class09_miniproject

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Class 9 Mini-Project

1. Exploratory data analysis

Preparing the data

```r
# Save your input data file into your Project directory
# (hid data with {r, results='hide'} to conserve pdf pages).
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)
wisc.df
```

```r
# Examine the data (hid data with {r, results='hide'} to conserve pdf pages).
wisc.df
```

```r
# Examine the data with 'head()'
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
# We can use -1 here to remove the first column (hid data with {r, results='hide'} to conserve pdf page
wisc.data <- wisc.df[,-1]
wisc.data
```

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

```
##   [1] M M M M M M M M M M M M M M M M M M M B B B M M M M M M M M M M M M M M M
##  [38] B M M M M M M M M B M B B B B B M M B M M B B B B M B M M B B B B M B M M
##  [75] B M B M M B B B M M B M M M B B B M B B M M B B B M M B B B B M B B M B B
## [112] B B B B B B M M M B M M B B B M M B M B M M B M M B B M B B M B B B B M B
## [149] B B B B B B B B M B B B B M M B M B B M M B B M M B B B B M B B M M M B M
## [186] B M B B B M B B M M B M M M M B M M M B M B M B B M B M M M M B B M M B B
## [223] B M B B B B B M M B B M B B M M B M B B B B M B B B B B M B M M M M M M M
## [260] M M M M M M M B B B B B B M B M B B M B B M B M M B B B B B B B B B B B B
## [297] B M B B M B M B B B B B B B B B B B B B B M B B B M B M B B B B M M M B B
## [334] B B M B M B M B B B M B B B B B B B M M M B B B B B B B B B B B M M B M M
## [371] M B M M B B B B B M B B B B B M B B B M B B M M B B B B B B M B B B B B B
## [408] B M B B B B B M B B M B B B B B B B B B B B M B M M B M B B B B B M B B
## [445] M B M B B M B M B B B B B B B B M M B B B B B B M B B B B B B B B B B M B
## [482] B B B B B B M B M B B M B B B B B M M B M B M B B B B B M B B M B M B M M
```

```
## [519] B B B M B B B B B B B B B B B M B M M B B B B B B B B B B B B B B B B B B
## [556] B B B B B B B M M M M M M B
## Levels: B M
```

Exploratory data analysis

Q1. How many observations are in this dataset?

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

There are 569 observations.

```
## [1] 569
```

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

212 have a malignant diagnosis.

```
table(diagnosis)
```

```
## diagnosis
##   B   M
## 357 212
```

```
colnames(wisc.df)
```

class examples on retrieving column names.

```
##  [1] "diagnosis"               "radius_mean"
##  [3] "texture_mean"            "perimeter_mean"
##  [5] "area_mean"               "smoothness_mean"
##  [7] "compactness_mean"        "concavity_mean"
##  [9] "concave.points_mean"     "symmetry_mean"
## [11] "fractal_dimension_mean"  "radius_se"
## [13] "texture_se"              "perimeter_se"
## [15] "area_se"                 "smoothness_se"
## [17] "compactness_se"          "concavity_se"
## [19] "concave.points_se"       "symmetry_se"
## [21] "fractal_dimension_se"    "radius_worst"
## [23] "texture_worst"           "perimeter_worst"
## [25] "area_worst"              "smoothness_worst"
## [27] "compactness_worst"       "concavity_worst"
## [29] "concave.points_worst"    "symmetry_worst"
## [31] "fractal_dimension_worst"
```

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

class example using 'grep' to help us find patterns we are interested in.

```
##  [1]  2  3  4  5  6  7  8  9 10 11
```

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

10.

```
length(grep("_mean", colnames(wisc.df)))
```

```
## [1] 10
```

2. Principal Component Analysis

Performing PCA

```
# Check column means and standard deviations
colMeans(wisc.data)
```

```
##             radius_mean            texture_mean          perimeter_mean
##            1.412729e+01            1.928965e+01            9.196903e+01
##               area_mean         smoothness_mean        compactness_mean
##            6.548891e+02            9.636028e-02            1.043410e-01
##          concavity_mean     concave.points_mean           symmetry_mean
##            8.879932e-02            4.891915e-02            1.811619e-01
##  fractal_dimension_mean               radius_se              texture_se
##            6.279761e-02            4.051721e-01            1.216853e+00
##            perimeter_se                 area_se           smoothness_se
##            2.866059e+00            4.033708e+01            7.040979e-03
##          compactness_se            concavity_se       concave.points_se
##            2.547814e-02            3.189372e-02            1.179614e-02
##             symmetry_se    fractal_dimension_se            radius_worst
##            2.054230e-02            3.794904e-03            1.626919e+01
##           texture_worst         perimeter_worst              area_worst
##            2.567722e+01            1.072612e+02            8.805831e+02
##        smoothness_worst       compactness_worst         concavity_worst
##            1.323686e-01            2.542650e-01            2.721885e-01
##    concave.points_worst          symmetry_worst fractal_dimension_worst
##            1.146062e-01            2.900756e-01            8.394582e-02
```

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

```
##             radius_mean            texture_mean          perimeter_mean
##            3.524049e+00            4.301036e+00            2.429898e+01
##               area_mean         smoothness_mean        compactness_mean
##            3.519141e+02            1.406413e-02            5.281276e-02
##          concavity_mean     concave.points_mean           symmetry_mean
##            7.971981e-02            3.880284e-02            2.741428e-02
##  fractal_dimension_mean               radius_se              texture_se
##            7.060363e-03            2.773127e-01            5.516484e-01
##            perimeter_se                 area_se           smoothness_se
##            2.021855e+00            4.549101e+01            3.002518e-03
##          compactness_se            concavity_se       concave.points_se
##            1.790818e-02            3.018606e-02            6.170285e-03
##             symmetry_se    fractal_dimension_se            radius_worst
##            8.266372e-03            2.646071e-03            4.833242e+00
##           texture_worst         perimeter_worst              area_worst
##            6.146258e+00            3.360254e+01            5.693570e+02
##        smoothness_worst       compactness_worst         concavity_worst
##            2.283243e-02            1.573365e-01            2.086243e-01
##    concave.points_worst          symmetry_worst fractal_dimension_worst
```

```
##             6.573234e-02             6.186747e-02             1.806127e-02
```

Q4. From your results, what proportion of the original variance is captured by the first principal components (PC1)?

0.4427

```
# Perform PCA on wisc.data by completing the following code
wisc.pr <- prcomp(wisc.data, scale = TRUE)
```

```
# 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
```

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

3 are required.

```
# Summary of wisc.pr and assigning to new vector.
x <- summary(wisc.pr)
x
```

```
## 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
```

```
str(x)
```

```
## List of 6
##  $ sdev      : num [1:30] 3.64 2.39 1.68 1.41 1.28 ...
##  $ rotation  : num [1:30, 1:30] -0.219 -0.104 -0.228 -0.221 -0.143 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:30] "radius_mean" "texture_mean" "perimeter_mean" "area_mean" ...
##   .. ..$ : chr [1:30] "PC1" "PC2" "PC3" "PC4" ...
##  $ center    : Named num [1:30] 14.1273 19.2896 91.969 654.8891 0.0964 ...
##   ..- attr(*, "names")= chr [1:30] "radius_mean" "texture_mean" "perimeter_mean" "area_mean" ...
##  $ scale     : Named num [1:30] 3.524 4.301 24.299 351.9141 0.0141 ...
##   ..- attr(*, "names")= chr [1:30] "radius_mean" "texture_mean" "perimeter_mean" "area_mean" ...
##  $ x         : num [1:569, 1:30] -9.18 -2.39 -5.73 -7.12 -3.93 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:569] "842302" "842517" "84300903" "84348301" ...
##   .. ..$ : chr [1:30] "PC1" "PC2" "PC3" "PC4" ...
##  $ importance: num [1:3, 1:30] 3.644 0.443 0.443 2.386 0.19 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:3] "Standard deviation" "Proportion of Variance" "Cumulative Proportion"
##   .. ..$ : chr [1:30] "PC1" "PC2" "PC3" "PC4" ...
##  - attr(*, "class")= chr "summary.prcomp"
```

```
# Determining how many principal components (PCs) are required to describe at least 70% of the original
x$importance[3,] >= 0.7
```

```
##   PC1   PC2   PC3   PC4   PC5   PC6   PC7   PC8   PC9  PC10  PC11  PC12  PC13
## FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  PC14  PC15  PC16  PC17  PC18  PC19  PC20  PC21  PC22  PC23  PC24  PC25  PC26
##  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  PC27  PC28  PC29  PC30
##  TRUE  TRUE  TRUE  TRUE
```

```
PC70 <- which(x$importance[3,] >= 0.7)
PC70[1]
```

```
## PC3
##   3
```

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

3 are required.

```
# Determining how many principal components (PCs) are required to describe at least 90% of the original
x$importance[3,] >= 0.9
```

```
##   PC1   PC2   PC3   PC4   PC5   PC6   PC7   PC8   PC9  PC10  PC11  PC12  PC13
## FALSE FALSE FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  PC14  PC15  PC16  PC17  PC18  PC19  PC20  PC21  PC22  PC23  PC24  PC25  PC26
##  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  PC27  PC28  PC29  PC30
##  TRUE  TRUE  TRUE  TRUE
```

```
PC90 <- which(x$importance[3,] >= 0.9)
PC90[1]
```

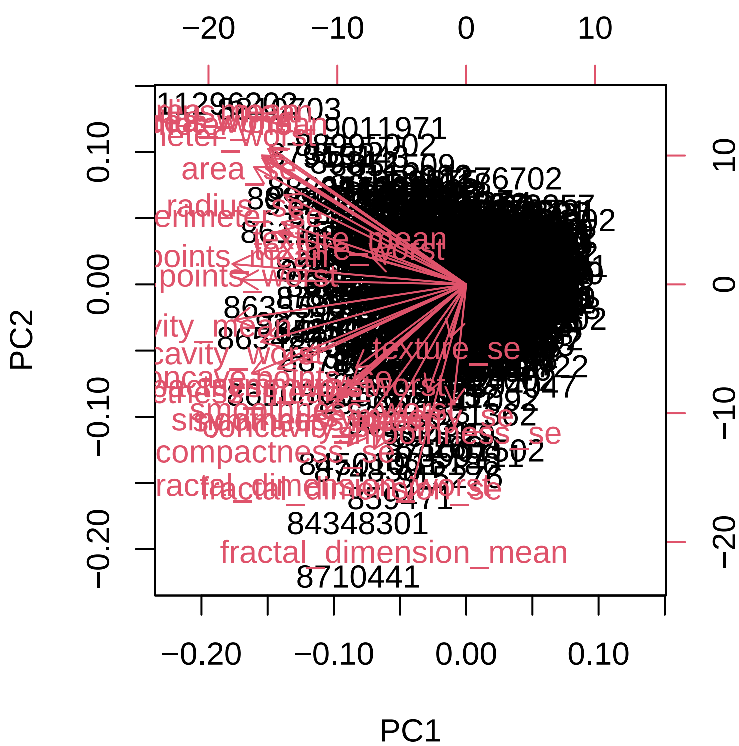
```
## PC7
##   7
```

Interpreting PCA results

Create a biplot of the wisc.pr using the biplot() function.

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

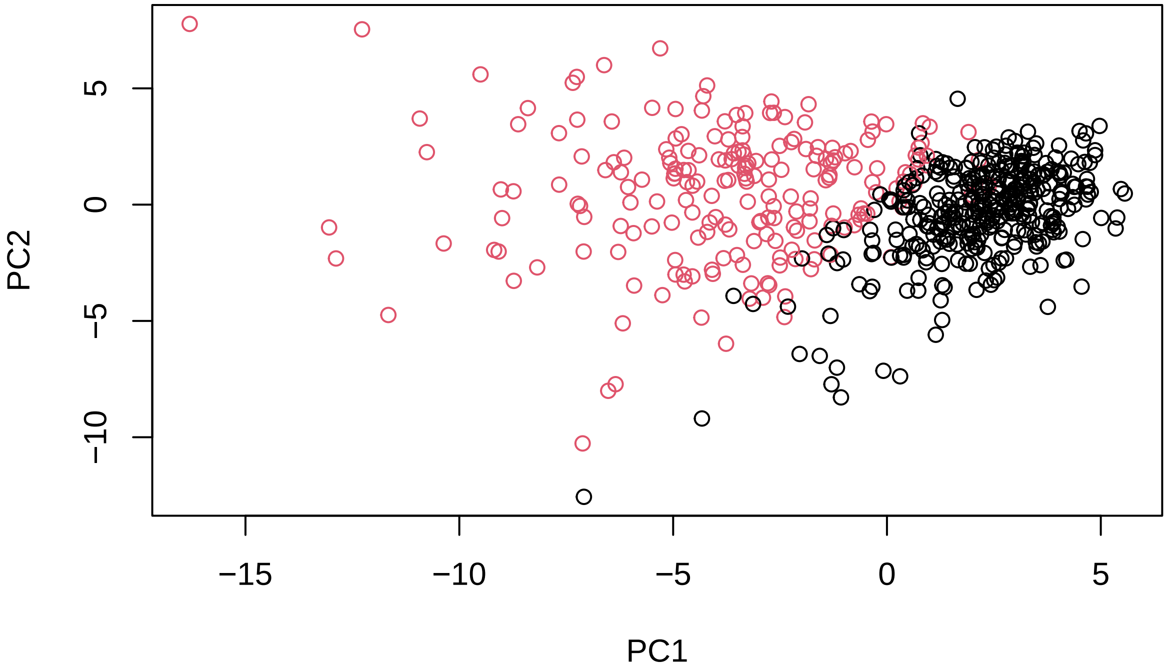
```
biplot(wisc.pr)
```



This plot is crowded and difficult to interpret.

```
# principal component (PC1/PC2)
# hid data with {r, results='hide'} to conserve pdf pages.
wisc.pr$x
```

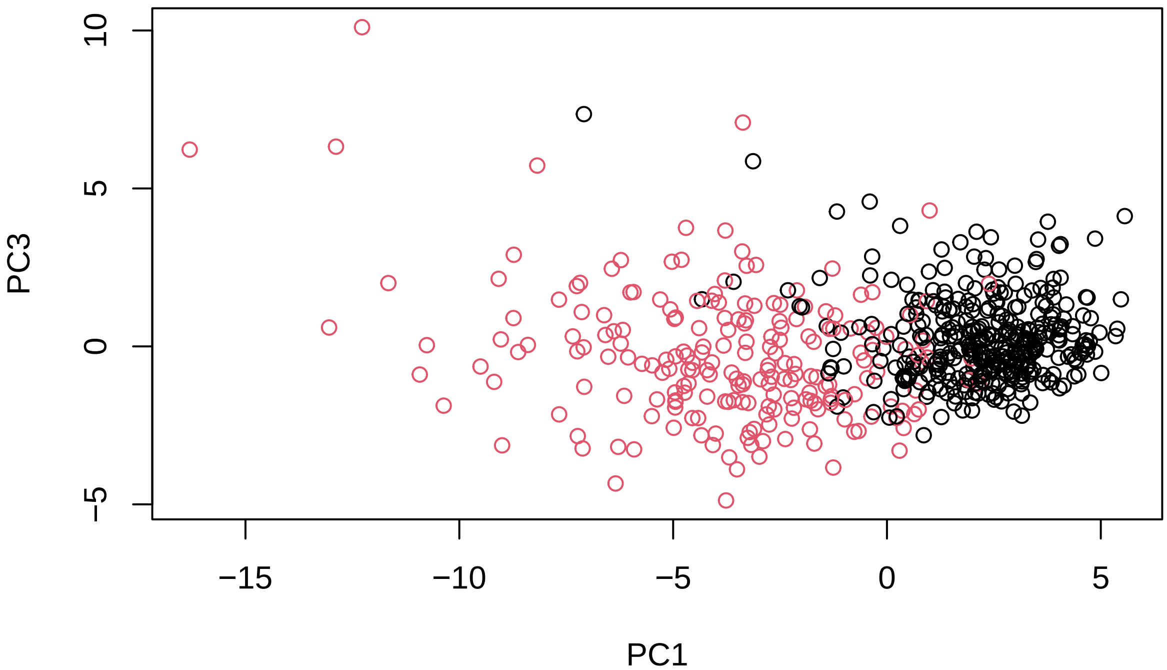
```
# Scatter plot observations by components 1 and 2
plot(wisc.pr$x, col = diagnosis ,
     xlab = "PC1", ylab = "PC2")
```



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

Although similar, PC1 vs PC2 displays less overlap between the data sets.

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

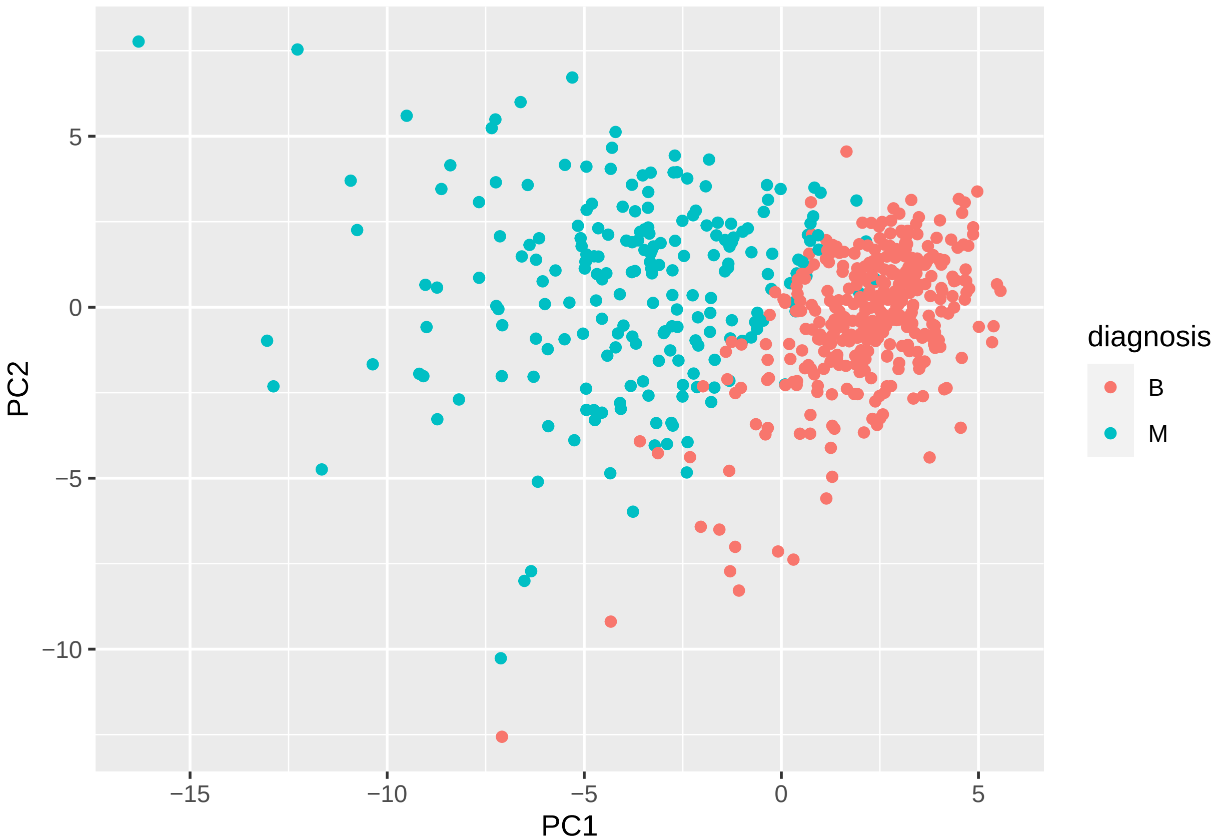


ggplot

```
# 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
```

```
sum.pr <- sum(pr.var)
```

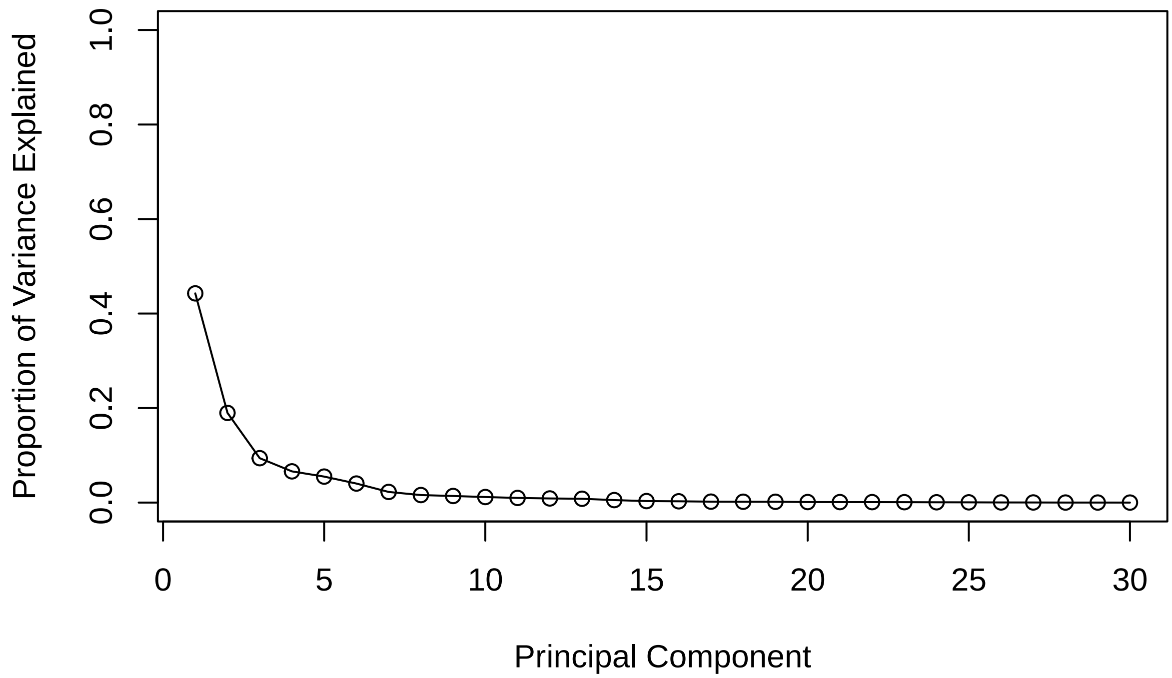
```
# Variance explained by each principal component: pve
pve <- pr.var/ sum.pr
pve
```

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

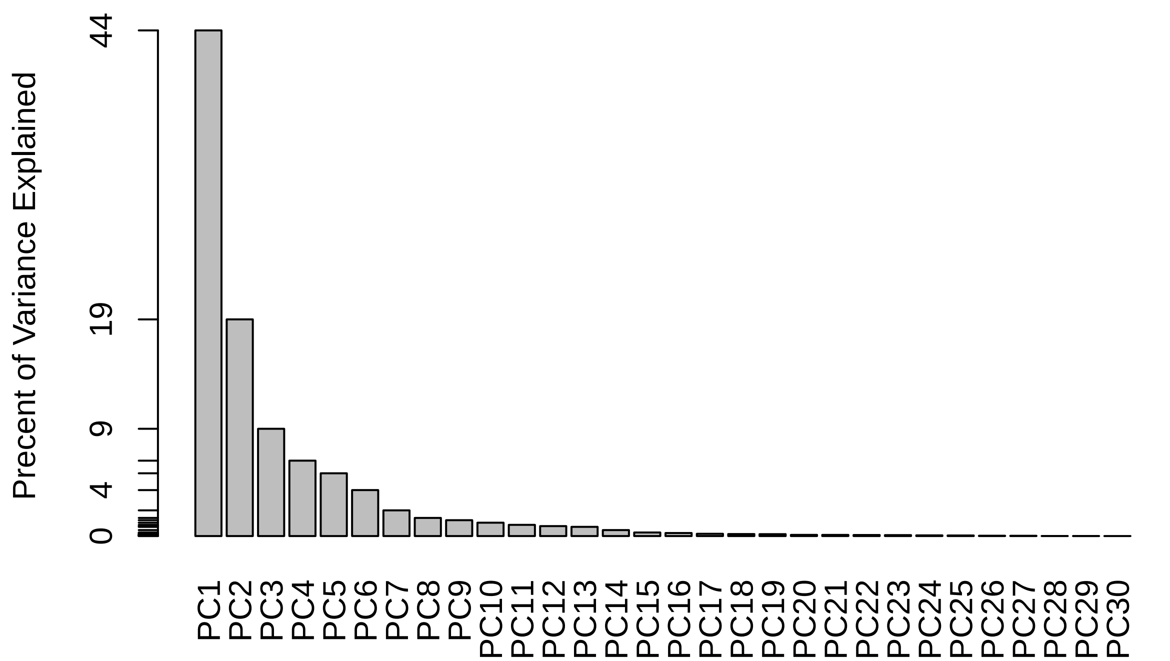
```
##  [1] 4.427203e-01 1.897118e-01 9.393163e-02 6.602135e-02 5.495768e-02
##  [6] 4.024522e-02 2.250734e-02 1.588724e-02 1.389649e-02 1.168978e-02
## [11] 9.797190e-03 8.705379e-03 8.045250e-03 5.233657e-03 3.137832e-03
## [16] 2.662093e-03 1.979968e-03 1.753959e-03 1.649253e-03 1.038647e-03
## [21] 9.990965e-04 9.146468e-04 8.113613e-04 6.018336e-04 5.160424e-04
## [26] 2.725880e-04 2.300155e-04 5.297793e-05 2.496010e-05 4.434827e-06
```

```
# Plot variance explained for each principal component
plot(pve, xlab = "Principal Component",
```

```r
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```



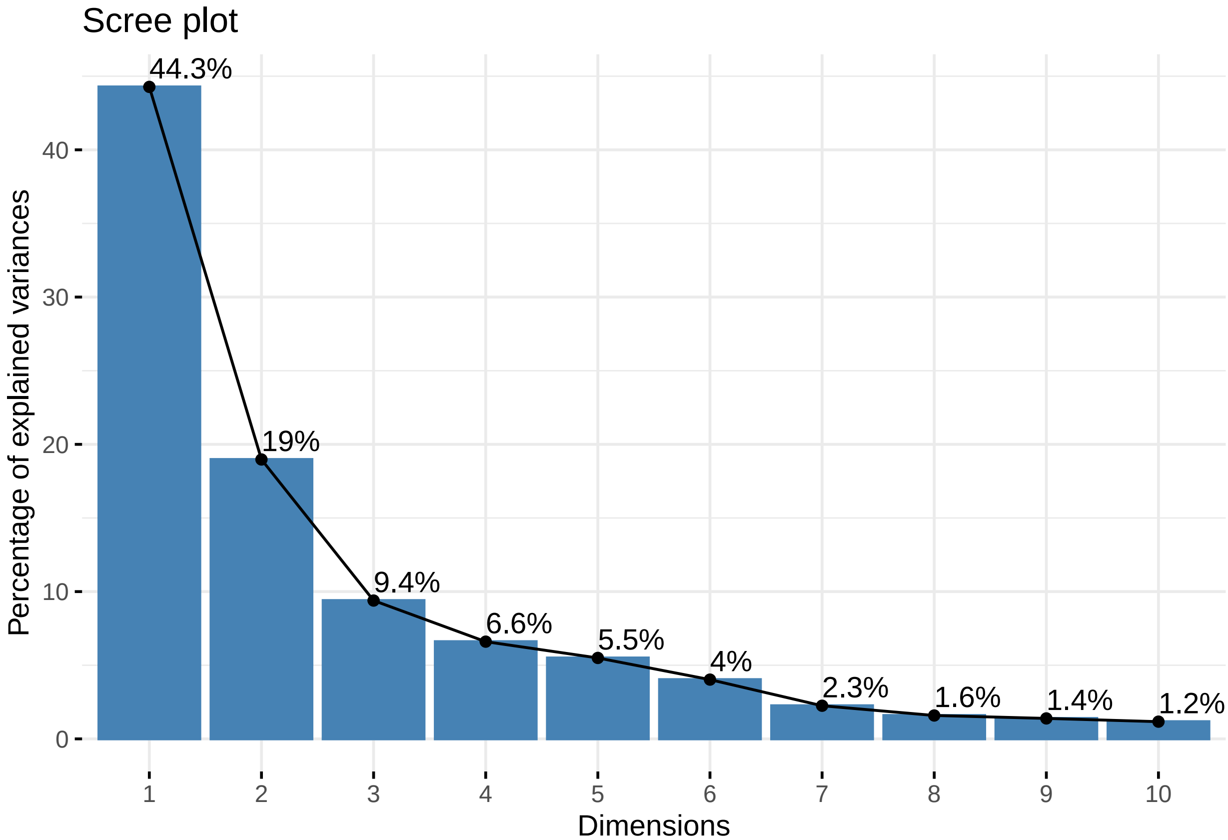

```r
# Alternative scree plot of the same data, note data driven y-axis
barplot(pve, ylab = "Precent of Variance Explained",
     names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```




```r
## ggplot based graph
#install.packages("factoextra")
library(factoextra)
```

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

```r
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?

```r
wisc.pr$rotation[,1]
```

concave.points_mean = -0.26085376

```
##             radius_mean            texture_mean          perimeter_mean 
##             -0.21890244             -0.10372458             -0.22753729 
##               area_mean         smoothness_mean        compactness_mean 
##             -0.22099499             -0.14258969             -0.23928535 
##          concavity_mean     concave.points_mean           symmetry_mean 
##             -0.25840048             -0.26085376             -0.13816696 
##  fractal_dimension_mean               radius_se              texture_se 
##             -0.06436335             -0.20597878             -0.01742803 
##            perimeter_se                 area_se           smoothness_se 
##             -0.21132592             -0.20286964             -0.01453145 
##          compactness_se            concavity_se       concave.points_se 
##             -0.17039345             -0.15358979             -0.18341740 
##             symmetry_se    fractal_dimension_se            radius_worst 
##             -0.04249842             -0.10256832             -0.22799663 
##           texture_worst         perimeter_worst              area_worst 
```

```
##            -0.10446933            -0.23663968            -0.22487053
##        smoothness_worst       compactness_worst         concavity_worst
##            -0.12795256            -0.21009588            -0.22876753
##    concave.points_worst          symmetry_worst fractal_dimension_worst
##            -0.25088597            -0.12290456            -0.13178394
```

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

```r
x$importance[3,] >= 0.8
```

Minimum number of principal components is 5.

```
##   PC1   PC2   PC3   PC4   PC5   PC6   PC7   PC8   PC9  PC10  PC11  PC12  PC13
## FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  PC14  PC15  PC16  PC17  PC18  PC19  PC20  PC21  PC22  PC23  PC24  PC25  PC26
##  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  PC27  PC28  PC29  PC30
##  TRUE  TRUE  TRUE  TRUE
```

```r
PC80 <- which(x$importance[3,] >= 0.8)
PC80[1]
```

```
## PC5
##   5
```

3. Hierarchical clustering

First scale the wisc.data data and assign the result to data.scaled.

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

Calculate the (Euclidean) distances between all pairs of observations in the new scaled dataset and assign the result to data.dist.

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

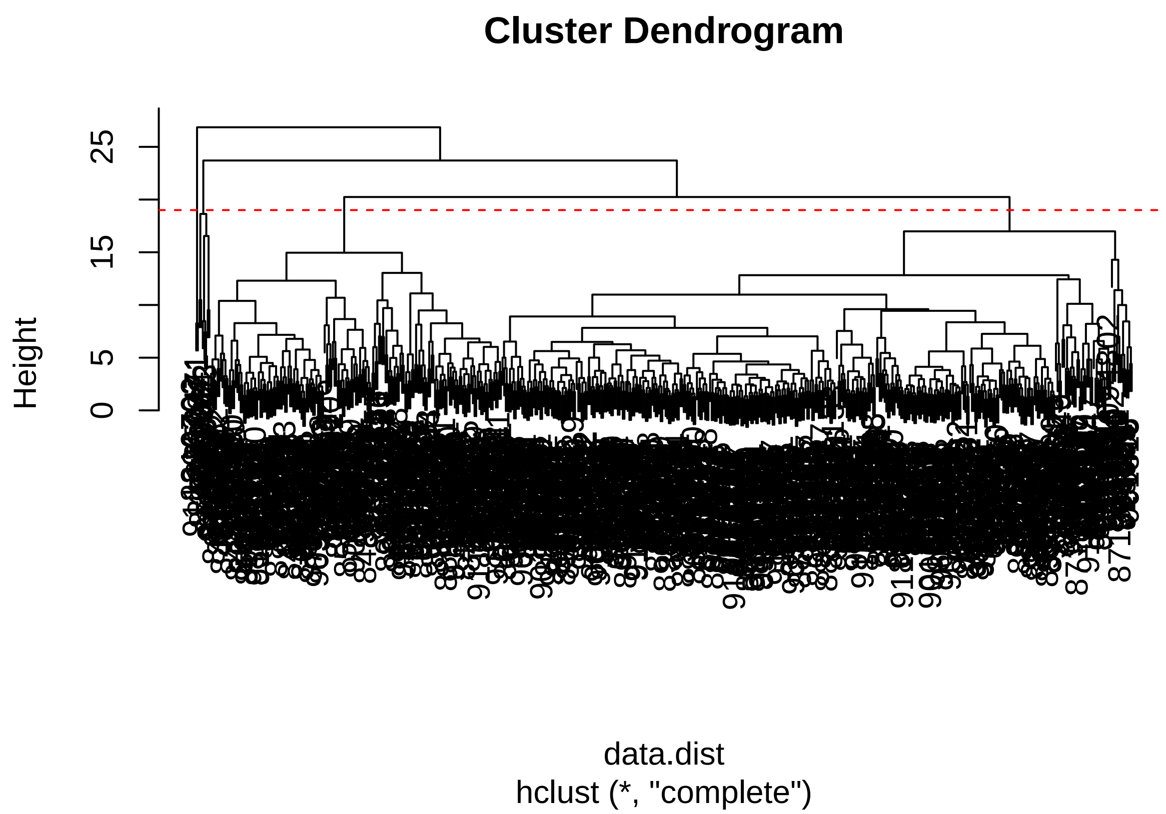
Create a hierarchical clustering model using complete linkage. Manually specify the method argument to hclust() and assign the results to wisc.hclust.

```r
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?

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



height = 19

Selecting number of clusters

Use cutree() to cut the tree so that it has 4 clusters. Assign the output to the variable wisc.hclust.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?

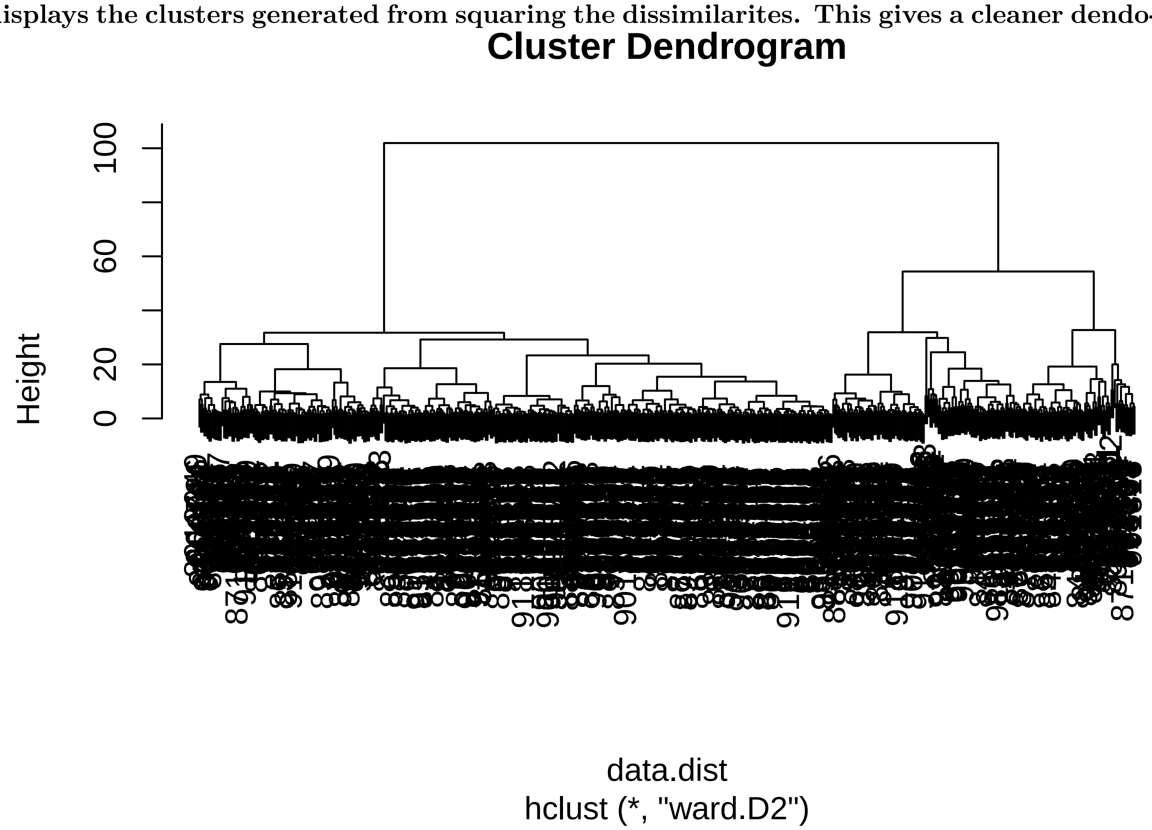
```
wisc.hclust.clusters2 <- cutree(wisc.hclust, k = 2, 10)
table(wisc.hclust.clusters2, diagnosis)
```

```
##                      diagnosis
## wisc.hclust.clusters2   B   M
##                     1 357 210
##                     2   0   2
```

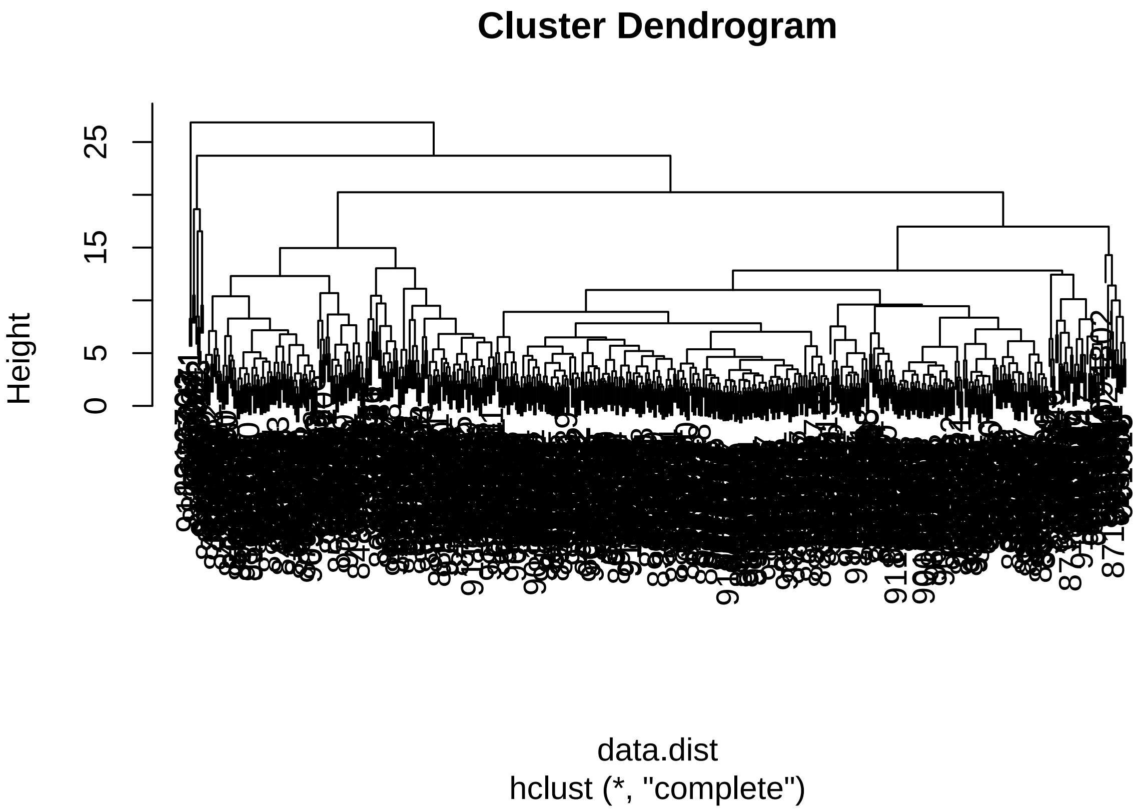
Q13. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning.

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

The 'ward.D2' method appears to give a better result of the same data.dist data set. The dendogram displays the clusters generated from squaring the dissimilarites. This gives a cleaner dendogram.




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



4. OPTIONAL: K-means clustering

```
wisc.km <- kmeans(scale(wisc.data), 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?

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

Fewer false positives/negatives.

```
##
## wisc.hclust.clusters   1   2
##                    1 160  17
##                    2   7   0
##                    3  20 363
##                    4   2   0
```

5. Combining methods

Clustering on PCA results

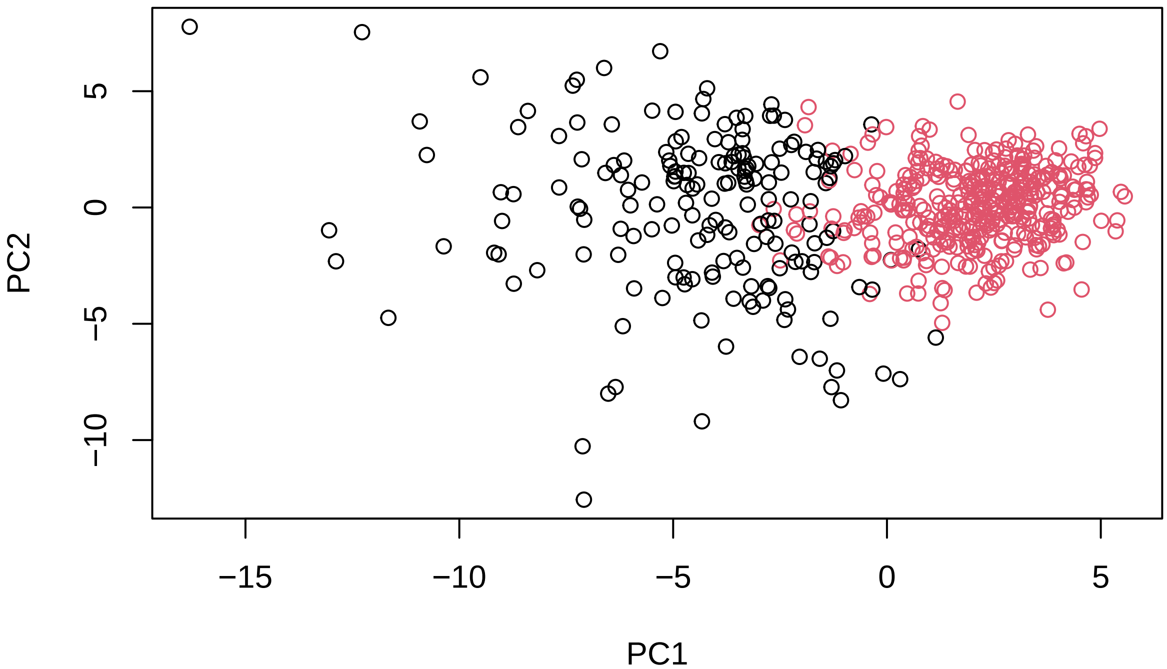
```
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

```
## grps
##   1   2
## 184 385
```

```
# We can do a cross-table by giving the table() function two inputs.
# TP (true positive = 164) FP (false positive = 20)
# TN (true negatives = 337) FP (false positive = 48)
table(grps, diagnosis)
```

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

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



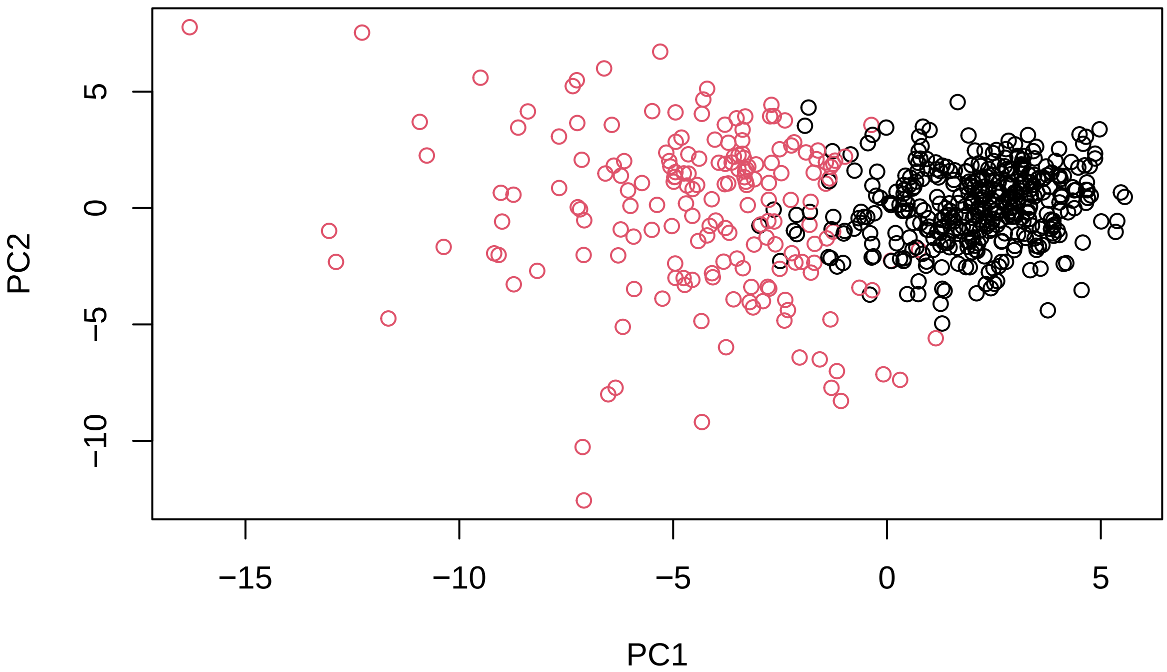

```
g <- as.factor(grps)
levels(g)
```

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

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

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

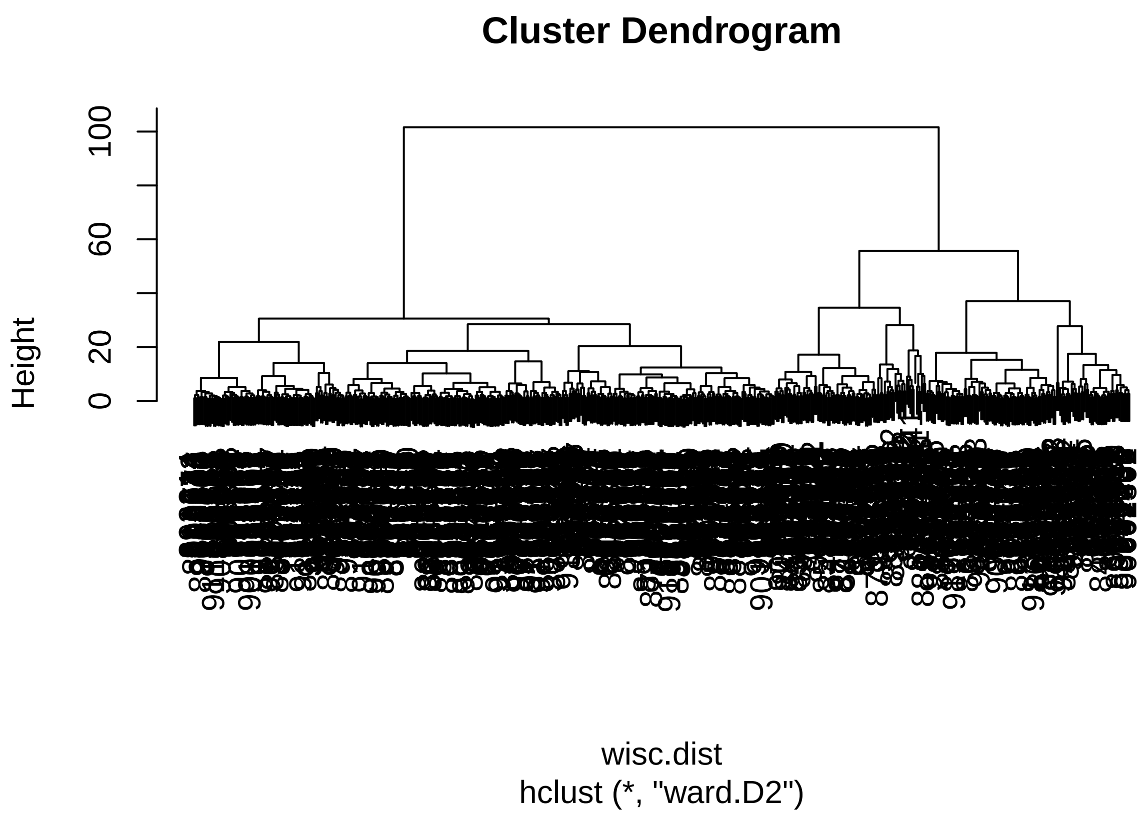
```
# Plot using our re-ordered factor
plot(wisc.pr$x[,1:2], col=g)
```



OPTIONAL

```
library(rgl)
plot3d(wisc.pr$x[,1:3], xlab="PC 1", ylab="PC 2", zlab="PC 3", cex=1.5, size=1, type="s", col=grps)
```

```
## Use the distance along the first 7 PCs for clustering i.e. wisc.pr$x[, 1:7]
wisc.dist <- dist(wisc.pr$x[, 1:7])
wisc.pr.hclust <- hclust(wisc.dist, method="ward.D2")
plot(wisc.pr.hclust)
```



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

```
wisc.pr.hclust.clusters <- cutree(wisc.pr.hclust, k=2)
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.km$cluster, diagnosis)
```

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

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

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

```
##                         4   0   2
```

#6. Sensitivity/Specificity ### **Q17.** Which of your analysis procedures resulted in a clustering model with the best specificity? How about sensitivity? #### It appears that the best specificity comes from using 'hclust' and we get the best sensitivity with 'kmeans'.

```
(175)/(175+14)
```

calculating sensitivity TP/(TP+FN)

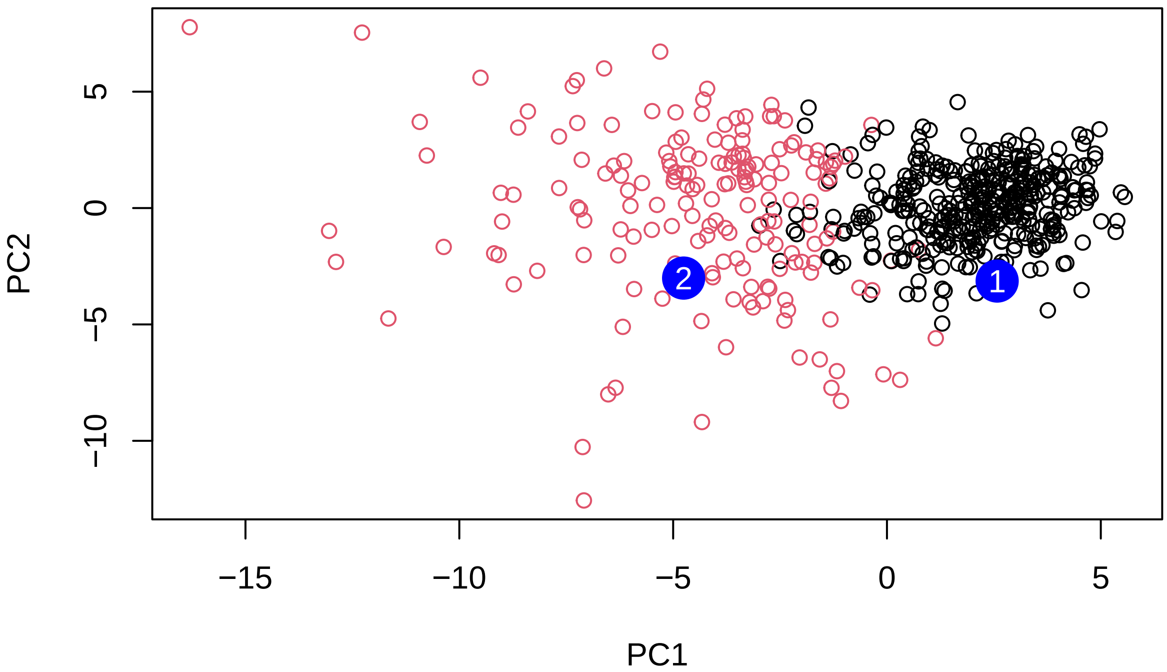
```
## [1] 0.9259259
```

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")
```



Q18. Which of these new patients should we prioritize for follow up based on your results?
patient 1.