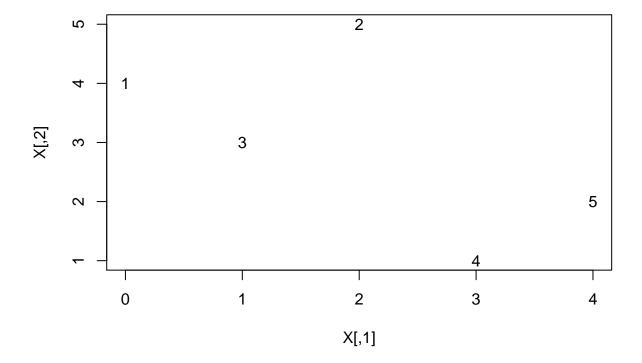
#### Dissimilarity

```
set.seed(1)
X <- cbind(c(0, 2, 1, 3, 4), c(4, 5, 3, 1, 2))
plot(X, pch = as.character(1:5))</pre>
```



```
d <- dist(X)
as.matrix(d)</pre>
```

```
## 1 2 3 4 5

## 1 0.00000 2.236068 1.414214 4.242641 4.472136

## 2 2.236068 0.00000 2.236068 4.123106 3.605551

## 3 1.414214 2.236068 0.00000 2.828427 3.162278

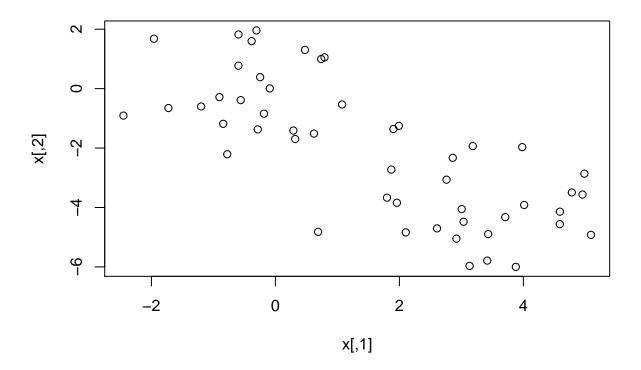
## 4 4.242641 4.123106 2.828427 0.000000 1.414214

## 5 4.472136 3.605551 3.162278 1.414214 0.000000
```

#### K-Mean

```
set.seed(2)
x <- matrix(rnorm(50 * 2), ncol = 2)
x[1:25, 1] <- x[1:25, 1] + 3</pre>
```

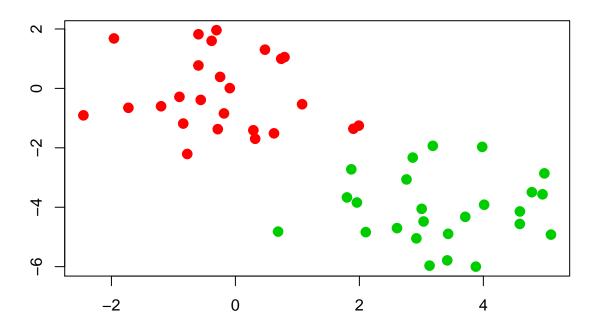
```
x[1:25, 2] \leftarrow x[1:25, 2] - 4
plot(x)
```



K <- 2

km\_out <- kmeans(x, K, nstart = 5)</pre>

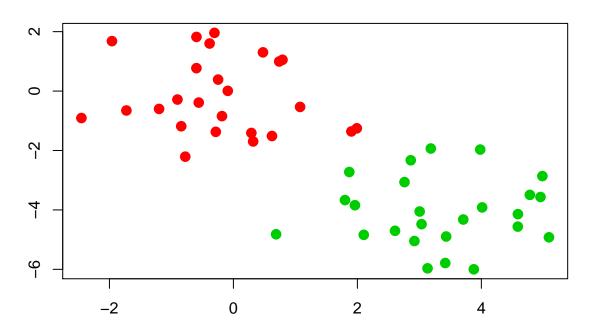
#### K-Means Clustering Results



```
km_out <- kmeans(x, K, nstart = 20)</pre>
km_out
## K-means clustering with 2 clusters of sizes 25, 25
##
## Cluster means:
          [,1]
## 1 -0.1956978 -0.1848774
## 2 3.3339737 -4.0761910
##
## Clustering vector:
## [36] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##
## Within cluster sum of squares by cluster:
## [1] 65.40068 63.20595
  (between_SS / total_SS = 72.8 %)
##
##
## Available components:
## [1] "cluster"
                   "centers"
                                "totss"
                                              "withinss"
## [5] "tot.withinss" "betweenss"
                                "size"
                                              "iter"
## [9] "ifault"
```

set.seed(4)

### **K-Means Clustering Results**



```
set.seed(3)
km_out <- kmeans(x, K, nstart = 1)
km_out$tot.withinss

## [1] 128.6066

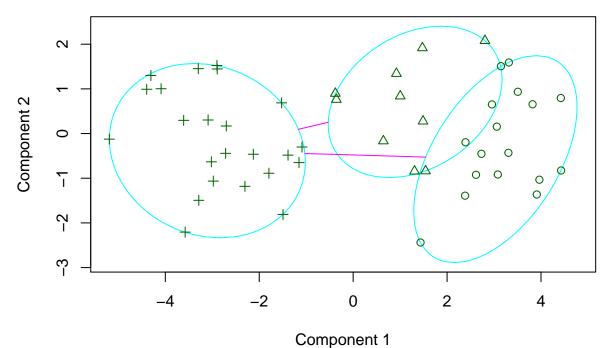
K <- 4
n <- nrow(x)
km_out <- kmeans(x, K, nstart = 20)
# CH index
(km_out$betweenss / (K - 1)) / (km_out$tot.withinss / (n - K))</pre>
```

#### K-Medoids

## [1] 88.77696

```
library(cluster)
pam.fit <- pam(x, 3)
clusplot(pam.fit)</pre>
```

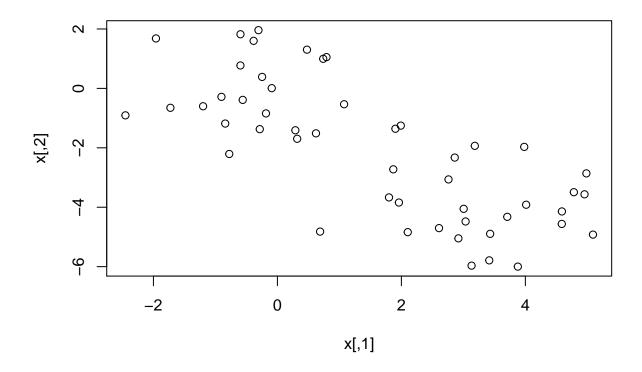
## clusplot(pam(x = x, k = 3))



These two components explain 100 % of the point variability.

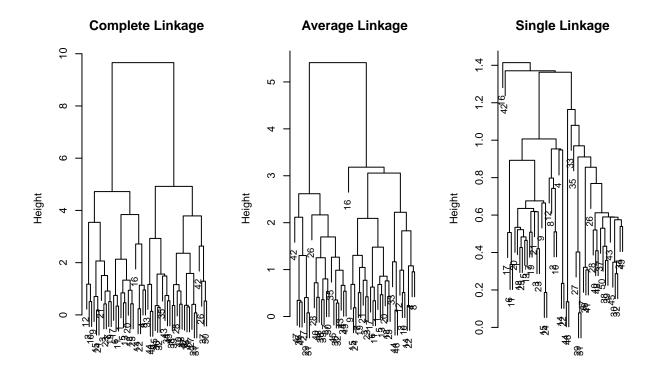
### Hierarchical clustering

```
set.seed(2)
x <- matrix(rnorm(50 * 2), ncol = 2)
x[1:25, 1] <- x[1:25, 1] + 3
x[1:25, 2] <- x[1:25, 2] - 4
plot(x)</pre>
```

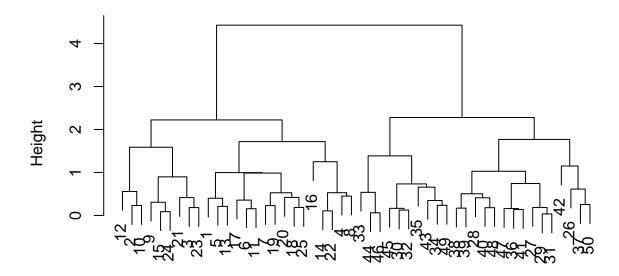


```
hc_complete <- hclust(dist(x), method = "complete")
hc_average <- hclust(dist(x), method = "average")
hc_single <- hclust(dist(x), method = "single")</pre>
```

```
par(mfrow = c(1, 3))
plot(hc_complete, main = "Complete Linkage", xlab = "", sub = "", cex = .9)
plot(hc_average, main = "Average Linkage", xlab = "", sub = "", cex = .9)
plot(hc_single, main = "Single Linkage", xlab = "", sub = "", cex = .9)
```



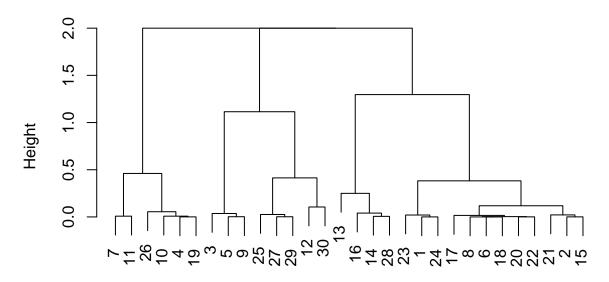
## **Hierarchical Clustering with Scaled Features**



dist(xsc) hclust (\*, "complete")

```
x <- matrix(rnorm(30 * 3), ncol = 3)
dd <- as.dist(1 - cor(t(x)))
plot(hclust(dd, method = "complete"), main = "Complete Linkage with Correlation-Based Distance", xlab =</pre>
```

#### **Complete Linkage with Correlation-Based Distance**



#### A Text mining example

```
library(stringr)
wiki <- "http://en.wikipedia.org/wiki/"
titles <- c(
    "Integral", "Riemann_integral", "Riemann-Stieltjes_integral", "Derivative",
    "Limit_of_a_sequence", "Edvard_Munch", "Vincent_van_Gogh", "Jan_Matejko",
    "Lev_Tolstoj", "Franz_Kafka", "J._R._R._Tolkien"
)
articles <- character(length(titles))

for (i in 1:length(titles)) {
    articles[i] <- str_flatten(readLines(pasteO(wiki, titles[i])), col = " ")
}</pre>
```

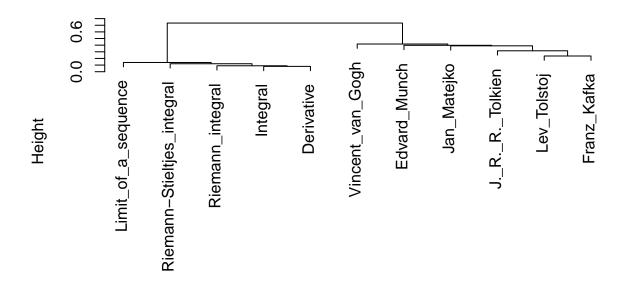
```
library(tm)
```

## Loading required package: NLP

```
docs <- Corpus(VectorSource(articles)) %>%
   tm_map(content_transformer(function(z) str_replace(z, "<.+?>", " "))) %>%
   tm_map(content_transformer(function(x) str_replace(x, fixed("\t"), " "))) %>%
```

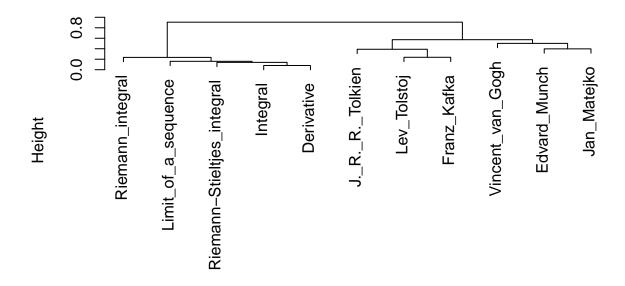
```
tm_map(PlainTextDocument) %>%
   tm_map(removePunctuation) %>%
   tm_map(stripWhitespace) %>%
    tm_map(content_transformer(tolower)) %>%
    tm_map(removeWords, stopwords("english"))
## Warning in tm_map.SimpleCorpus(., content_transformer(function(z)
## str_replace(z, : transformation drops documents
## Warning in tm_map.SimpleCorpus(., content_transformer(function(x)
## str_replace(x, : transformation drops documents
## Warning in tm_map.SimpleCorpus(., PlainTextDocument): transformation drops
## documents
## Warning in tm_map.SimpleCorpus(., content_transformer(tolower)):
## transformation drops documents
## Warning in tm_map.SimpleCorpus(., removeWords, stopwords("english")):
## transformation drops documents
docsTDM <- TermDocumentMatrix(docs)</pre>
t(as.matrix(docsTDM))[, sample(10000, 3)]
##
       Terms
## Docs classtoclevel3 tdtr stylepadding03em
##
                     2
##
     2
                     0
                          0
                                            1
##
    3
                     0
                          0
                                            0
##
     4
                     0
                          0
                                            1
##
                     0
                          5
     5
                                            0
##
     6
                     0
                          0
                                            0
##
    7
                    13
                         0
                                            0
##
                     0
                        26
                                            0
    8
##
     9
                     0
                          0
                                            1
##
     10
                     3
                         25
                                            0
##
                    27
     11
library(proxy)
##
## Attaching package: 'proxy'
## The following objects are masked from 'package:stats':
##
##
       as.dist, dist
## The following object is masked from 'package:base':
##
##
       as.matrix
```

```
docsdissim <- dist(t(as.matrix(docsTDM)), method = "cosine")
h <- hclust(docsdissim, method = "single")
plot(h, labels = titles)</pre>
```



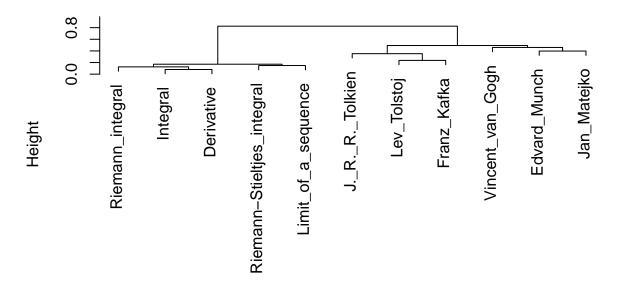
docsdissim hclust (\*, "single")

```
h <- hclust(docsdissim, method = "complete")
plot(h, labels = titles)</pre>
```



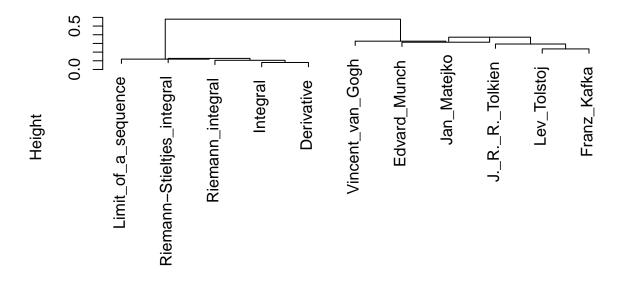
docsdissim hclust (\*, "complete")

```
h <- hclust(docsdissim, method = "average")
plot(h, labels = titles)</pre>
```



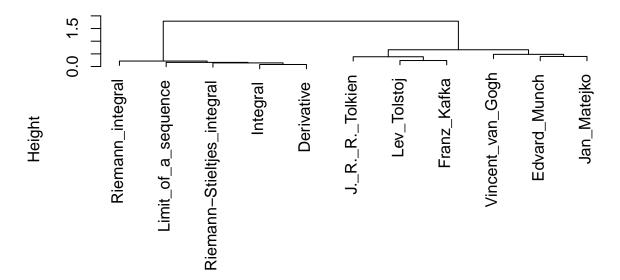
docsdissim hclust (\*, "average")

```
h <- hclust(docsdissim, method = "centroid")
plot(h, labels = titles)</pre>
```



docsdissim hclust (\*, "centroid")

```
h <- hclust(docsdissim, method = "ward.D2")
plot(h, labels = titles)</pre>
```



docsdissim hclust (\*, "ward.D2")