Unsupervised Learning Analysis of Human Breast Cancer Cells

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Preparing the Data

```
# Save your input data file into your Project directory
fna.data <- "https://bioboot.github.io/bimm143_W24/class-material/WisconsinCancer.csv"

# Complete the following code to input the data and store as 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
```

We want to exclude the first column, which is a pathologist provided expert diagnosis, which assigns whether the cancer is malignant or benign.

```
# Creating a new data frame that omits the first column with the diagnosis
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
```

```
#Creating a diagnosis vector for later
diagnosis <- wisc.df[,"diagnosis"]
head(diagnosis)
```

```
[1] "M" "M" "M" "M" "M" "M"
```

Exploratory Data Analysis

Useful functions for Q1-Q3: dim(), nrow(), table(), length(), and grep()

Q1. How many observations are in this data set?

There are 569 cases that were observed in the data set. This can solved using the dim() function or the nrow() function.

```
# The dim() function returns the dimensions of the data frame
dim(wisc.data)
```

```
[1] 569  30
```

```
# The length() function returns the number of columns that are in the data frame
length(wisc.data)
```

```
[1] 30
```

```
# The nrow() function returns the number of rows that are in the data frame
nrow(wisc.data)
```

```
[1] 569
```

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

There are 212 observations with a malignant diagnosis.

```
# Using the table() function, I am able to extract the frequency of the two variables, M a

table(wisc.df$diagnosis)
```

```
  B   M
357 212
```

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

There are 10 variables/features with the suffix "_mean", which was solved with the col.names() function, grep() function, and the length() function.

```
# Retrives all of the column names of the data frame, within a new vector
column_names <- colnames(wisc.data)
# Retrieves all of the column names with "_mean" in the title
mean_columns <- grep("_mean", column_names, value = TRUE)
# Calculates the number of columns with "_mean" in the title
total_mean_columns <- length(mean_columns)
# Returns the number of columns with the phrase "_mean" in the title
total_mean_columns
```

```
[1] 10
```

If I were to makes this a function:

```
phrase_appearance_calc <- function(dataset, PhraseOfInterest) {
  column_names <- colnames(dataset)
```

```
  mean_columns <- grep(PhraseOfInterest, column_names, value = TRUE)
  total_mean_columns <- length(mean_columns)
  total_mean_columns
}
```

```
phrase_appearance_calc(wisc.data, "_mean")
```

```
[1] 10
```

Principle Component Analysis

We will first see if the data needs to be scaled before 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)?

0.4427

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

At least 3 principal components are required - PC1, PC2, and PC3

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

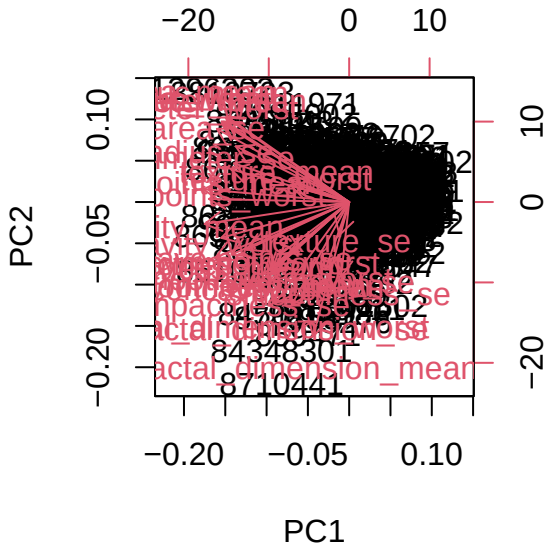
At least 6 principal components (PCs) are required to describe at least 90% of the original variance – PC1, PC2, PC3, PC4, PC5, and PC6

Interpreting PCA Results

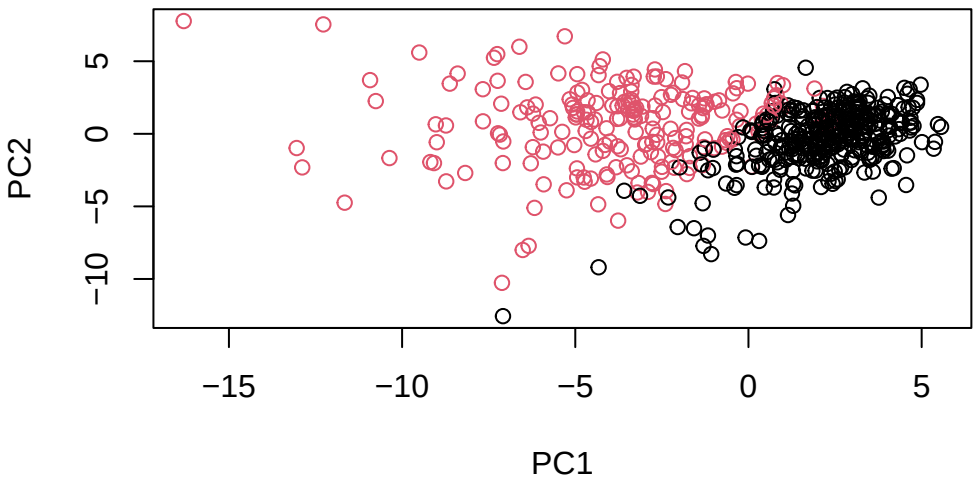
Q7.What stands out to you about this plot? Is it easy or difficult to understand? Why?

The plot seems very cluttered and crowded, so much so that is it almost impossible to discern the different points and words.

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



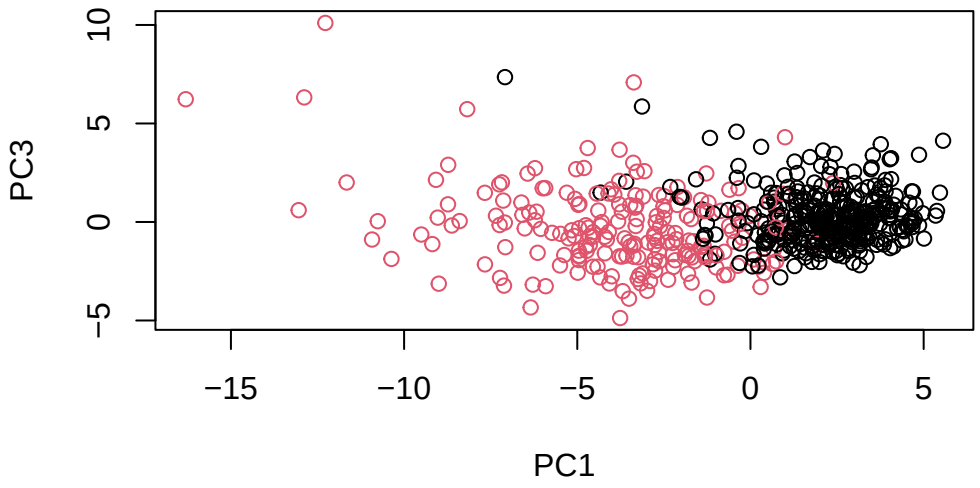

```
plot(wisc.pr$x[,1:2], col = as.factor(diagnosis),
     xlab = "PC1", ylab = "PC2")
```



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

The plot points for PC1 and PC2, as shown in the graph above, are much more 'intertwined' and overlapping with one another, compared to PC1 vs PC3. This is due to greater variance found in PC2.

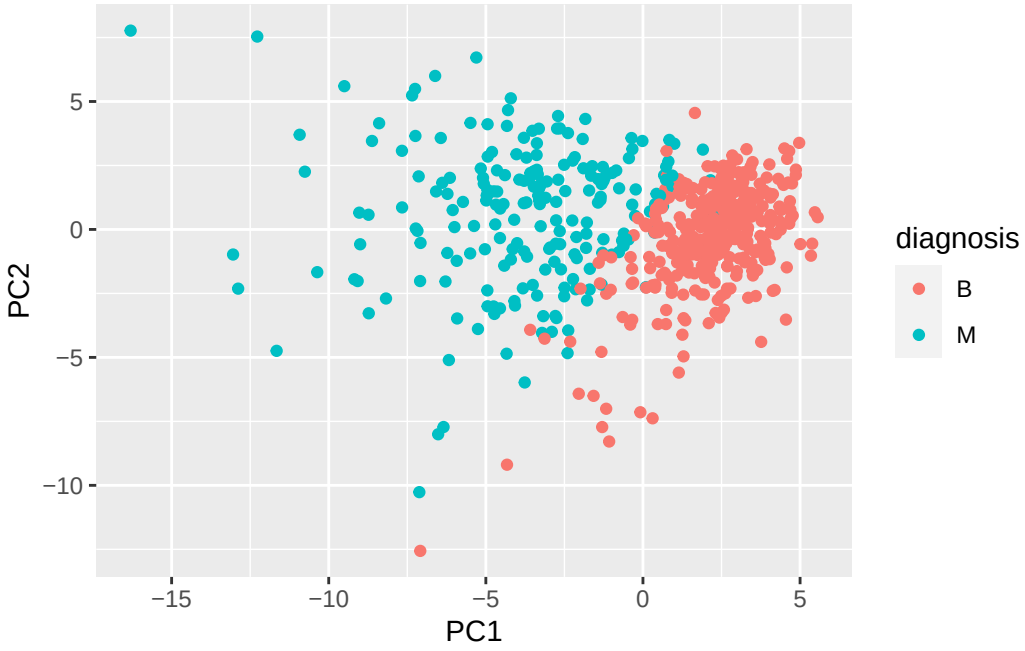
```
plot(wisc.pr$x[,1], wisc.pr$x[,3], col = as.factor(diagnosis),
     xlab = "PC1", ylab = "PC3")
```




```
# Using ggplot2
df <- as.data.frame(wisc.pr$x)
df$diagnosis <- diagnosis

library(ggplot2)

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



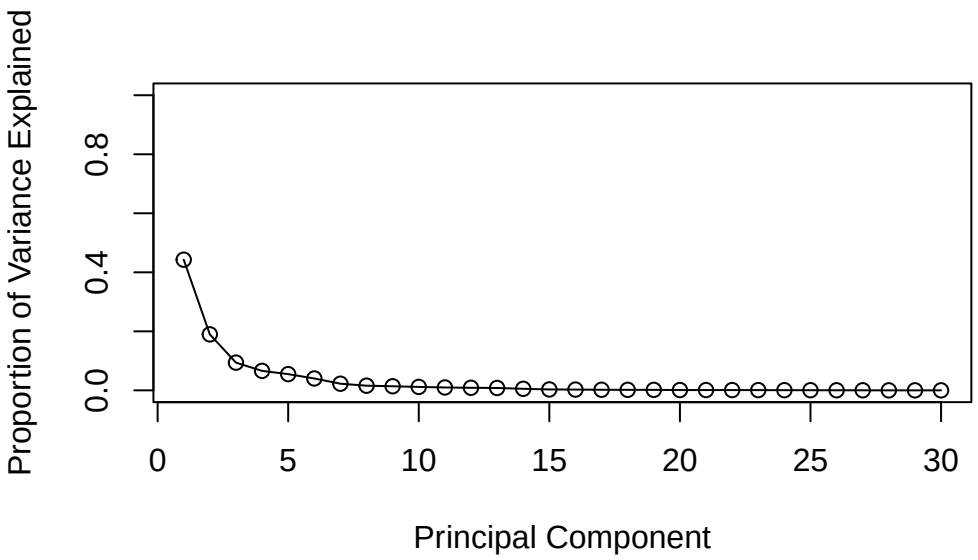
Variance Explained

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

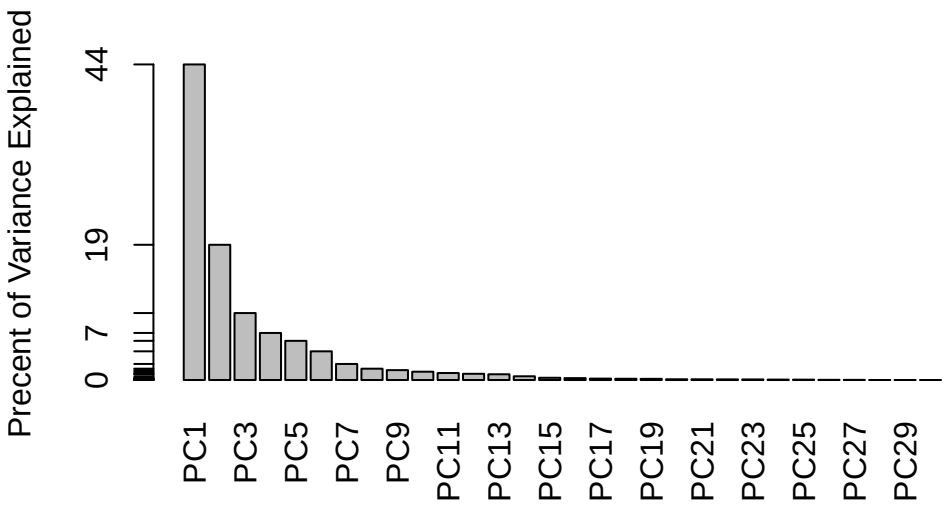
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
# 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")
```



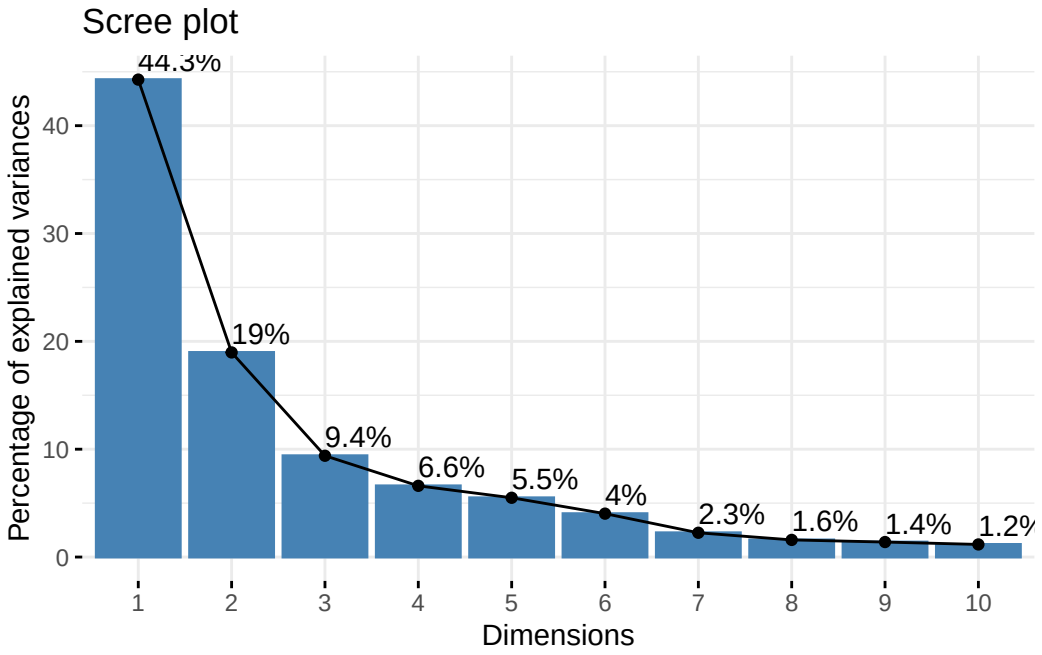

```
# Alternative scree plot of the same data
barplot(pve, ylab = "Precent of Variance Explained",
     names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```




```
library(factoextra)
```

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

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



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`?

-0.2608538

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

```
concave.points_mean
         -0.2608538
```

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

The minimum number of PCs needed to cover 80% of variance is 5 – PC1, PC2, PC3, PC4, & PC5

Hierarchical Clustering

Hierarchical clustering does not assume the number of natural groups that exist in the data – so it would not know that we are looking at two groups: benign and malignant.

```
# Scaling the data using scale()
data.scaled <- scale(wisc.data)
```

```
# Calculating the Euclidean distance between all pairs of observations of scaled data set
data.dist <- dist(data.scaled)
```

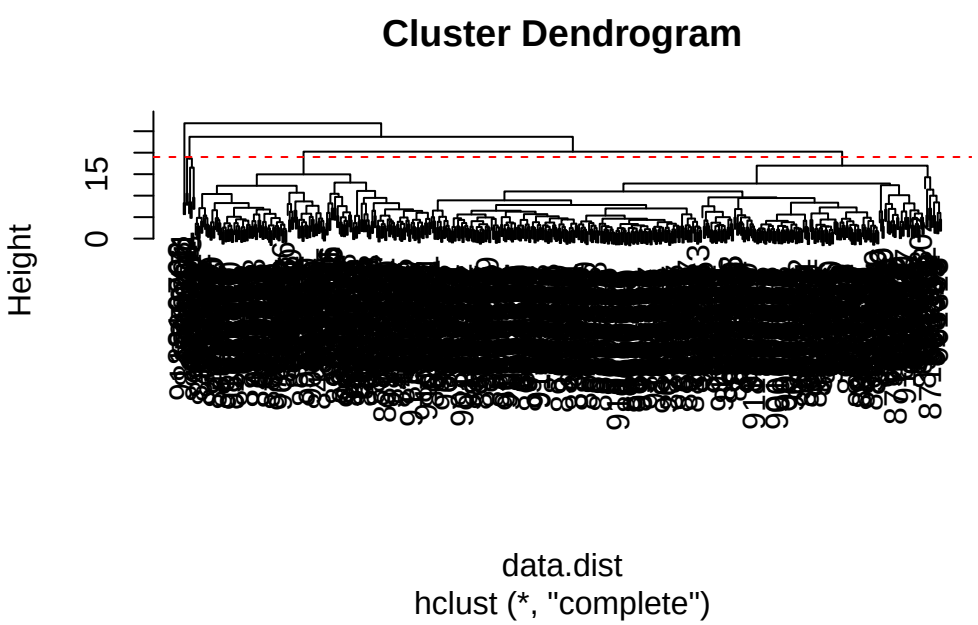
Complete linkage:

```
# Creating a hierarchical clustering model using complete linkage.
wisc.hclust <- hclust(data.dist, method = "complete")
```

Results of Hierarchical Clustering

> **Q11. Using the `plot()` and `abline()` functions, what is the height at which the clustering model has 4 clusters?**
>
> h = 19

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



Selecting Number of 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?

I don't think there is a better cluster because at 4 clusters there are two distinct groups of benign and malignant classifications at cluster 3 and cluster 1 respectively. By adding more clusters, the algorithm is splitting up those classifications into more separate groups, thereby making the classification of malignant vs benign harder to interpret.

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

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

```r
wisc.hclust.clusters.3 <- cutree(wisc.hclust, k = 3)
table(wisc.hclust.clusters.3, diagnosis)
```

```
                     diagnosis
wisc.hclust.clusters.3   B   M
                     1 355 205
                     2   2   5
                     3   0   2
```

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

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

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

```
                     diagnosis
wisc.hclust.clusters.6   B   M
                     1  12 165
                     2   0   5
                     3 331  39
                     4   2   0
                     5  12   1
                     6   0   2
```

```r
wisc.hclust.clusters.7 <- cutree(wisc.hclust, k = 7)
table(wisc.hclust.clusters.7, diagnosis)
```

```
                     diagnosis
wisc.hclust.clusters.7   B   M
                     1  12 165
                     2   0   3
                     3 331  39
                     4   2   0
                     5  12   1
                     6   0   2
                     7   0   2
```

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

```
                     diagnosis
wisc.hclust.clusters.8   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
```

```r
wisc.hclust.clusters.9 <- cutree(wisc.hclust, k = 9)
table(wisc.hclust.clusters.9, diagnosis)
```

```
                     diagnosis
wisc.hclust.clusters.9   B   M
                     1  12  86
                     2   0  79
                     3   0   3
                     4 331  39
                     5   2   0
                     6  12   0
                     7   0   2
```

```
  8   0   2
  9   0   1
```

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

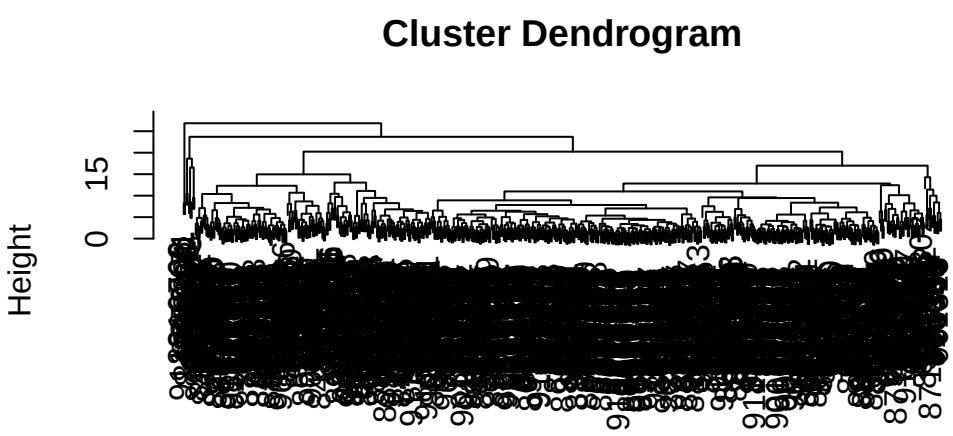
```
                      diagnosis
wisc.hclust.clusters.10   B   M
                     1   12  86
                     2    0  59
                     3    0   3
                     4  331  39
                     5    0  20
                     6    2   0
                     7   12   0
        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

Using Different Methods

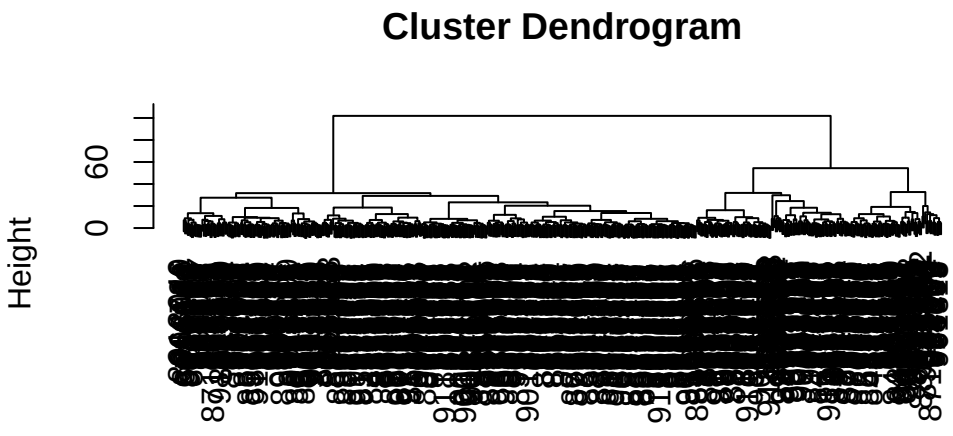
Q13. Which method gives your favorite results for the same `data.dist` dataset? Explain your reasoning.

I think the best methods for analyzing the data set, in my opinion, would be there "complete" and "ward.D2" approaches. As someone who is not an expert in PC analysis, the plots generated by these two approaches are easiest to read and interpret, as the first layers which separate the data into two clusters are most distinct. The lineages and sizes of the clusters are more comparable as they are evenly sized. With the "single" method, the data is grouped too closely together, so it is difficult to understand the distinctions/classifications of the data points.

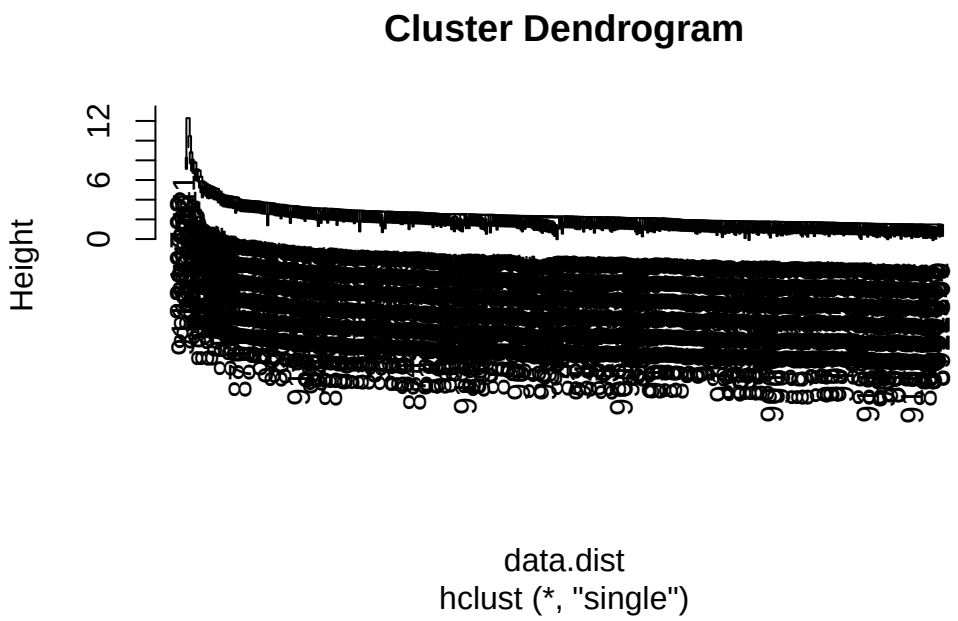
```
wisc.hclust <- hclust(data.dist, method = "complete")
plot(wisc.hclust)
```



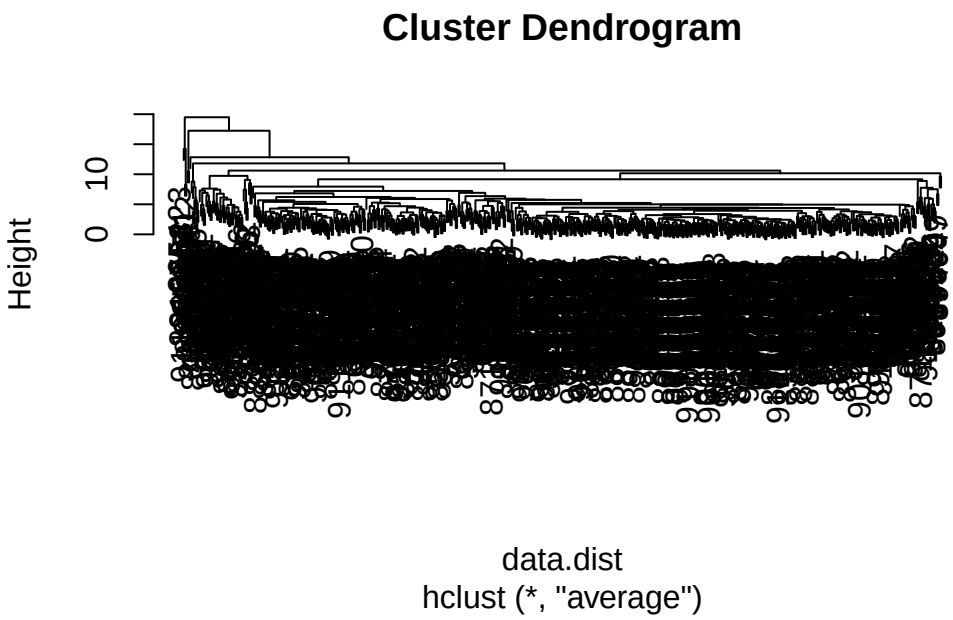

```
wisc.hclust.ward <- hclust(data.dist, method = "ward.D2")
plot(wisc.hclust.ward)
```



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




```
wisc.hclust.avg <- hclust(data.dist, method = "average")
plot(wisc.hclust.avg)
```



OPTIONAL: K-means clustering

```
wisc.km <- kmeans(wisc.data, centers = 2, nstart = 20)

table(wisc.km$cluster, diagnosis)
```

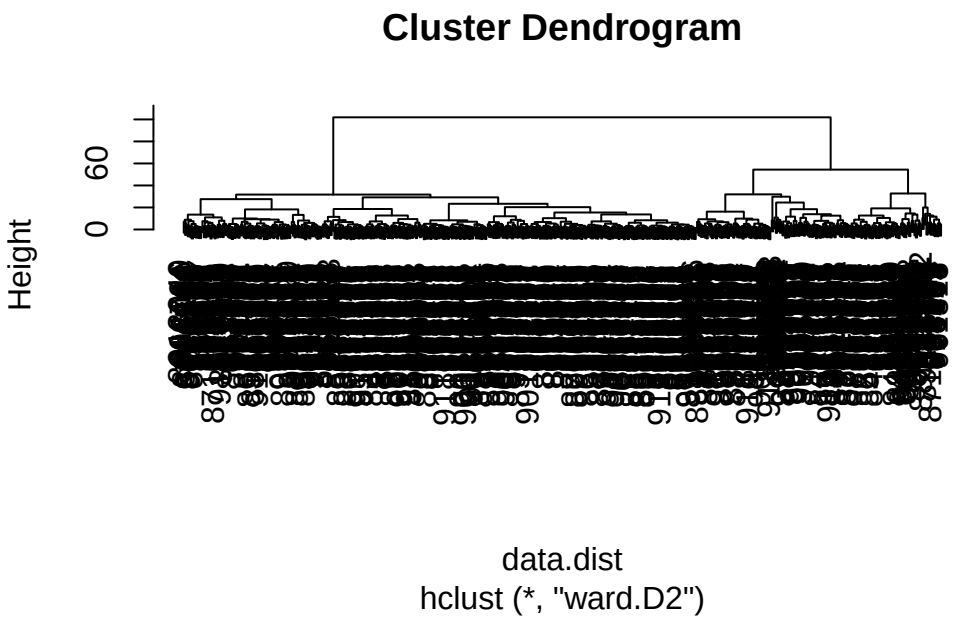
```
   diagnosis
      B   M
  1 356  82
  2   1 130
```

```
table(wisc.hclust.clusters, wisc.km$cluster)
```

```
wisc.hclust.clusters   1   2
                   1  68 109
                   2   5   2
                   3 365  18
                   4   0   2
```

Combining Methods: Clustering on PCA Results

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



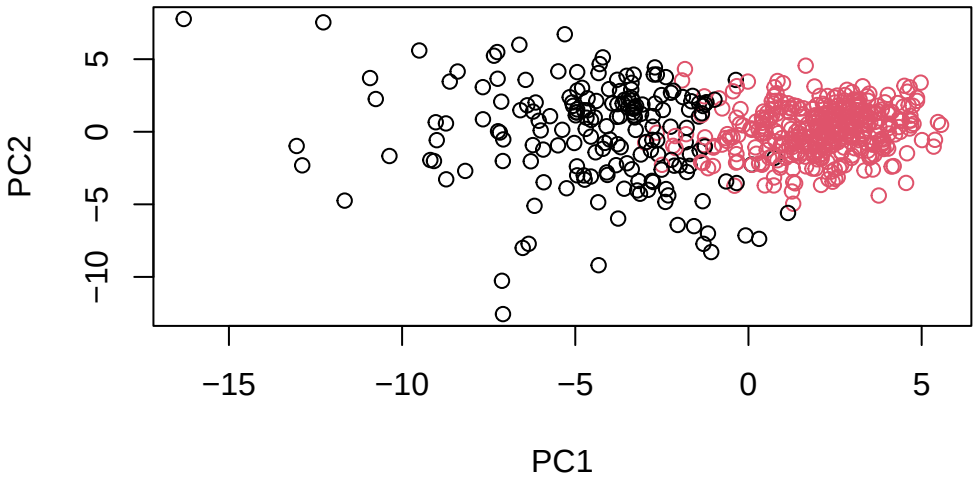

```
grps <- cutree(wisc.hclust.ward, k=2)
table(grps)
```

```
grps
  1   2
184 385
```

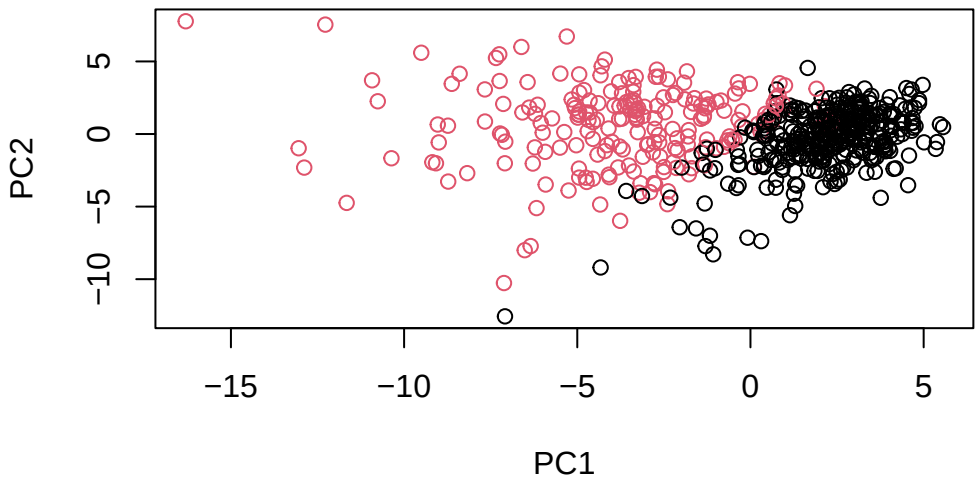
```
table(grps, diagnosis)
```

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

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




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



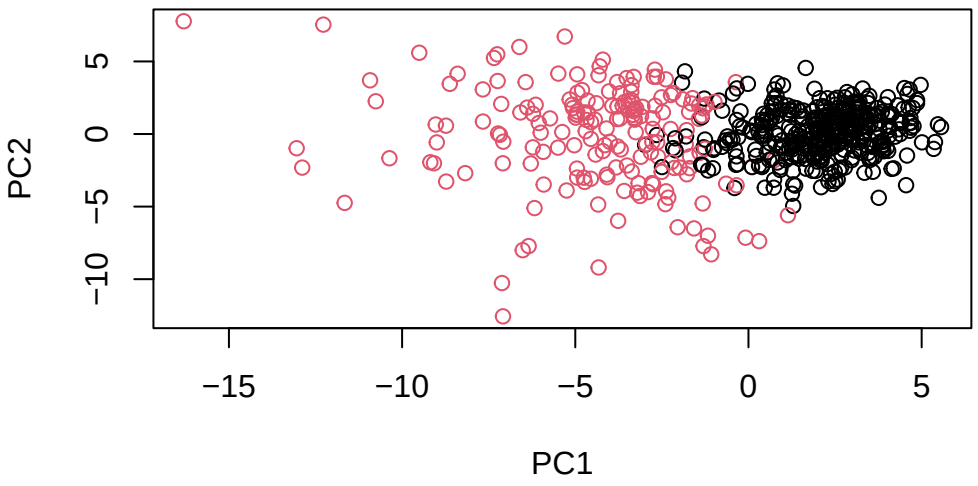

```
g <- as.factor(grps)
levels(g)
```

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

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

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

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




```
sc.pr.hclust.clusters <- hclust(data.dist, method = "ward.D2")
wisc.pr.hclust.clusters <- cutree(wisc.pr.hclust, k=2)
table(wisc.pr.hclust.clusters, diagnosis)
```

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

Q16. How well do the k-means and 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.hclust.clusters`) with the vector containing the actual diagnoses.

I think the clustering models are relatively comparable, in the sense that I think for both the data points all seem to be pretty spread out from one another into distinct benign vs malignant clusters (which we can see when compared with the actual diagnoses). I think either could be used, both may just require some trial and error with the number of clusters.

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

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

Sensitivity/Specificity

Q17. Which of your analysis procedures resulted in a clustering model with the best specificity? How about sensitivity? Sensitivity = malignant, Specificity = Benign

True values: Benign: 357, Malignant: 212

Sensitivity: Combined PCA with hierarchical clustering performed the best, with 188/212

Specificity: K means and hierarchical clustering performed equally well, with 343/357

```
kmeans_specificty <- 175/212
kmeans_specificty
```

```
[1] 0.8254717
```

```
kmeans_selectivity <- 343/357
kmeans_selectivity
```

```
[1] 0.9607843
```

```
hcluster_specificity <- 165/212
hcluster_specificity
```

```
[1] 0.7783019
```

```
hcluster_sensitivity <- 343/357
hcluster_sensitivity
```

```
[1] 0.9607843
```

```
combined_specificity <- 188/212
combined_specificity
```

```
[1] 0.8867925
```

```
combined_selectivity <- 329/357
combined_selectivity
```

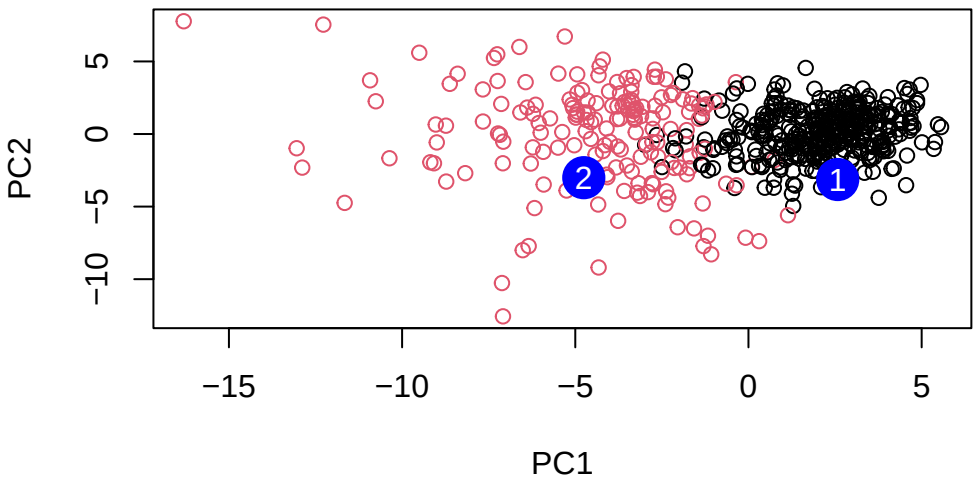
```
[1] 0.9215686
```

Prediction

```
#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
```

```
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")
```



Q18. Which of these new patients should we prioritize for follow up based on your results?

Assuming the red and black are still associated with malignant and benign diagnoses, respectively, I think patient 1 should be prioritized, as it is clustered together with other malignant cells.