CLASS08

Joshua Lau

Preparing the data

```
# 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)

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
```

```r
#let us remove the diagnosis column from our dataset
wisc.data <- wisc.df[,-1]

#but save it into another varaiable just in case
diagnosis <- factor(wisc.df$diagnosis)
```

Q1 How many observations are in this dataset?

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

```
[1] 569
```

569 observations are in this dataset

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

```
table(diagnosis)
```

```
diagnosis
  B   M 
357 212 
```

212 observations are diagnosed malignant

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

```
paste(length(grep("_mean", colnames(wisc.df))), "variables are suffixed with _mean, which
```

```
[1] "10 variables are suffixed with _mean, which are:"
```

```
colnames(wisc.df)[grep("_mean", colnames(wisc.df))]
```

```
 [1] "radius_mean"            "texture_mean"           "perimeter_mean"        
 [4] "area_mean"              "smoothness_mean"        "compactness_mean"      
 [7] "concavity_mean"         "concave.points_mean"    "symmetry_mean"         
[10] "fractal_dimension_mean"
```

10 variables are suffixed with `_mean`

2. PCA

Let's see if we need to scale the data before PCA, by looking at the distribution of the variables

```r
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 
```

```r
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
```

Since the variables have different distributions, let's try scaling our data

```
wisc.data.scaled <- as.data.frame(scale(wisc.data))
```

The variables should now be centered around ~0 with a sd of ~1 now

```
head(colMeans(wisc.data.scaled))
```

```
    radius_mean     texture_mean   perimeter_mean        area_mean
  -1.383450e-16     6.151104e-17    -1.193179e-16     1.219428e-16
smoothness_mean compactness_mean
   1.620945e-16    -7.617540e-17
```

```
head(apply(wisc.data.scaled,2,sd))
```

```
    radius_mean     texture_mean   perimeter_mean        area_mean
              1                1                1                1
smoothness_mean compactness_mean
              1                1
```

looks good!

Now we execute PCA and look at the summary

```
wisc.pr <- prcomp( wisc.data.scaled )
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)?

From the summary table above, 44.27% of the original 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?

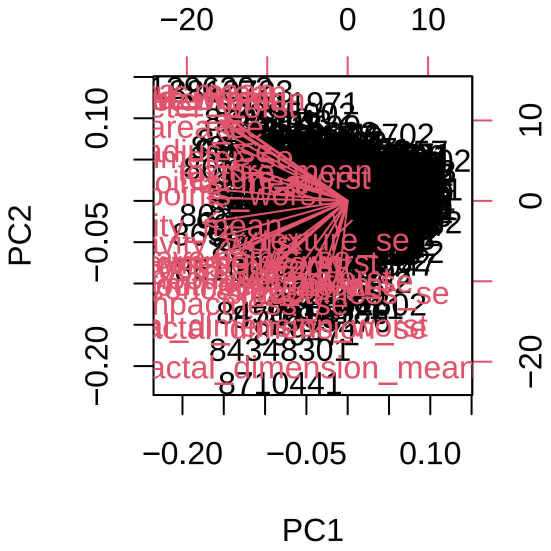
From the summary table above, looking at the cumulative proportion, 3 principal components are needed to describe 70% of the original variance in the data (PC1, PC2, PC3 contribute to 72.6%)

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

From the summary table above, looking at the cumulative proportion, 7 principal components are needed to describe 90% of the original variance in the data (PC1, PC2, PC3, PC4, PC5, PC6, and PC7 contribute to 91.0%)

Interpreting PCA Results

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

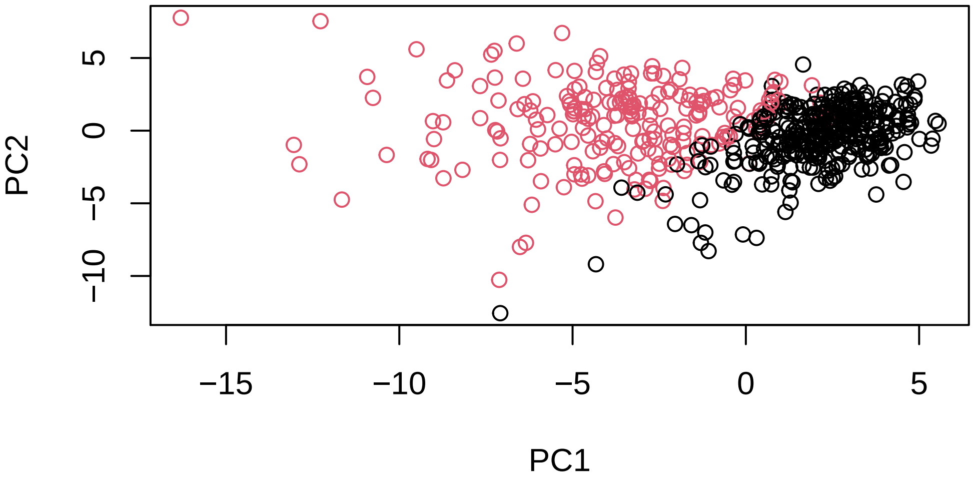


Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why?

It stands out to me that I cannot interpret much about the dataset from this biplot. There is far too much text and labelling due to the large number of observations and thus everything is overlapping and nothing is legible

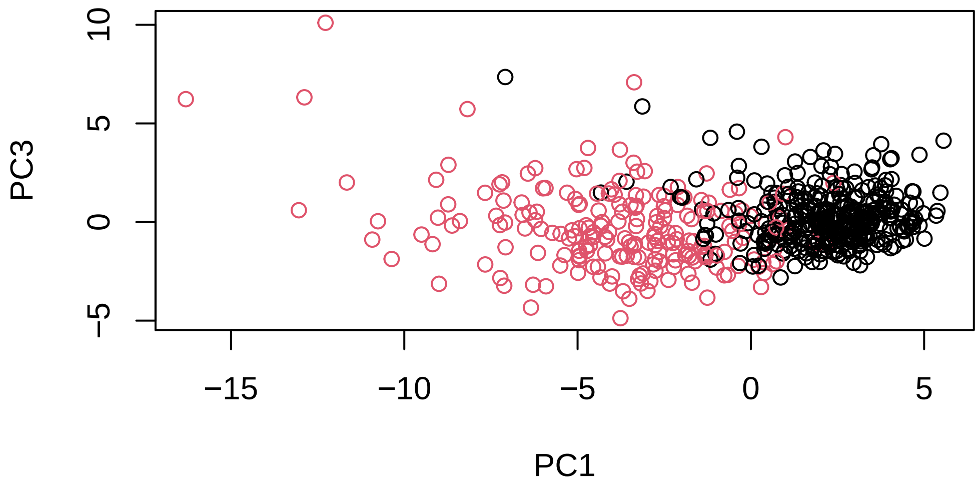
Let's plot a better scatterplot for PC1 and PC2

```
plot(wisc.pr$x, col = diagnosis ,
     xlab = "PC1", ylab = "PC2")
```



And for PC1 and PC3

```
plot(wisc.pr$x[,-2], col = diagnosis ,
     xlab = "PC1", ylab = "PC3")
```



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

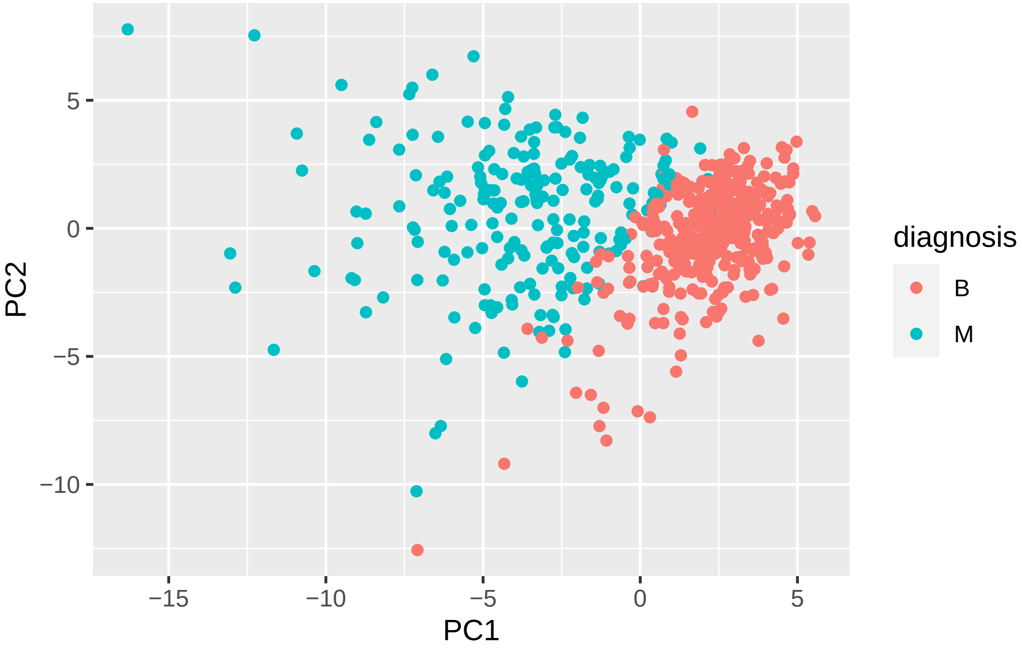
I notice that PC1 and PC2/PC3 are able to segragate the Benign and Malignant samples quite well based on the data. This is seen from how there are two distinct/separated groups of colored points which are based on the diagnosis by the physician. I see that the plot of PC1 and PC2 separates these two conditions slightly better which makes sense as PC2 accounts for more of the variation within the data.

Let's try using ggplot to create better plots

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

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

```
Warning: package 'ggplot2' was built under R version 4.0.5
```

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



Variance Explained

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

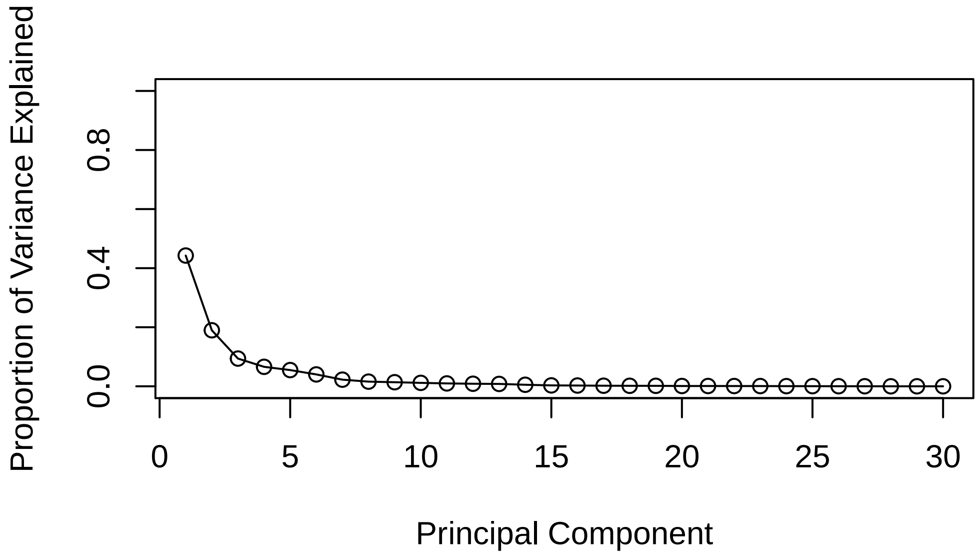
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```r
#divide by the sum of variances
pve <- pr.var/ sum(wisc.pr$sdev^2)
head(pve)
```

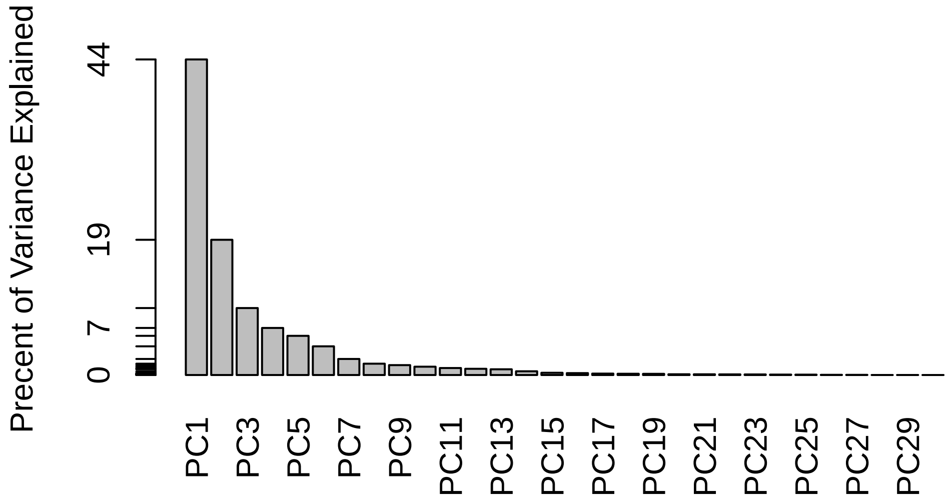
```
[1] 0.44272026 0.18971182 0.09393163 0.06602135 0.05495768 0.04024522
```

Plotting variance explained by each PC

```
plot(pve, xlab = "Principal Component",
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```



```
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 )
```



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]["concave.points_mean"]
```

```
concave.points_mean
         -0.2608538
```

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

```
sum(pve[1:4])
```

```
[1] 0.7923851
```

```
sum(pve[1:5])
```

```
[1] 0.8473427
```

5 principal components are needed to describe 90% of the original variance in the data (PC1, PC2, PC3, PC4, PC5 together contribute to 84.0% of the original variation)

Hierarchial Clustering

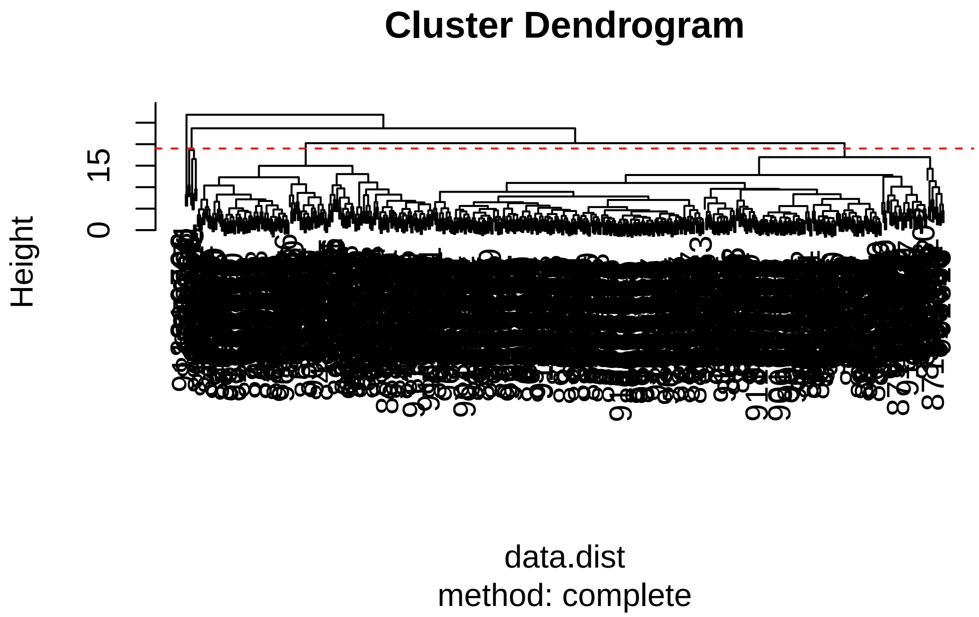
Scaling data and calculating pairwise distance matrix and performing `hclust()`

```
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?

plotting results

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



19 is one value of height for which the dendrogram is segregated into 4 custers

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?

```
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
```

```
wisc.hclust.clusters_10 <- cutree(wisc.hclust, k=10)

table(wisc.hclust.clusters_10, diagnosis)
```

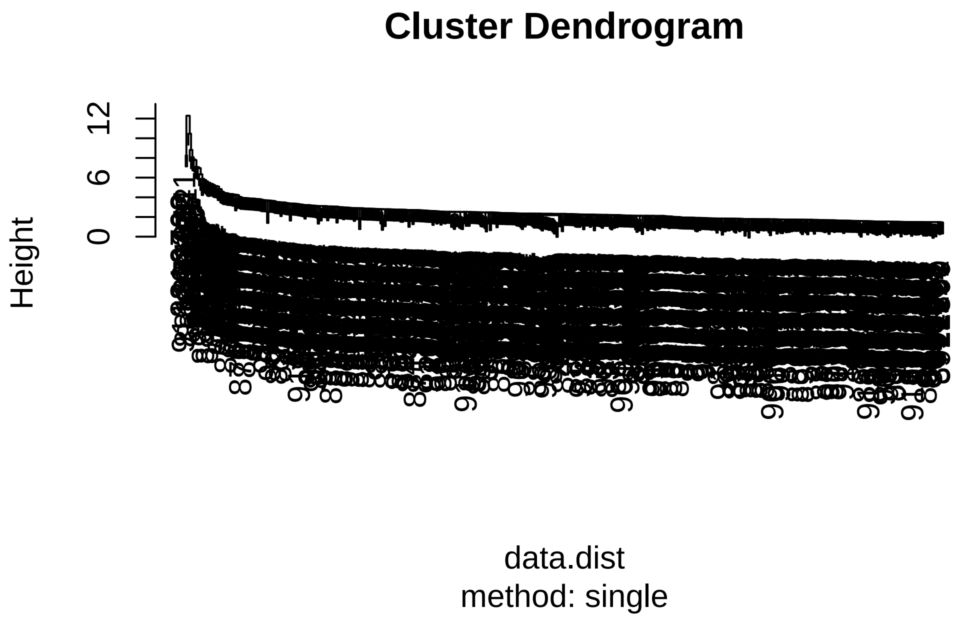
```
                       diagnosis
wisc.hclust.clusters_10   B   M
                     1   12  86
                     2    0  59
                     3    0   3
                     4  331  39
                     5    0  20
                     6    2   0
                     7   12   0
                     8    0   2
                     9    0   2
                     10   0   1
```

We see that for k<4 there is poor separation of clusters into benign and malignant groups. Therefore, k=4 is the minimum number of clusters needed to separate these two conditions. However, as we increase k beyond 4, up until even k=10 we see that there is only a very marignal improvement in the separation of these B and M clusters. Therefore, k=4 should be an optimal number of clusters for this data.

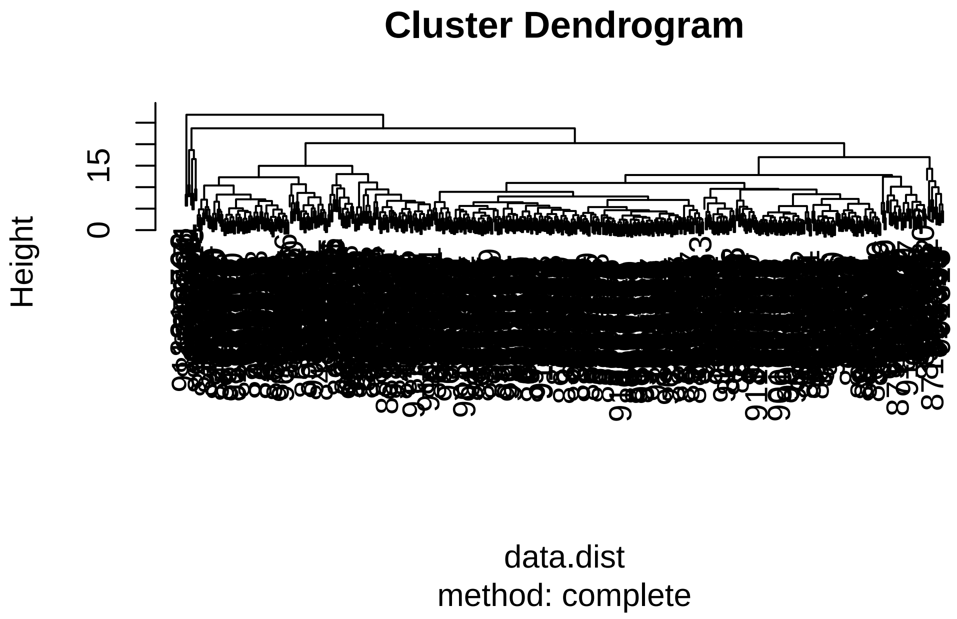
Q13. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning.

Using different methods

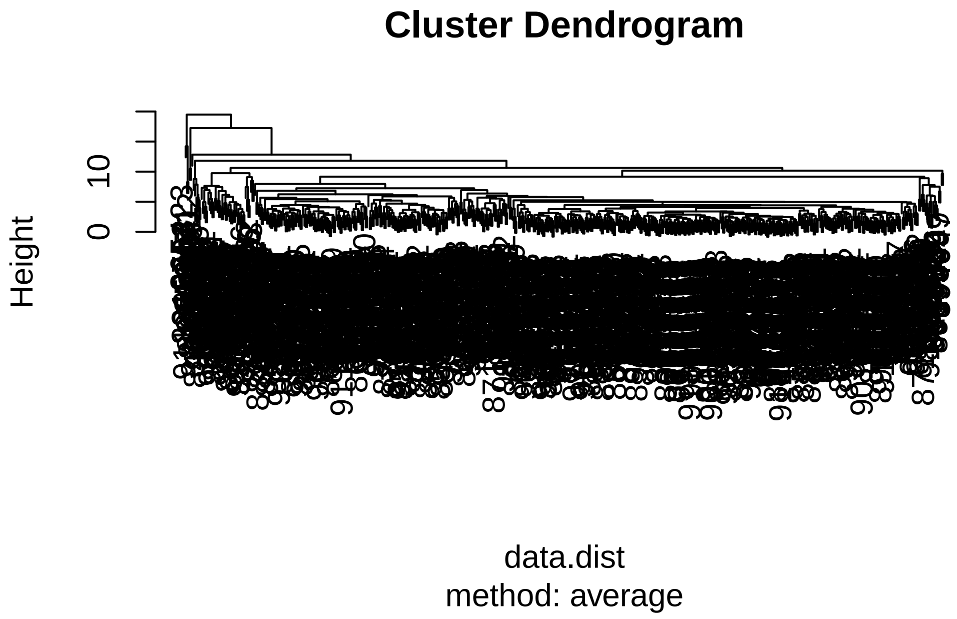
```
plot(hclust(data.dist, method = "single"), sub = "method: single")
```



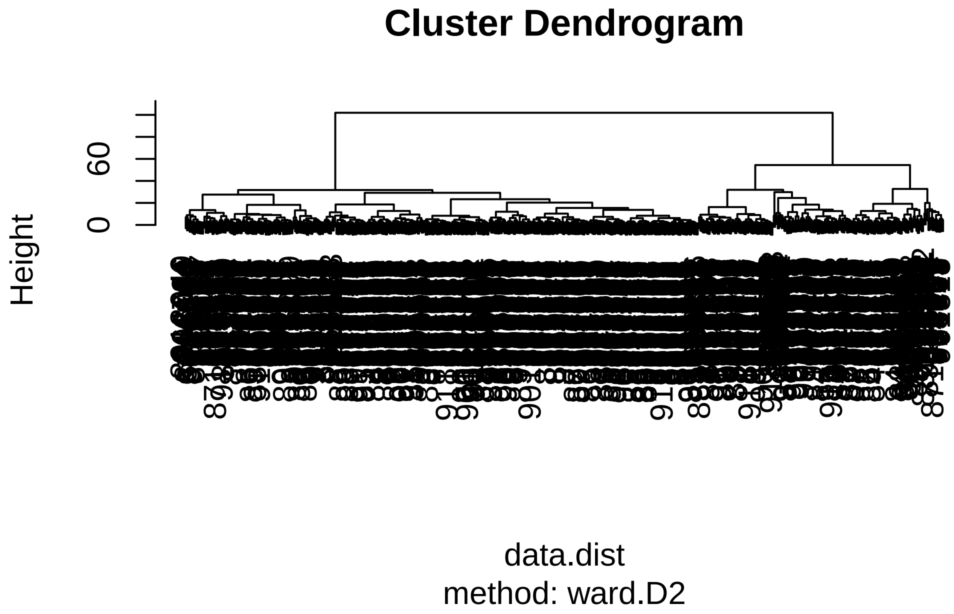
```
plot(hclust(data.dist, method = "complete"), sub = "method: complete")
```



```
plot(hclust(data.dist, method = "average"), sub = "method: average")
```



```r
plot(hclust(data.dist, method = "ward.D2"), sub = "method: ward.D2")
```



```r
#examining the ward.D2 method better
wisc.hclust.clusters.ward <- cutree(hclust(data.dist, method = "ward.D2"), k=2)

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

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

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

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

the method ward.D2 looks the best to me because there is a clear separation of the two clusters in the dataset, which represent the two disease conditions (B/M) quite well, as seen in the table above. It is good to have the number of clusters equal to the number of diagnostic conditions as that means that the data naturally segregates in such a way that supports the initial diagnosis. On the other hand, looking at the dendrograms obtained using the other methods, it seems that more clusters (a higher k) are necessary before the same level of separation is achieved. With that being said, if the desired measure is accuracy then the original method of "complete" works best as it only produces 14 misdiagnosed benign samples (12 from grp 1 and 2 from grp 2), and 40 misdiagnosed malignant samples from grp 3. However, a limitation with more clusters is that when you have small cluster sizes with not very distinct separation, e.g. clusters 2 and 4, you cannot be statistically very certain as to whether or not such a cluster actually represents, in this case,the M diagnosis, and it is more likely that clusters 2 and 4 should be assigned an "unknown" diagnosis

k-means

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

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

```
   diagnosis
      B   M
  1  14 175
  2 343  37
```

Q14. How well does k-means separate the two diagnoses? How does it compare to your hclust results?

k-means performs reasonably well to separate the two diagnoses, with 343 true positives and 175 true negatives, and only 37 false negatives and 14 false positives. It is slightly improved over the hclust results from ward.D2 method which yields slightly poorer truth measures (TP = 337, TN = 164, FP = 20, FN = 48).

5. Combining methods

Clustering on PCA results

Create a hclust model of the PCs that describe 90% of the variability of the data with `method = "ward.D2"`

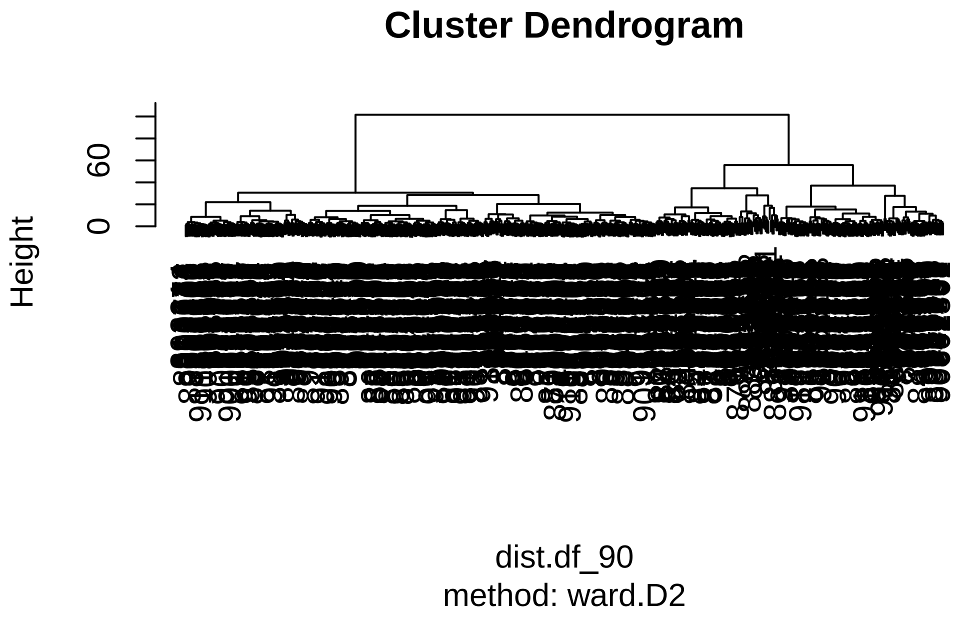
```
summary(wisc.pr)
```

```
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
```

PC1 - PC7 is needed to account for 90% of the variation

```
df_90 <- wisc.pr$x[,1:7]
dist.df_90 <- dist(df_90)
```

```
wisc.pr.hclust <- hclust(dist.df_90, method = "ward.D2")
plot(wisc.pr.hclust, sub = "method: ward.D2")
```



looking at two main branches, compare results to ground truth of actual diagnosis

```
grps_2 <- cutree(wisc.pr.hclust, k=2)
table(grps_2,diagnosis)
```

```
      diagnosis
grps_2   B   M
     1  28 188
     2 329  24
```

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

```
grps_4 <- cutree(wisc.pr.hclust, k=4)
table(grps_4,diagnosis)
```

```
      diagnosis
grps_4   B   M
     1   0  45
     2   2  77
     3  26  66
     4 329  24
```

This newly created model with 4 clusters performs the same as the original model with 2 clusters. If we consider that clusters 1,2, and 3 represent the M diagnosis; and cluster 4 represents the B diagnosis, we can still see that there are 28 (2 from grp 2 and 26 from grp 3) benign samples assigned to a malignant cluster, and still 24 (all from grp 4) malignant samples assigned to benign cluster (cluster 4)

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(grps_2,diagnosis)
```

```
      diagnosis
grps_2   B   M
     1  28 188
     2 329  24
```

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

```
   diagnosis
      B   M
  1  14 175
  2 343  37
```

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

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

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

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

It appears that these methods, whether it be the hclust on the PCA, the hclust with ward.D2 method, or the hclust with the complete method, all perform rather similarly achieving a relatively good separation of the B and M diagnoses

Q17. Which of your analysis procedures resulted in a clustering model with the best specificity? How about sensitivity?

FN: Predicted B, is M FP: Predicted M, is B

Looking at the combined PCA(90%) -> hclust model first

```
table(grps_2,diagnosis)
```

```
      diagnosis
grps_2   B   M
     1  28 188
     2 329  24
```

```
sens_1 <- 188/(188+28)
spec_1 <- 329/(329+24)

sens_1
```

```
[1] 0.8703704
```

```
spec_1
```

```
[1] 0.9320113
```

Then the kmeans model (k=2)

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

```
   diagnosis
      B   M
  1  14 175
  2 343  37
```

```
sens_2 <- 175/(175+14)
spec_2 <- 343/(343+37)

sens_2
```

```
[1] 0.9259259
```

```
spec_2
```

```
[1] 0.9026316
```

Then the hclust model with method = ward.D2 and k = 2

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

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

```
sens_3 <- 164/(164+20)
spec_3 <- 337/(337+48)

sens_3
```

```
[1] 0.8913043
```

```
spec_3
```

```
[1] 0.8753247
```

then the hclust model with complete method and k = 4. (Let clusters 2 and 4 be assigned to M)

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

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

```
sens_4 <- (165+5+2)/(165+5+2+12+2+0)
spec_4 <- (343) / (343+40)

sens_4
```

```
[1] 0.9247312
```

```
spec_4
```

```
[1] 0.8955614
```

it appears that the model with the highest specificity is the first model, which performs a hclust with the method ward.D2 on the first 7 Principal Components of the PCA. It has a specificity of 93.2 %. The model with the highest sensitivity is the kmeans model (k=2) with a sensitivity of 92.59 %

7. Prediction

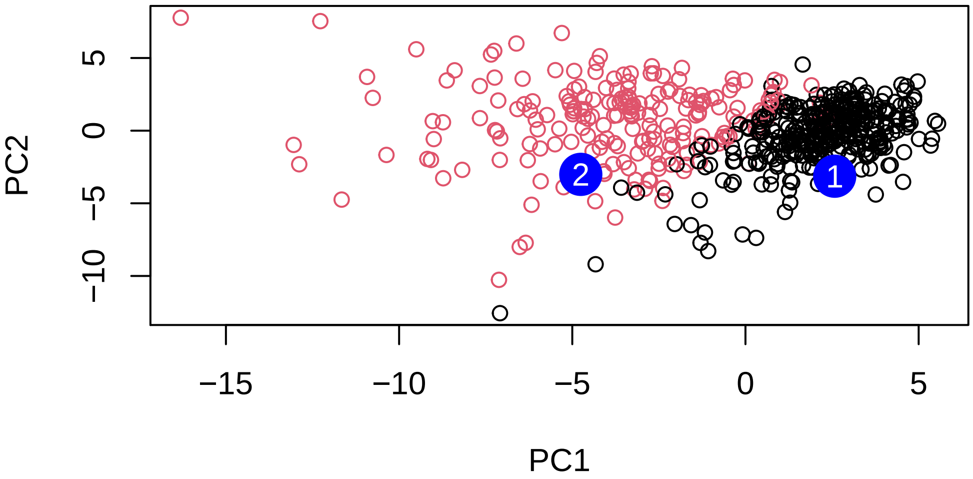
We will use the predict() function that will take our PCA model from before and new cancer cell data and project that data onto our PCA space.

```
url <- "https://tinyurl.com/new-samples-CSV"
new <- read.csv(url)
```

```r
#need to scale data first as wisc.pr was trained on scaled data
new.scaled <- scale(new, center = colMeans(wisc.data), scale = apply(wisc.data,2,sd))
npc <- predict(wisc.pr, newdata=new.scaled)
head(npc)
```

```
           PC1       PC2        PC3        PC4       PC5        PC6        PC7
[1,]  2.576616 -3.135913  1.3990492 -0.7631950  2.781648 -0.8150185 -0.3959098
[2,] -4.754928 -3.009033 -0.1660946 -0.6052952 -1.140698 -1.2189945  0.8193031
            PC8       PC9       PC10      PC11      PC12      PC13     PC14
[1,] -0.2307350 0.1029569 -0.9272861 0.3411457  0.375921 0.1610764 1.187882
[2,] -0.3307423 0.5281896 -0.4855301 0.7173233 -1.185917 0.5893856 0.303029
          PC15       PC16        PC17        PC18        PC19       PC20
[1,] 0.3216974 -0.1743616 -0.07875393 -0.11207028 -0.08802955 -0.2495216
[2,] 0.1299153  0.1448061 -0.40509706  0.06565549  0.25591230 -0.4289500
           PC21       PC22       PC23       PC24        PC25         PC26
[1,]  0.1228233 0.09358453 0.08347651  0.1223396  0.02124121  0.078884581
[2,] -0.1224776 0.01732146 0.06316631 -0.2338618 -0.20755948 -0.009833238
             PC27        PC28         PC29         PC30
[1,]  0.220199544 -0.02946023 -0.015620933  0.005269029
[2,] -0.001134152  0.09638361  0.002795349 -0.019015820
```

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

Based on our new results, we should prioritize follow up of Patient 2 as they fall into the red (malignant) cluster based on the PCA transformation