mini-project

Alyssa Hayashi

##Preparing the data

```
# Save your input data file into your Project directory
fna.data <- "https://bioboot.github.io/bimm143_S20/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)
```

```
View(wisc.df)
```

```
# We can use -1 here to remove the first column
wisc.data <- wisc.df[,-1]
```

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

Exploratory data analysis

Q1. How many observations are in this dataset? Q2. How many of the observations have a malignant diagnosis? Q3. How many variables/features in the data are suffixed with _mean?

```
Q1 <- nrow(wisc.df)
Q1
```

```
[1] 569
```

```
Q2 <- sum(wisc.df$diagnosis=="M")
Q2
```

```
[1] 212
```

```
mean_variables <- grep("_mean$", colnames(wisc.df))
num_mean_variables <- length(mean_variables)
num_mean_variables
```

```
[1] 10
```

##Principle 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
```

```
# Check column means
means <- colMeans(wisc.data)
cat("Column Means:\n")
```

```
Column Means:
```

```
print(means)
```

```
           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
```

```
# Check column standard deviations
sds <- apply(wisc.data, 2, sd)
cat("\nColumn Standard Deviations:\n")
```

```
Column Standard Deviations:
```

```
print(sds)
```

```
          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
# Scale parameter is set to TRUE to scale the variables
```

```
wisc.pr <- prcomp( wisc.data, scale. = T )
```

```
# Look at summary of results
summary(wisc.pr)
```

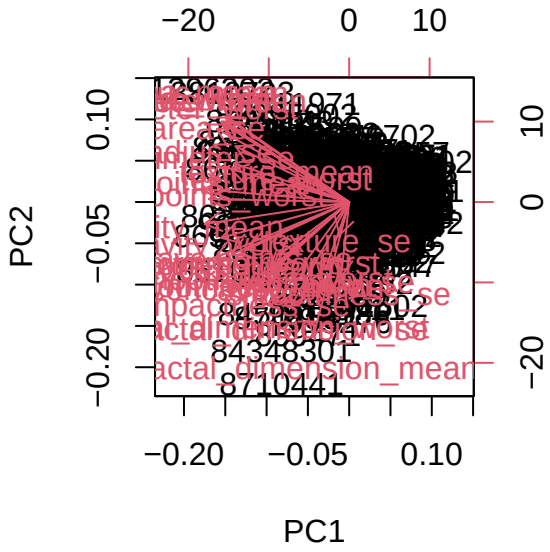
```
Importance of components:
                          PC1    PC2     PC3     PC4     PC5     PC6     PC7
Standard deviation     3.6444 2.3857 1.67867 1.40735 1.28403 1.09880 0.82172
Proportion of Variance 0.4427 0.1897 0.09393 0.06602 0.05496 0.04025 0.02251
Cumulative Proportion  0.4427 0.6324 0.72636 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)? A:44.27% Q5. How many principal components (PCs) are required to describe at least 70% of the original variance in the data? A:3 PCs Q6. How many principal components (PCs) are required to describe at least 90% of the original variance in the data? A:7 PCs

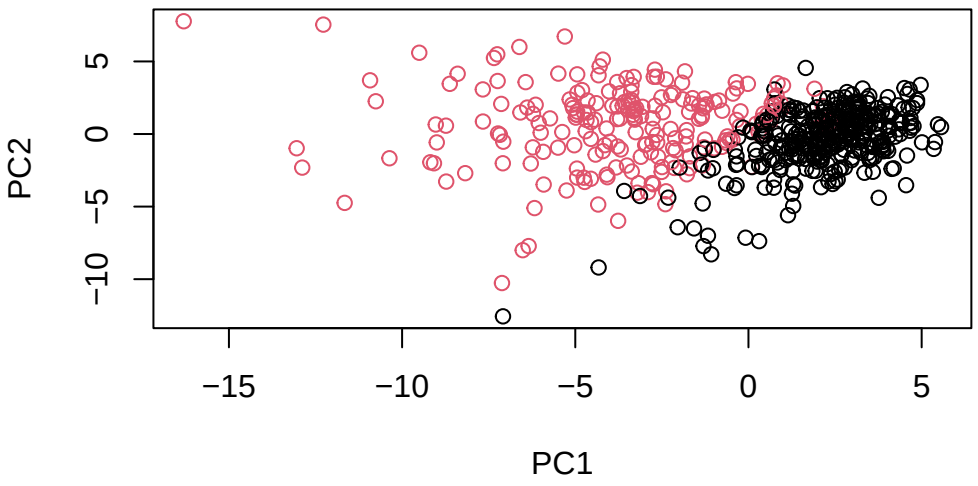
Interpreting PCA results

Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why? A:there is too much going on and is hard to understand what's going on. we will need to make our own to make sense of the pca results

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

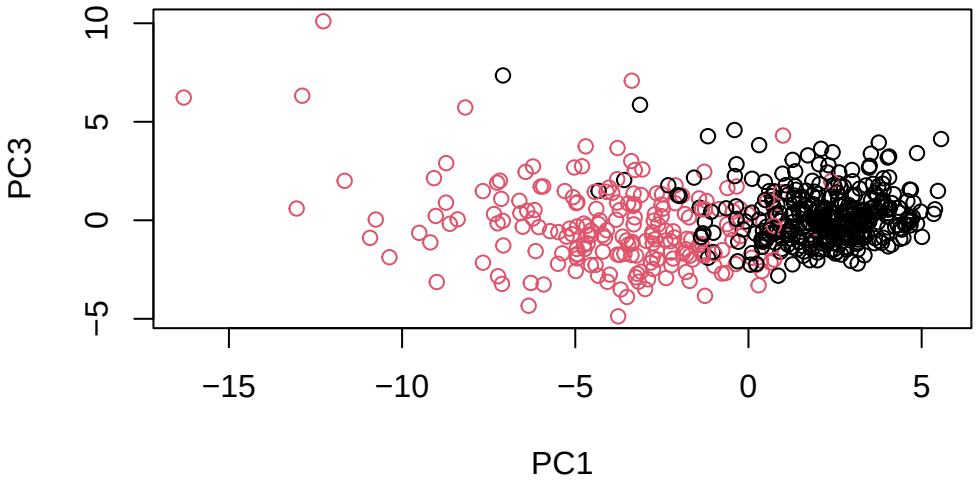



```
# Scatter plot observations by components 1 and 2
plot( wisc.pr$x , col = diagnosis ,
     xlab = "PC1", ylab = "PC2")
```



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[, c(1,3)], col = as.integer(diagnosis),
     xlab = "PC1", ylab = "PC3")
```

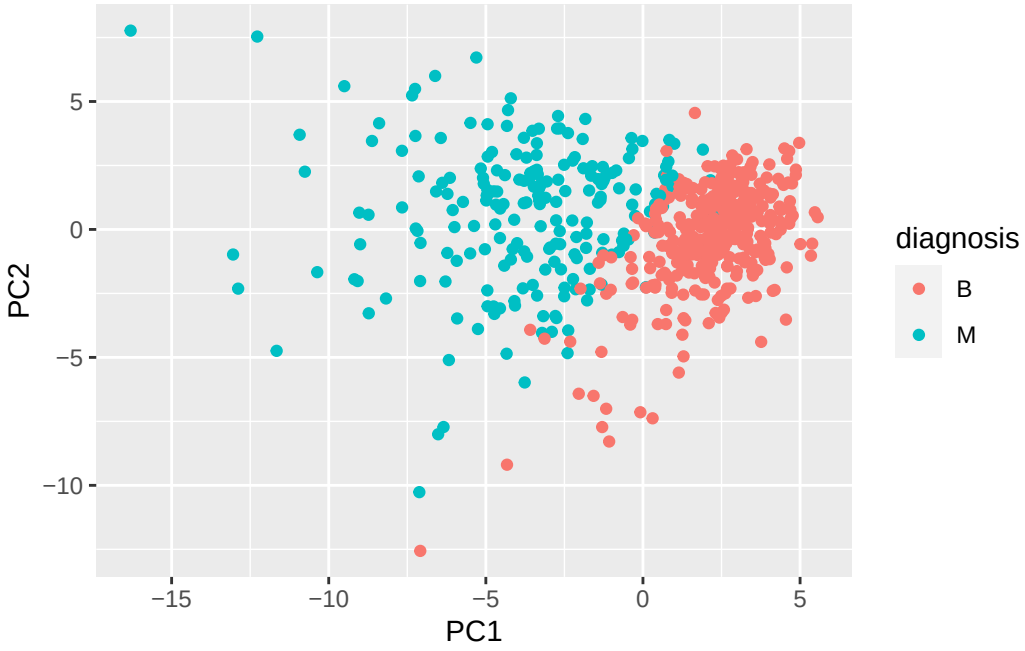


A: Both plots have very similar distributions with both having the majority of the points being centered around 0. However the scales are different

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



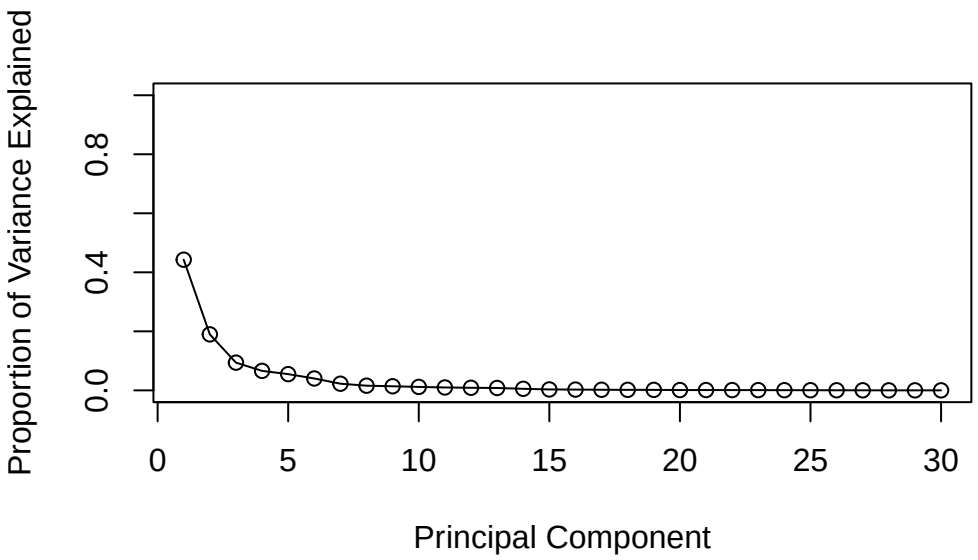
##Variance explained

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

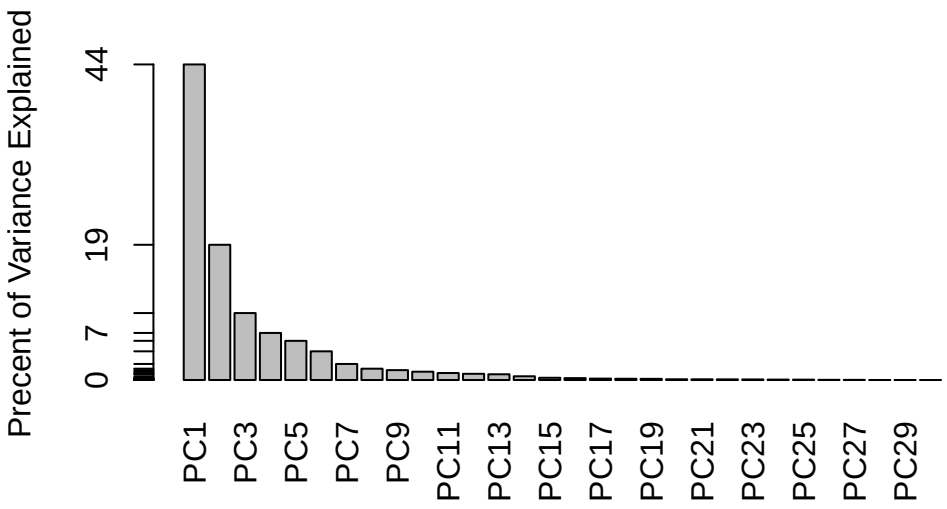
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
# Variance explained by each principal component: pve
pve <- 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 )
```



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? A: it takes the loading for the feature concave.points_mean in PC1 Q10. What is the minimum number of principal components required to explain 80% of the variance of the data? A: 5 PCs are required to explain 80% of the variance

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

```
[1] -0.2608538
```

```
cumulative_variance <- cumsum(pve)
which(cumulative_variance >= 0.8)[1]
```

```
[1] 5
```

3. Hierarchical Clustering

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

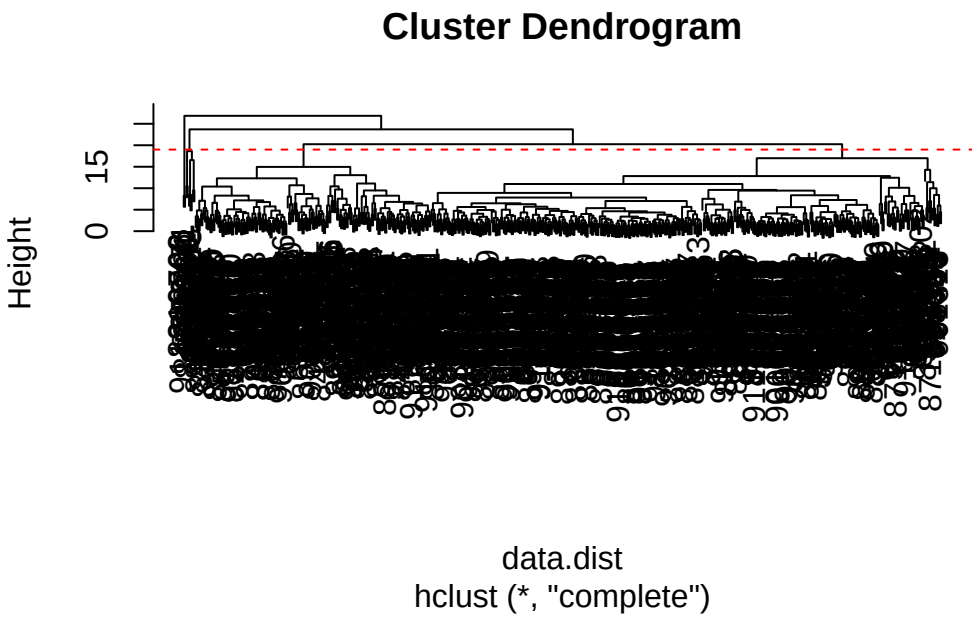
```
data.dist <- dist(data.scaled)
```

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

Results of hierarchical clustering

Q11. Using the plot() and abline() functions, what is the height at which the clustering model has 4 clusters? around 18-19?

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




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

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

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

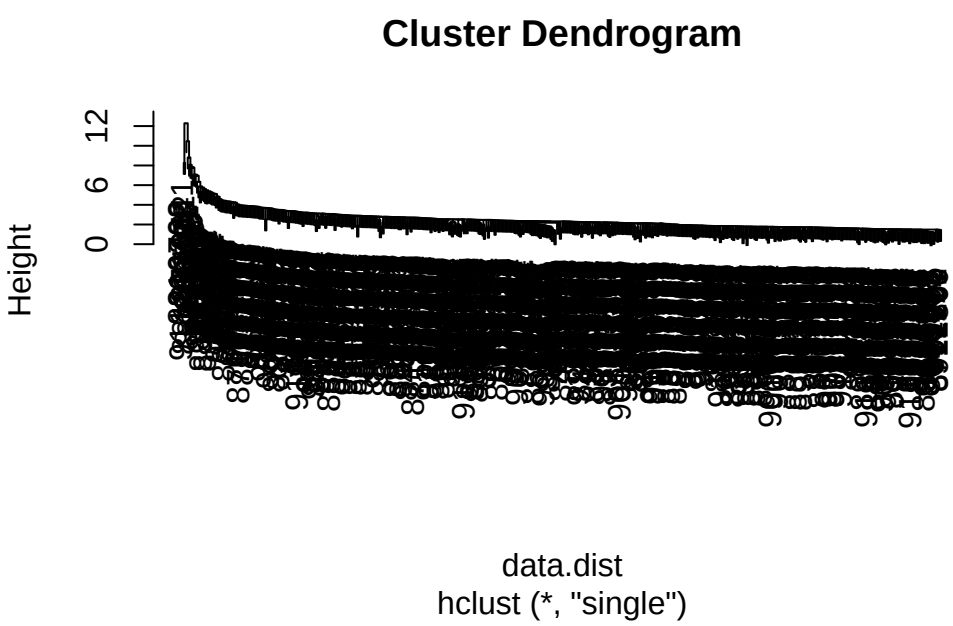
```
                    diagnosis
wisc.hclust.clusters   B   M
                   1 357 210
                   2   0   2
```

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

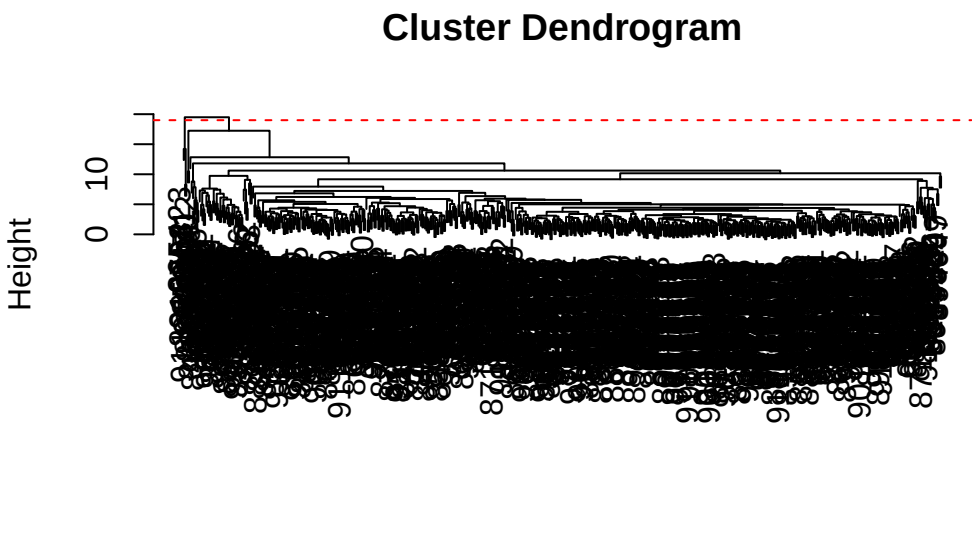
```
                    diagnosis
wisc.hclust.clusters   B   M
                   1   12  86
                   2    0  59
                   3    0   3
                   4  331  39
                   5    0  20
                   6    2   0
                   7   12   0
                   8    0  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

##Using different methods

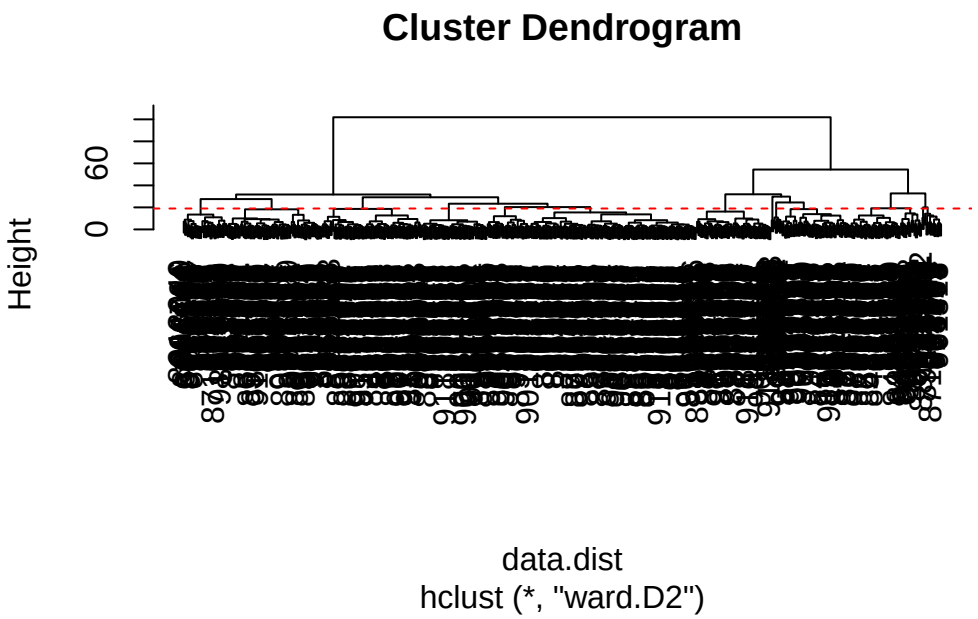
```
wisc.hclust <- hclust(data.dist, method="single")
plot(wisc.hclust)
abline(h=19, col="red", lty=2)
```




```
wisc.hclust <- hclust(data.dist, method="average")
plot(wisc.hclust)
abline(h=19, col="red", lty=2)
```




```
wisc.hclust <- hclust(data.dist, method="ward.D2")
plot(wisc.hclust)
abline(h=19, col="red", lty=2)
```



Q13. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning. A: My favorite is ward.D2 since it minimizes variance in the clustering.

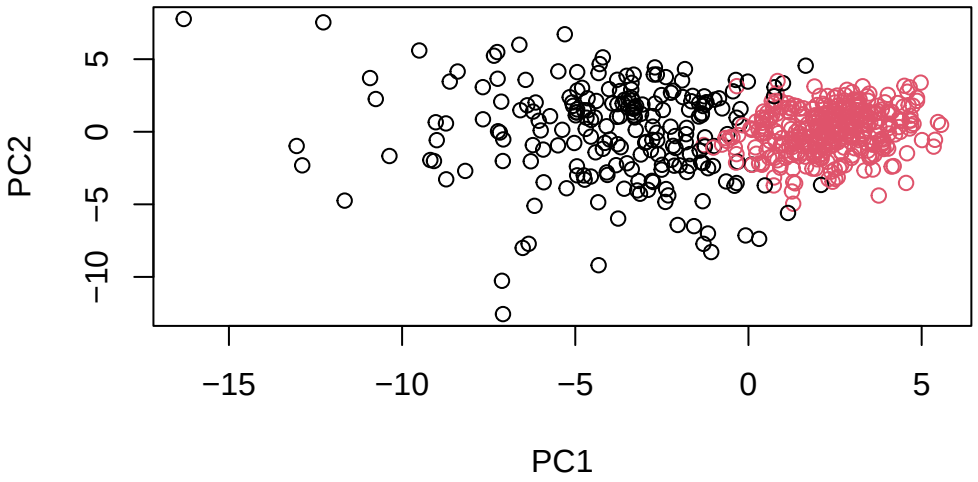
```
cumulative_variance<- cumsum(pve)
min_components_90<-which(cumulative_variance>=.9)[1]
wisc.pr_reduced<- wisc.pr$x[, 1:min_components_90]
wisc.pr.hclust <- hclust(dist(wisc.pr_reduced), method="ward.D2")
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

```
grps
  1   2
216 353
```

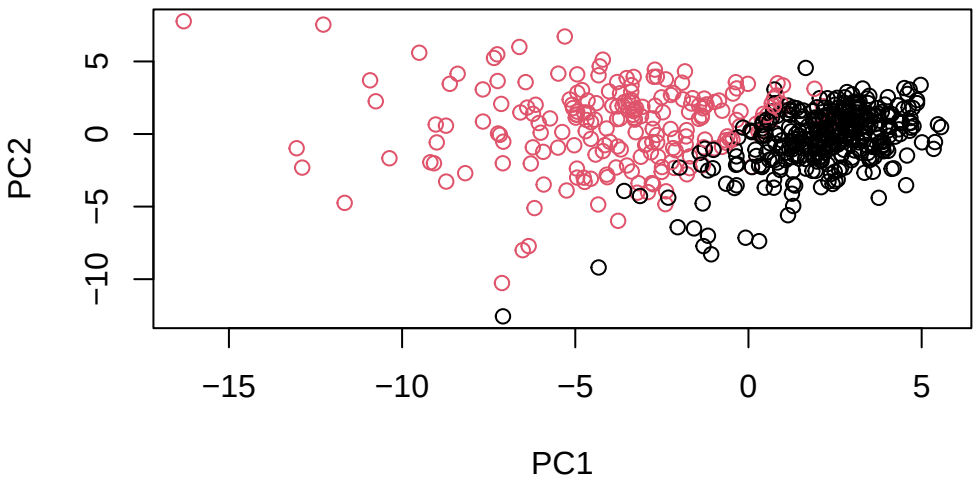
```
table(grps, diagnosis)
```

```
    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)
```




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

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

```
# Compare to actual diagnoses
table(wisc.pr.hclust.clusters, diagnosis)
```

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

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

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

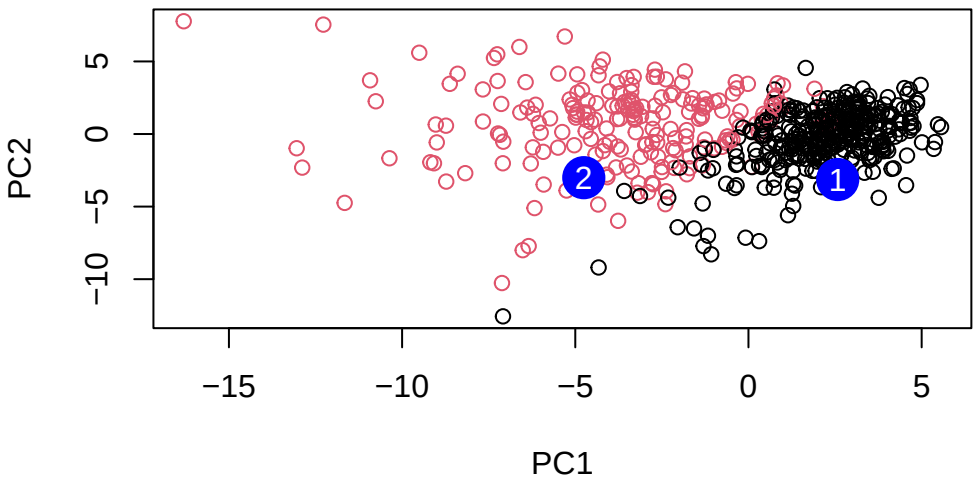
```
                    diagnosis
```

```
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
```

```
#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=diagnosis)
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?

1