Class 8 Mini-Project

Mari Williams (A15858833)

Table of contents

Data prep

```r
fna.data <- "WisconsinCancer.csv"
wisc.df <- read.csv(fna.data, row.names=1)
head(wisc.df)
```

```
         diagnosis radius_mean texture_mean perimeter_mean area_mean
842302           M       17.99        10.38         122.80    1001.0
842517           M       20.57        17.77         132.90    1326.0
84300903         M       19.69        21.25         130.00    1203.0
84348301         M       11.42        20.38          77.58     386.1
84358402         M       20.29        14.34         135.10    1297.0
843786           M       12.45        15.70          82.57     477.1
         smoothness_mean compactness_mean concavity_mean concave.points_mean
842302           0.11840          0.27760         0.3001             0.14710
842517           0.08474          0.07864         0.0869             0.07017
84300903         0.10960          0.15990         0.1974             0.12790
84348301         0.14250          0.28390         0.2414             0.10520
84358402         0.10030          0.13280         0.1980             0.10430
```

```
843786           0.12780           0.17000         0.1578             0.08089
         symmetry_mean fractal_dimension_mean radius_se texture_se perimeter_se
842302          0.2419                0.07871    1.0950     0.9053        8.589
842517          0.1812                0.05667    0.5435     0.7339        3.398
84300903        0.2069                0.05999    0.7456     0.7869        4.585
84348301        0.2597                0.09744    0.4956     1.1560        3.445
84358402        0.1809                0.05883    0.7572     0.7813        5.438
843786          0.2087                0.07613    0.3345     0.8902        2.217
         area_se smoothness_se compactness_se concavity_se concave.points_se
842302    153.40      0.006399        0.04904      0.05373           0.01587
842517     74.08      0.005225        0.01308      0.01860           0.01340
84300903   94.03      0.006150        0.04006      0.03832           0.02058
84348301   27.23      0.009110        0.07458      0.05661           0.01867
84358402   94.44      0.011490        0.02461      0.05688           0.01885
843786     27.19      0.007510        0.03345      0.03672           0.01137
         symmetry_se fractal_dimension_se radius_worst texture_worst
842302       0.03003             0.006193        25.38         17.33
842517       0.01389             0.003532        24.99         23.41
84300903     0.02250             0.004571        23.57         25.53
84348301     0.05963             0.009208        14.91         26.50
84358402     0.01756             0.005115        22.54         16.67
843786       0.02165             0.005082        15.47         23.75
         perimeter_worst area_worst smoothness_worst compactness_worst
842302            184.60     2019.0           0.1622            0.6656
842517            158.80     1956.0           0.1238            0.1866
84300903          152.50     1709.0           0.1444            0.4245
84348301           98.87      567.7           0.2098            0.8663
84358402          152.20     1575.0           0.1374            0.2050
843786            103.40      741.6           0.1791            0.5249
         concavity_worst concave.points_worst symmetry_worst
842302            0.7119               0.2654         0.4601
842517            0.2416               0.1860         0.2750
84300903          0.4504               0.2430         0.3613
84348301          0.6869               0.2575         0.6638
84358402          0.4000               0.1625         0.2364
843786            0.5355               0.1741         0.3985
         fractal_dimension_worst
842302                   0.11890
842517                   0.08902
84300903                 0.08758
84348301                 0.17300
84358402                 0.07678
843786                   0.12440
```

```r
wisc.data <- wisc.df[,-1]
diagnosis <- wisc.df$diagnosis
diagnosis <-as.factor(diagnosis)
```

Q1. How many observations are in this dataset?

```r
dim(wisc.data)
```

```
[1] 569  30
```

569 observations

Q2. How many of the observations have a malignant diagnosis?

```r
sum(diagnosis=="M")
```

```
[1] 212
```

212 observations are diagnosed as malignant

Q3. How many variables/features in the data are suffixed with _mean

```r
length(grep("_mean", colnames(wisc.data)))
```

```
[1] 10
```

10 variables are suffixed with _mean

Principal Component Analysis

```r
colMeans(wisc.data)
```

```
            radius_mean            texture_mean          perimeter_mean
           1.412729e+01            1.928965e+01            9.196903e+01
              area_mean         smoothness_mean        compactness_mean
           6.548891e+02            9.636028e-02            1.043410e-01
         concavity_mean     concave.points_mean           symmetry_mean
           8.879932e-02            4.891915e-02            1.811619e-01
```

```
 fractal_dimension_mean               radius_se              texture_se
           6.279761e-02            4.051721e-01            1.216853e+00
           perimeter_se                 area_se           smoothness_se
           2.866059e+00            4.033708e+01            7.040979e-03
         compactness_se            concavity_se       concave.points_se
           2.547814e-02            3.189372e-02            1.179614e-02
            symmetry_se    fractal_dimension_se            radius_worst
           2.054230e-02            3.794904e-03            1.626919e+01
          texture_worst         perimeter_worst              area_worst
           2.567722e+01            1.072612e+02            8.805831e+02
       smoothness_worst       compactness_worst         concavity_worst
           1.323686e-01            2.542650e-01            2.721885e-01
   concave.points_worst          symmetry_worst fractal_dimension_worst
           1.146062e-01            2.900756e-01            8.394582e-02
```

```
apply(wisc.data,2,sd)
```

```
            radius_mean            texture_mean          perimeter_mean
           3.524049e+00            4.301036e+00            2.429898e+01
              area_mean         smoothness_mean        compactness_mean
           3.519141e+02            1.406413e-02            5.281276e-02
         concavity_mean     concave.points_mean           symmetry_mean
           7.971981e-02            3.880284e-02            2.741428e-02
 fractal_dimension_mean               radius_se              texture_se
           7.060363e-03            2.773127e-01            5.516484e-01
           perimeter_se                 area_se           smoothness_se
           2.021855e+00            4.549101e+01            3.002518e-03
         compactness_se            concavity_se       concave.points_se
           1.790818e-02            3.018606e-02            6.170285e-03
            symmetry_se    fractal_dimension_se            radius_worst
           8.266372e-03            2.646071e-03            4.833242e+00
          texture_worst         perimeter_worst              area_worst
           6.146258e+00            3.360254e+01            5.693570e+02
       smoothness_worst       compactness_worst         concavity_worst
           2.283243e-02            1.573365e-01            2.086243e-01
   concave.points_worst          symmetry_worst fractal_dimension_worst
           6.573234e-02            6.186747e-02            1.806127e-02
```

```
wisc.pr <- prcomp(wisc.data, center = TRUE, scale. = TRUE)
summary(wisc.pr)
```

```
Importance of components:
```

```
                          PC1    PC2     PC3     PC4     PC5     PC6     PC7
Standard deviation     3.6444 2.3857 1.67867 1.40735 1.28403 1.09880 0.82172
Proportion of Variance 0.4427 0.1897 0.09393 0.06602 0.05496 0.04025 0.02251
Cumulative Proportion  0.4427 0.6324 0.72636 0.79239 0.84734 0.88759 0.91010
                           PC8    PC9    PC10   PC11    PC12    PC13    PC14
Standard deviation     0.69037 0.6457 0.59219 0.5421 0.51104 0.49128 0.39624
Proportion of Variance 0.01589 0.0139 0.01169 0.0098 0.00871 0.00805 0.00523
Cumulative Proportion  0.92598 0.9399 0.95157 0.9614 0.97007 0.97812 0.98335
                          PC15    PC16    PC17    PC18    PC19    PC20   PC21
Standard deviation     0.30681 0.28260 0.24372 0.22939 0.22244 0.17652 0.1731
Proportion of Variance 0.00314 0.00266 0.00198 0.00175 0.00165 0.00104 0.0010
Cumulative Proportion  0.98649 0.98915 0.99113 0.99288 0.99453 0.99557 0.9966
                          PC22    PC23   PC24    PC25    PC26    PC27    PC28
Standard deviation     0.16565 0.15602 0.1344 0.12442 0.09043 0.08307 0.03987
Proportion of Variance 0.00091 0.00081 0.0006 0.00052 0.00027 0.00023 0.00005
Cumulative Proportion  0.99749 0.99830 0.9989 0.99942 0.99969 0.99992 0.99997
                          PC29    PC30
Standard deviation     0.02736 0.01153
Proportion of Variance 0.00002 0.00000
Cumulative Proportion  1.00000 1.00000
```

Q4. From your results, what proportion of the original variance is captured by the first principal components (PC1)?

44% of the variance is explained by PC1

Q5. How many principal components (PCs) are required to describe at least 70% of the original variance in the data?

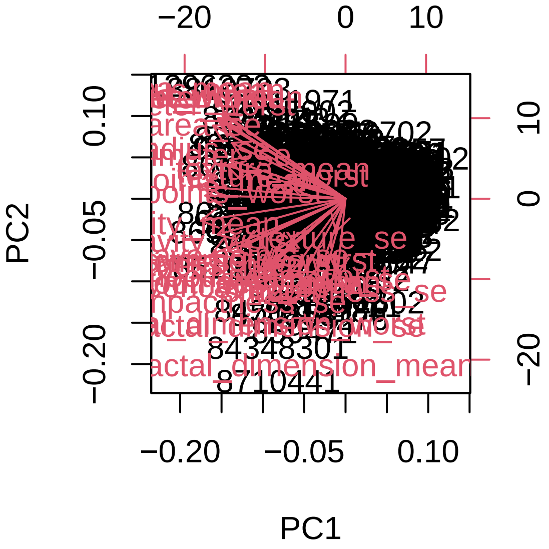
3 PCs

Q6. How many principal components (PCs) are required to describe at least 90% of the original variance in the data?

7 PCs

Interpreting PCA results

```r
biplot(wisc.pr)
```

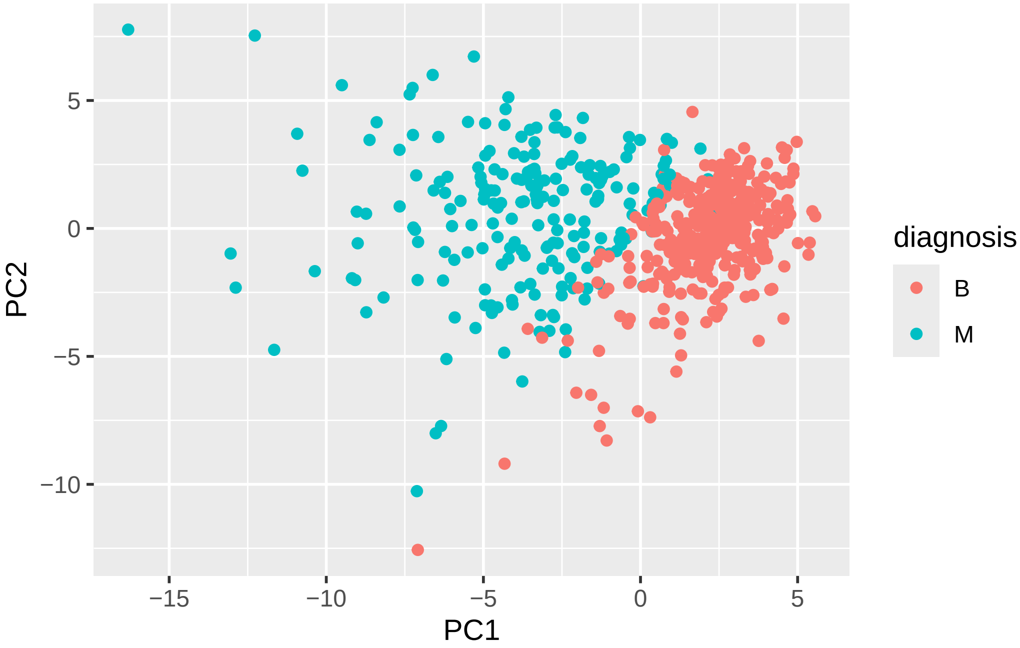


Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why? Text and numbers are indecipherable

```
library(ggplot2)
```

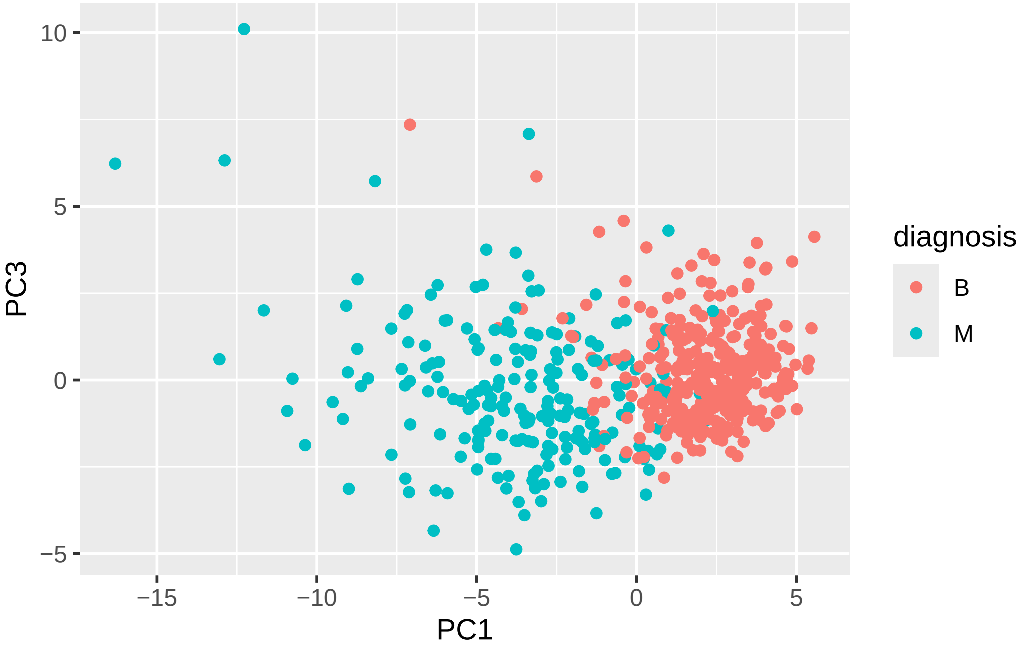
```
Warning: package 'ggplot2' was built under R version 4.3.3
```

```
ggplot(wisc.pr$x) + aes(PC1, PC2, col = diagnosis, xlab = "PC1", ylab= "PC2") + geom_point()
```



Q8. Generate a similar plot for principal components 1 and 3. What do you notice about these plots?

```
ggplot(wisc.pr$x) + aes(PC1, PC3, col = diagnosis, xlab = "PC1", ylab= "PC3") + geom_point()
```



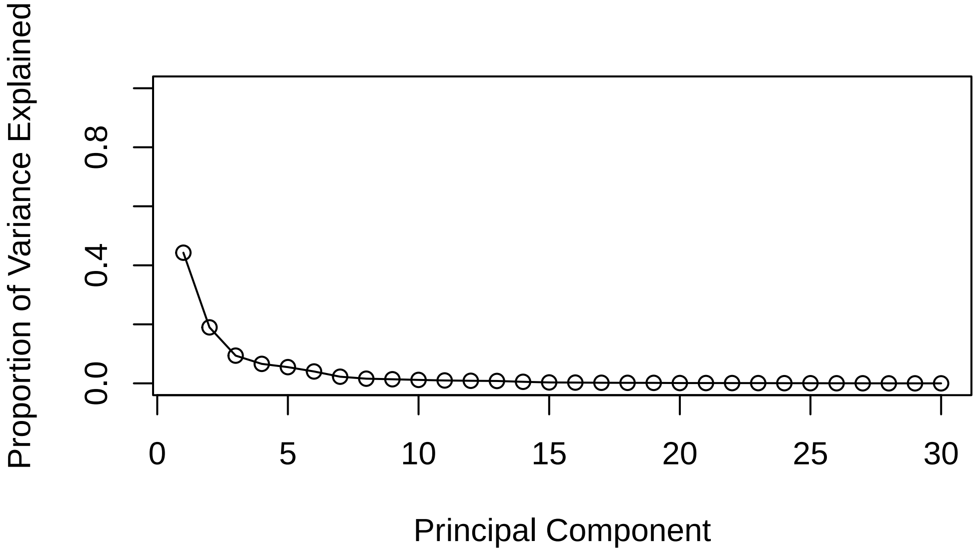
Both plots have pretty good separation between diagnoses but the first one is a little cleaner. Similar x distributions, the y distributions are shifted.

Variance explained

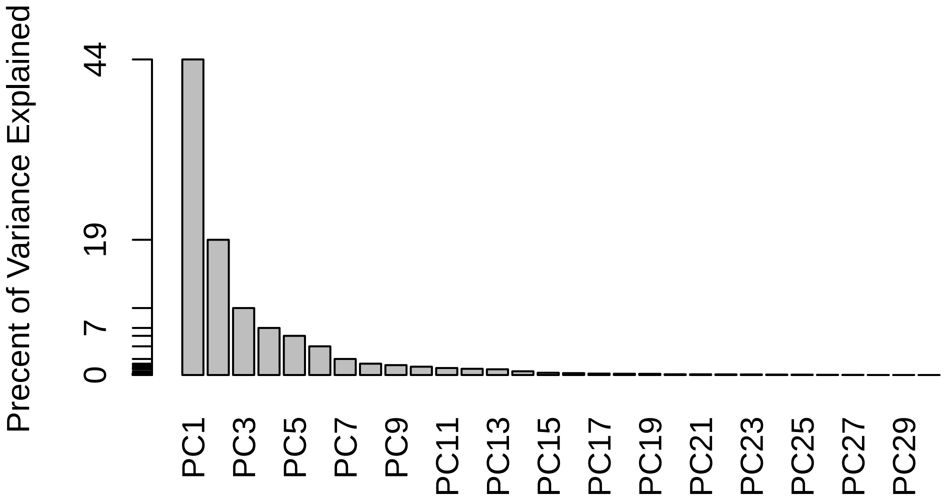
```
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
pve <- pr.var / sum(pr.var)
plot(pve, xlab = "Principal Component",
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```



```
barplot(pve, ylab = "Precent of Variance Explained",
     names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```



Communicating PCA Results

Q9. For the first principal component, what is the component of the loading vector (i.e. wisc.pr$rotation[,1]) for the feature concave.points_mean? This tells us how much this original feature contributes to the first PC.

```
lv <- wisc.pr$rotation[,1]
lv["concave.points_mean"]
```

```
concave.points_mean
         -0.2608538
```

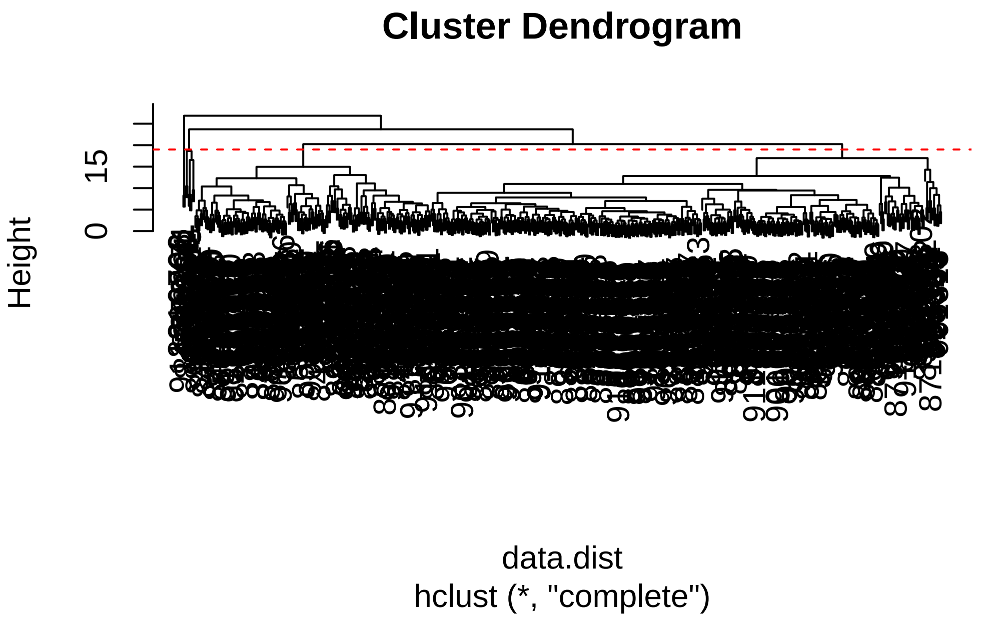
-0.261

Hierarchical clustering

```
data.scaled <- scale(wisc.data)
data.dist <- dist(data.scaled)
wisc.hclust <- hclust(data.dist, method= "complete")
```

Q10. Using the plot() and abline() functions, what is the height at which the clustering model has 4 clusters?

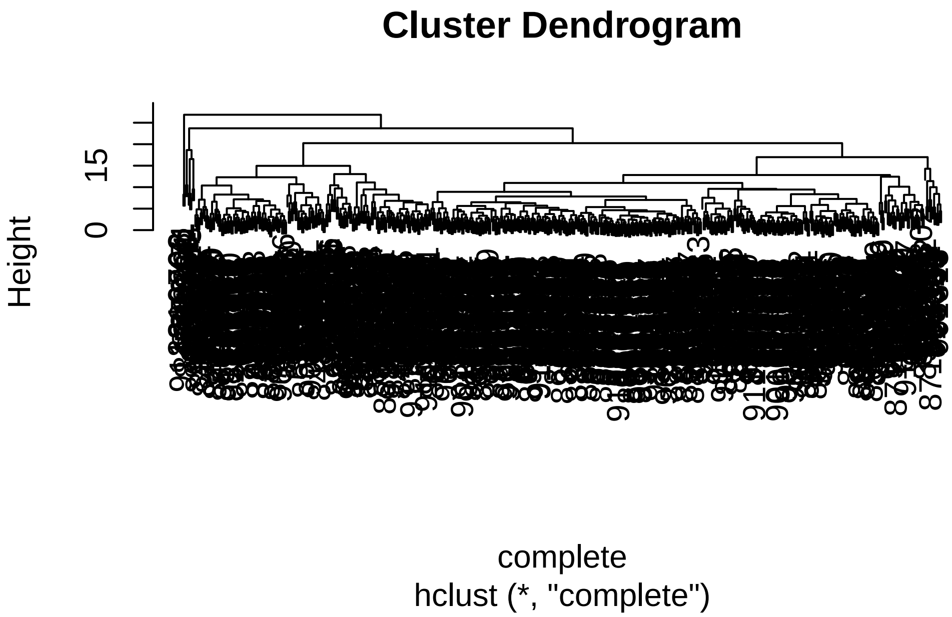
```
plot(wisc.hclust)
abline(a=19, b=0, col="red", lty=2)
```

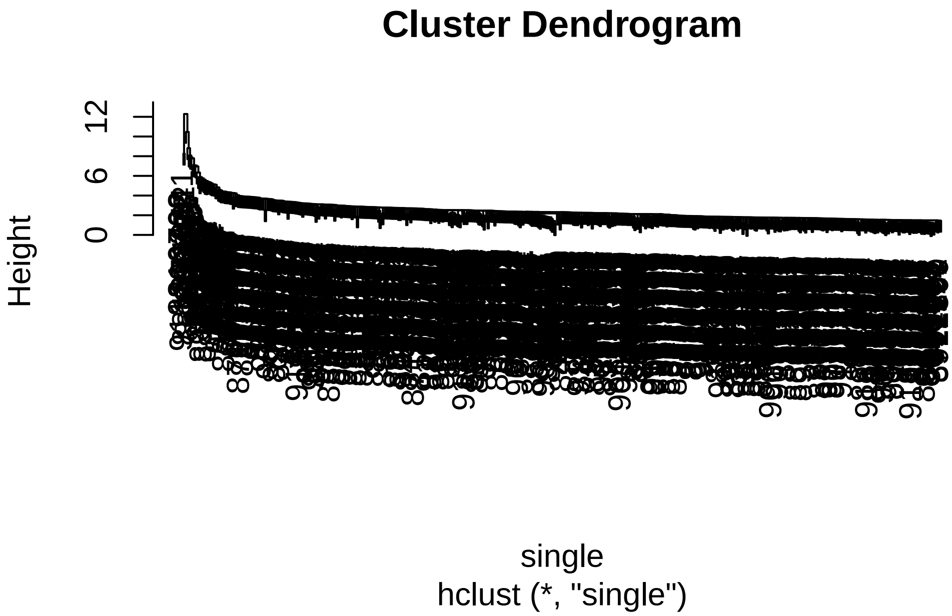


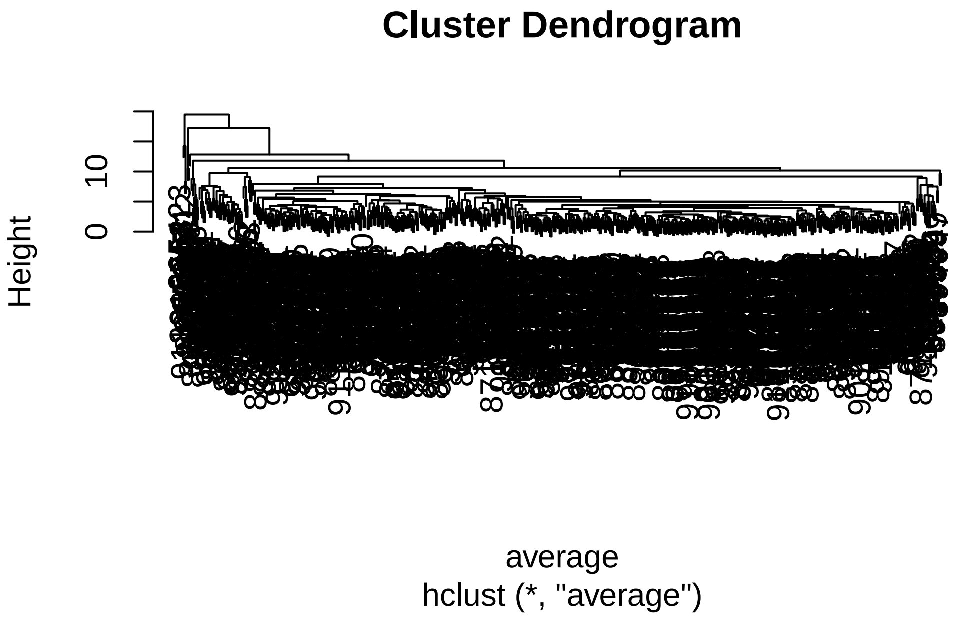
height=19

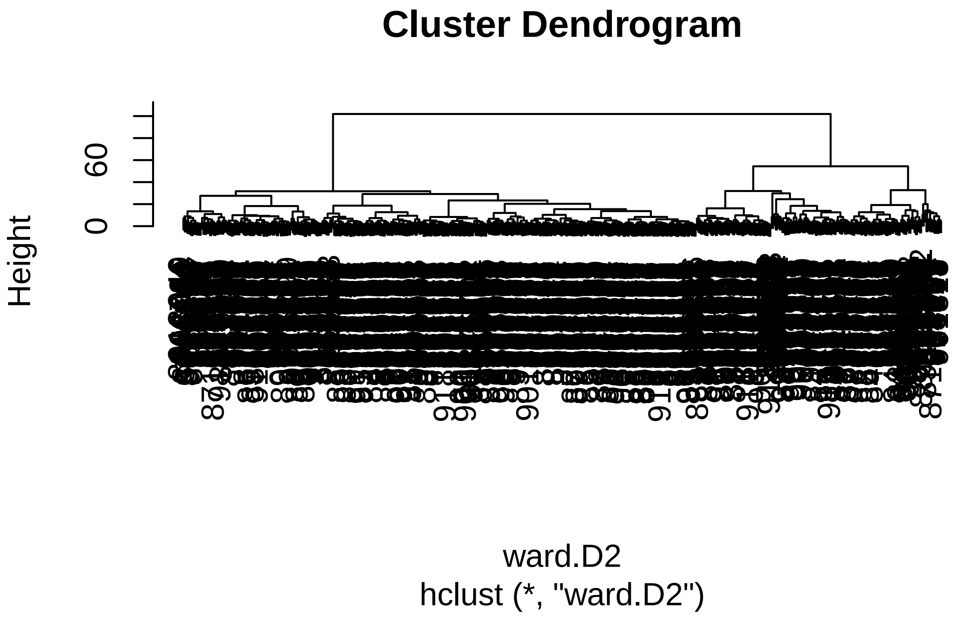
Q12. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning.

```
clust <- function(data, way) {
  wisc.hclust <- hclust(data, method= way)
  plot(wisc.hclust, xlab=way)

}
sapply(c("complete", "single", "average", "ward.D2"), function(m) clust(data.dist, m))
```


Cluster Dendrogram
Height
0
15
complete
hclust (*, "complete")


Cluster Dendrogram
Height
0
6
12
single
hclust (*, "single")





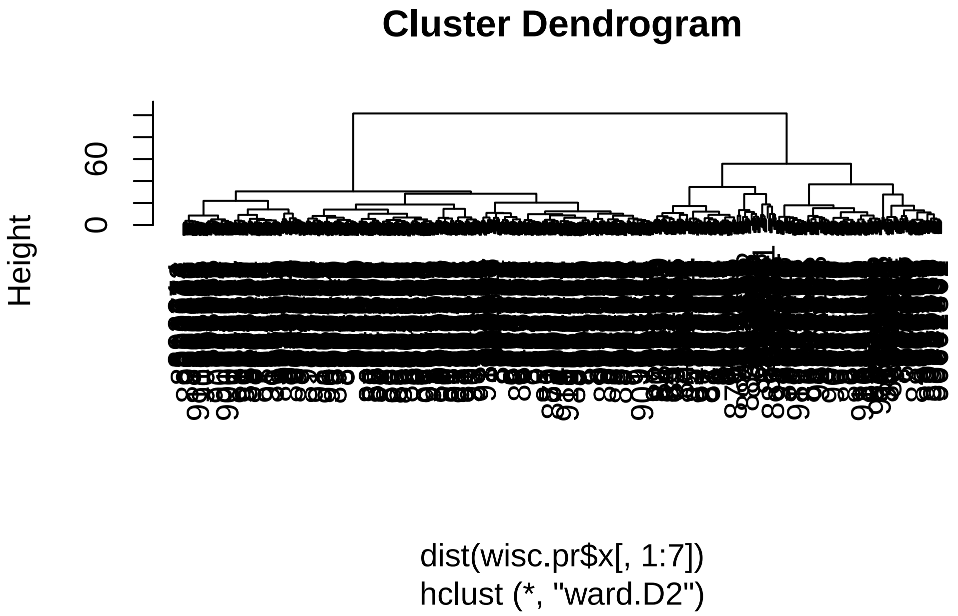
```
$complete
NULL
```

```
$single
NULL

$average
NULL

$ward.D2
NULL
```

I like ward.D2 as well, because of the clean separation of the clusters

Combining methods

```
d<- dist(wisc.pr$x[,1:3])
wisc.pr.hclust <- hclust(dist(wisc.pr$x[,1:7]), method= "ward.D2")
plot(wisc.pr.hclust)
```



```
wisc.pr.hclust <- hclust(dist(wisc.pr$x[,1:3]), method= "ward.D2")
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

```
grps
  1   2 
203 366 
```

```
table(grps, diagnosis)
```

```
    diagnosis
grps   B   M
   1  24 179
   2 333  33
```

TP: 179 FP:33

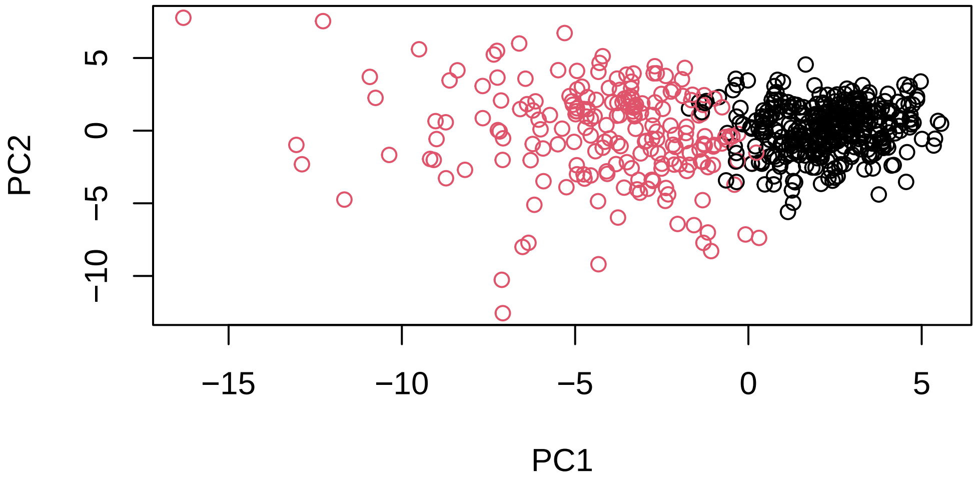
```
g <- as.factor(grps)
levels(g)
```

```
[1] "1" "2"
```

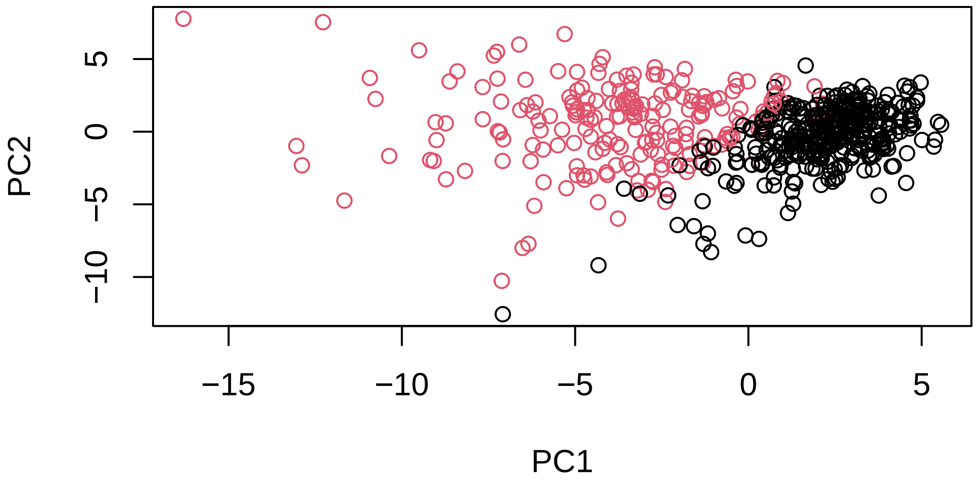
```
g <- relevel(g,2)
levels(g)
```

```
[1] "2" "1"
```

```
plot(wisc.pr$x[,1:2], col=g)
```



```r
plot(wisc.pr$x[,1:2], col=diagnosis)
```



```r
wisc.pr.hclust <- hclust(dist(wisc.pr$x[, 1:7]), method="ward.D2")

wisc.pr.hclust.clusters <- cutree(wisc.pr.hclust, k=2)
table(wisc.pr.hclust.clusters)
```

```
wisc.pr.hclust.clusters
  1   2 
216 353 
```

Q13. How well does the newly created model with four clusters separate out the two diagnoses?

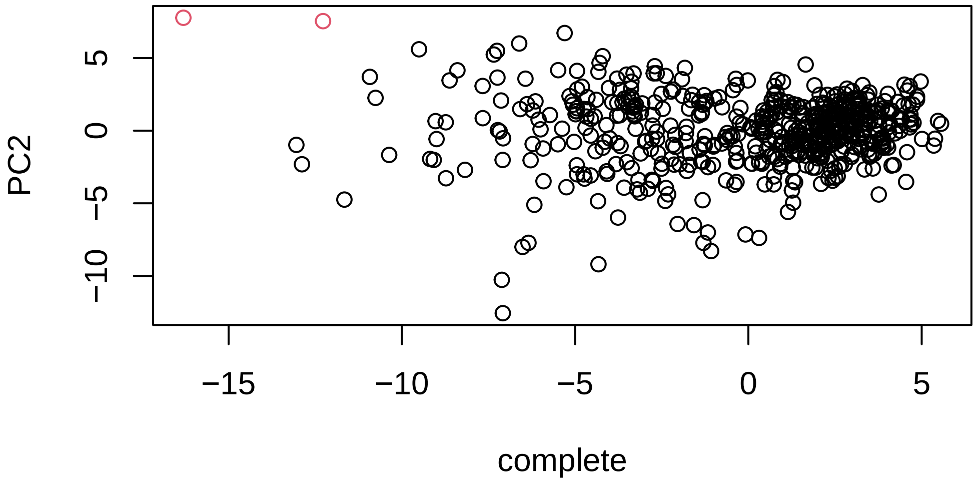
```r
table(wisc.pr.hclust.clusters, diagnosis)
```

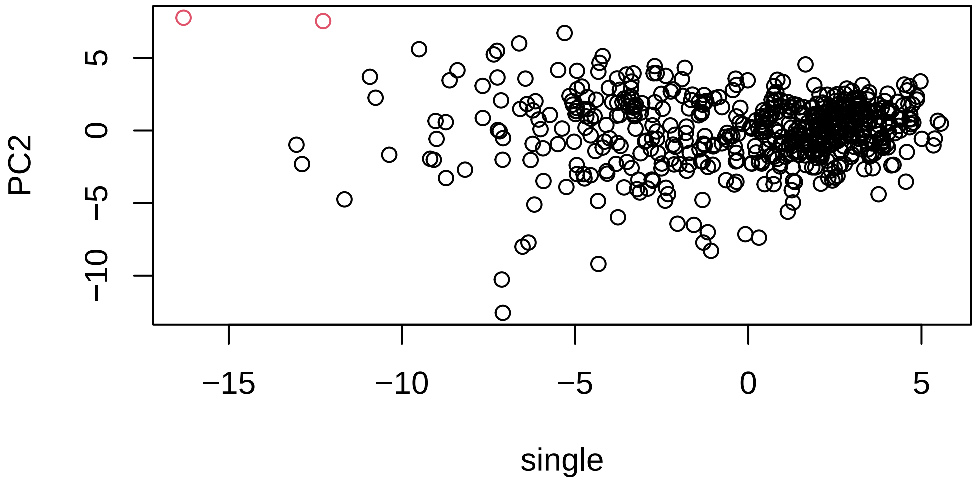
```
                       diagnosis
wisc.pr.hclust.clusters   B   M
                      1  28 188
                      2 329  24
```

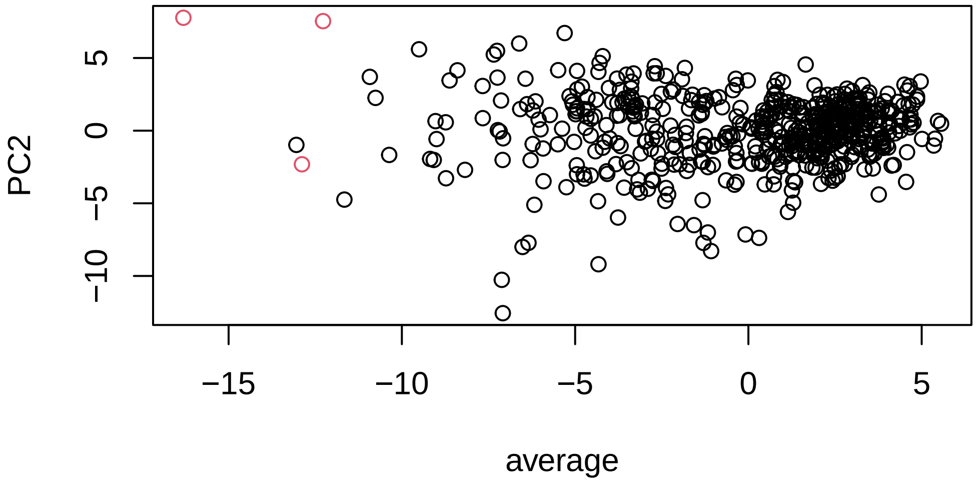
Pretty well! 9% of the assignments do not agree, but the rest do.

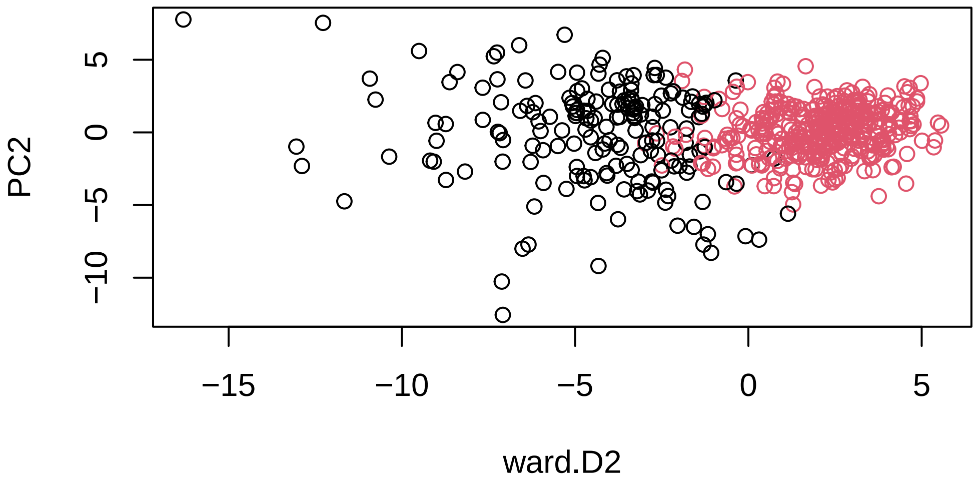
Q14. How well do the hierarchical clustering models you created in previous sections (i.e. before PCA) do in terms of separating the diagnoses? Again, use the table() function to compare the output of each model (wisc.km$cluster and wisc.hclust.clusters) with the vector containing the actual diagnoses.

```r
clust <- function(data, way) {
wisc.hclust <- hclust(data, method= way)
wisc.pr.hclust.clusters <- cutree(wisc.hclust, k=2)

tbl<- (table(wisc.pr.hclust.clusters, diagnosis))
plt<- (plot(wisc.pr$x[,1:2], col=wisc.pr.hclust.clusters, xlab=way))

return(list(table = tbl, plot = plt))

}

result <- sapply(c("complete", "single", "average", "ward.D2"), function(m) clust(data.dist,
```


PC2
5
0
−5
−10
−15
−10
−5
0
5
complete


PC2
5
0
−5
−10
−15
−10
−5
0
5
single





```
result[1,1:4]
```

```
$complete
```

```
                       diagnosis
wisc.pr.hclust.clusters   B   M
                      1 357 210
                      2   0   2

$single
                       diagnosis
wisc.pr.hclust.clusters   B   M
                      1 357 210
                      2   0   2

$average
                       diagnosis
wisc.pr.hclust.clusters   B   M
                      1 357 209
                      2   0   3

$ward.D2
                       diagnosis
wisc.pr.hclust.clusters   B   M
                      1  20 164
                      2 337  48
```

```
result$plot
```

```
NULL
```

Most of the methods except ward.D2 have very innacurate categorization that does not overlap with the diagnosis.