class08 mini-project

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Table of contents

1. Exploratory data analysis

```
#Data files were saved in my project folder
fna.data <- "WisconsinCancer.csv"

#will store the data in a dataframe called wisc.df
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
```

```
#omitting the diagnosis column as we will not be using it for our analysis
# We can use -1 here to remove the first column
wisc.data <- wisc.df[,-1]
head(wisc.data)
```

```
         radius_mean texture_mean perimeter_mean area_mean smoothness_mean
842302         17.99        10.38         122.80    1001.0         0.11840
842517         20.57        17.77         132.90    1326.0         0.08474
84300903       19.69        21.25         130.00    1203.0         0.10960
84348301       11.42        20.38          77.58     386.1         0.14250
84358402       20.29        14.34         135.10    1297.0         0.10030
843786         12.45        15.70          82.57     477.1         0.12780
         compactness_mean concavity_mean concave.points_mean symmetry_mean
842302            0.27760         0.3001             0.14710        0.2419
842517            0.07864         0.0869             0.07017        0.1812
84300903          0.15990         0.1974             0.12790        0.2069
84348301          0.28390         0.2414             0.10520        0.2597
```

```
84358402          0.13280         0.1980             0.10430        0.1809
843786            0.17000         0.1578             0.08089        0.2087
         fractal_dimension_mean radius_se texture_se perimeter_se area_se
842302                  0.07871    1.0950     0.9053        8.589  153.40
842517                  0.05667    0.5435     0.7339        3.398   74.08
84300903                0.05999    0.7456     0.7869        4.585   94.03
84348301                0.09744    0.4956     1.1560        3.445   27.23
84358402                0.05883    0.7572     0.7813        5.438   94.44
843786                  0.07613    0.3345     0.8902        2.217   27.19
         smoothness_se compactness_se concavity_se concave.points_se
842302        0.006399        0.04904      0.05373           0.01587
842517        0.005225        0.01308      0.01860           0.01340
84300903      0.006150        0.04006      0.03832           0.02058
84348301      0.009110        0.07458      0.05661           0.01867
84358402      0.011490        0.02461      0.05688           0.01885
843786        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
```

```
# setup a separate new vector called diagnosis that contains the data from the diagnosis c
diagnosis <- as.factor(wisc.df$diagnosis)
head(diagnosis)
```

```
[1] M M M M M M
Levels: B M
```

Q1. How many observations are in this dataset?

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

```
[1] 569
```

There are 569 observations in this dataset.

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

```
table(diagnosis)
```

```
diagnosis
  B   M
357 212
```

There are 212 observations with a malignant diagnosis.

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

```
wisc.colnames <- colnames(wisc.data)
wisc.colnames
```

```
 [1] "radius_mean"             "texture_mean"
 [3] "perimeter_mean"          "area_mean"
 [5] "smoothness_mean"         "compactness_mean"
 [7] "concavity_mean"          "concave.points_mean"
 [9] "symmetry_mean"           "fractal_dimension_mean"
[11] "radius_se"               "texture_se"
[13] "perimeter_se"            "area_se"
[15] "smoothness_se"           "compactness_se"
[17] "concavity_se"            "concave.points_se"
[19] "symmetry_se"             "fractal_dimension_se"
[21] "radius_worst"            "texture_worst"
[23] "perimeter_worst"         "area_worst"
[25] "smoothness_worst"        "compactness_worst"
[27] "concavity_worst"         "concave.points_worst"
[29] "symmetry_worst"          "fractal_dimension_worst"
```

```
#find the columns that have _mean in their names
grep("_mean", wisc.colnames)
```

```
 [1]  1  2  3  4  5  6  7  8  9 10
```

```
#count the number of columns that have _mean in their names
length(grep("_mean", wisc.colnames))
```

```
[1] 10
```

10 variables/features are suffixed with "_mean".

2. Principal Component Analysis

Let's try PCA on this data to see what major features might be hidden in this high dimensional data that are hard to see any other way.

First, we need to check if the data need to be scaled. Two reasons for scaling data include.

- The input variables use different units of measurement.
- The input variables have significantly different variances.

```r
# check the mean and stdev of the features to determine if the data should be scaled
#check column means and stdevs
round(colMeans(wisc.data))
```

```
            radius_mean            texture_mean          perimeter_mean 
                     14                      19                      92 
              area_mean         smoothness_mean        compactness_mean 
                    655                       0                       0 
         concavity_mean     concave.points_mean           symmetry_mean 
                      0                       0                       0 
 fractal_dimension_mean               radius_se              texture_se 
                      0                       0                       1 
           perimeter_se                 area_se           smoothness_se 
                      3                      40                       0 
         compactness_se            concavity_se       concave.points_se 
                      0                       0                       0 
            symmetry_se    fractal_dimension_se            radius_worst 
                      0                       0                      16 
          texture_worst         perimeter_worst              area_worst 
                     26                     107                     881 
       smoothness_worst       compactness_worst         concavity_worst 
                      0                       0                       0 
   concave.points_worst          symmetry_worst fractal_dimension_worst 
                      0                       0                       0 
```

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

```
            radius_mean            texture_mean          perimeter_mean 
                      4                       4                      24 
              area_mean         smoothness_mean        compactness_mean 
                    352                       0                       0 
         concavity_mean     concave.points_mean           symmetry_mean 
                      0                       0                       0 
 fractal_dimension_mean               radius_se              texture_se 
                      0                       0                       1 
           perimeter_se                 area_se           smoothness_se 
                      2                      45                       0 
         compactness_se            concavity_se       concave.points_se 
                      0                       0                       0 
            symmetry_se    fractal_dimension_se            radius_worst 
```

```
                      0                       0                       5
          texture_worst         perimeter_worst              area_worst
                      6                      34                     569
       smoothness_worst       compactness_worst         concavity_worst
                      0                       0                       0
   concave.points_worst          symmetry_worst fractal_dimension_worst
                      0                       0                       0
```

```r
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
```

```r
#shows that PC1 captured 44.3% of the variance in the original data
```

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

PC1 captured 44.27% of the variance in the original data.

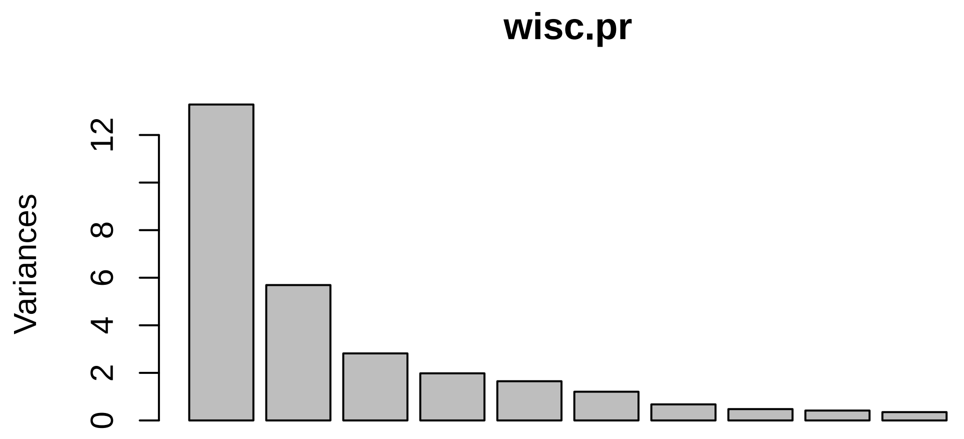
Q5. How many principal components (PCs) are required to describe at least 70% of the original variance in the data?

Three principle components are required to describe at least 70% of the original variance (as shown by the cumulative proportion row).

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

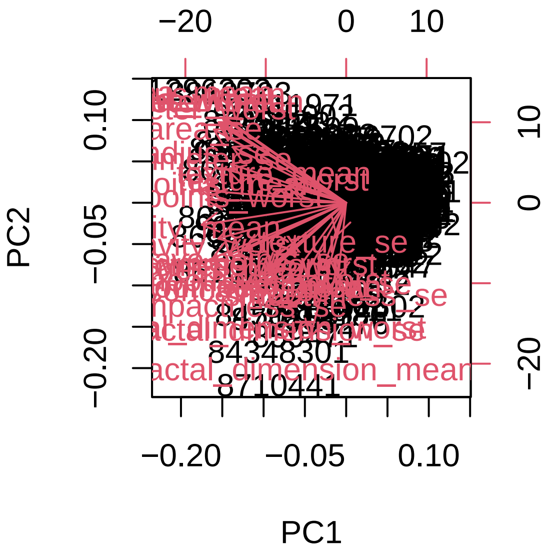
Seven are required.

```r
plot(wisc.pr)
```



One of our main results from methods like PCA is a so called “score plots” aka ’PC plots”, “ordination plot”, PC1 vs PC2...

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



Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why?

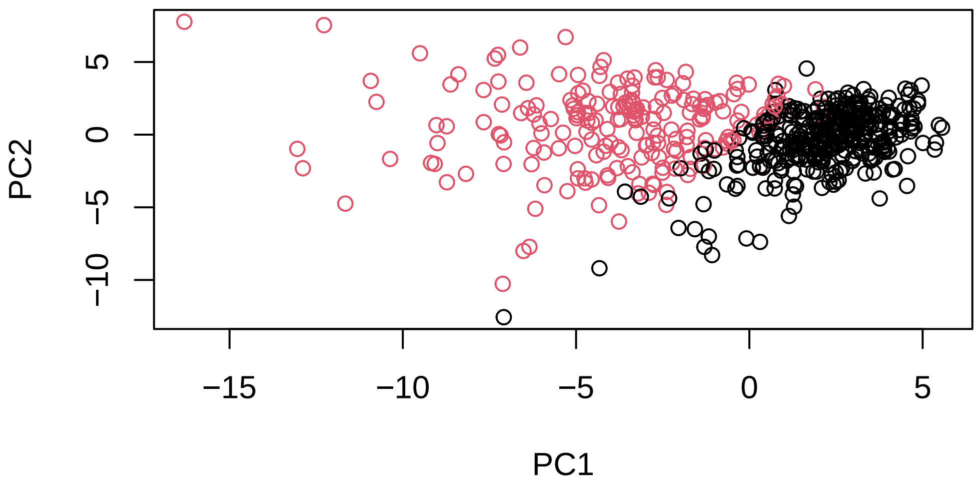
It's very messy and difficult to understand. There are a lot of labelled things that make it impossible to see the plot.

```
head(wisc.pr$x)
```

```
               PC1        PC2        PC3       PC4        PC5         PC6
842302   -9.184755  -1.946870 -1.1221788 3.6305364  1.1940595  1.41018364
842517   -2.385703   3.764859 -0.5288274 1.1172808 -0.6212284  0.02863116
84300903 -5.728855   1.074229 -0.5512625 0.9112808  0.1769302  0.54097615
84348301 -7.116691 -10.266556 -3.2299475 0.1524129  2.9582754  3.05073750
84358402 -3.931842   1.946359  1.3885450 2.9380542 -0.5462667 -1.22541641
843786   -2.378155  -3.946456 -2.9322967 0.9402096  1.0551135 -0.45064213
                 PC7         PC8         PC9       PC10       PC11       PC12
842302    2.15747152  0.39805698 -0.15698023 -0.8766305 -0.2627243 -0.8582593
842517    0.01334635 -0.24077660 -0.71127897  1.1060218 -0.8124048  0.1577838
```

```
84300903 -0.66757908 -0.09728813  0.02404449  0.4538760  0.6050715  0.1242777
84348301  1.42865363 -1.05863376 -1.40420412 -1.1159933  1.1505012  1.0104267
84358402 -0.93538950 -0.63581661 -0.26357355  0.3773724 -0.6507870 -0.1104183
843786    0.49001396  0.16529843 -0.13335576 -0.5299649 -0.1096698  0.0813699
                PC13         PC14         PC15        PC16        PC17
842302    0.10329677 -0.690196797  0.601264078  0.74446075 -0.26523740
842517   -0.94269981 -0.652900844 -0.008966977 -0.64823831 -0.01719707
84300903 -0.41026561  0.016665095 -0.482994760  0.32482472  0.19075064
84348301 -0.93245070 -0.486988399  0.168699395  0.05132509  0.48220960
84358402  0.38760691 -0.538706543 -0.310046684 -0.15247165  0.13302526
843786   -0.02625135  0.003133944 -0.178447576 -0.01270566  0.19671335
                PC18       PC19        PC20         PC21        PC22
842302   -0.54907956  0.1336499  0.34526111  0.096430045 -0.06878939
842517    0.31801756 -0.2473470 -0.11403274 -0.077259494  0.09449530
84300903 -0.08789759 -0.3922812 -0.20435242  0.310793246  0.06025601
84348301 -0.03584323 -0.0267241 -0.46432511  0.433811661  0.20308706
84358402 -0.01869779  0.4610302  0.06543782 -0.116442469  0.01763433
843786   -0.29727706 -0.1297265 -0.07117453 -0.002400178  0.10108043
                PC23         PC24         PC25         PC26        PC27
842302    0.08444429  0.175102213  0.150887294 -0.201326305 -0.25236294
842517   -0.21752666 -0.011280193  0.170360355 -0.041092627  0.18111081
84300903 -0.07422581 -0.102671419 -0.171007656  0.004731249  0.04952586
84348301 -0.12399554 -0.153294780 -0.077427574 -0.274982822  0.18330078
84358402  0.13933105  0.005327110 -0.003059371  0.039219780  0.03213957
843786    0.03344819 -0.002837749 -0.122282765 -0.030272333 -0.08438081
                  PC28         PC29          PC30
842302   -0.0338846387  0.045607590  0.0471277407
842517    0.0325955021 -0.005682424  0.0018662342
84300903  0.0469844833  0.003143131 -0.0007498749
84348301  0.0424469831 -0.069233868  0.0199198881
84358402 -0.0347556386  0.005033481 -0.0211951203
843786    0.0007296587 -0.019703996 -0.0034564331
```

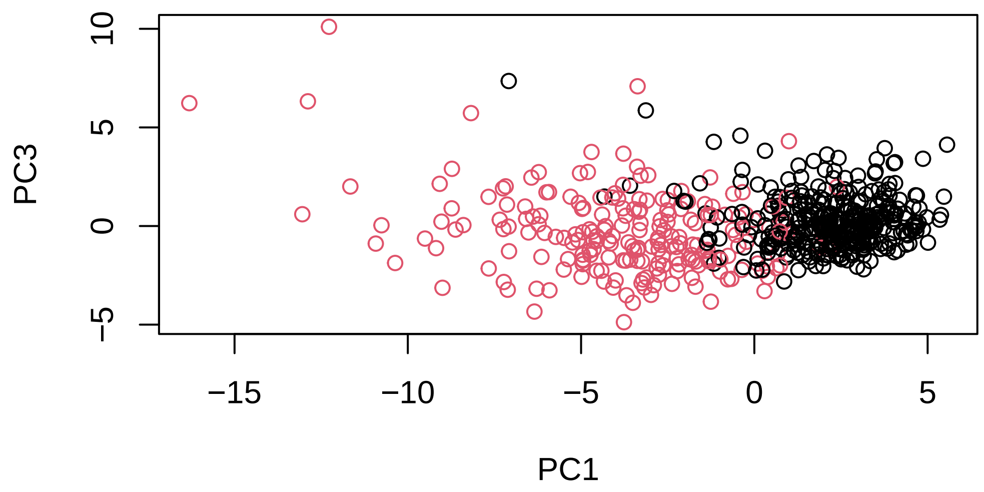
```
#plot PC1 vs PC2
plot(wisc.pr$x[,1], wisc.pr$x[,2], col=diagnosis,
     xlab= "PC1", ylab="PC2")
```



```
#each dot is a patient sample
```

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

```
plot(wisc.pr$x[,1], wisc.pr$x[,3], col=diagnosis,
     xlab= "PC1", ylab="PC3")
```

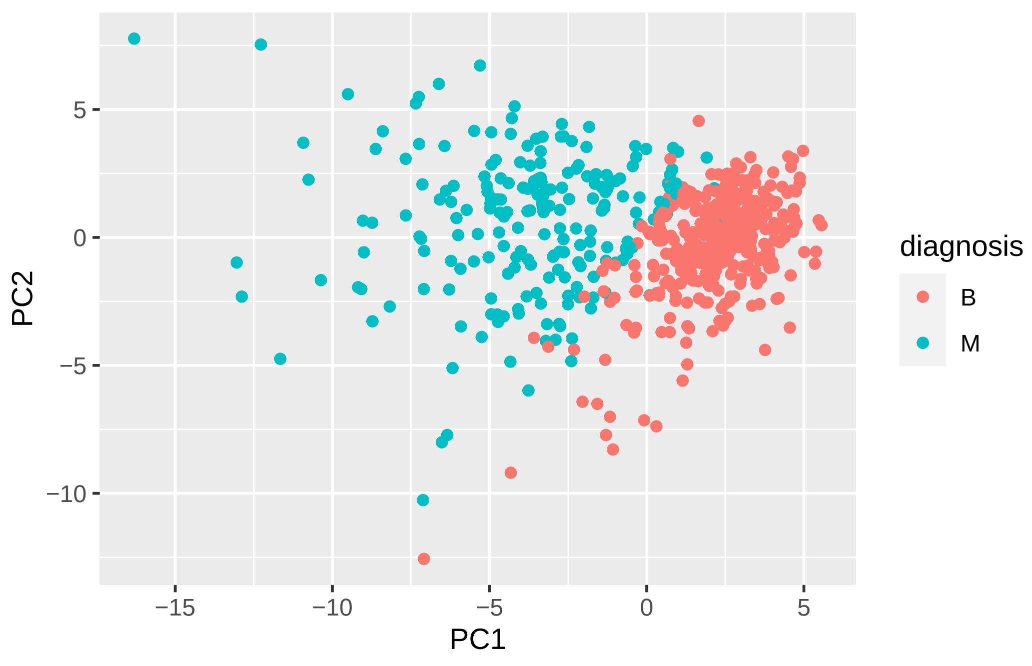


The groups in this plot are not as separated as in the PC1 vs PC2 plot since PC3 doesn't capture as much variance as PC2. But the two groups are still distinct, so PC1 is enough to distinguish for the most part between benign and malignant.

```r
# Create a data.frame for ggplot
df <- as.data.frame(wisc.pr$x)
df$diagnosis <- diagnosis
```

```r
# Load the ggplot2 package
library(ggplot2)
```

```r
# Make a scatter plot colored by diagnosis
ggplot(df) +
  aes(PC1, PC2, col=diagnosis) +
  geom_point() +
  labs(x="PC1", y="PC2")
```



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.

```r
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
```

-0.26085376 is the component of the loading vector for the feature concave.points_mean.

3. Hierarchical clustering

```
# Scale the wisc.data data using the "scale()" function
data.scaled <- scale(wisc.data)
```

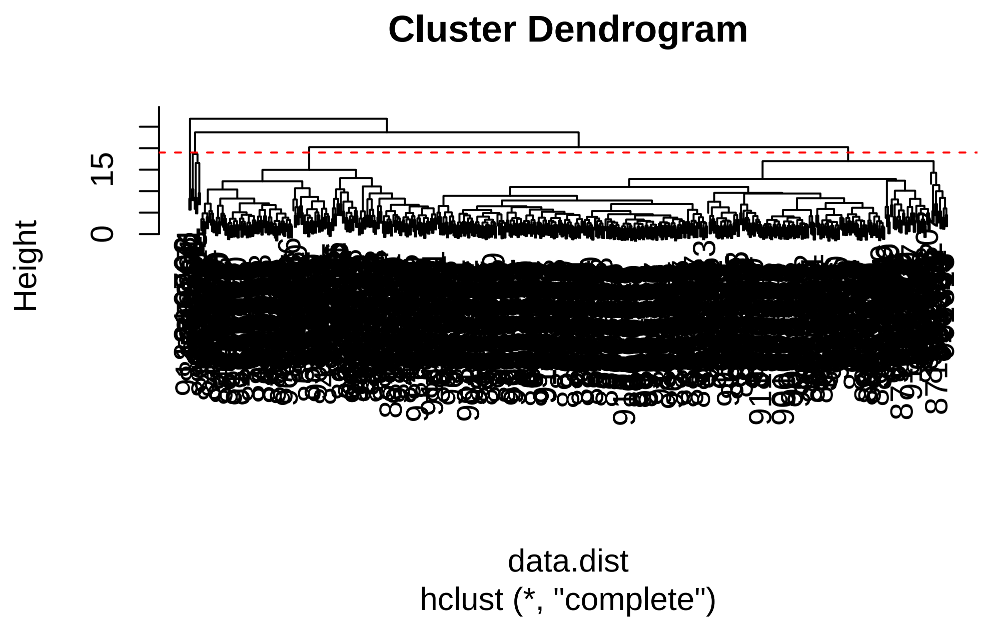
```
#Calculate the (Euclidean) distances between all pairs of observations in the new scaled d
data.dist <- dist(data.scaled, method="euclidean")
head(data.dist)
```

```
[1] 10.309426  6.771675 10.463467  8.663413  8.402233  9.843286
```

```
#Create a hierarchical clustering model using complete linkage. Manually specify the metho
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?

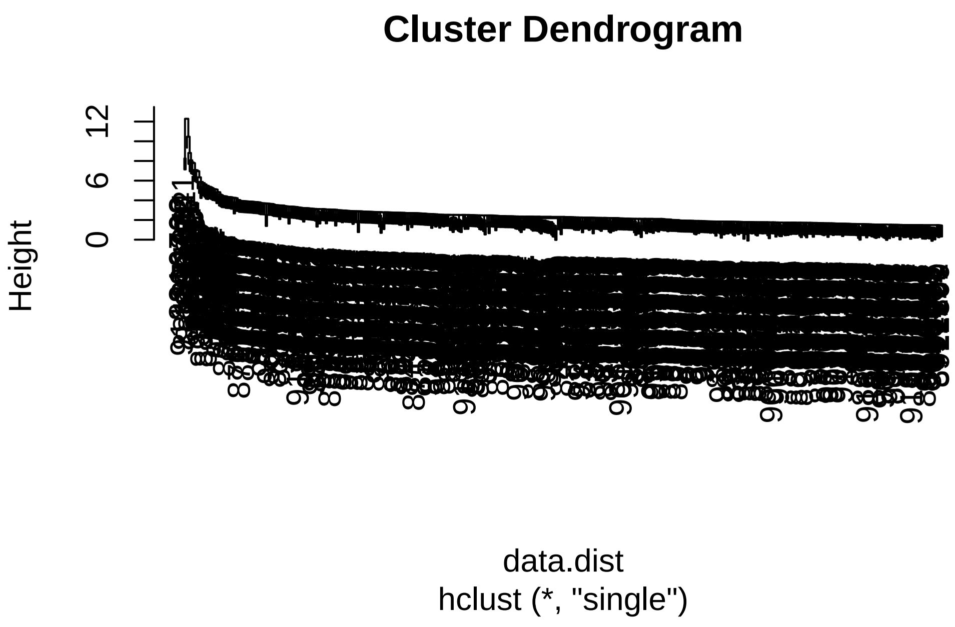
```
plot(wisc.hclust)
abline(h=19, col="red", lty=2)
```



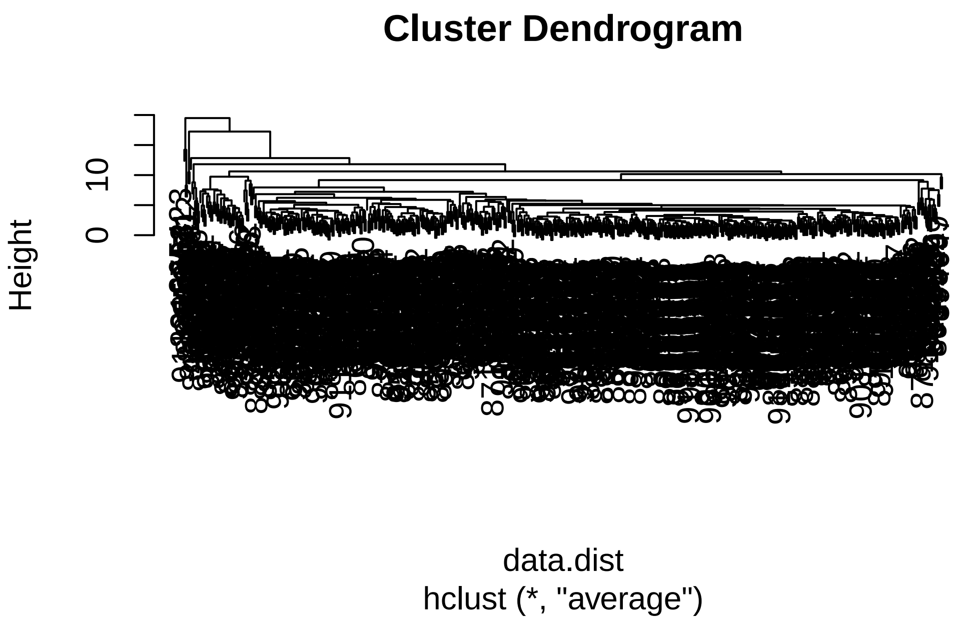
Height = 19

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

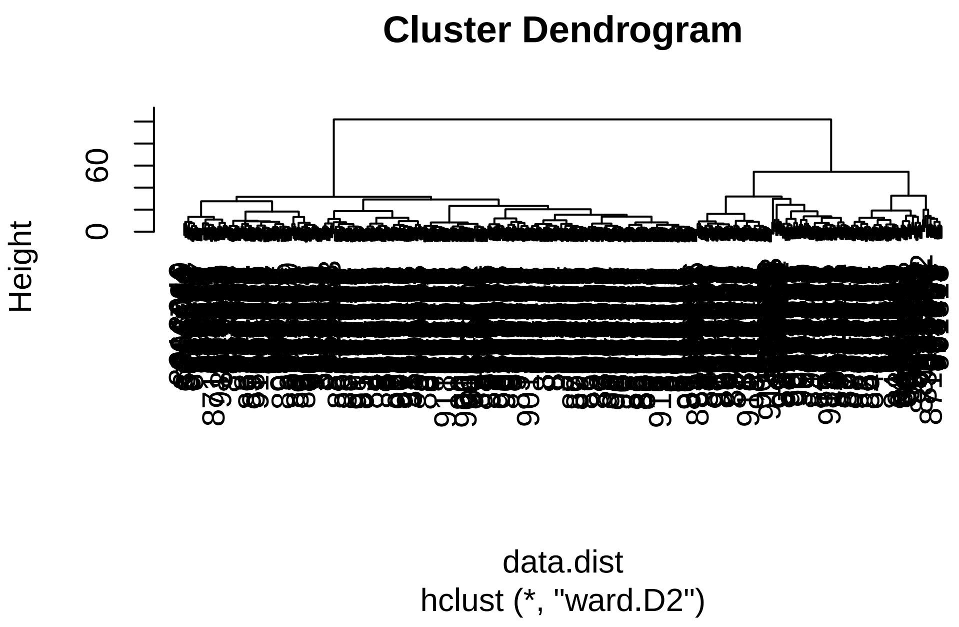
```
single_method <- hclust(data.dist, method="single")
plot(single_method)
```



```r
average_method <- hclust(data.dist, method="average")
plot(average_method)
```



```r
ward.D2_method <- hclust(data.dist, method="ward.D2")
plot(ward.D2_method)
```



Ward.D2 gives my favorite results because it produces the clearest looking groupings. It's nice that it minimizes variance within the clusters.

4. Combining methods

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

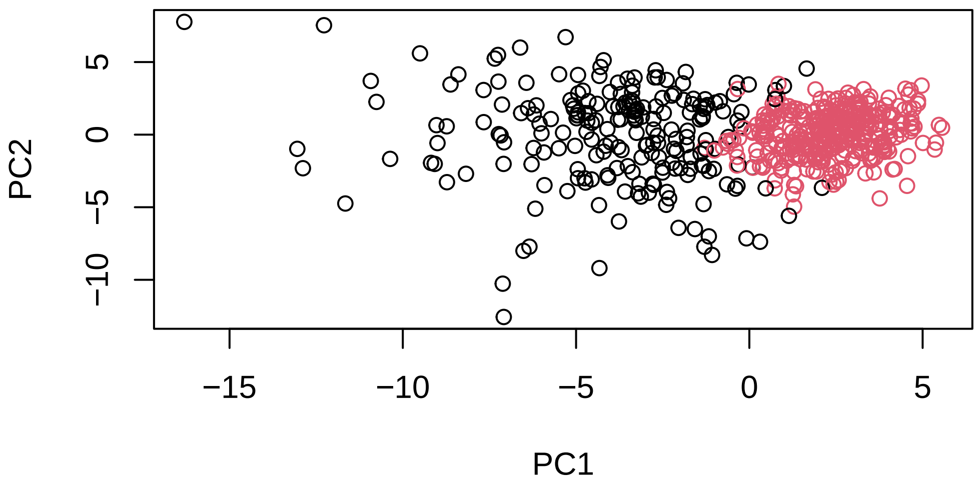
```r
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

```
grps
  1   2
216 353
```

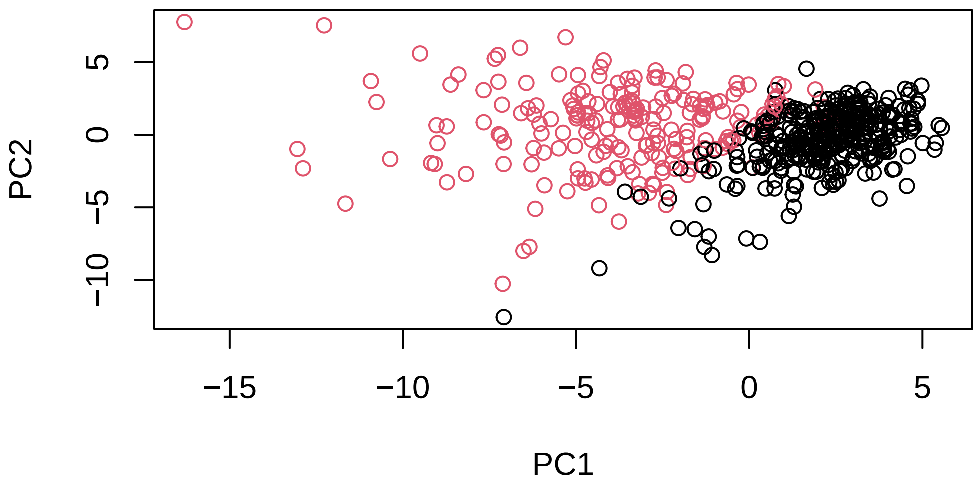
```r
table(grps, diagnosis)
```

```
    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)
```



Note the color swap here as the hclust cluster 1 is mostly "M" and cluster 2 is mostly "B" as we saw from the results of calling table(grps, diagnosis). To match things up we can turn our groups into a factor and reorder the levels so cluster 2 comes first and thus gets the first color (black) and cluster 1 gets the second color (red).

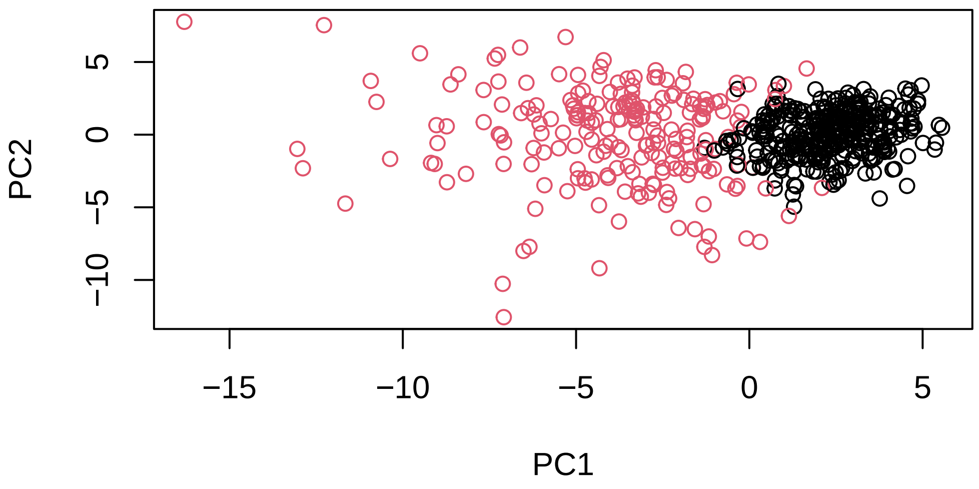
```
g <- as.factor(grps)
levels(g)
```

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

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

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

```
# Plot using our re-ordered factor
plot(wisc.pr$x[,1:2], col=g)
```



We can be fancy and look in 3D with the rgl or plotly packages.

```
#install.packages("rgl")
```

```
library(rgl)
```

```
plot3d(wisc.pr$x[,1:3], xlab="PC 1", ylab="PC 2", zlab="PC 3", cex=1.5, size=1, type="s",
```

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

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

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

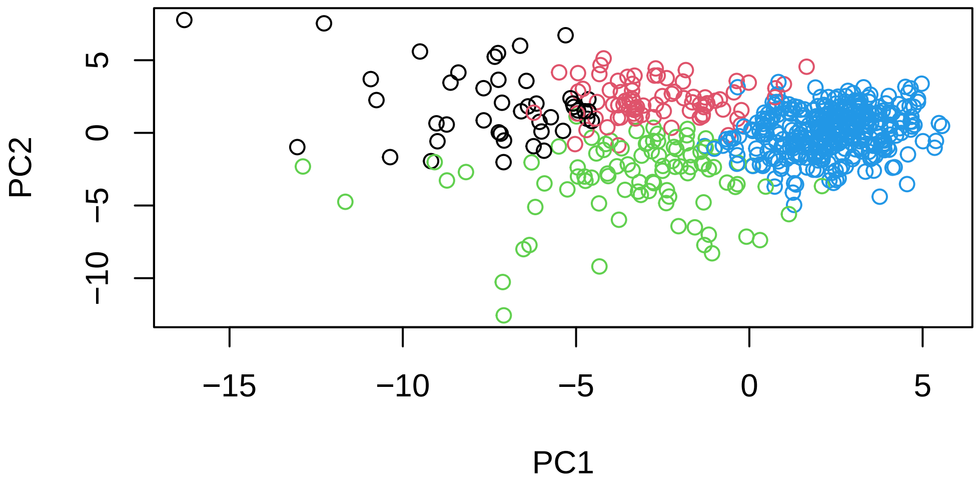
```r
grps4 <- cutree(wisc.pr.hclust, k=4)
table(grps4)
```

```
grps4
  1   2   3   4 
 45  79  92 353 
```

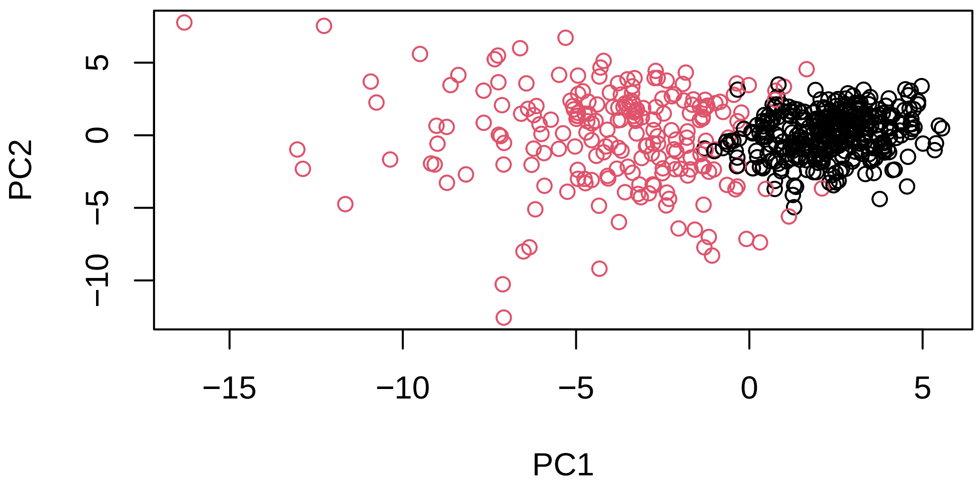
```r
table(grps4, diagnosis)
```

```
     diagnosis
grps4   B   M
    1   0  45
    2   2  77
    3  26  66
    4 329  24
```

```r
plot(wisc.pr$x[,1:7], col=grps4)
```



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



It separates out very similarly to when two clusters were made–with there being 28 and 24 samples in the Benign and Malignant groups being "misdiagnosed".

Q14. How well do the hierarchical clustering models you created in previous sections (i.e. before PCA) do in terms of separating the diagnoses?

```
#k-means clustering method
km_method <- kmeans(wisc.data, centers=2)
km_method$cluster
```

```
  842302    842517  84300903  84348301  84358402    843786    844359  84458202
       1         1         1         2         1         2         1         2
  844981  84501001    845636  84610002    846226    846381  84667401  84799002
       2         2         2         1         1         2         2         2
  848406  84862001    849014   8510426   8510653   8510824   8511133    851509
       2         1         1         2         2         2         2         1
  852552    852631    852763    852781    852973    853201    853401    853612
       1         1         2         1         1         1         1         2
```

85382601	854002	854039	854253	854268	854941	855133	855138
1	1	1	1	2	2	2	2
855167	855563	855625	856106	85638502	857010	85713702	85715
2	2	1	2	2	1	2	2
857155	857156	857343	857373	857374	857392	857438	85759902
2	2	2	2	2	1	2	2
857637	857793	857810	858477	858970	858981	858986	859196
1	2	2	2	2	2	2	2
85922302	859283	859464	859465	859471	859487	859575	859711
2	2	2	2	2	2	1	2
859717	859983	8610175	8610404	8610629	8610637	8610862	8610908
1	2	2	1	2	1	1	2
861103	8611161	8611555	8611792	8612080	8612399	86135501	86135502
2	2	1	1	2	1	2	1
861597	861598	861648	861799	861853	862009	862028	86208
2	2	2	2	2	2	2	1
86211	862261	862485	862548	862717	862722	862965	862980
2	2	2	2	2	2	2	2
862989	863030	863031	863270	86355	864018	864033	86408
2	2	2	2	1	2	2	2
86409	864292	864496	864685	864726	864729	864877	865128
2	2	2	2	2	2	1	1
865137	86517	865423	865432	865468	86561	866083	866203
2	1	1	2	2	2	2	1
866458	866674	866714	8670	86730502	867387	867739	868202
2	1	2	2	2	2	1	2
868223	868682	868826	868871	868999	869104	869218	869224
2	2	2	2	2	1	2	2
869254	869476	869691	86973701	86973702	869931	871001501	871001502
2	2	2	2	2	2	2	2
8710441	87106	8711002	8711003	8711202	8711216	871122	871149
2	2	2	2	1	2	2	2
8711561	8711803	871201	8712064	8712289	8712291	87127	8712729
2	1	1	2	1	2	2	1
8712766	8712853	87139402	87163	87164	871641	871642	872113
1	2	2	2	2	2	2	2
872608	87281702	873357	873586	873592	873593	873701	873843
2	2	2	2	1	1	1	2
873885	874158	874217	874373	874662	874839	874858	875093
2	2	1	2	2	2	2	2
875099	875263	87556202	875878	875938	877159	877486	877500
2	2	2	2	2	1	1	2
877501	877989	878796	87880	87930	879523	879804	879830

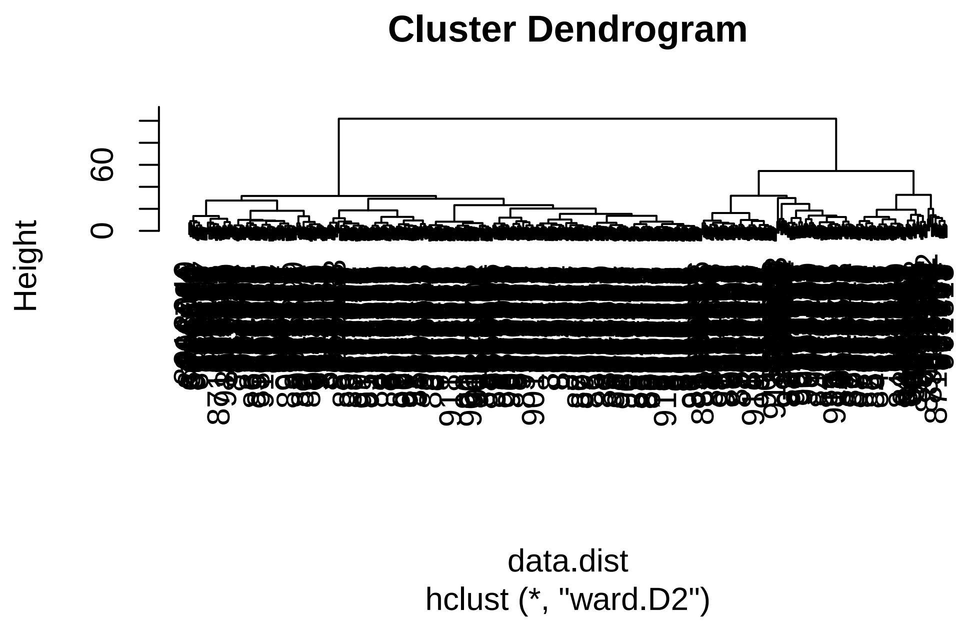
```
        2         1         1         2         2         2         2         1 
  8810158   8810436 881046502   8810528   8810703 881094802   8810955   8810987 
        2         2         1         2         1         2         2         2 
  8811523   8811779   8811842  88119002   8812816   8812818   8812844   8812877 
        2         2         1         1         2         2         2         2 
  8813129  88143502  88147101  88147102  88147202    881861    881972  88199202 
        2         2         2         2         2         2         1         2 
 88203002  88206102    882488  88249602  88299702    883263    883270  88330202 
        2         1         2         2         1         1         2         1 
 88350402    883539    883852  88411702    884180    884437    884448    884626 
        2         2         2         2         1         2         2         2 
 88466802    884689    884948  88518501    885429   8860702    886226    886452 
        2         2         1         2         1         1         1         2 
 88649001    886776    887181  88725602    887549    888264    888570    889403 
        1         2         1         2         1         1         1         2 
   889719  88995002   8910251   8910499   8910506   8910720   8910721   8910748 
        1         1         2         2         2         2         2         2 
  8910988   8910996   8911163   8911164   8911230   8911670   8911800   8911834 
        1         2         1         2         2         1         2         2 
  8912049   8912055     89122   8912280   8912284   8912521   8912909      8913 
        1         2         1         2         2         2         2         2 
  8913049  89143601  89143602      8915    891670    891703    891716    891923 
        2         2         2         2         2         2         2         2 
   891936    892189    892214    892399    892438    892604  89263202    892657 
        2         2         2         2         1         2         1         2 
    89296    893061     89344     89346    893526    893548    893783  89382601 
        2         2         2         2         2         2         2         2 
 89382602    893988    894047    894089    894090    894326    894329    894335 
        2         2         2         2         2         1         2         2 
   894604    894618    894855    895100  89511501  89511502     89524    895299 
        2         1         2         1         2         2         2         2 
  8953902    895633    896839    896864    897132    897137    897374  89742801 
        2         2         2         2         2         2         2         1 
   897604    897630    897880     89812     89813    898143     89827    898431 
        2         1         2         1         2         2         2         1 
 89864002    898677    898678     89869    898690    899147    899187    899667 
        2         2         2         2         2         2         2         2 
   899987   9010018    901011   9010258   9010259    901028   9010333 901034301 
        1         2         2         2         2         2         2         2 
901034302    901041   9010598   9010872   9010877    901088   9011494   9011495 
        2         2         2         2         2         1         1         2 
  9011971   9012000   9012315   9012568   9012795    901288   9013005    901303 
        1         1         2         2         1         1         2         2 
   901315   9013579   9013594   9013838    901549    901836     90250     90251 
        2         2         2         2         2         2         2         2 
   902727     90291    902975    902976    903011     90312  90317302    903483 
        2         2         2         2         2         1         2         2 
   903507    903516    903554    903811  90401601  90401602    904302    904357 
        1         1         2         2         2         2         2         2 
 90439701    904647    904689      9047    904969    904971    905189    905190 
        1         2         2         2         2         2         2         2 
 90524101    905501    905502    905520    905539    905557    905680    905686 
        1         2         2         2         2         2         2         2 
   905978  90602302    906024    906290    906539    906564    906616    906878 
        2         1         2         2         2         2         2         2 
   907145    907367    907409     90745  90769601  90769602    907914    907915 
        2         2         2         2         2         2         2         2 
   908194    908445    908469    908489    908916    909220    909231    909410 
        1         1         2         2         2         2         2         2 
   909411    909445  90944601    909777   9110127   9110720   9110732   9110944 
        2         1         2         2         1         2         1         2 
   911150 911157302   9111596   9111805   9111843    911201    911202   9112085 
        2         1         2         1         2         2         2         2 
  9112366   9112367   9112594   9112712 911296201 911296202   9113156 911320501 
        2         2         2         2         1         1         2         2 
911320502   9113239   9113455   9113514   9113538    911366   9113778   9113816 
        2         2         2         2         1         2         2         2 
   911384   9113846    911391    911408    911654    911673    911685    911916 
        2         2         2         2         2         2         2         2 
   912193     91227    912519    912558    912600    913063    913102    913505 
        2         2         2         2         2         2         2         1 
   913512    913535  91376701  91376702    914062    914101    914102    914333 
        2         2         2         1         1         2         2         2 
   914366    914580    914769     91485    914862     91504     91505    915143 
        2         2         1         1         2         2         2         1 
   915186    915276  91544001  91544002    915452    915460     91550    915664 
        2         2         2         2         2         2         2         2 
   915691    915940  91594602    916221    916799    916838    917062    917080 
        2         2         2         2         1         1         2         2 
   917092  91762702     91789    917896    917897     91805  91813701  91813702 
        2         1         2         2         2         2         2         2 
   918192    918465     91858  91903901  91903902  91930402    919537    919555 
        2         2         2         2         2         1         2         1 
 91979701    919812    921092    921362    921385    921386    921644    922296 
        2         2         2         2         2         2         2         2 
   922297    922576    922577    922840    923169    923465    923748    923780 
```

```
      2        2        2        2        2        2        2        2
 924084   924342   924632   924934   924964   925236   925277   925291
      2        2        2        2        2        2        2        2
 925292   925311   925622   926125   926424   926682   926954   927241
      2        2        2        1        1        1        2        1
  92751
      2
```

```
table(km_method$cluster, diagnosis)
```

```
 diagnosis
    B   M
1   1 130
2 356  82
```

```
#using the hierarchical clustering method
#ward.D2_method is the dataframe from earlier where I applied the Ward.D2 method of cluste
plot(ward.D2_method)
```



```r
#ward.D2_method <- hclust(data.dist, method="ward.D2")
hclust_method <- cutree(ward.D2_method, k=2)
table(hclust_method, diagnosis)
```

```
             diagnosis
hclust_method   B   M
            1  20 164
            2 337  48
```

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

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

```r
table(hclust_method, diagnosis)
```

```
             diagnosis
hclust_method   B   M
            1  20 164
            2 337  48
```

```r
table(km_method$cluster, diagnosis)
```

```
   diagnosis
      B   M
  1   1 130
  2 356  82
```

Overall, the PCA clustering model seems to do the best (has the least total samples being "misdiagnosed"), but the kmeans and hierarchical clustering models also do a good job of clustering them, with hierarchical clustering being better than kmeans.

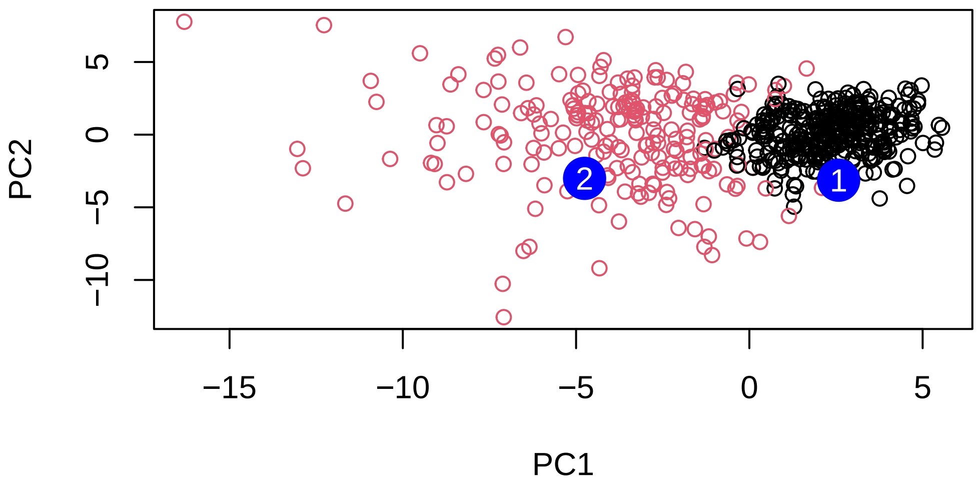
5. Sensitivity/Specificity

6. Prediction

```r
#url <- "new_samples.csv"
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
```

```r
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. Which of these new patients should we prioritize for follow up based on your results?

Patient 2 because they are in the cluster where the majority of samples are malignant.