Class 08 Lab

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1. Exploratory Data Analysis

```
#First, save the input data file into the Project Directory
fna.data <- read.csv("WisconsinCancer.csv")

# Input the data and store as wisc.df
wisc.df <- data.frame(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
```

```
# Remove the first column (diagnosis) from the data.frame
wisc.data <- wisc.df[,-1]

# View the dataset
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
```

```
# Create diagnosis vector for later
diagnosis <- factor(wisc.df$diagnosis)
```

Question 1

How many observations are in this dataset?

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

```
[1] 569
```

There are 569 observations in this dataset.

Question 2

How many of the observations have a malignant diagnosis?

```
table(diagnosis)
```

```
diagnosis
  B   M
357 212
```

There are 212 malignant diagnoses.

Question 3

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

```
sum(grepl("_mean$", names(wisc.data)))
```

```
[1] 10
```

There are 10 features that are suffixed with _mean.

2. Principal Component Analysis

```
# 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
```

The data does appear to use different units of measurement and to have slightly different variances, so scaling is necessary.

```
# 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
```

Question 4

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

```
# Using wisc.pr:

#find proportion of the original variance
prop_var <- wisc.pr$sdev^2 / sum(wisc.pr$sdev^2)

#find which `prop_var` is represented by PC1 (1)
prop_var[1]
```

```
[1] 0.4427203
```

The first principal components capture ~44% of the original variance.

Question 5

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

```
# Using `prop_var` from above:

# find cumulative variance
cum_var <- cumsum(prop_var)

# find the number of PCs required to reach at least 70% variance
which(cum_var >= 0.70)[1]
```

```
[1] 3
```

Three principal components are required to describe at least 70% of the data's.

Question 6

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

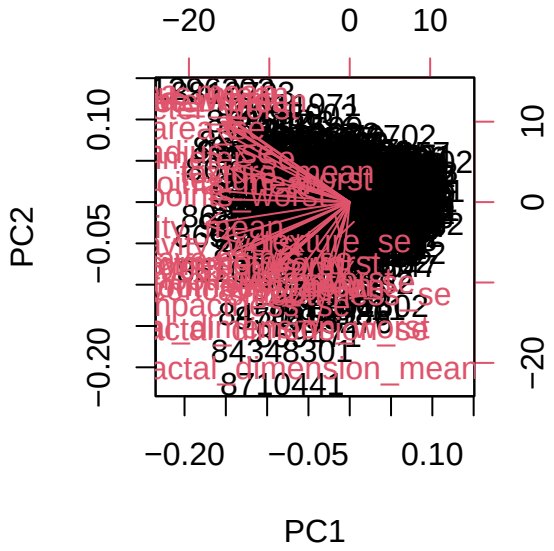
```
# find the number of PCs required to reach at least 90% variance
which(cum_var >= 0.90)[1]
```

```
[1] 7
```

Seven principal components are required to describe at least 90% of the data's variance.

Now, I will create a biplot of the `wisc.pr` using the `biplot()` function.

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



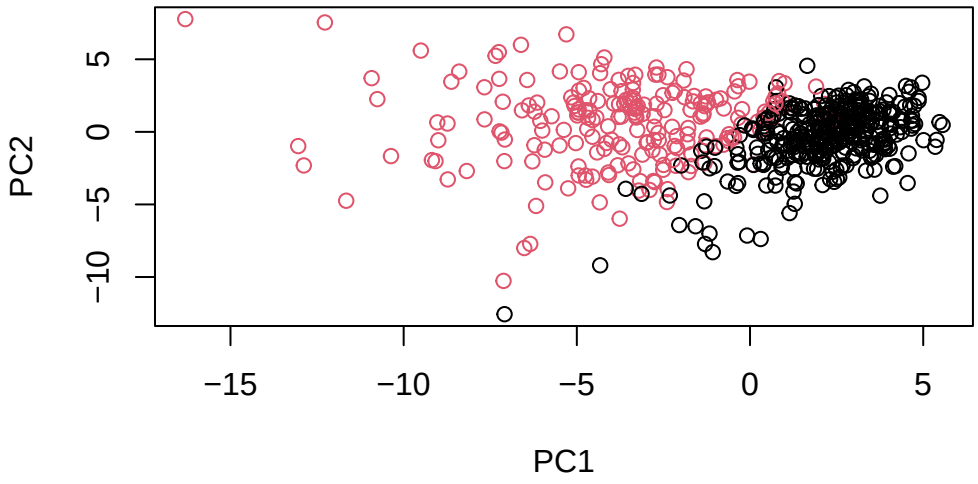
Question 7

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

This plot seems unorganized to me. The data is hard to interpret because you cannot read the labels for each plot, and all the labels crowd the data so you can't see the datapoints- making it difficult to understand. The plot also has no units.

To start fixing this:

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

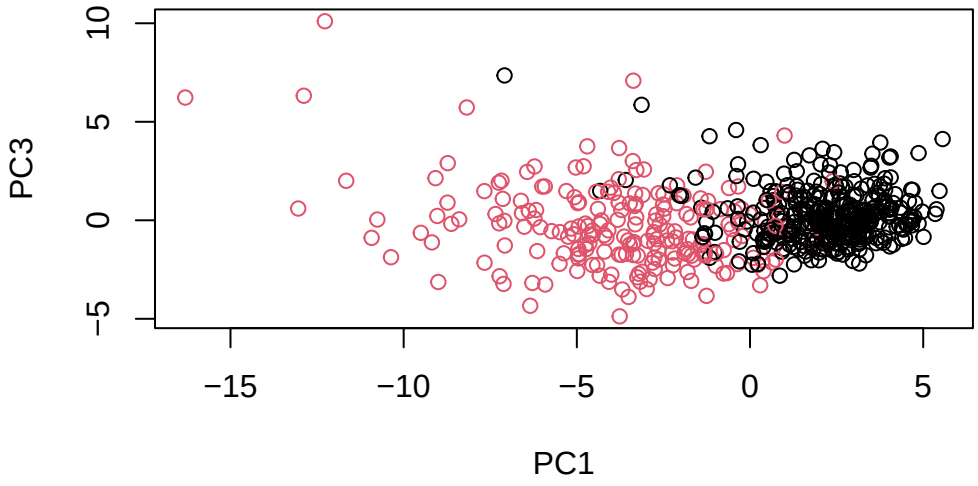


Question 8

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

For the plots below: I notice that the new plots have slightly less clear separation when comparing them to those created by comparing PC1 vs PC2. The original plots have better separation between the data because they cover more of the variance.

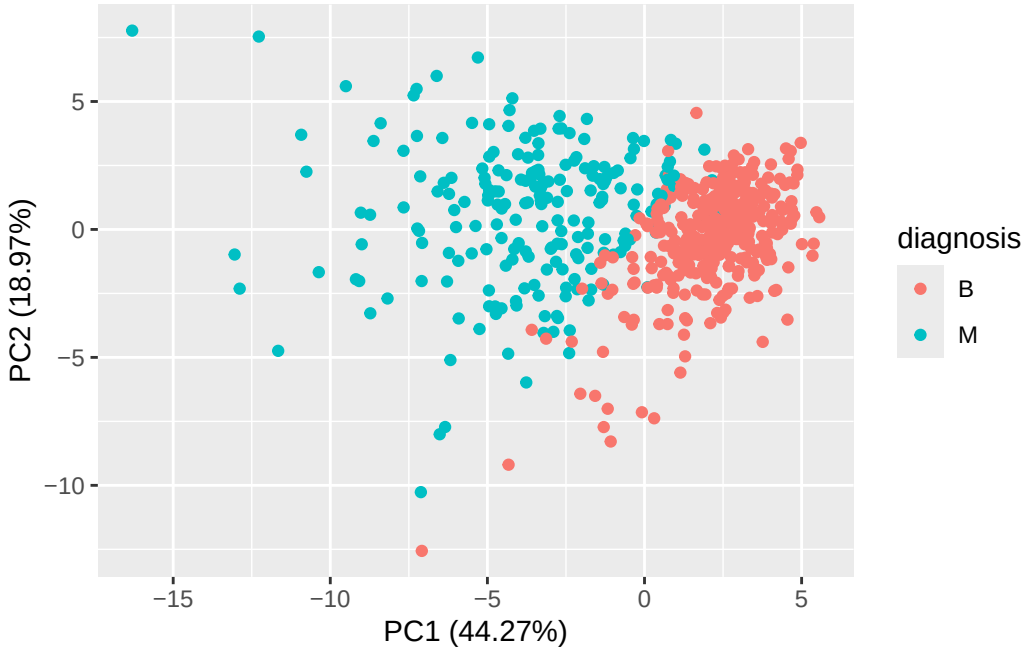
```
# Repeat for components 1 and 3
plot(wisc.pr$x[, c(1, 3) ], col = diagnosis ,
     xlab = "PC1", ylab = "PC3")
```



The separation between the two groups appears to be less clear in the above graph. This is because PC2 explains more variance than PC3.

Using ggplot to make it fancier:

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

# Load the ggplot2 package
library(ggplot2)

# Make a scatter plot colored by diagnosis
ggplot(wisc.pr$x) +
  aes(PC1, PC2, col= diagnosis ) +
  labs(x="PC1 (44.27%)", y="PC2 (18.97%)") +
  geom_point()
```

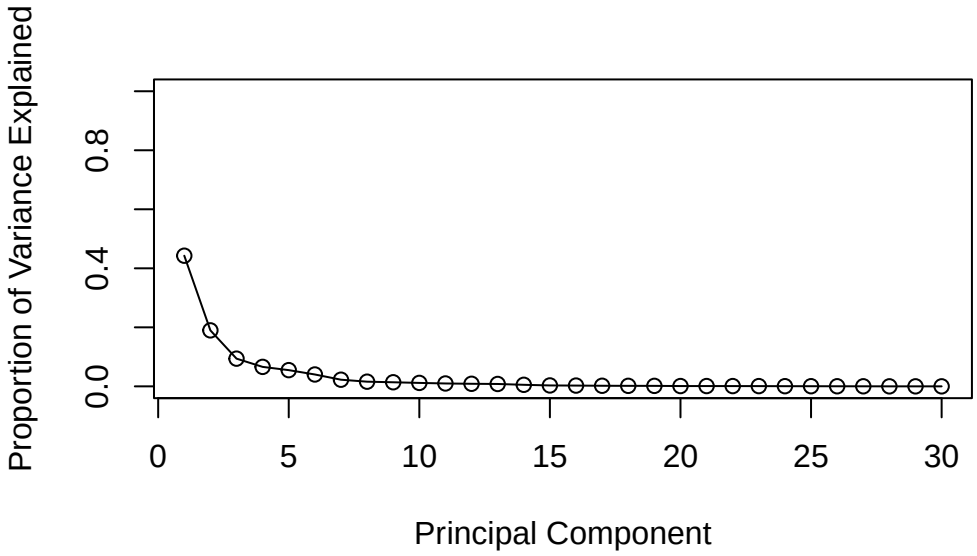



```
# Calculate variance of each component
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

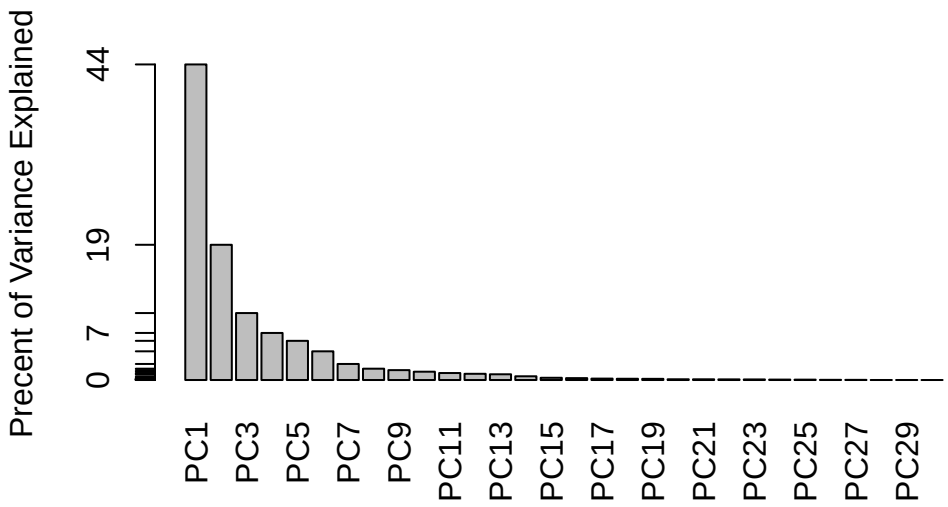
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

Calculate the variance explained by each principal component by dividing by the total variance explained by all principal components. Assign this to a variable called pve and create a plot of variance explained for each principal component.

```
# Variance explained by each principal component: pve
pve <- wisc.pr$sdev^2 / sum(wisc.pr$sdev^2)

# 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 )
```



skipped the cran example

Question 9

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?

```
# Get the component of the loading vector for concave.points_mean (PC1)

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

loading_concave_points_mean
```

```
[1] -0.2608538
```

The component of the loading vector for `concave.points_mean` is -0.26.

Question 10

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

```
which(cum_var >= 0.80)[1]
```

```
[1] 5
```

There are 5 principal components required to explain 80% of the data's variance.

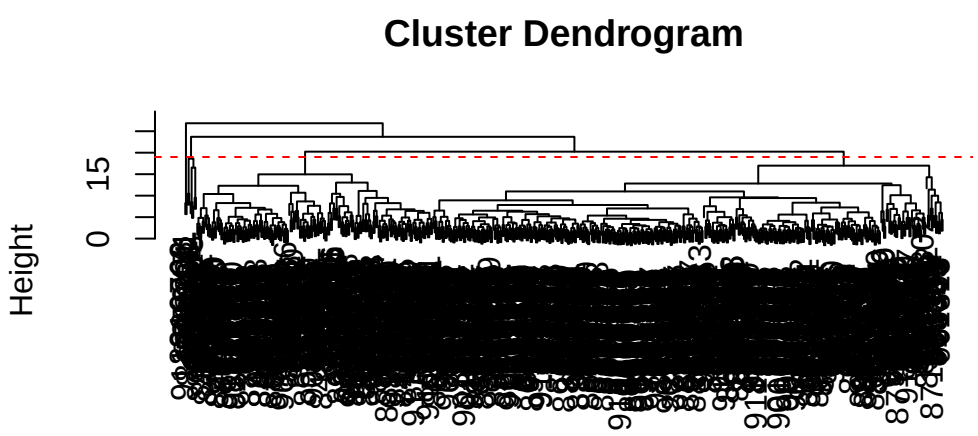
3. Hierarchical Clustering

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

# Calculate distances between all pairs in `data.scaled`
data.dist <- dist(data.scaled)

# Use complete linkage to create a hierarchical clustering model. Specify the method argumen
wisc.hclust <- hclust(data.dist, method = "complete")
```

Question 11

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

```
# plot the dendrogram of the clustering model
plot(wisc.hclust)

# find where h = x has 4 clusters, done by trial and error
abline(h = 19, col="red", lty=2)
```



The clustering model has 4 clusters when h = 19.

```
# use cutree to cut the tree down to 4 clusters
wisc.hclust.clusters <- cutree(wisc.hclust, k = 4)

# make a table to compare cluster membership to diagnoses
table(wisc.hclust.clusters, diagnosis)
```

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

When four clusters were picked, cluster 1 appears to correspond with mostly malignant cells (M = 165, B = 12) and cluster 3 largely corresponds to benign cells (M = 40, B = 343), but not perfectly.

Question 12

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

```
# use cutree to cut the tree down to 2 - 10 clusters, done by trial and error
wisc.hclust.clusters <- cutree(wisc.hclust, k = 5)

# make a table to compare cluster membership to diagnoses
table(wisc.hclust.clusters, diagnosis)
```

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

Based on the options (k = 2-10) I tried, I ended up liking the arrangement when cutting the tree down to 5 clusters.

In this result, we have a relatively clear separation between beningn and malignant cell populations, like when k = 4. The numbers of benign and malignant cells in clusters 1 and 3 are consistent.

However, we have the additional benefit of a more clear separation in the other three clusters (2, 4, and 5) with all three containing either only malignant or only benign cells.

So, I believe k = 5 presents a better diagnoses versus clusters match.

There are a number of different methods that can be used to combine points during the hierarchical clustering procedure. These include “single”, “complete”, “average” and (Prof. Grant’s favorite) “ward.D2”.

Question 13

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

```
# Trying hierarchical clustering with different methods

# "single"
wisc.hclust.s <- hclust(data.dist, method = "single")

wisc.hclust.s.clusters <- cutree(wisc.hclust.s, k = 5)

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

```
                      diagnosis
wisc.hclust.s.clusters   B   M
                     1 356 209
                     2   1   0
                     3   0   1
                     4   0   1
                     5   0   1
```

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

wisc.hclust.comp.clusters <- cutree(wisc.hclust.comp, k = 5)

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

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

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

wisc.hclust.avg.clusters <- cutree(wisc.hclust.avg, k = 5)

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

```
                       diagnosis
wisc.hclust.avg.clusters   B   M
                       1 355 208
                       2   2   0
                       3   0   1
                       4   0   2
                       5   0   1
```

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

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

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

```
                          diagnosis
wisc.hclust.ward.clusters   B   M
                        1   0  59
                        2   0  56
                        3   6  48
                        4 337  48
                        5  14   1
```

I decided to use k = 5 for all my comparisons, because it was what I liked most in the original method. I ended up liking "ward.D2" the most, because I believe it displayed a more thorough separation, with potentially another variable clustering them. There are several clusters that have only benign or malignant cells, with larger populations in each of the clusters than the other methods, which I just like more, visually.

4. K-means clustering (skipped)

Question 14 (skipped)

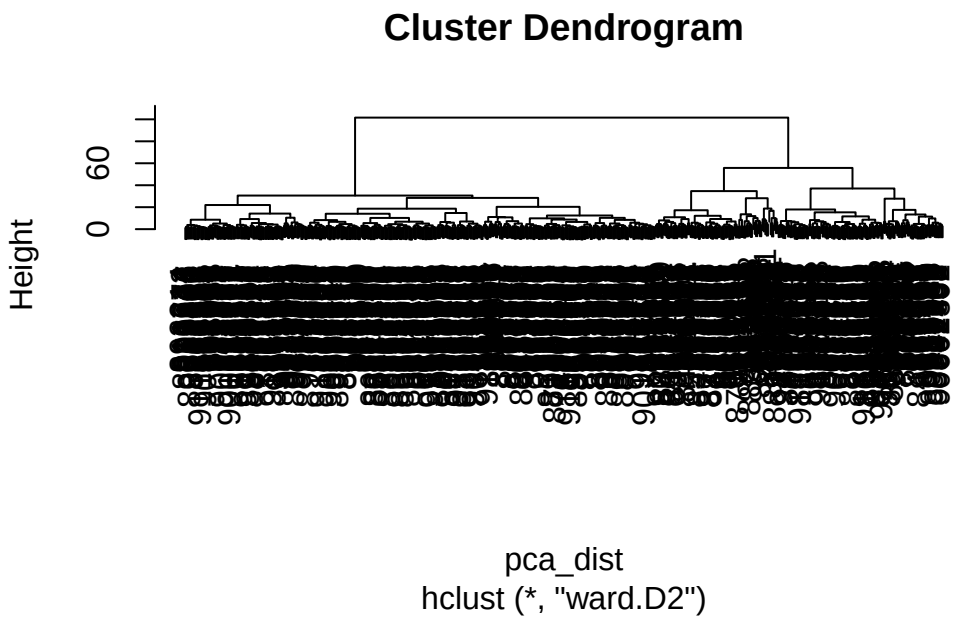
5. Combining Methods

Using the minimum number of principal components required to describe at least 90% of the variability in the data, create a hierarchical clustering model with the linkage method = "ward.D2". (Ward's criterion is used here because it is based on multidimensional variance like principal components analysis)

Assign the results to wisc.pr.hclust.

```r
# Obtain cumulative proportion
cum_var <- cumsum(pve)

# Find number of PCs needed to reach 90%
num_pcs_90 <- which(cum_var >= 0.90)[1]

# Subset PCA-transformed data to those components
pca_subset <- wisc.pr$x[, 1:num_pcs_90]
```

```r
# Compute distances using Euclidean metric on PCA scores
pca_dist <- dist(pca_subset)

# Perform hierarchical clustering with Ward's method
wisc.pr.hclust <- hclust(pca_dist, method = "ward.D2")

#Plot the new subset
plot(wisc.pr.hclust)
```



What do the two main branches of dendrogram (indicating two main clusters) show? Are the malignant and benign?

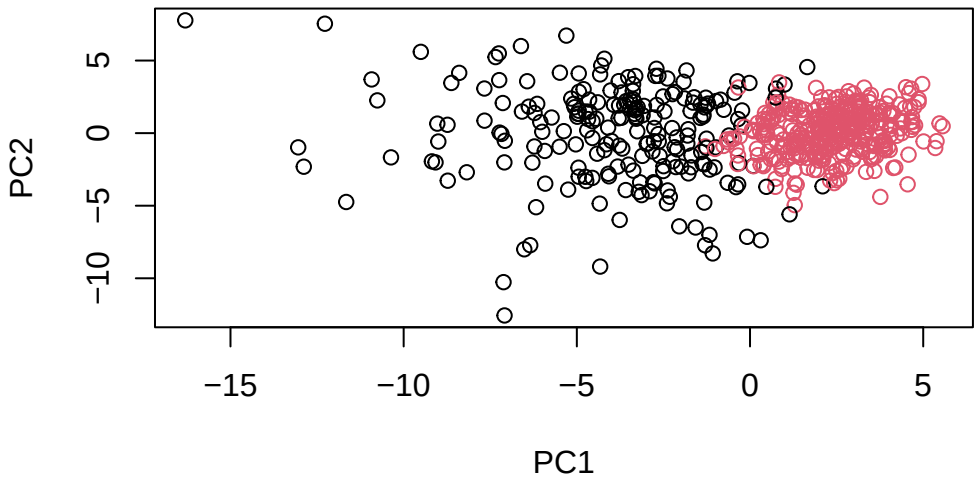
```r
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

```
grps
  1   2
216 353
```

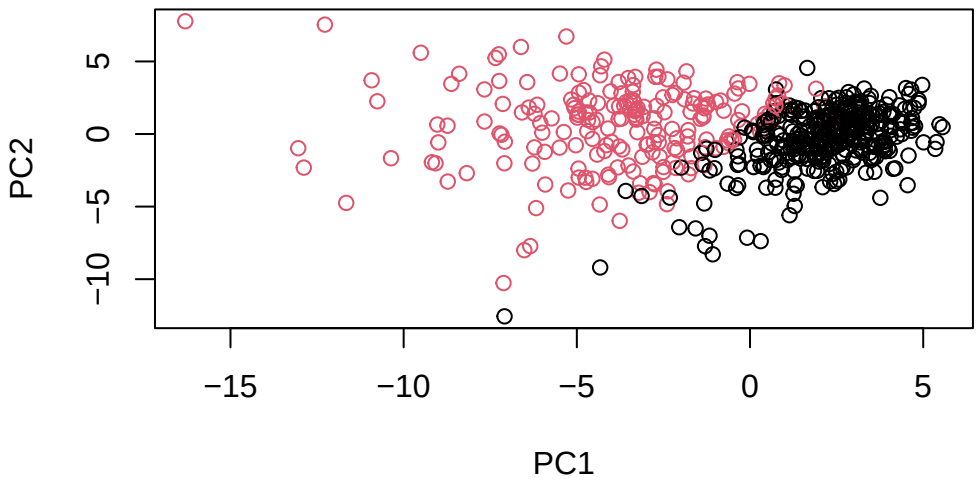
```r
table(grps , diagnosis)
```

```
    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)
```



There is a color swap here indicating 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).

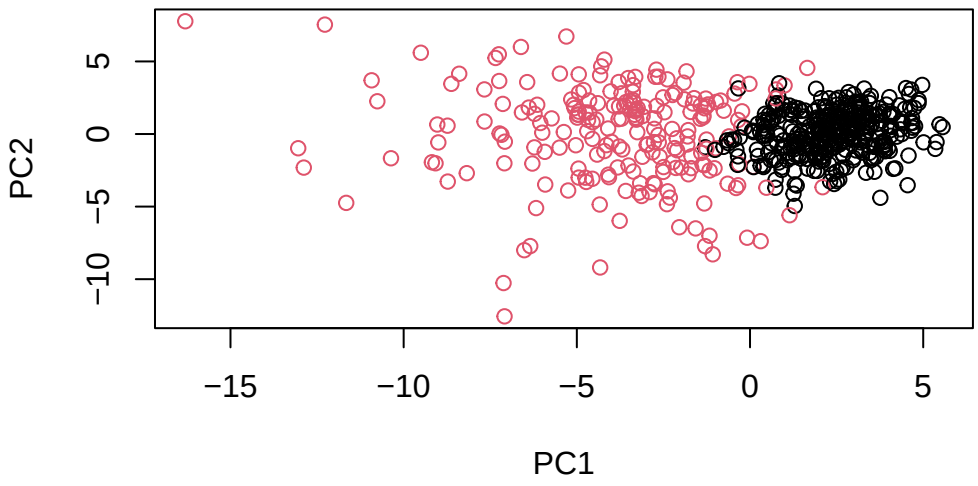
```
g <- as.factor(grps)
levels(g)
```

```
[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)
```



I skipped the rest of the fancy stuff...

Question 15

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

```
# Compare to actual diagnoses
grps <- cutree(wisc.pr.hclust, k=2)

table(grps , diagnosis)
```

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

It separates them relatively well, but not perfectly as it has grouped a small population of benign cells with the larger population of malignant cells, and vice versa.

Question 16

> 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.km$cluster and wisc.hclust.clusters) with the vector containing the actual diagnoses.

```
# No table created for wisc.km$cluster because that section was labeled "Optional" and I did

# Create table for `wisc.hclust.clusters`
table(wisc.hclust.clusters , diagnosis)
```

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

According to my classmates (source: Grace), the k-means model did not do well. I think the hierarchical clustering model does a pretty decent job.

6. Sensitivity / Specificity

Sensitivity: refers to a test's ability to correctly detect ill patients who do have the condition. In our example, the sensitivity = the total number of samples in the cluster identified as predominantly malignant (TP) (cancerous) divided by the total number of known malignant samples (TP+FN). In other words: TP/(TP+FN).

Specificity: relates to a test's ability to correctly reject healthy patients without a condition. In our example, specificity is the proportion of benign (not cancerous) samples in the cluster identified as predominantly benign that are known to be benign. In other words: TN/(TN+FN).

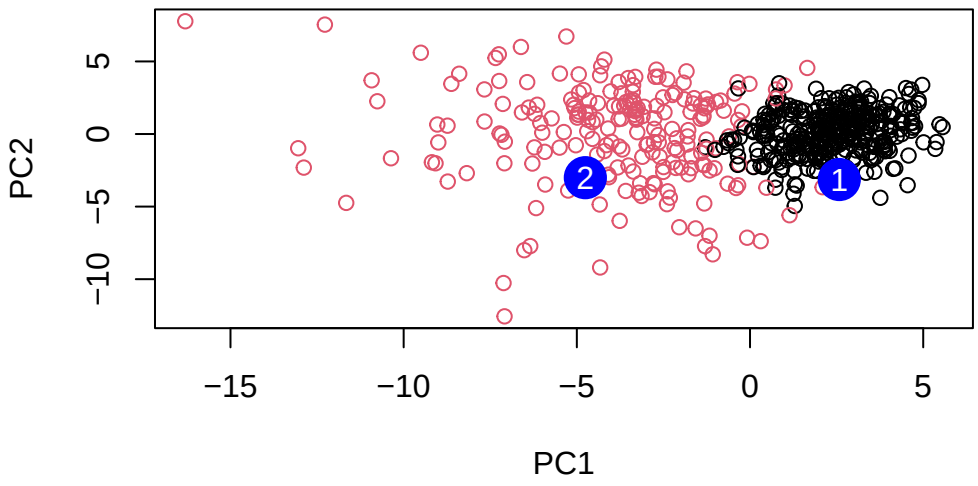
Question 17 (skipped, running out of time)

7. 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")
```



Question 18

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

According to the data above, the largely benign cells should be black and the largely malignant cells should be red. Therefore, because we aim to prioritize patients that are more at risk for malignant cells (red), we should prioritize patient 2 because they are located in a cluster of largely malignant cells.