Class08

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In today's mini project we will explore a complete analysis using the unsupervised learning techniques covered in class specifically looking at breast FNA biopsies of tissue to see if tumors are benign or malignant.

Exploratory data analysis

Save your input data file into your Project directory

```
fna.data <- "WisconsinCancer.csv"
```

Complete the following code to input the data and store as wisc.df

```
wisc.df <- read.csv(fna.data, row.names=1)
# We can use -1 here to remove the first column
wisc.data <- wisc.df[,-1]
# Create diagnosis vector for later
diagnosis <- factor(wisc.df[,1])
```

Q1. How many observations are in this dataset?

```
nrow(diagnosis)
```

```
NULL
```

There are 569 diagnoses

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

```
table(wisc.df$diagnosis)
```

```
  B   M
357 212
```

There are 212 malignant diagnosis

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

```
meancount <- wisc.data[grepl("_mean",colnames(wisc.data))]
length(meancount)
```

```
[1] 10
```

There are 10 variables suffixed with _mean.

Prinicpal Component Analysis

Now we are performing PCA

```
# Check column means and standard deviations
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
```

```
# Perform PCA on wisc.data by completing the following code
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. From your results, what proportion of the original variance is captured by the first principal components (PC1)?

44.3% of variance is captured by PC1

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

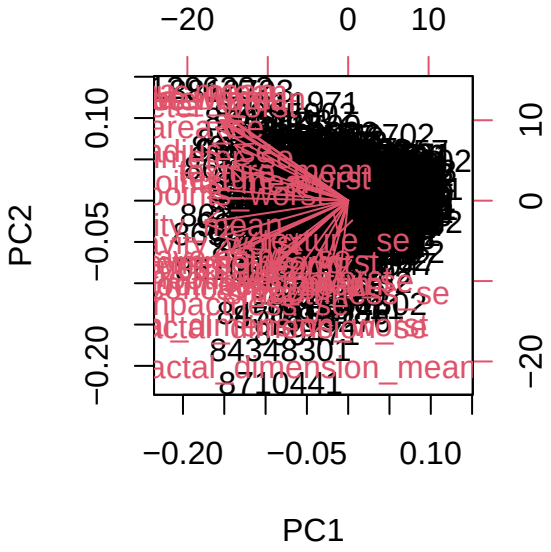
3 Principal components is required to describe at least 70% of the original variance.

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

7 Principal components

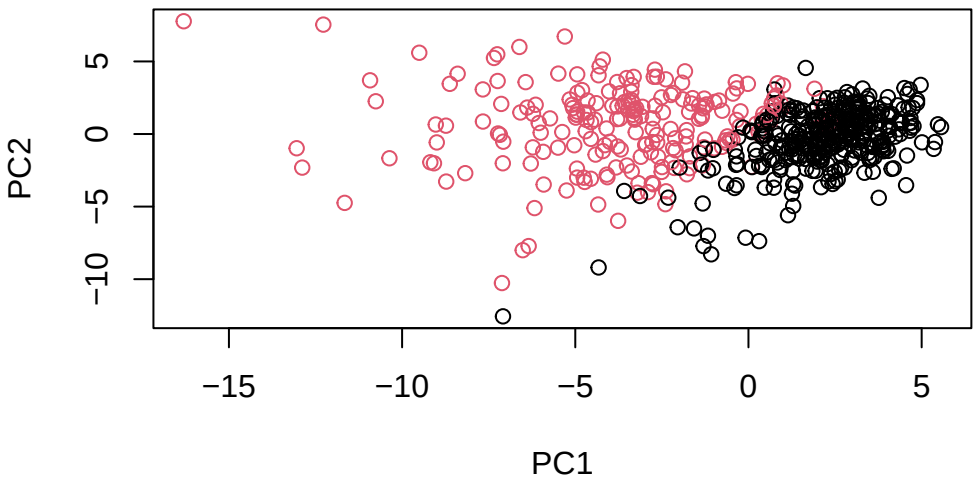
Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why?

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



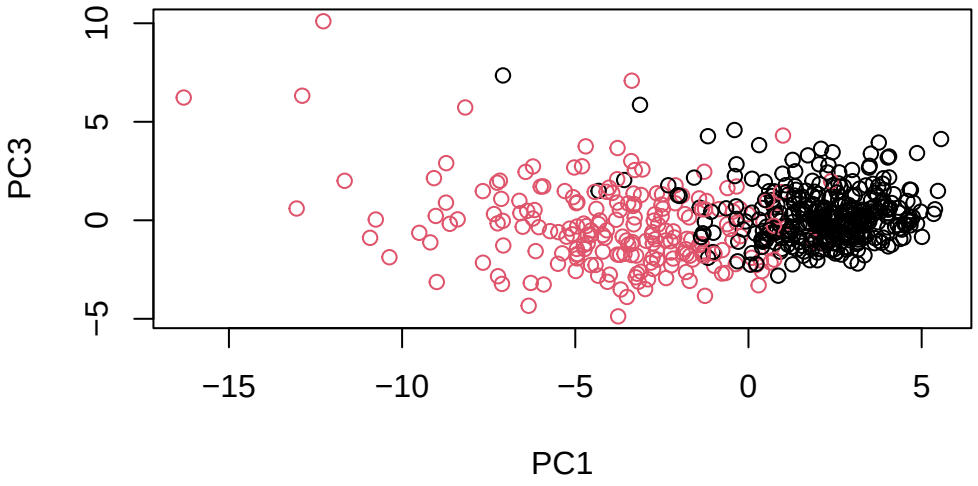
The plot is difficult to understand and is really messy due to the amount of samples(rows) and variables (columns) that are present in the data set.

```
# Scatter plot observations by components 1 and 2
plot(wisc.pr$x[,1], wisc.pr$x[,2], col = diagnosis , xlab = "PC1", ylab = "PC2")
```



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

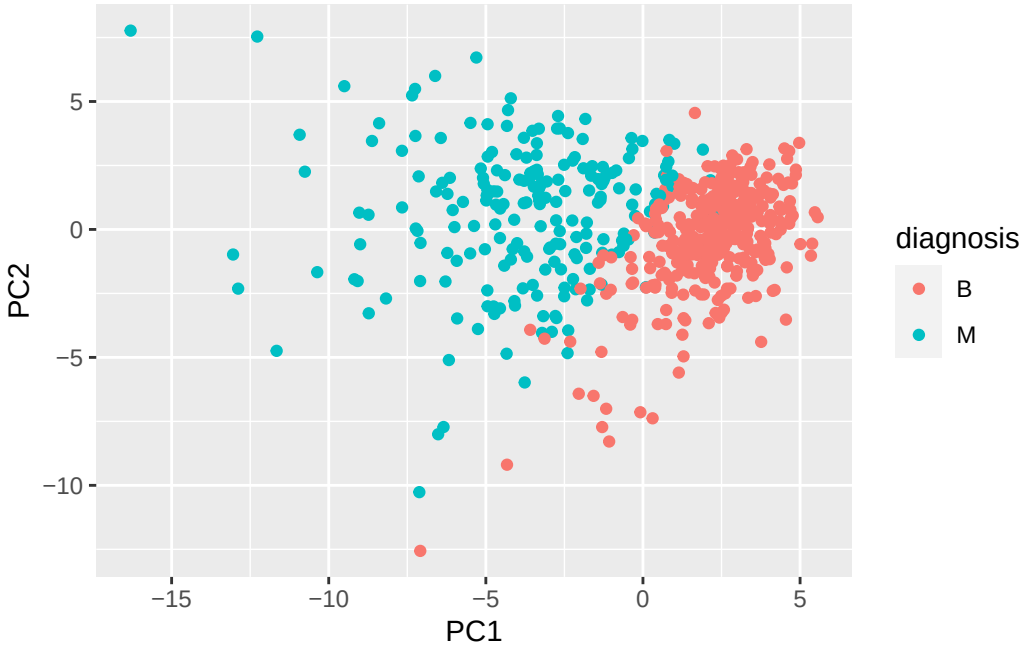
```
# Repeat for components 1 and 3
plot(wisc.pr$x[,1], wisc.pr$x[,3], col = diagnosis,
     xlab = "PC1", ylab = "PC3")
```



The separation between malignant and the benign diagnoses are more mixed together and do not have as clear of a separation in the diagnoses.

```
library(ggplot2)
pc <- as.data.frame(wisc.pr$x)
pc$diagnosis <- diagnosis

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

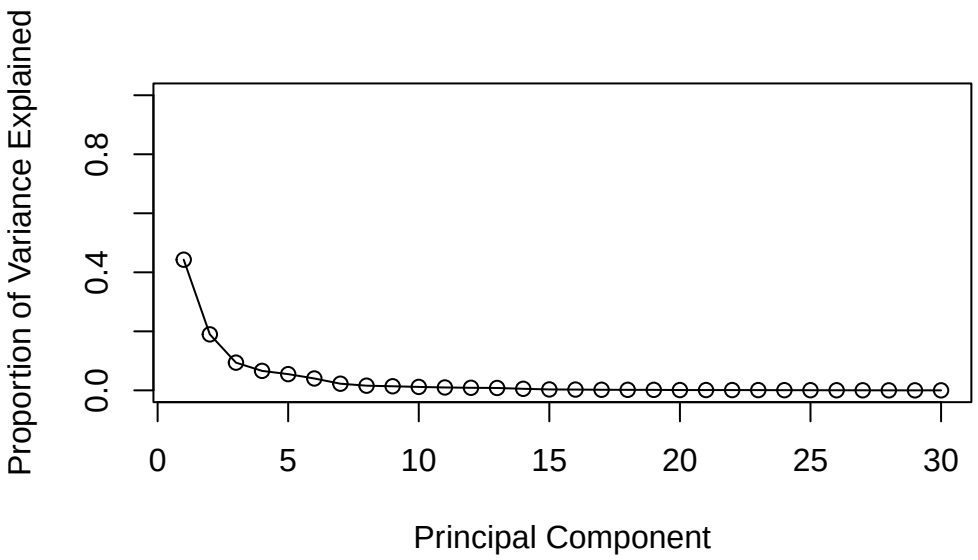



```
# Calculate variance of each component
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

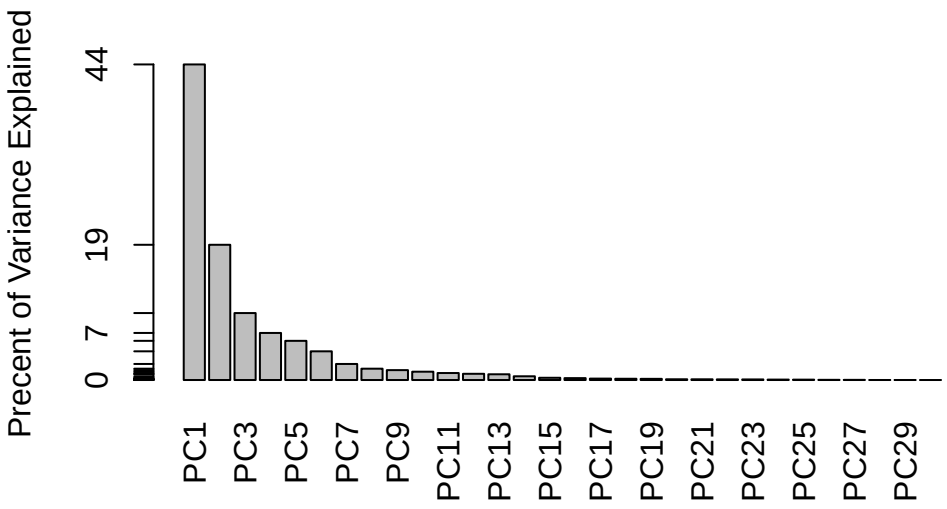
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
# Variance explained by each principal component: pve
pve <- pr.var / sum(pr.var)

# Plot variance explained for each principal component
plot(pve, xlab = "Principal Component",
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```



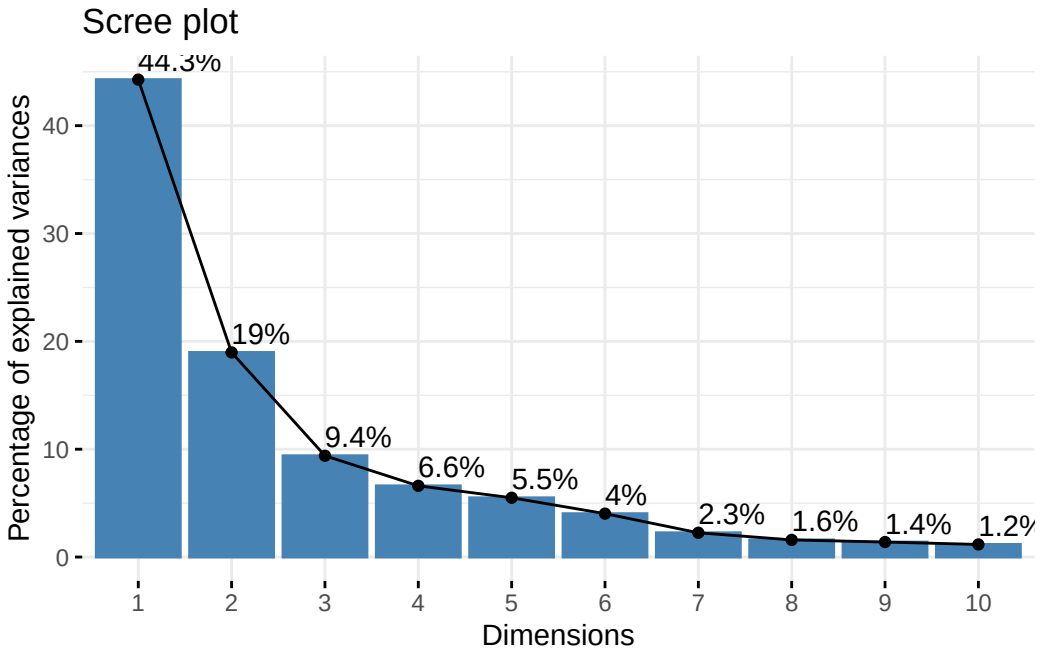

```
# Alternative scree plot of the same data, note data driven y-axis
barplot(pve, ylab = "Precent of Variance Explained",
     names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```




```
## ggplot based graph
#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)
```



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?

```
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
```

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

```
concave.points_mean
         -0.2608538
```

The loading vector for concave.points_mean in PC1 is -0.261

Q10. What is the minimum number of principal components required to explain 80% of the variance of the data?

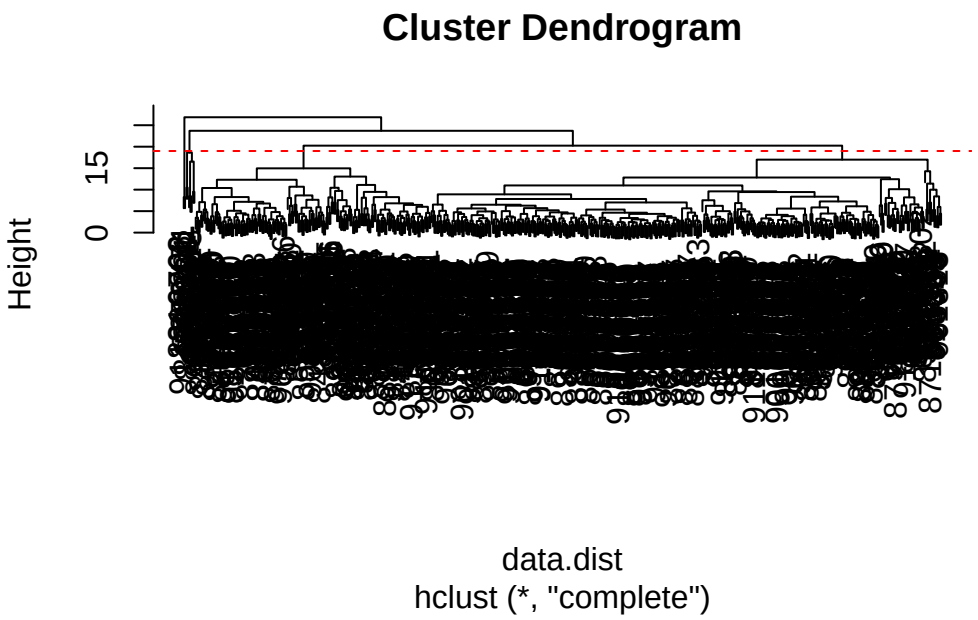
The minimum number is 5 principal components

3. Hiearchial Clustering

```
# Scale the wisc.data data using the "scale()" function
data.scaled <- scale(wisc.data)
data.dist <- dist(data.scaled)
wisc.hclust <- hclust(data.dist, method="complete")
```

Q11. 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)
```



The height is about 19 for which the model has 4 clusters

```
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
```

Q12. Can you find a better cluster vs diagnoses match by cutting into a different number of clusters between 2 and 10?

A better cluster vs diagnoses match would be 10 as evidenced by the following code where most clusters are highly associated with either benign or malignant diagnoses

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

```
                    diagnosis
wisc.hclust.clusters   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
```

Q13. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning.

The best results came from complete since it had much tigheter clusters even though they are closer together.

5. Combining methods

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

This is our cluster dendrogram which has two distinct groups

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

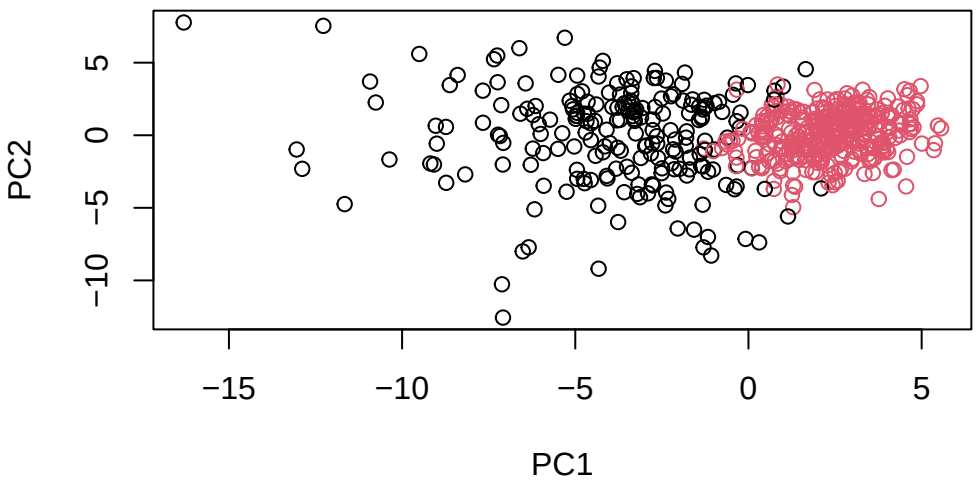
```
grps
  1   2
216 353
```

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

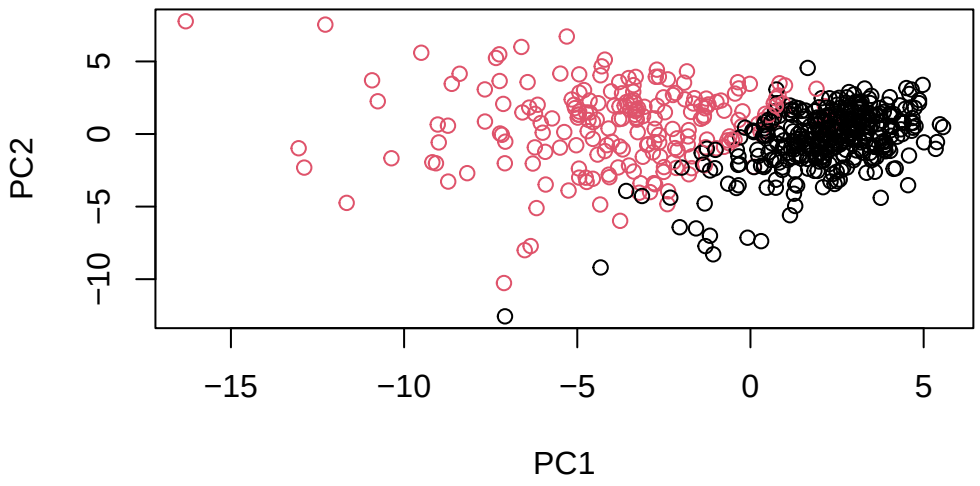
```
    diagnosis
grps   B   M
   1  28 188
```

```
 2 329  24
```

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




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




```
(179+333)/nrow(wisc.data)
```

```
[1] 0.8998243
```

This is the amount of successful identifications of benign or malignant breast cancer

Q15. How well does the newly created model with four clusters separate out the two diagnoses?

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

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

The four clusters seem a bit worse since in cluster 3 there are a noninsignificant amount of false positives