Revision 7

Example PCA

Question 5.

```r
# We create the points in R
x1 <- c(1, 7)
x2 <- c(4, 2)
x3 <- c(3, 8.5)
x4 <- c(6.6, 9)
x5 <- c(1, 9.5)
x6 <- c(4, 7)

d <- rbind(x1, x2, x3, x4, x5, x6) # a, b and c are combined per row
colnames(d) <- c("x", "y") # rename columns

d # display the points
```

```
##      x   y
## x1 1.0 7.0
## x2 4.0 2.0
## x3 3.0 8.5
## x4 6.6 9.0
## x5 1.0 9.5
## x6 4.0 7.0
```

```r
# The distance is found using the dist() function:
d.dist <- dist(d, method = "euclidean")
d.dist # display the distance matrix
```

```
##          x1       x2       x3       x4       x5
## x2 5.830952
## x3 2.500000 6.576473
## x4 5.946427 7.467262 3.634556
## x5 2.500000 8.077747 2.236068 5.622277
## x6 3.000000 5.000000 1.802776 3.280244 3.905125
```
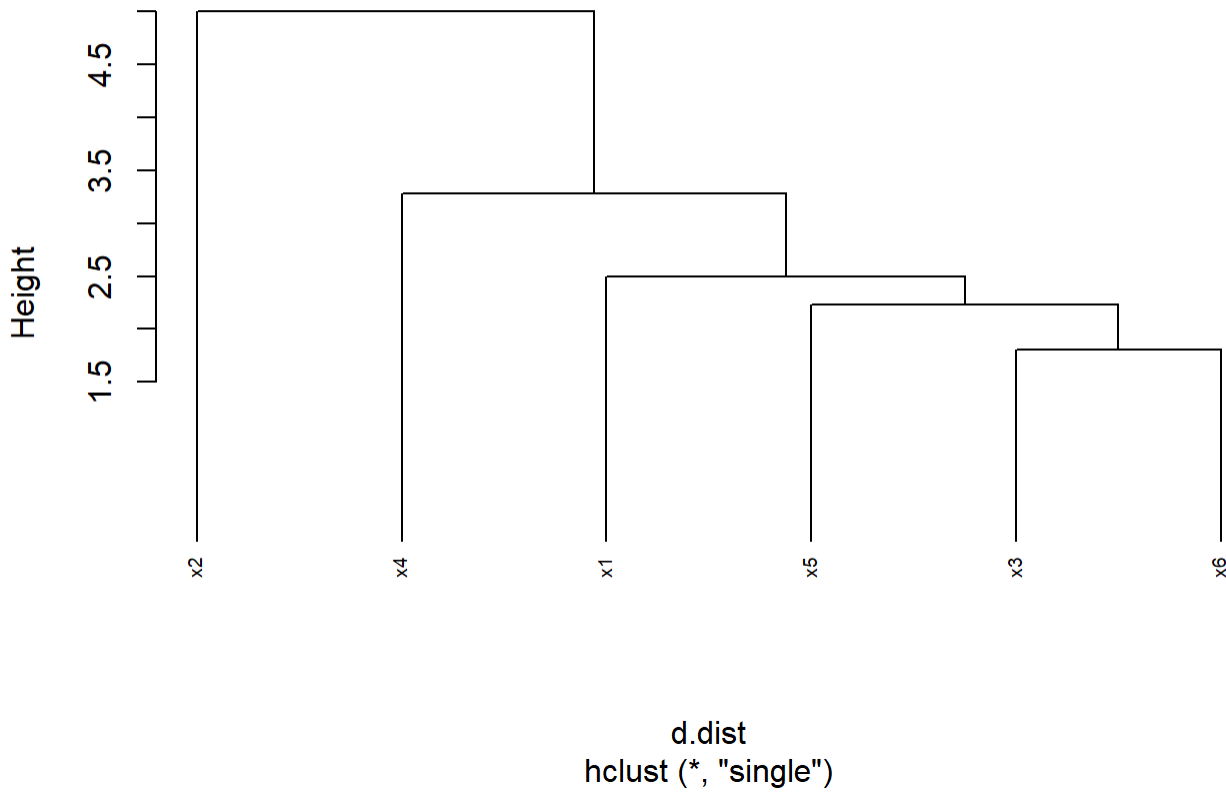
```r
# Agglomerative Hierarchical Clustering for single linkage

ahc.s <- hclust(d.dist, method="single")
ahc.s
```

```
##
## Call:
## hclust(d = d.dist, method = "single")
##
## Cluster method   : single
## Distance         : euclidean
## Number of objects: 6
```

```r
# Plotting a dendrogram for single linkage
plot(ahc.s, hang = -1, cex = 0.6)
```


Cluster Dendrogram

d.dist
hclust (*, "single")

```r
# Agglomerative Hierarchical Clustering for single linkage

ahc.c <- hclust(d.dist, method="complete")
ahc.c
```

```
##
## Call:
## hclust(d = d.dist, method = "complete")
##
## Cluster method   : complete
## Distance         : euclidean
## Number of objects: 6
```

```r
# Plotting a dendrogram for single linkage
plot(ahc.c, hang = -1, cex = 0.6)
```


Cluster Dendrogram

d.dist
hclust (*, "complete")