Class 08 Mini Project

Zijing

```
# Save input data file into Project directory
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
```

```
wisc.data <- wisc.df[,-1]
```

```
diagnosis <- as.factor(wisc.df$diagnosis)
```

Q1, Q2, Q3

```
nrow(wisc.data)
```

```
[1] 569
```

```
table(diagnosis)
```

```
diagnosis
  B   M
357 212
```

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

```
[1] 10
```

The data have 569 observations in total, among wich 212 are diagnosed as malignant. There are 10 variables in the data suffixed with "_mean".

```
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, 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

0.4427 of the original variance is explained by the first principle component.

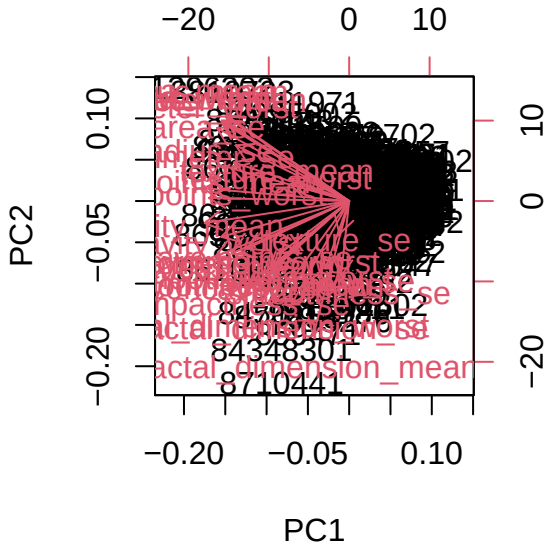
Q5

Three principle components is required to explain at least 70% of the original variance in the data.

Q6

Seven principle components is required to explain at least 90% of the original variance in the data.

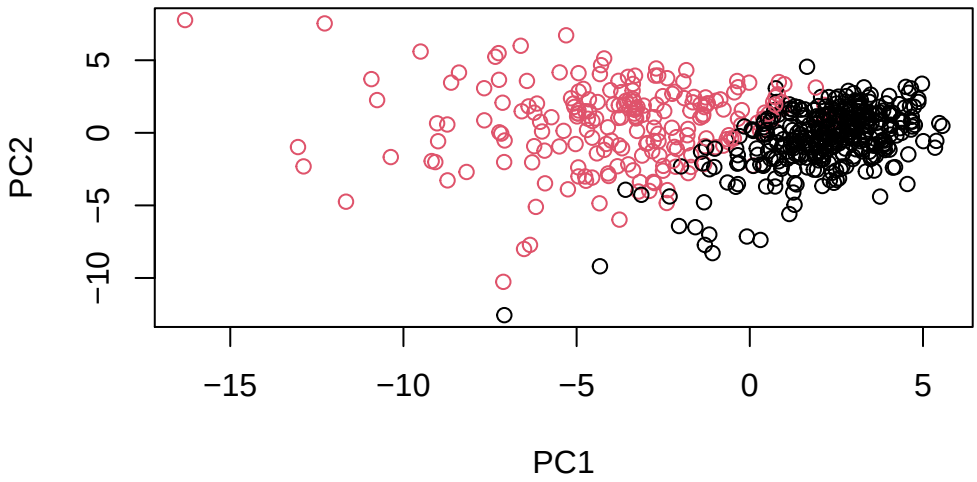
```
biplot(wisc.pr)
```



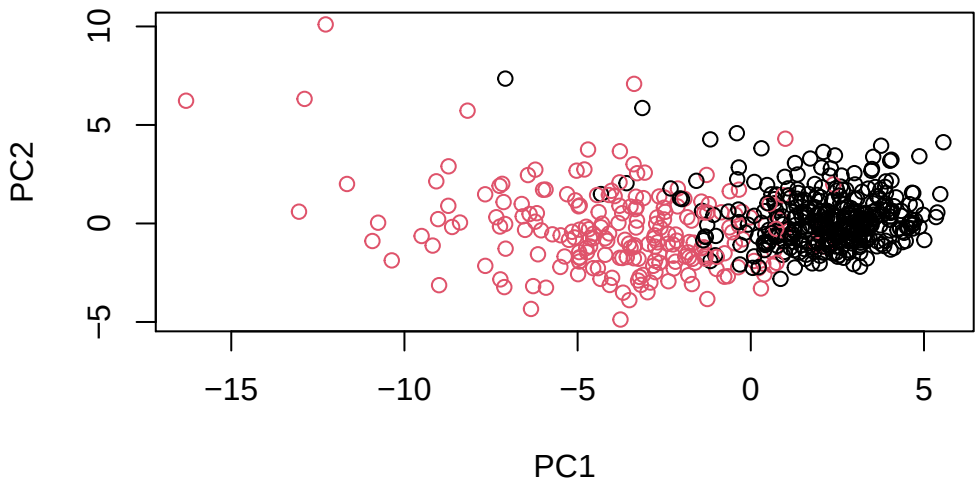
Q7

This plot is extremely hard to read as all the information are squashed together, making it impossible to read any useful information.

```
plot( wisc.pr$x[,1:2], col = diagnosis ,
     xlab = "PC1", ylab = "PC2")
```



```
plot(wisc.pr$x[,1], wisc.pr$x[,3], col = diagnosis ,
     xlab = "PC1", ylab = "PC2")
```



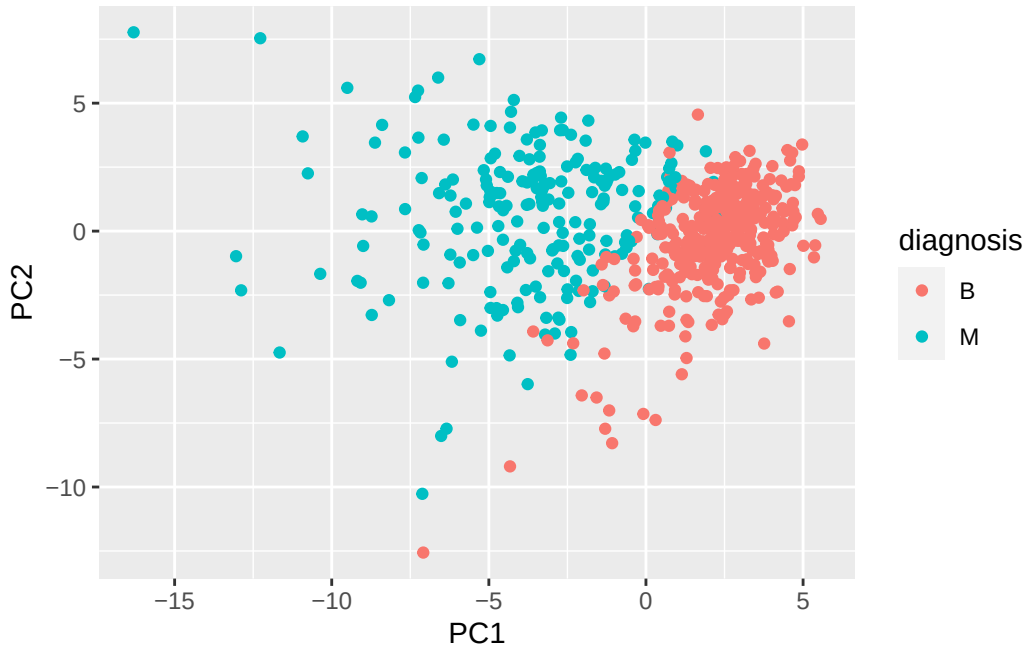
Q8

The two plots show that principle component 1 accounts for the most of the distinction between two diagnosis, showing that PC1 is the factor contributing more to the different diagnosis.

```
df <- as.data.frame(wisc.pr$x)
df$diagnosis <- diagnosis

library(ggplot2)

ggplot(df) +
  aes(PC1, PC2, col=diagnosis) +
  geom_point()
```

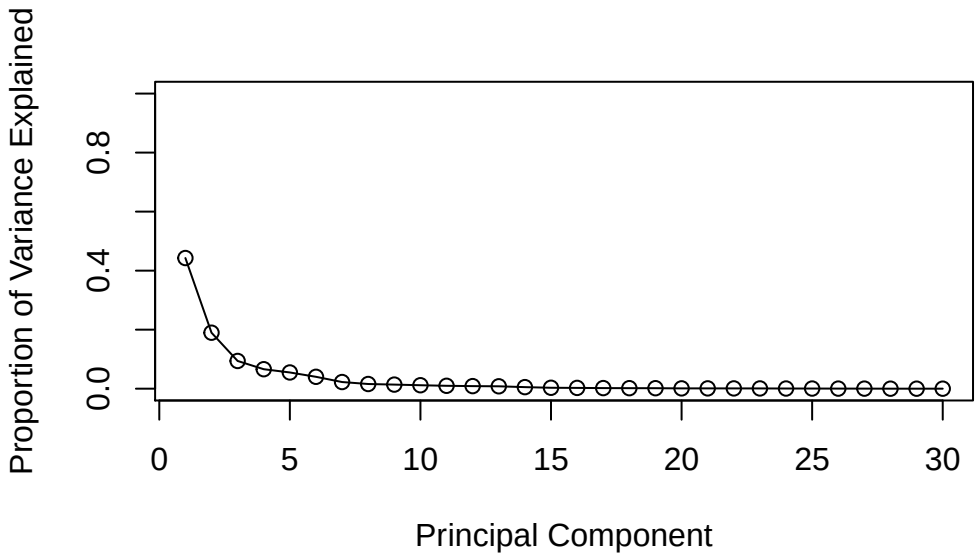



```
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

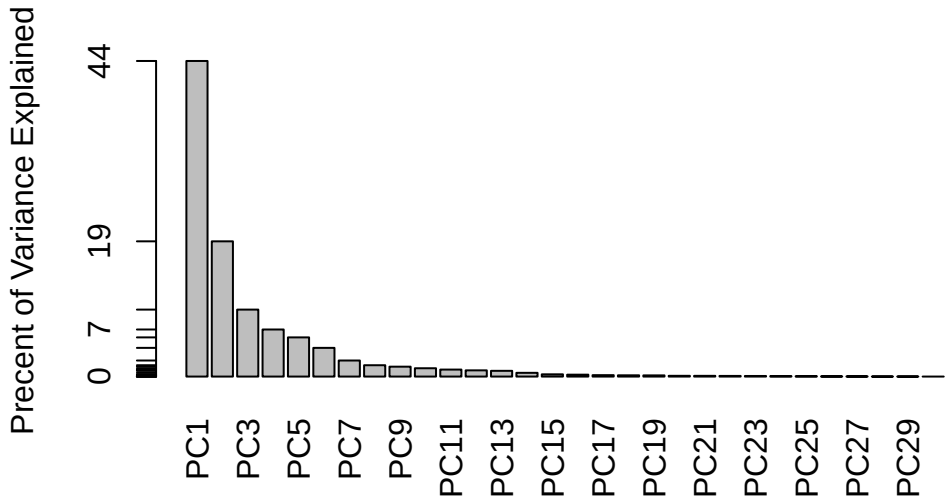
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
pve <- pr.var / sum(pr.var)

plot(pve, xlab = "Principal Component",
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```



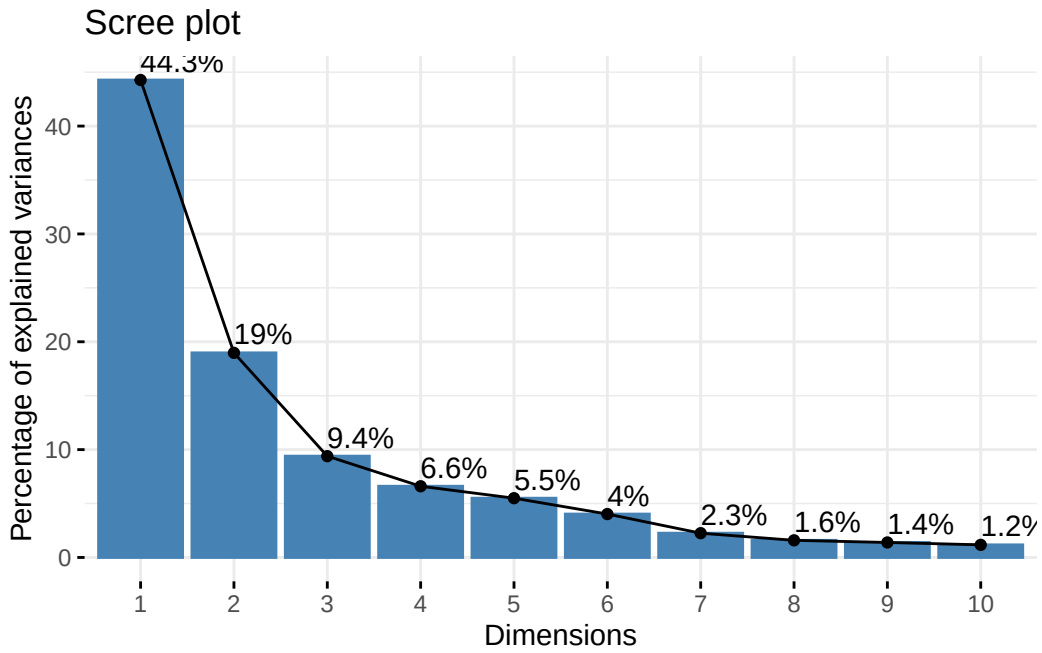

```
barplot(pve, ylab = "Precent of Variance Explained",
     names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```




```
#install.packages("factoextra")
library(factoextra)
```

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

```
fviz_eig(wisc.pr, addlabels = TRUE)
```




```
wisc.pr$rotation[,1]
```

```
            radius_mean            texture_mean          perimeter_mean
             -0.21890244              -0.10372458              -0.22753729
              area_mean         smoothness_mean        compactness_mean
             -0.22099499              -0.14258969              -0.23928535
         concavity_mean     concave.points_mean           symmetry_mean
             -0.25840048              -0.26085376              -0.13816696
 fractal_dimension_mean               radius_se              texture_se
             -0.06436335              -0.20597878              -0.01742803
           perimeter_se                 area_se           smoothness_se
             -0.21132592              -0.20286964              -0.01453145
        compactness_se            concavity_se       concave.points_se
             -0.17039345              -0.15358979              -0.18341740
          symmetry_se     fractal_dimension_se            radius_worst
             -0.04249842              -0.10256832              -0.22799663
        texture_worst          perimeter_worst               area_worst
             -0.10446933              -0.23663968              -0.22487053
      smoothness_worst        compactness_worst          concavity_worst
```

```
          -0.12795256            -0.21009588            -0.22876753
concave.points_worst          symmetry_worst fractal_dimension_worst
          -0.25088597            -0.12290456            -0.13178394
```

Q9

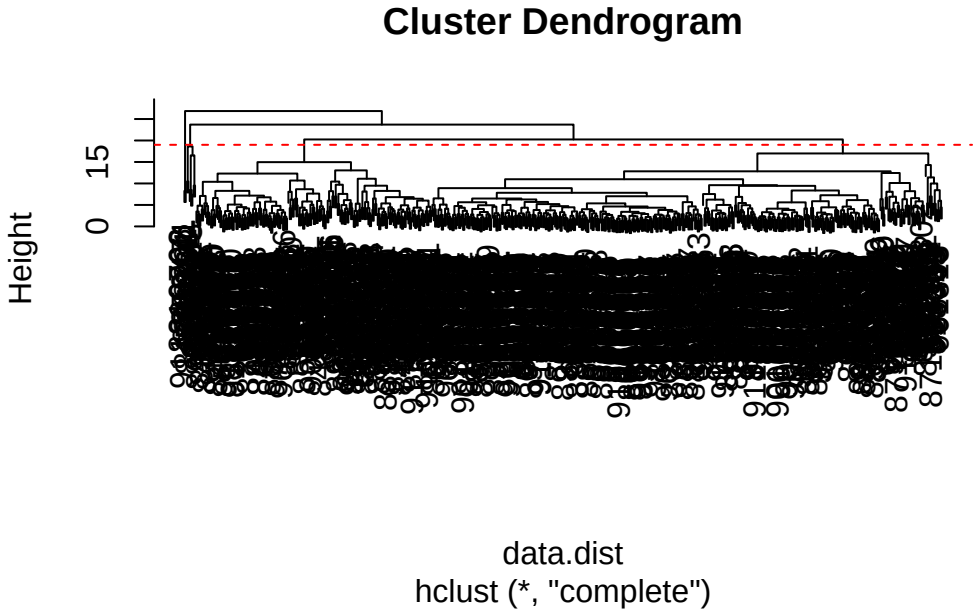
The component of the loading vector for the feature concave.points_mean is -0.2608. This feature contributes the most to the first principle component, as this feature has the highest absolute value in this leading vector.

```
data.scaled <- scale(wisc.data)
```

```
data.dist <- dist(data.scaled,"euclidean")
```

```
wisc.hclust <- hclust(data.dist, "complete")
```

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



Q10

The clutering model has 4 clusters at height 19.

```
  wisc.hclust.clusters <- cutree(wisc.hclust,k=4)
  table(wisc.hclust.clusters, diagnosis)
```

```
                   diagnosis
wisc.hclust.clusters   B   M
                   1  12 165
                   2   2   5
                   3 343  40
                   4   0   2
```

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

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

```
  wisc.hclust.5clusters <- cutree(wisc.hclust,k=5)
  table(wisc.hclust.5clusters, diagnosis)
```

```
                    diagnosis
wisc.hclust.5clusters   B   M
                    1  12 165
                    2   0   5
                    3 343  40
                    4   2   0
                    5   0   2
```

```
  wisc.hclust.8clusters <- cutree(wisc.hclust,k=8)
  table(wisc.hclust.8clusters, diagnosis)
```

```
                     diagnosis
wisc.hclust.8clusters   B   M
                    1  12  86
                    2   0  79
                    3   0   3
                    4 331  39
                    5   2   0
                    6  12   1
                    7   0   2
                    8   0   2
```

```
wisc.hclust.10clusters <- cutree(wisc.hclust,k=10)
table(wisc.hclust.10clusters, diagnosis)
```

```
                      diagnosis
wisc.hclust.10clusters   B   M
                    1   12  86
                    2    0  59
                    3    0   3
                    4  331  39
                    5    0  20
                    6    2   0
                    7   12   0
                    8    0   2
                    9    0   2
                    10   0   1
```

Q11

Cluster with number less than 4 does a bad job at matching with dianosis result, while cluster with number higher than 4 show really trivial improvement. The distinction between cases diagnosed as M vs B does improve, with more clusters converging to just one type of diagnosis. However, clusters including both diagnosis still exist even at 10 clusters.

```
wisc.hclust.single <- hclust(data.dist, "single")
wisc.hclust.average <- hclust(data.dist, "average")
wisc.hclust.ward <- hclust(data.dist, "ward.D2")
```

```r
wisc.hclust.single.clusters <- cutree(wisc.hclust.single,k=6)
table(wisc.hclust.single.clusters, diagnosis)
```

```
                           diagnosis
wisc.hclust.single.clusters   B   M
                          1 356 208
                          2   0   1
                          3   1   0
                          4   0   1
                          5   0   1
                          6   0   1
```

```r
wisc.hclust.average.clusters <- cutree(wisc.hclust.average,k=6)
table(wisc.hclust.average.clusters, diagnosis)
```

```
                            diagnosis
wisc.hclust.average.clusters   B   M
                           1 355 202
                           2   0   6
                           3   2   0
                           4   0   1
                           5   0   2
                           6   0   1
```

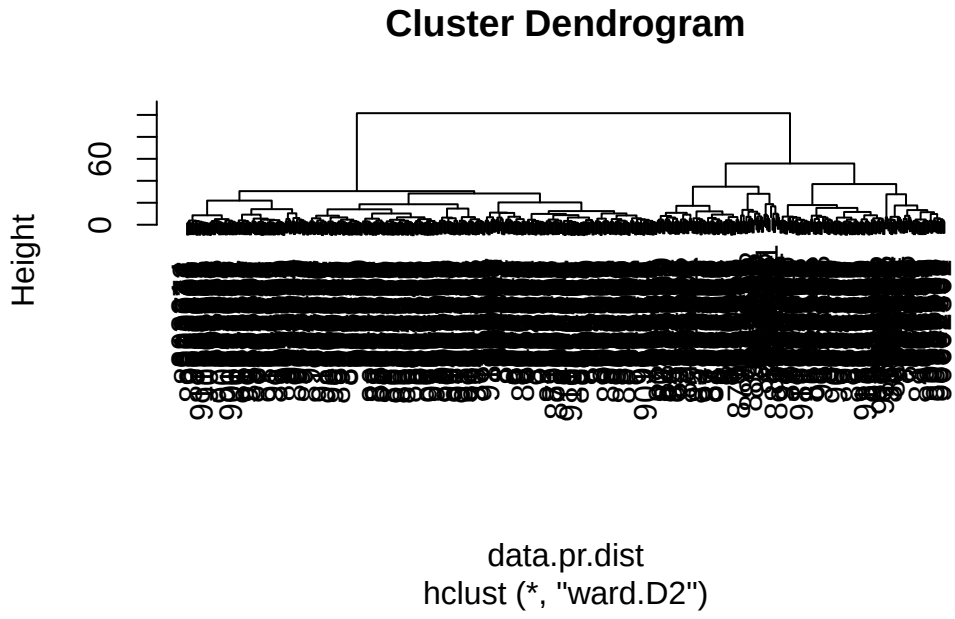
```r
wisc.hclust.ward.clusters <- cutree(wisc.hclust.ward,k=2)
table(wisc.hclust.ward.clusters, diagnosis)
```

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

Q12

I like the result from ward.D2 the most, as it is able to achieve a relatively good clear distinction between M and B diagnosis even just at k=2, while data from all other methods are not able to do that.

```
wisc.pr.90 <- wisc.pr$x[,1:7]
data.pr.dist <- dist(wisc.pr.90,"euclidean")
wisc.pr.hclust <- hclust(data.pr.dist, "ward.D2")
plot(wisc.pr.hclust)
```



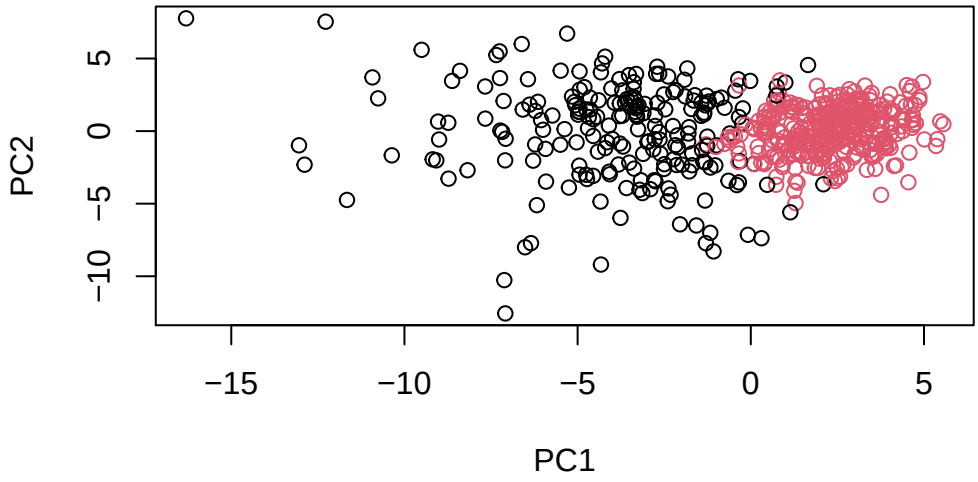

```
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

```
grps
  1   2
216 353
```

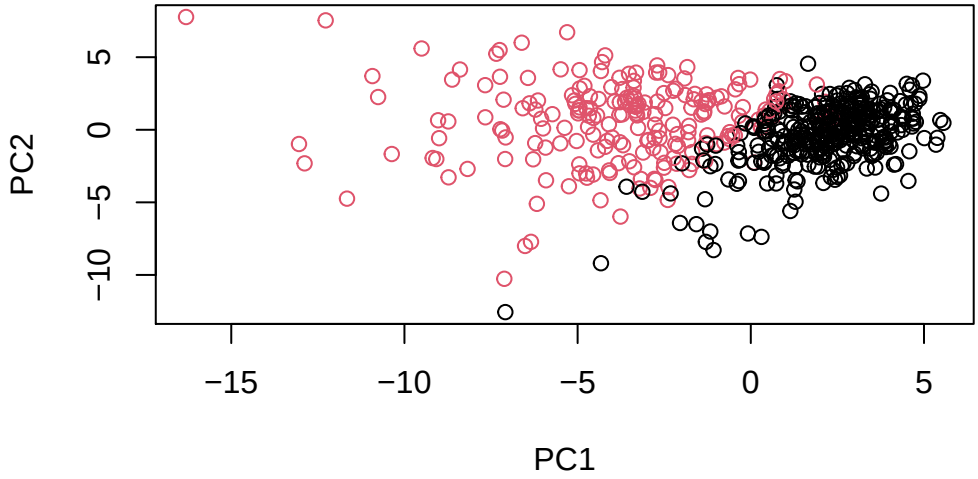
```
table(grps, diagnosis)
```

```
    diagnosis
grps   B   M
   1  28 188
   2 329  24
```

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



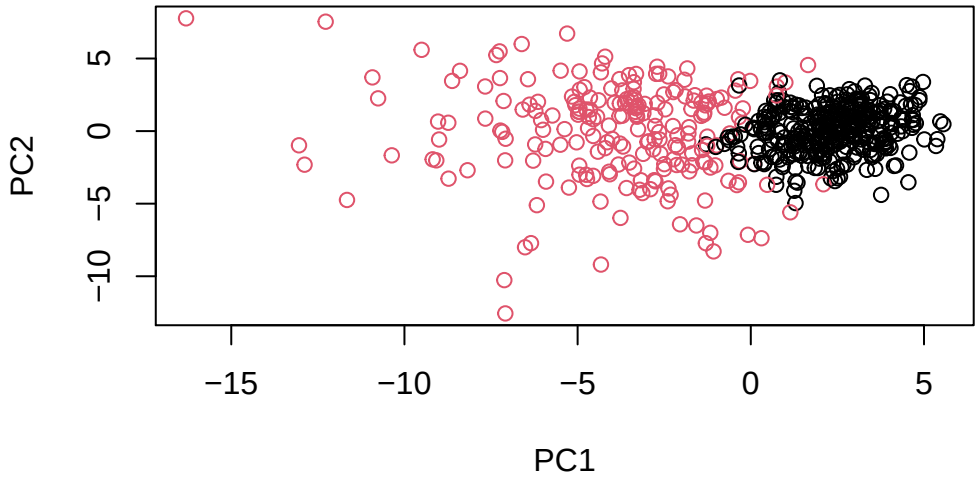

```
plot(wisc.pr$x[,1:2], col=diagnosis)
```




```
g <- as.factor(grps)
g <- relevel(g,2)
levels(g)
```

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

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




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

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

Q13

Although not completely neat, this newly created model separates out the two diagnosis pretty good.

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

```
                   diagnosis
wisc.hclust.clusters   B   M
                   1  12 165
                   2   2   5
                   3 343  40
                   4   0   2
```

Q14

This result from the previous model did not do as good as the model after PCA, especially with more M diagnosis in the majorly B diagnosis group.

```
# ward.D2 with PCA
188/(188+24)
```

```
[1] 0.8867925
```

```
329/(329+28)
```

```
[1] 0.9215686
```

```
#ward.D2 without PCA
164/(164+48)
```

```
[1] 0.7735849
```

```
337/(337+20)
```

```
[1] 0.9439776
```

```
#complete without PCA
(165+5+2)/(165+5+2+40)
```

```
[1] 0.8113208
```

```
343/(343+2+12)
```

```
[1] 0.9607843
```

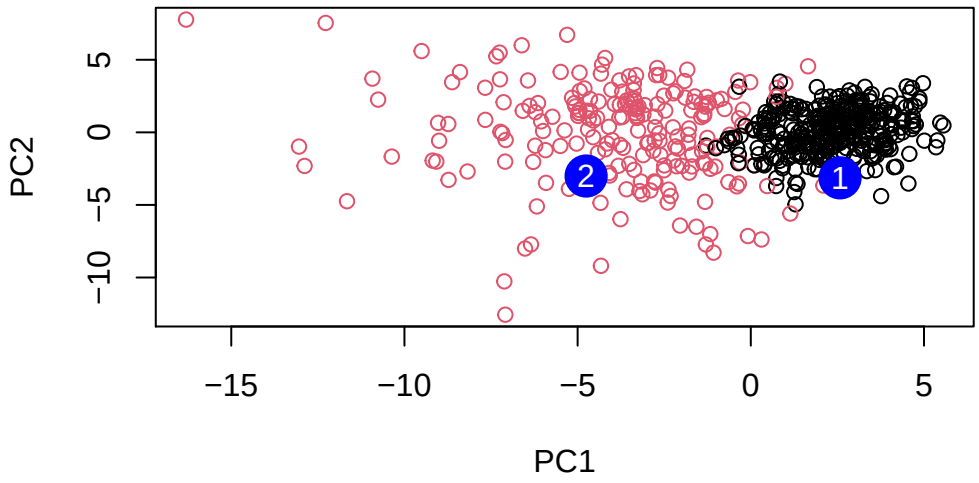
Q15

Among the three models being evaluated above, the model using PCA and the 'ward.D2' method achieves the best sensitivity. The model without PCA using the 'complete' method achieves the best specificity.

```
url <- "https://tinyurl.com/new-samples-CSV"
new <- read.csv(url)
npc <- predict(wisc.pr, newdata=new)
npc
```

```
          PC1       PC2        PC3        PC4       PC5        PC6        PC7
[1,]  2.576616 -3.135913  1.3990492 -0.7631950  2.781648 -0.8150185 -0.3959098
[2,] -4.754928 -3.009033 -0.1660946 -0.6052952 -1.140698 -1.2189945  0.8193031
           PC8       PC9       PC10       PC11      PC12      PC13     PC14
[1,] -0.2307350 0.1029569 -0.9272861 0.3411457  0.375921 0.1610764 1.187882
[2,] -0.3307423 0.5281896 -0.4855301 0.7173233 -1.185917 0.5893856 0.303029
          PC15       PC16        PC17        PC18        PC19       PC20
[1,] 0.3216974 -0.1743616 -0.07875393 -0.11207028 -0.08802955 -0.2495216
[2,] 0.1299153  0.1448061 -0.40509706  0.06565549  0.25591230 -0.4289500
          PC21       PC22       PC23       PC24        PC25         PC26
[1,]  0.1228233 0.09358453 0.08347651  0.1223396  0.02124121  0.078884581
[2,] -0.1224776 0.01732146 0.06316631 -0.2338618 -0.20755948 -0.009833238
             PC27        PC28         PC29         PC30
[1,]  0.220199544 -0.02946023 -0.015620933  0.005269029
[2,] -0.001134152  0.09638361  0.002795349 -0.019015820
```

```
plot(wisc.pr$x[,1:2], col=g)
points(npc[,1], npc[,2], col="blue", pch=16, cex=3)
text(npc[,1], npc[,2], c(1,2), col="white")
```



Q16

Patient 2 should be prioritized for followup as its data is more similar to that of previous patients with malignant diagnosis, so patient 2 is more likely to be a malignant case.