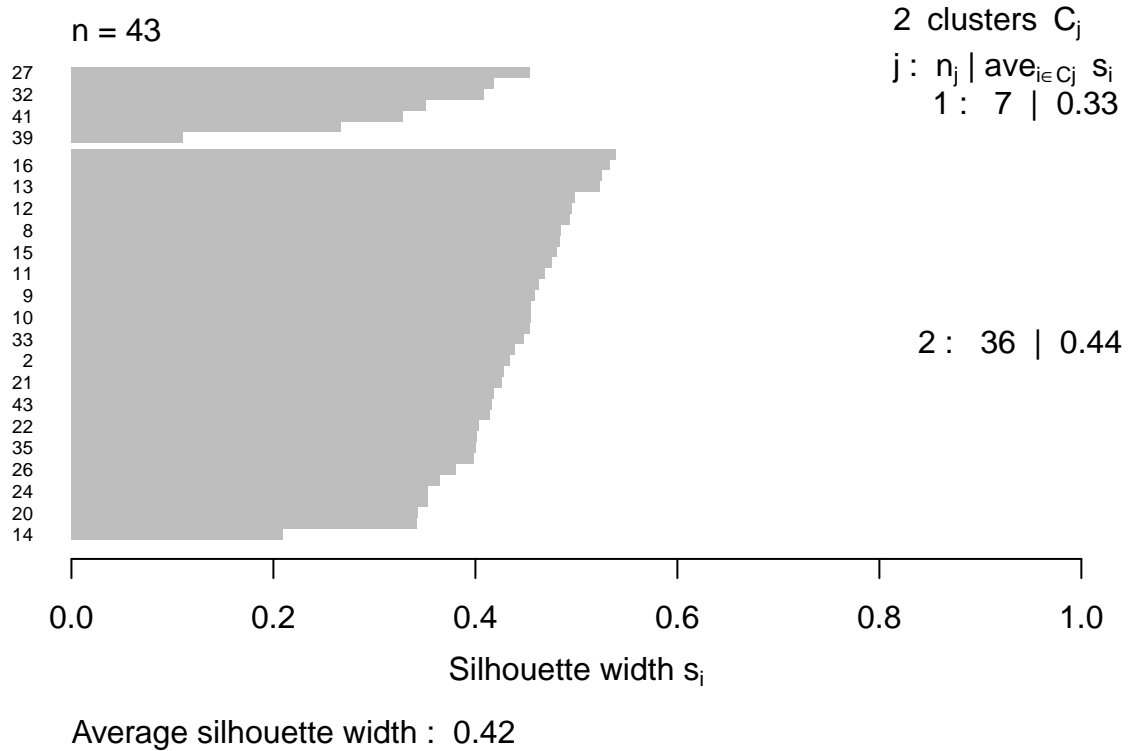
```
si <- silhouette(kmeans_coffee$cluster, dist(x_scaled))
head(si)
```

```
##      cluster neighbor sil_width
## [1,]      2        1 0.5252373
## [2,]      2        1 0.4346060
## [3,]      2        1 0.4143200
## [4,]      2        1 0.4932787
## [5,]      2        1 0.4632535
## [6,]      2        1 0.4832208
```

```
#average Silhouette width
mean(si[, 3])
```

```
## [1] 0.4186062
```

```
plot(si, nmax= 80, cex.names=0.6, main = "")
```

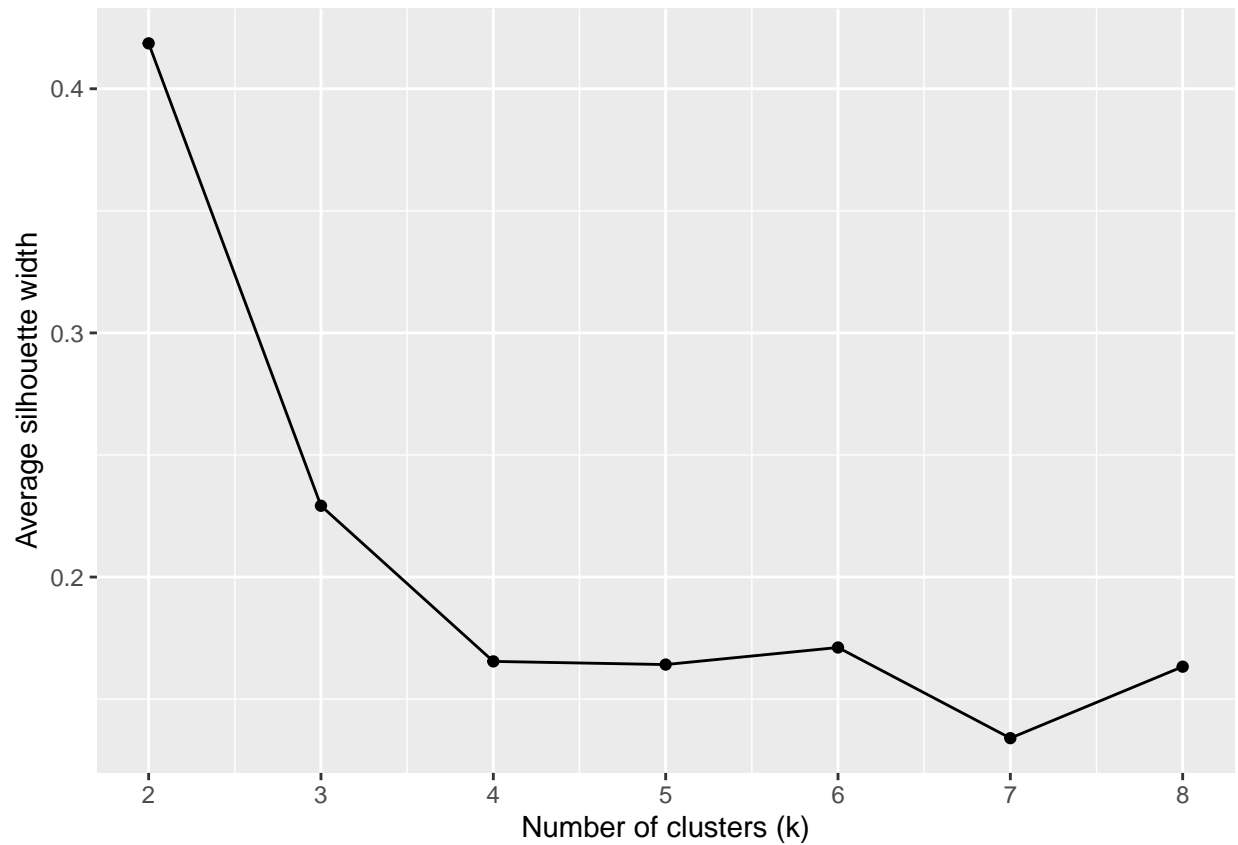


```
# Let's select K using average Silhouette width
avgSilhouette <- function(K,x) {
  km_cl <- kmeans(x, K)
  sil <- silhouette(km_cl$cluster, dist(x))
  return(mean(sil[, 3]))
}

K <- 2:8

avgSil <- numeric()
for(i in K){
  avgSil[(i-1)] <- avgSilhouette(i, x_scaled)
}

ggplot(tibble(K = K, avgSil = avgSil), aes(x = K, y = avgSil)) +
  geom_point() +
  geom_line() +
  xlab("Number of clusters (k)") +
  ylab("Average silhouette width") +
  scale_x_continuous(breaks=c(seq(1,K[length(K)])))
```

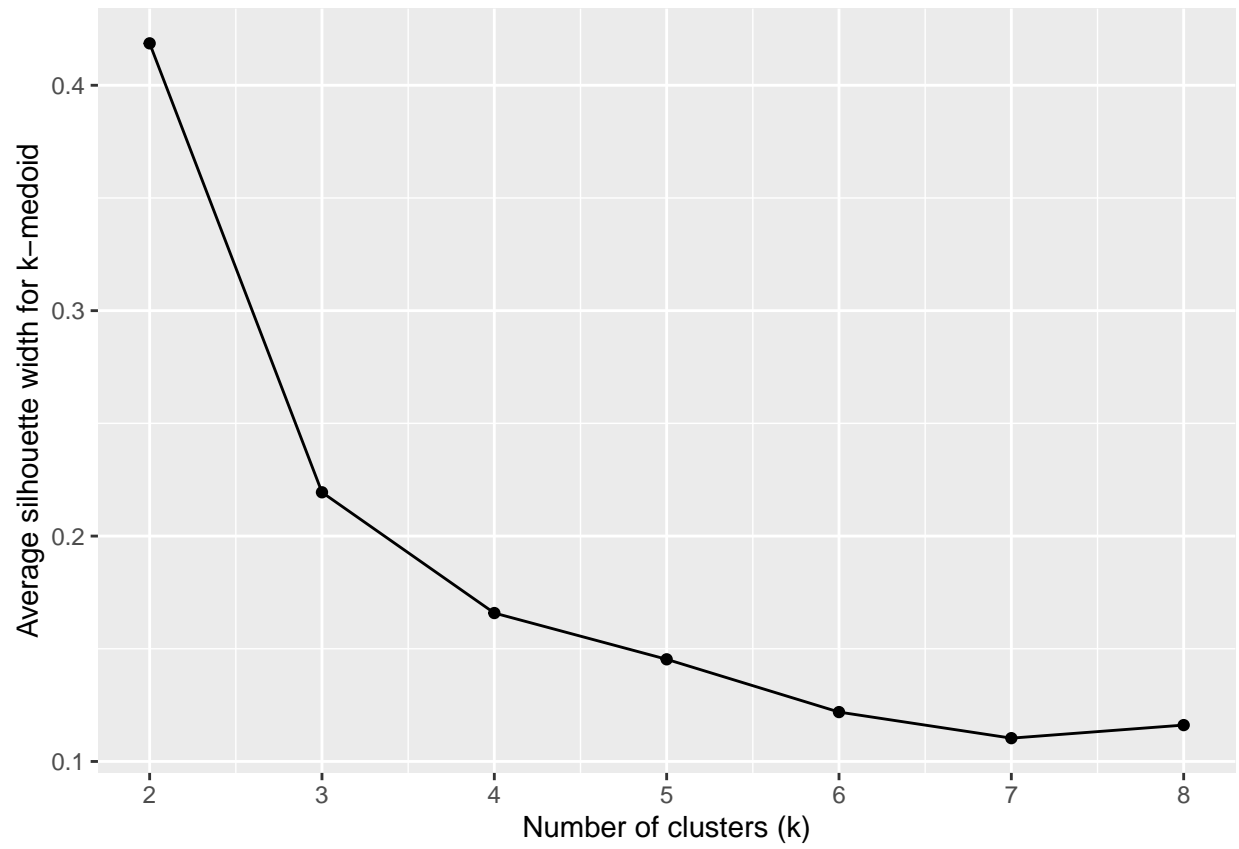


```
kmedoid_coffee <- pam(x_scaled, 2)
kmedoid_coffee$silinfo$avg.width
```

```
## [1] 0.4186062
```

```
avgSil <- lapply(as.list(2:8), function(k){
  kmedoid_coffee <- pam(x_scaled, k)
  kmedoid_coffee$silinfo$avg.width
}) %>% unlist()

ggplot(tibble(K = 2:8, avgSil = avgSil), aes(x = K, y = avgSil)) +
  geom_point() +
  geom_line() +
  xlab("Number of clusters (k)") +
  ylab("Average silhouette width for k-medoid") +
  scale_x_continuous(breaks=c(seq(1,K[length(K)])))
```

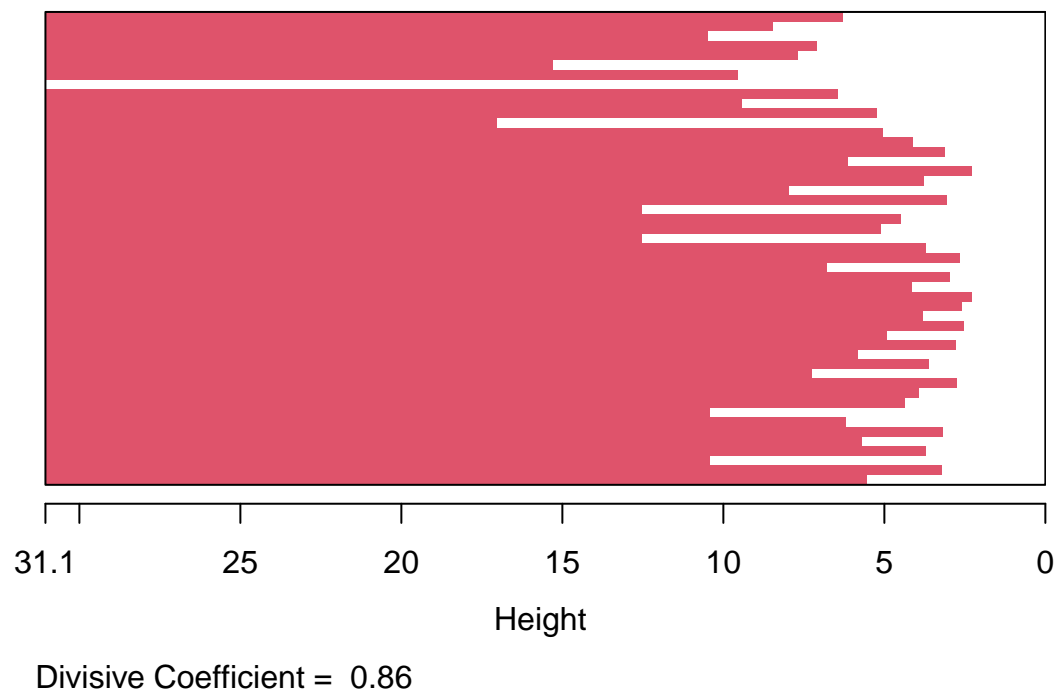


```
library(cluster)
library(factoextra)

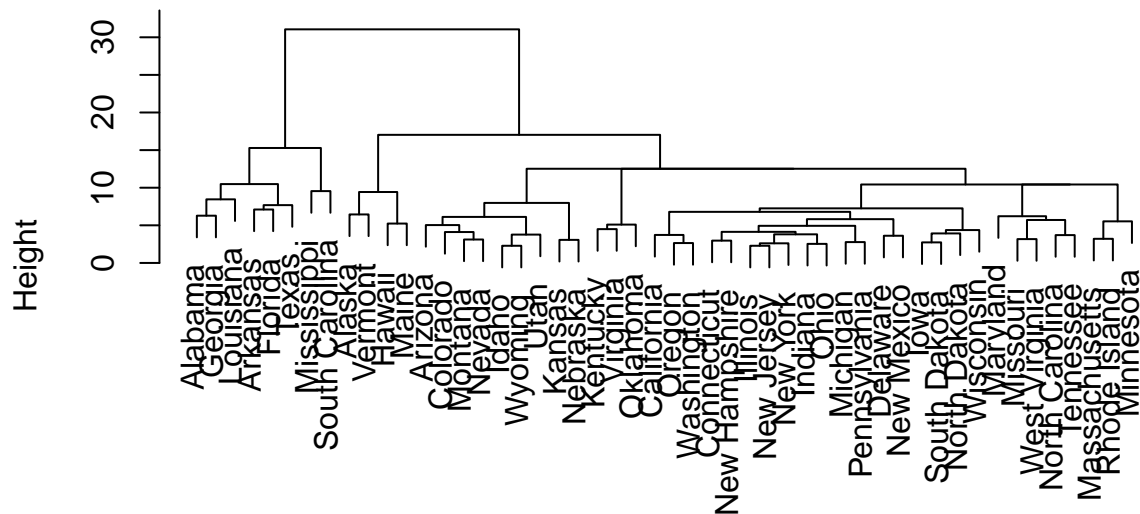
data(votes.repub)
divisive_votes <- diana(
  votes.repub,
  metric = "euclidean",
  stand = TRUE
)

plot(divisive_votes)
```

Banner of `diana(x = votes.repub, metric = "euclidean", stand`



Dendrogram of `diana(x = votes.repub, metric = "euclidean", stand = "T`



votes.repub
Divisive Coefficient = 0.86

```
cut_divisive_votes <- cutree(as.hclust(divisive_votes), k = 2)
table(cut_divisive_votes) # 8 and 42 group members
```

```
## cut_divisive_votes
## 1 2
## 8 42
```

```
rownames(votes.repub)[cut_divisive_votes == 1]
```

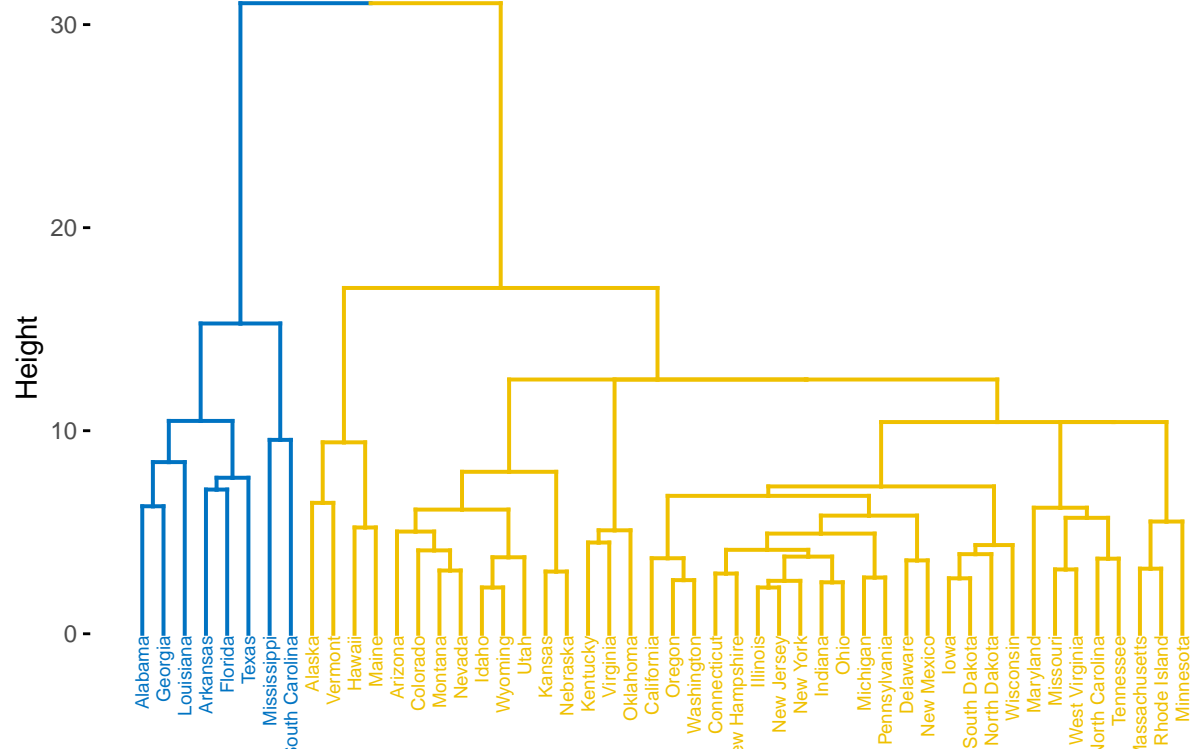
```
## [1] "Alabama"      "Arkansas"      "Florida"      "Georgia"
## [5] "Louisiana"    "Mississippi"   "South Carolina" "Texas"
```

```
# rownames(votes.repub)[cut_divisive_votes == 2]
```

```
#make a nice dendrogram
```

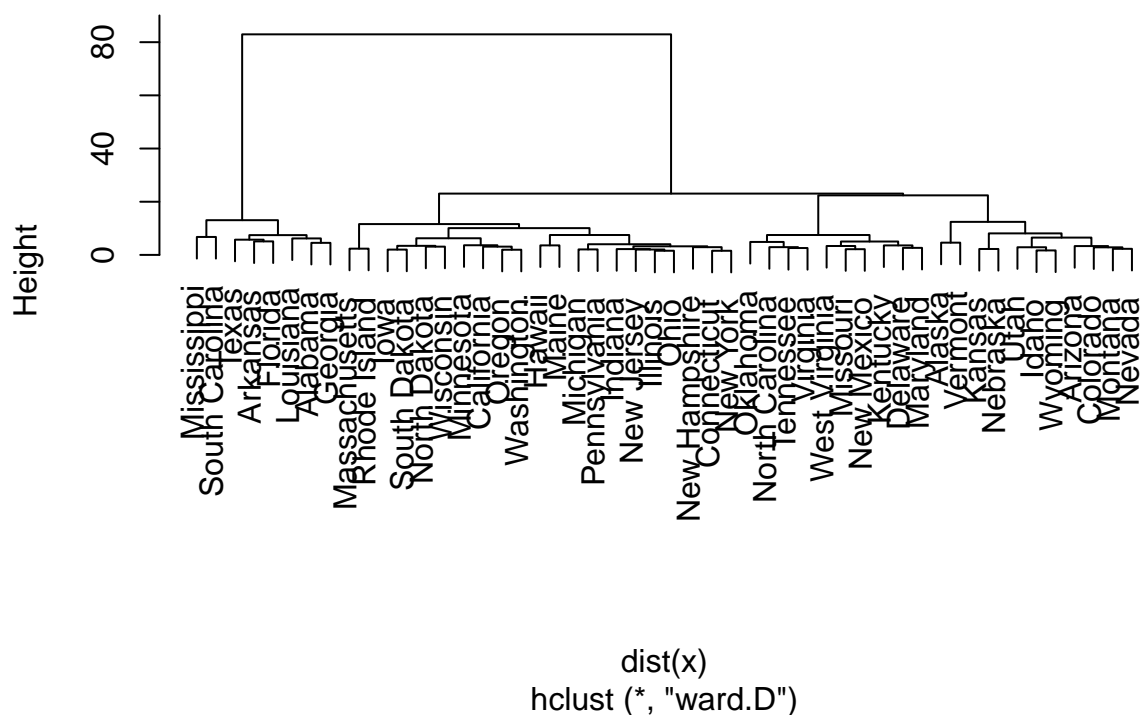
```
fviz_dend(
  divisive_votes,
  cex = 0.5,
  k = 2, # Cut in 2 groups
  palette = "jco", # Color palette
  main = "Dendrogram for votes data (divisive clustering)")
```

Dendrogram for votes data (divisive clustering)



```
x <- votes.repub %>%
  scale()
hc_vote <- hclust(dist(x), "ward.D")
plot(hc_vote)
```

Cluster Dendrogram



```
#make a nice dendrogram
fviz_dend(
  hc_vote,
  k = 2, # Cut in 2 groups
  cex = 0.5,
  color_labels_by_k = TRUE,
  rect = TRUE,
  main = "Dendrogram for votes data (agglomerative clustering)"
)
```


Dendrogram for votes data (agglomerative clustering)

