Class08 mini-project

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```
# 1) Exploratory Data Analysis
# Input data

fna.data <- "WisconsinCancer.csv"
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
```

```
# Alter dataframe to remove "diagnosis" column
wisc.data <- wisc.df[,-1]
head(wisc.data)
```

```
##          radius_mean texture_mean perimeter_mean area_mean smoothness_mean
## 842302        17.99        10.38         122.80    1001.0         0.11840
## 842517        20.57        17.77         132.90    1326.0         0.08474
## 84300903      19.69        21.25         130.00    1203.0         0.10960
## 84348301      11.42        20.38          77.58     386.1         0.14250
## 84358402      20.29        14.34         135.10    1297.0         0.10030
## 843786        12.45        15.70          82.57     477.1         0.12780
##          compactness_mean concavity_mean concave.points_mean symmetry_mean
## 842302            0.27760         0.3001             0.14710        0.2419
## 842517            0.07864         0.0869             0.07017        0.1812
## 84300903          0.15990         0.1974             0.12790        0.2069
## 84348301          0.28390         0.2414             0.10520        0.2597
## 84358402          0.13280         0.1980             0.10430        0.1809
## 843786            0.17000         0.1578             0.08089        0.2087
##          fractal_dimension_mean radius_se texture_se perimeter_se area_se
## 842302                  0.07871    1.0950     0.9053        8.589  153.40
## 842517                  0.05667    0.5435     0.7339        3.398   74.08
## 84300903                0.05999    0.7456     0.7869        4.585   94.03
## 84348301                0.09744    0.4956     1.1560        3.445   27.23
## 84358402                0.05883    0.7572     0.7813        5.438   94.44
## 843786                  0.07613    0.3345     0.8902        2.217   27.19
##          smoothness_se compactness_se concavity_se concave.points_se
## 842302        0.006399        0.04904      0.05373           0.01587
## 842517        0.005225        0.01308      0.01860           0.01340
## 84300903      0.006150        0.04006      0.03832           0.02058
## 84348301      0.009110        0.07458      0.05661           0.01867
## 84358402      0.011490        0.02461      0.05688           0.01885
## 843786        0.007510        0.03345      0.03672           0.01137
##          symmetry_se fractal_dimension_se radius_worst texture_worst
## 842302       0.03003             0.006193        25.38         17.33
## 842517       0.01389             0.003532        24.99         23.41
## 84300903     0.02250             0.004571        23.57         25.53
## 84348301     0.05963             0.009208        14.91         26.50
## 84358402     0.01756             0.005115        22.54         16.67
## 843786       0.02165             0.005082        15.47         23.75
##          perimeter_worst area_worst smoothness_worst compactness_worst
## 842302            184.60     2019.0           0.1622            0.6656
## 842517            158.80     1956.0           0.1238            0.1866
## 84300903          152.50     1709.0           0.1444            0.4245
## 84348301           98.87      567.7           0.2098            0.8663
## 84358402          152.20     1575.0           0.1374            0.2050
## 843786            103.40      741.6           0.1791            0.5249
##          concavity_worst concave.points_worst symmetry_worst
## 842302            0.7119               0.2654         0.4601
## 842517            0.2416               0.1860         0.2750
## 84300903          0.4504               0.2430         0.3613
## 84348301          0.6869               0.2575         0.6638
## 84358402          0.4000               0.1625         0.2364
## 843786            0.5355               0.1741         0.3985
##          fractal_dimension_worst
## 842302                   0.11890
## 842517                   0.08902
```

```
## 84300903                0.08758
## 84348301                0.17300
## 84358402                0.07678
## 843786                  0.12440
```

```
# Store Diagnosis column as vector
# First store as factor and then as vector
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.5     v purrr   0.3.4
## v tibble  3.1.6     v dplyr   1.0.7
## v tidyr   1.2.0     v stringr 1.4.0
## v readr   2.1.2     v forcats 0.5.1
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
diagnosis_list <- wisc.df[,1]
diagnosis_level <- c("B", "M")
diagnosis <- factor(diagnosis_list, level=diagnosis_level)
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
```

```
# Factor with warning
diagnosis2 <- parse_factor(diagnosis_list, level=diagnosis_level)
```

```
# [Q1] How many observations are in this dataset?
nrow(wisc.data)
```

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

```
# There are 569 observations in the dataset.

# [Q2] How many of the observations have a malignant diagnosis?
table(diagnosis)
```

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

```
# There are 212 malignant diagnosis observations.

# [Q3] How many variables/features in the data are suffixed with _mean?
length(grep("_mean", colnames(wisc.df)))
```

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

```
# There are 10 variables in the data suffixed with _mean.
```

```
# 2) Principal Component Analysis

# Check if wisc.data needs to be scaled
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)
```

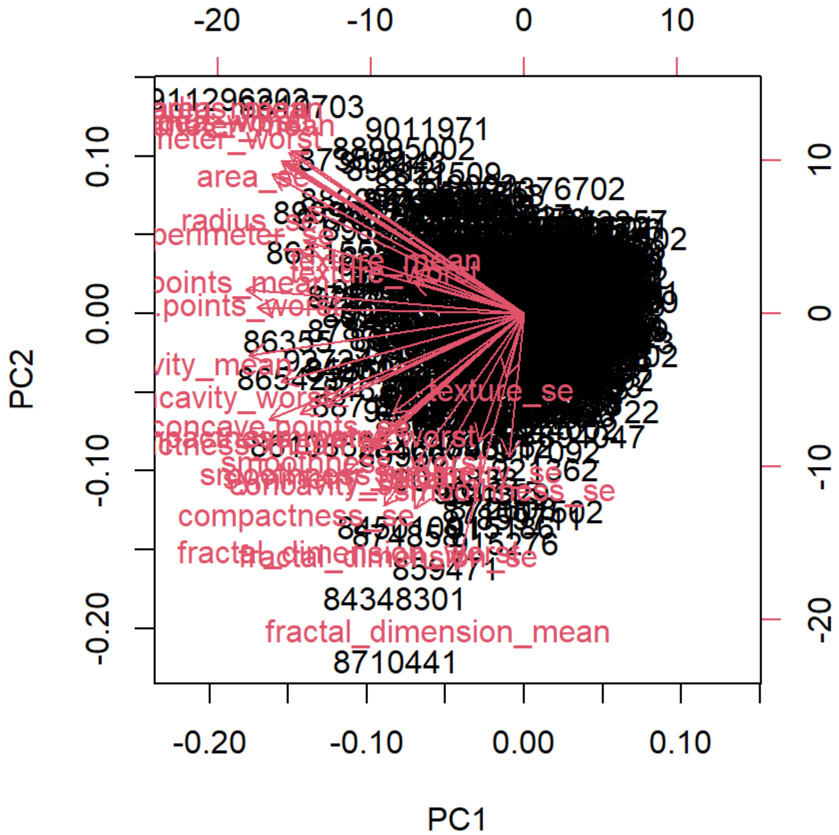
```
##             radius_mean            texture_mean          perimeter_mean 
##            3.524049e+00            4.301036e+00            2.429898e+01 
##               area_mean         smoothness_mean        compactness_mean 
##            3.519141e+02            1.406413e-02            5.281276e-02 
##          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
```

```
# Does need to be scaled due to high variance.

# Perform PCA on wisc.data
wisc.pr <- prcomp(wisc.data, scale=TRUE)
summary(wisc.pr)
```

```
## Importance of components:
##                           PC1    PC2     PC3     PC4     PC5     PC6     PC7
## Standard deviation     3.6444 2.3857 1.67867 1.40735 1.28403 1.09880 0.82172
## Proportion of Variance 0.4427 0.1897 0.09393 0.06602 0.05496 0.04025 0.02251
## Cumulative Proportion  0.4427 0.6324 0.72636 0.79239 0.84734 0.88759 0.91010
##                            PC8    PC9    PC10   PC11    PC12    PC13    PC14
## Standard deviation     0.69037 0.6457 0.59219 0.5421 0.51104 0.49128 0.39624
## Proportion of Variance 0.01589 0.0139 0.01169 0.0098 0.00871 0.00805 0.00523
## Cumulative Proportion  0.92598 0.9399 0.95157 0.9614 0.97007 0.97812 0.98335
##                           PC15    PC16    PC17    PC18    PC19    PC20   PC21
## Standard deviation     0.30681 0.28260 0.24372 0.22939 0.22244 0.17652 0.1731
## Proportion of Variance 0.00314 0.00266 0.00198 0.00175 0.00165 0.00104 0.0010
## Cumulative Proportion  0.98649 0.98915 0.99113 0.99288 0.99453 0.99557 0.9966
##                           PC22    PC23   PC24    PC25    PC26    PC27    PC28
## Standard deviation     0.16565 0.15602 0.1344 0.12442 0.09043 0.08307 0.03987
## Proportion of Variance 0.00091 0.00081 0.0006 0.00052 0.00027 0.00023 0.00005
## Cumulative Proportion  0.99749 0.99830 0.9989 0.99942 0.99969 0.99992 0.99997
##                           PC29    PC30
## Standard deviation     0.02736 0.01153
## Proportion of Variance 0.00002 0.00000
## Cumulative Proportion  1.00000 1.00000
```

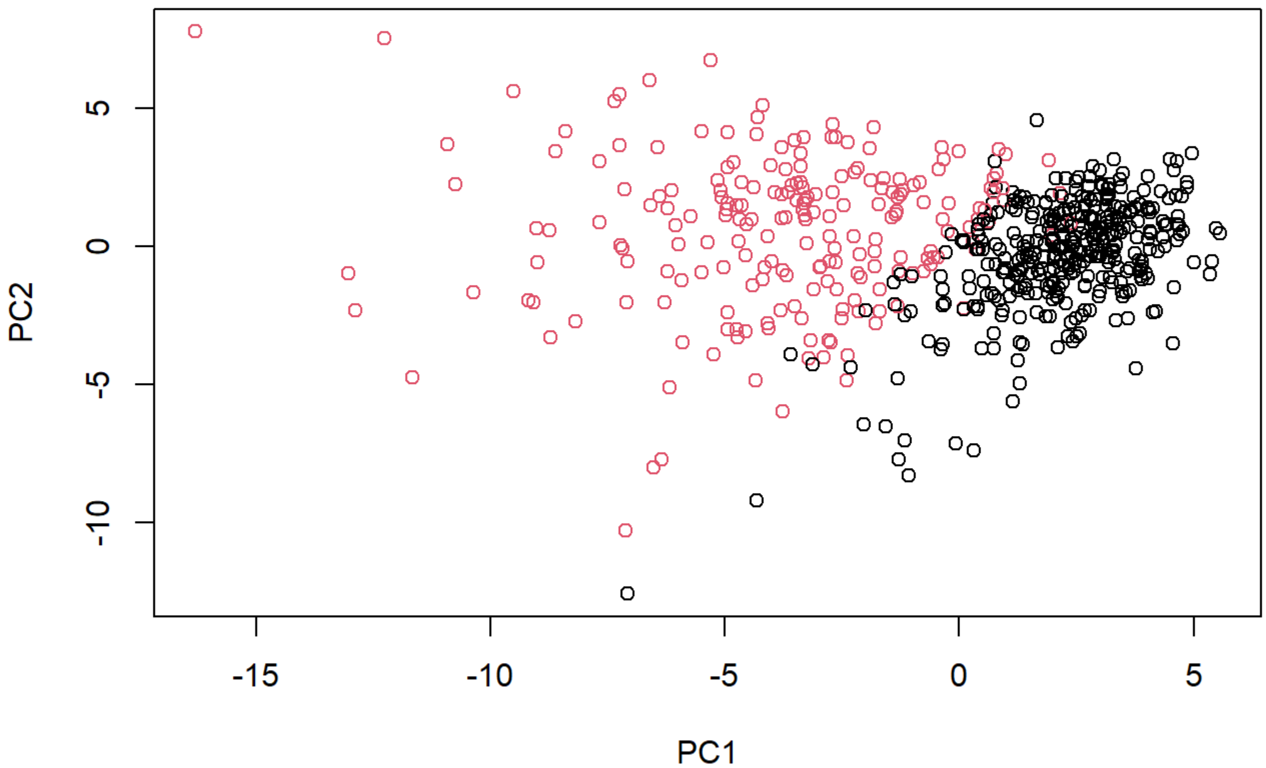
```
# [Q4] From your results, what proportion of the original variance is captured by the first prin
cipal components (PC1)?
# On the summary(wisc.pr), the proportion of variance that PC1 captures is 0.4427.

# [Q5] How many principal components (PCs) are required to describe at least 70% of the original
variance in the data?
# Based on the summary(wisc.pr), 3 principal components are required to describe at least 70% of
the original variance in the data.

# [Q6] How many principal components (PCs) are required to describe at least 90% of the original
variance in the data?
# Based on the summary(wisc.pr), 7 principal components are required to describe at least 90% of
the original variance in the data.
```

```
#Biplot of PCA results
biplot(wisc.pr)
```

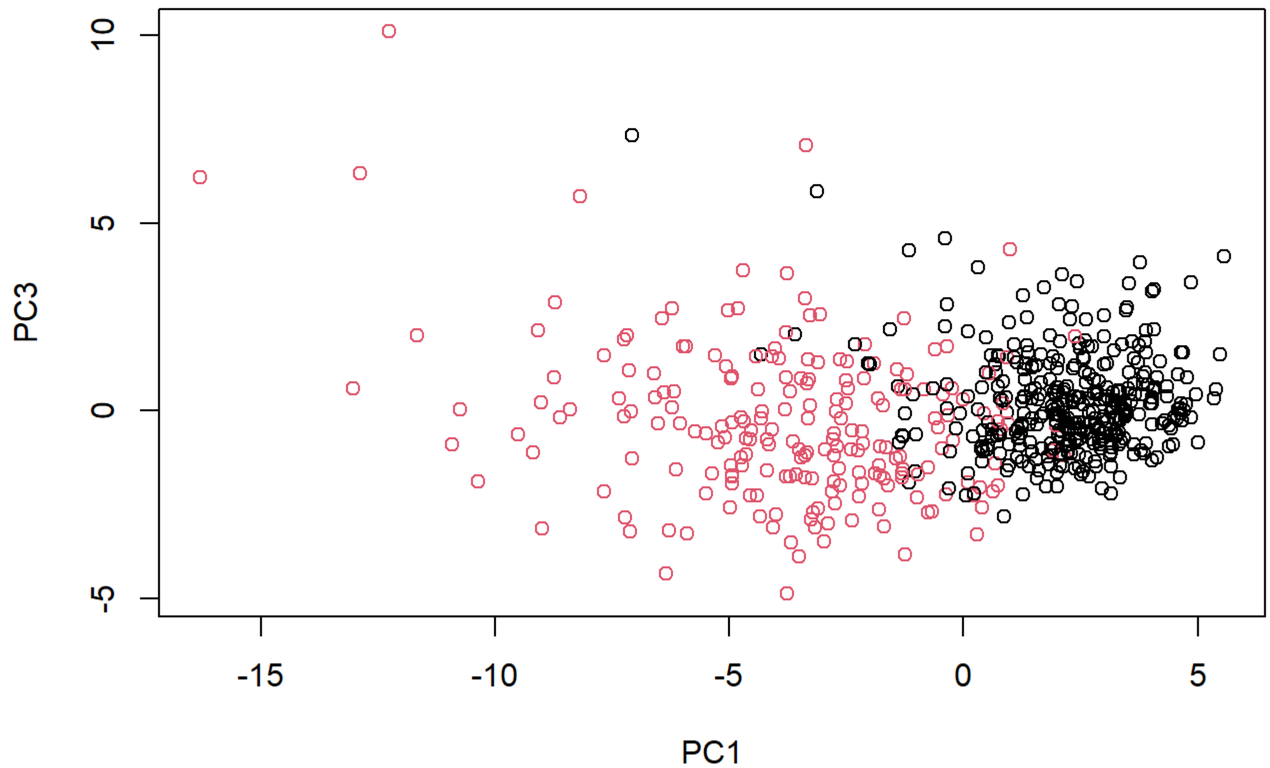



```
# [Q7] What stands out to you about this plot? Is it easy or difficult to understand? Why?
# Based on observations of the plot, a majority of PC1 and PC2 have variances that fall in betwe
en -0.1 and 0.1. However, a few IDs, such as 8710441, have variances not between -0.1 and 0.1. T
he biplot is difficult to understand because of how compact all the data is, making it difficult
to read.
```

```
# Scatterplot of PC1 and PC2
plot(wisc.pr$x[,1:2], col=diagnosis,
  xlab="PC1", ylab="PC2")
```




```
# [Q8] Generate a similar plot for principal components 1 and 3. What do you notice about these
 plots?
plot(wisc.pr$x[,1], wisc.pr$x[,3], col=diagnosis,
  xlab="PC1", ylab="PC3")
```




```
#It appears that PC3  has less variance than the PC2 plot since the more variance points for PC3 fall between -5 and 5 than PC2.
```

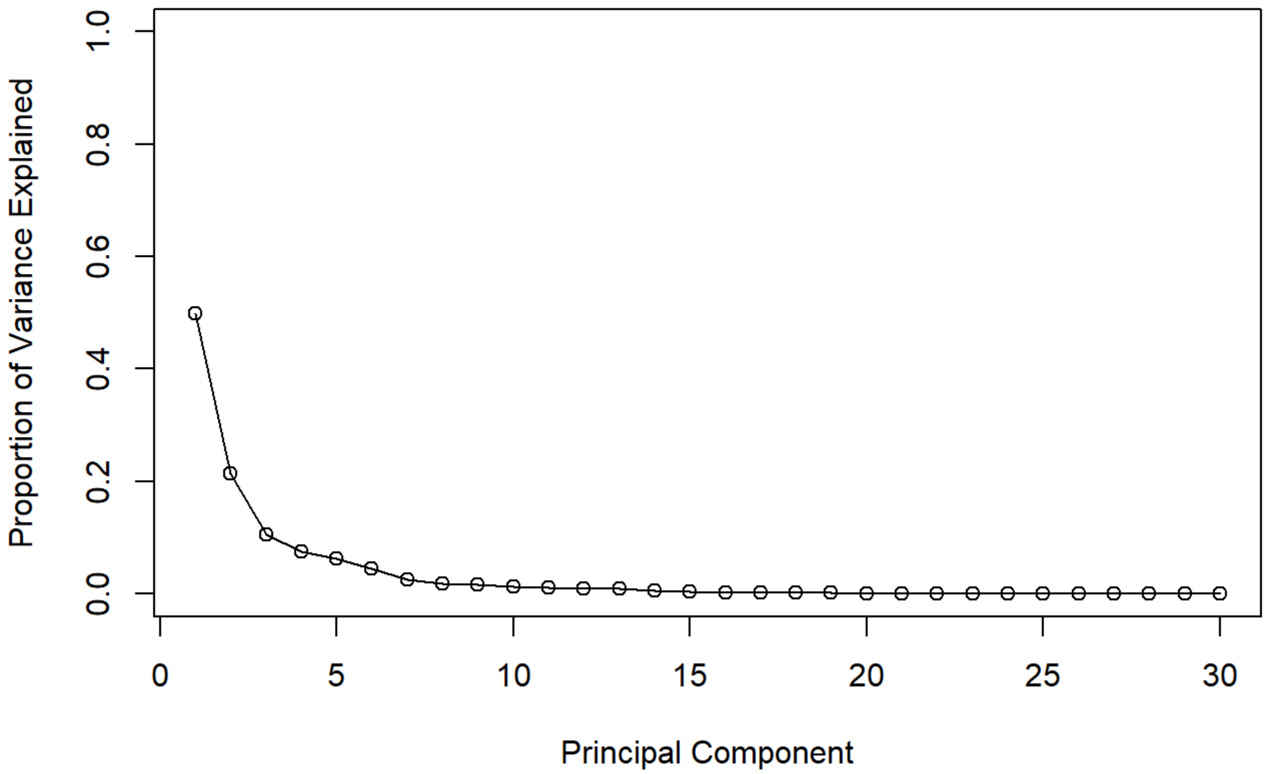
```
# Create a data.frame for ggplot
df <- as.data.frame(wisc.pr$x)
df$diagnosis <- diagnosis

# Load the ggplot2 package
library(ggplot2)

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

```
## Warning: Use of `df$diagnosis` is discouraged. Use `diagnosis` instead.
```

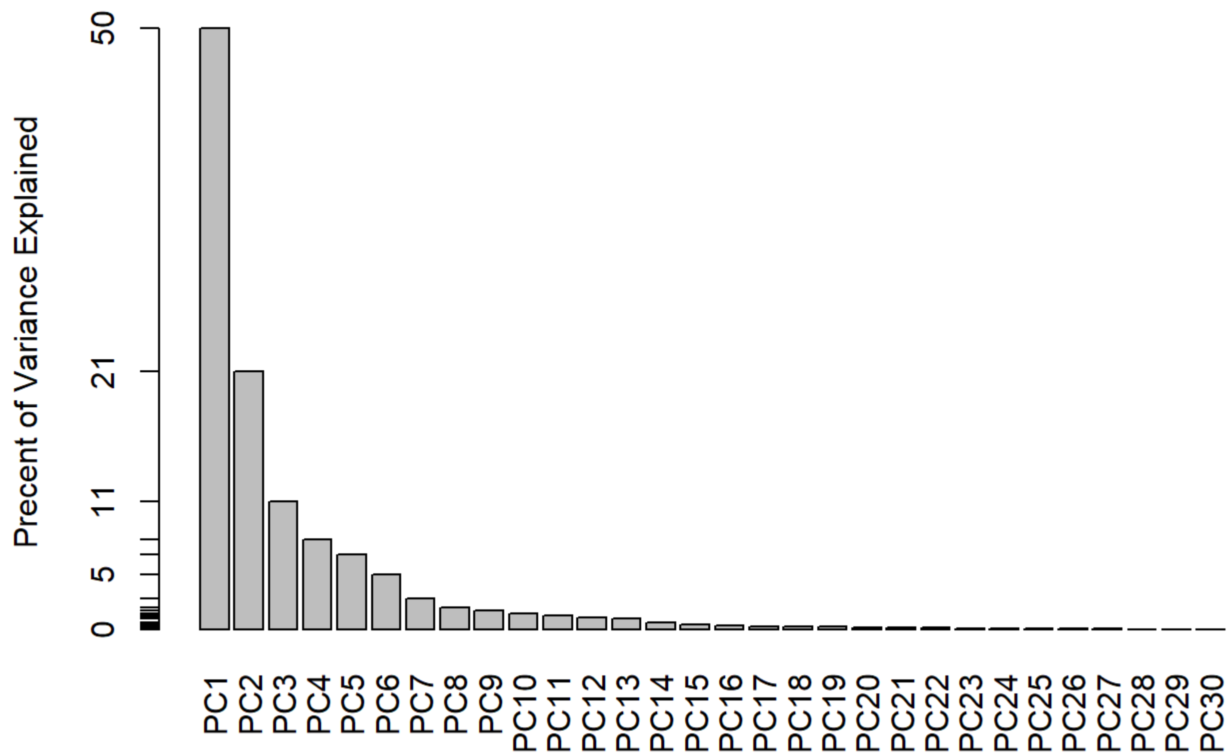

```
#Calculate variance of each components
var.pr <- wisc.pr$sdev^2
head(var.pr)
```

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

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

# Plot variance explained for each principal component
plot(pve, xlab = "Principal Component",
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```



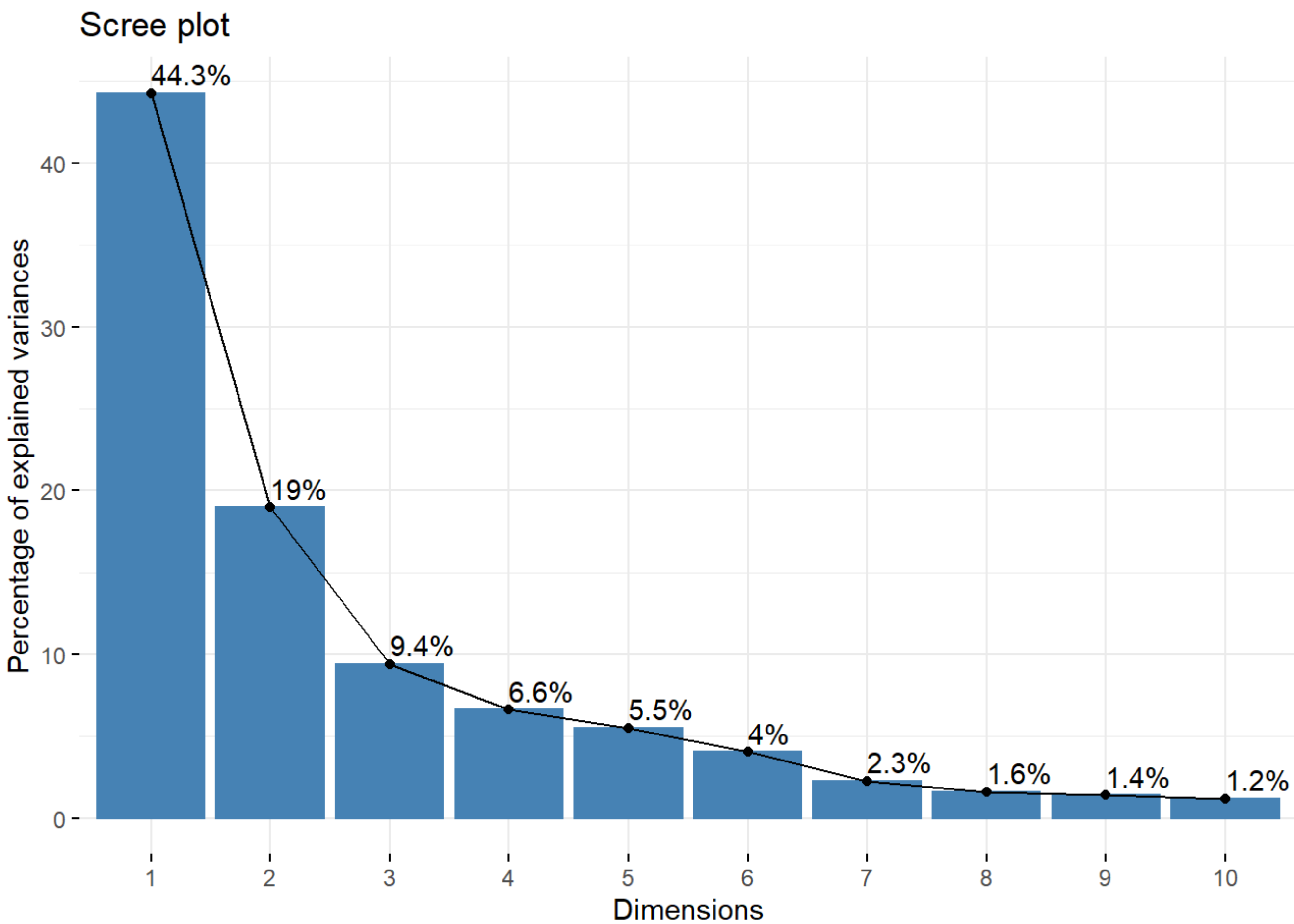

```
# Alternative scree plot of the same data, note data driven y-axis
barplot(pve, ylab = "Precent of Variance Explained",
     names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```




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

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

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




```
# [Q9] For the first principal component, what is the component of the loading vector (i.e. wis
c.pr$rotation[,1]) for the feature concave.points_mean?
wisc.pr$rotation[,1]
```

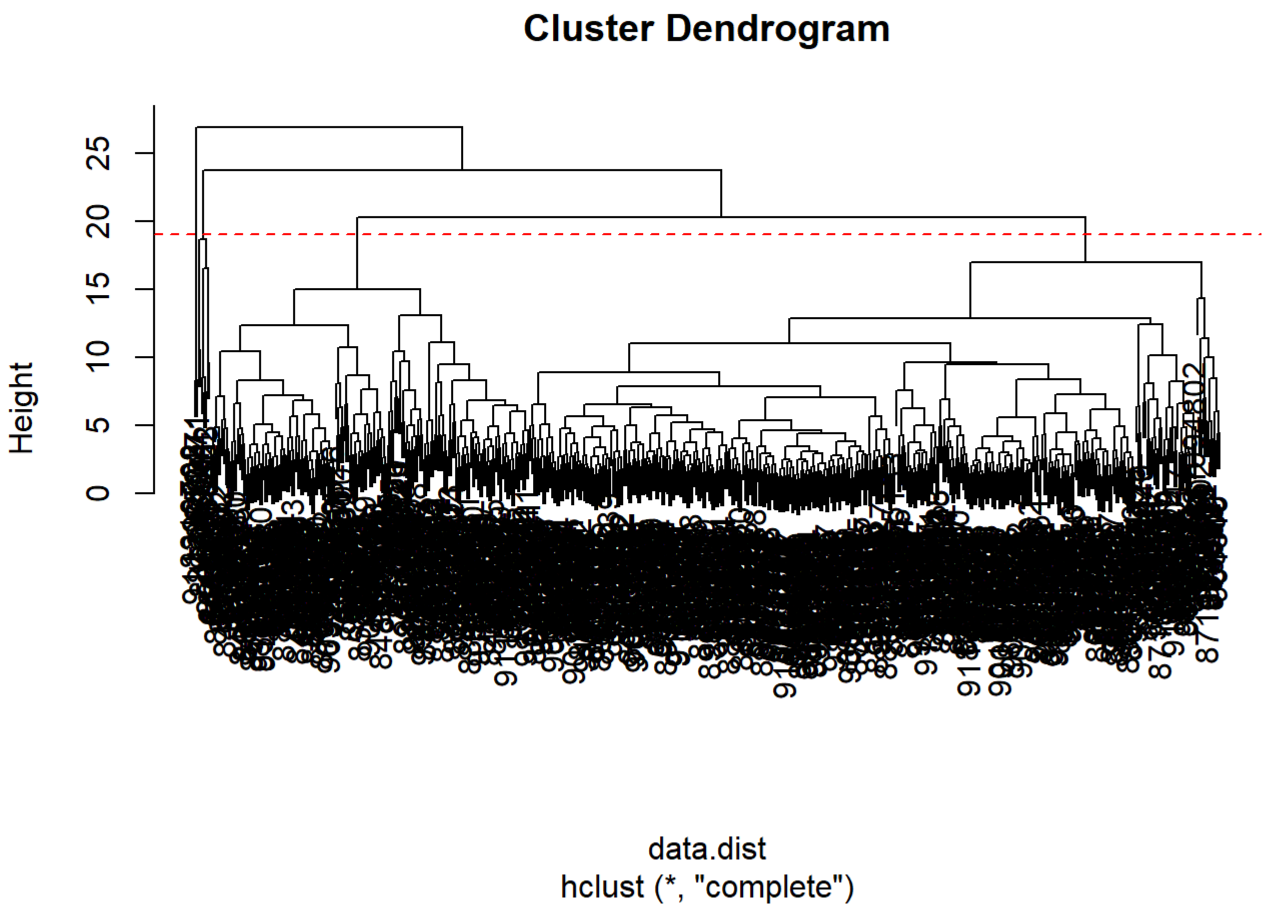
```
##            radius_mean            texture_mean          perimeter_mean
##            -0.21890244             -0.10372458             -0.22753729
##              area_mean         smoothness_mean        compactness_mean
##            -0.22099499             -0.14258969             -0.23928535
##         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
```

```
# The component of the loading vector for concave.poins_mean is -0.26085376.

# [Q10] What is the minimum number of principal components required to explain 80% of the varian
ce of the data?
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
```

```
# 5 prinicipal components are required to explain 80% of the variance of the data.
```

```
# 3) Hierarchial Clustering

#Scale wisc.data
data.scaled <- scale(wisc.data)

# Calculate Euclidean distances between all pairs of observations in scaled dataset
data.dist <- dist(data.scaled)

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

# [Q11] Using the plot() and abline() functions, what is the height at which the clustering mode
l has 4 clusters?
plot(wisc.hclust)
  abline(h=19, col="red", lty=2)
```




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

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

```
#[Q12] Can you find a better cluster vs diagnoses match by cutting into a different number of cl
usters between 2 and 10?
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
```

```
# The best cluster vs diagnoses match is found by cutting into 4 clusters
```

```
wisc.hclust.single <- hclust(data.dist, method="single")
wisc.hclust.singles <- cutree(wisc.hclust.single, k=3)
table(wisc.hclust.singles, diagnosis)
```

```
##                    diagnosis
## wisc.hclust.singles   B   M
##                   1 356 210
##                   2   1   0
##                   3   0   2
```

```
wisc.hclust.average <- hclust(data.dist, method="average")
wisc.hclust.averages <- cutree(wisc.hclust.average, k=3)
table(wisc.hclust.averages, diagnosis)
```

```
##                     diagnosis
## wisc.hclust.averages   B   M
##                    1 355 209
##                    2   2   0
##                    3   0   3
```

```
wisc.hclust.wardD2 <- hclust(data.dist, method="ward.D2")
wisc.hclust.ward.D2 <- cutree(wisc.hclust.wardD2, k=9)
table(wisc.hclust.ward.D2, diagnosis)
```

```
##                    diagnosis
## wisc.hclust.ward.D2   B   M
##                   1   0  57
##                   2   0  56
##                   3   6  48
##                   4  34  41
##                   5 201   5
##                   6  69   2
##                   7  33   0
##                   8  14   1
##                   9   0   2
```

```
# [Q13] Which method gives your favorite results for the same data.dist dataset? Explain your re
asoning.
# The ward.D2 method gave the better results as it was able to separate the data.dist dataset in
to respective clusters based on diagnosis.
```

```
# K-means clustering
wisc.km <- kmeans(scale(wisc.data), centers=2, nstart=20)
table(wisc.km$cluster, diagnosis)
```

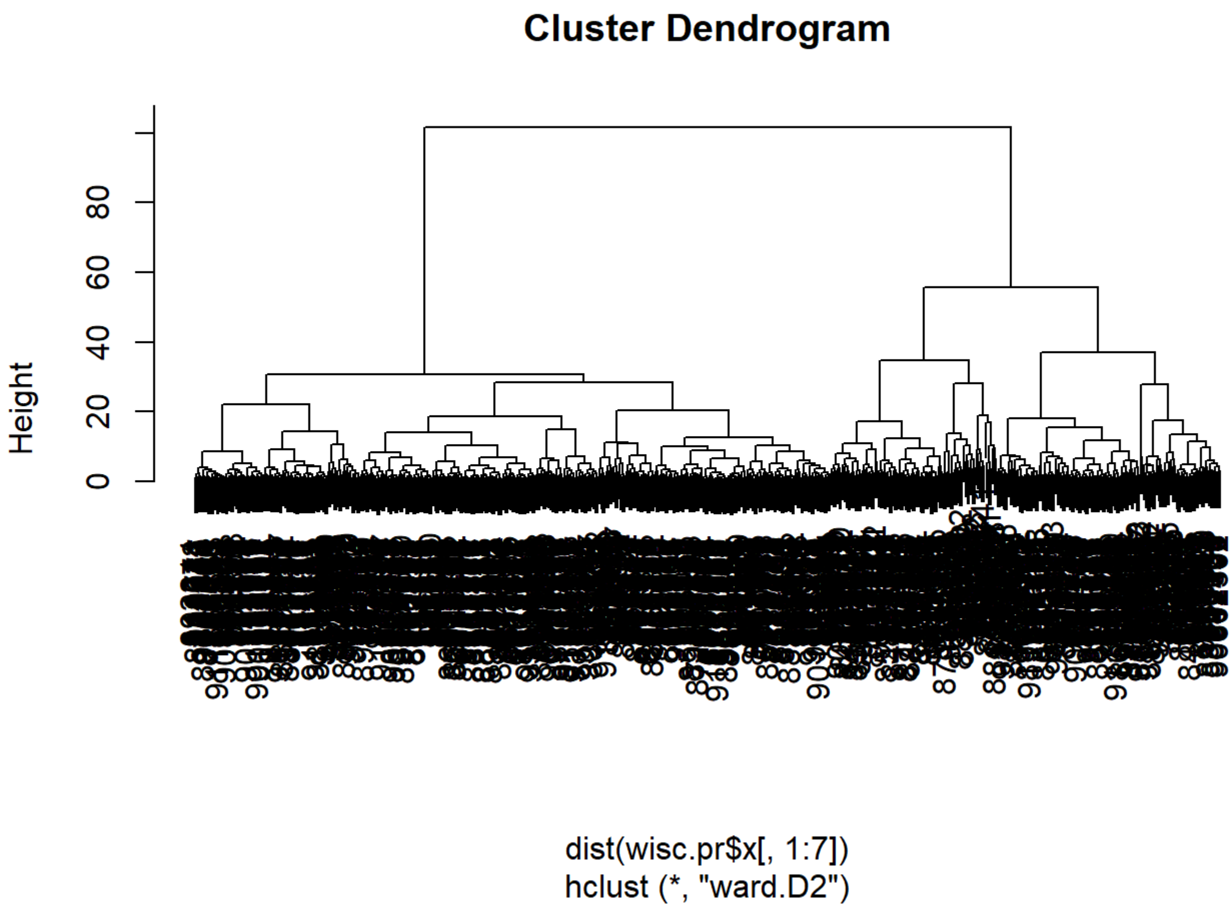
```
##    diagnosis
##       B   M
##   1  14 175
##   2 343  37
```

```
#Compare to hclust results
table(wisc.hclust.clusters, wisc.km$cluster)
```

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

```
# [Q14] How well does k-means separate the two diagnoses? How does it compare to your hclust res
ults?
# The k-means method separates the two diagnoses fairly well as it designates the benign and mal
ignant diagnoses into separate
```

```
# 5) Combining methods

# Use ward.D2 method to create hierarchical clustering model
dist <- data.dist
wisc.pr.hclust <- hclust(dist(wisc.pr$x[, 1:7]), method="ward.D2")
plot(wisc.pr.hclust)
```



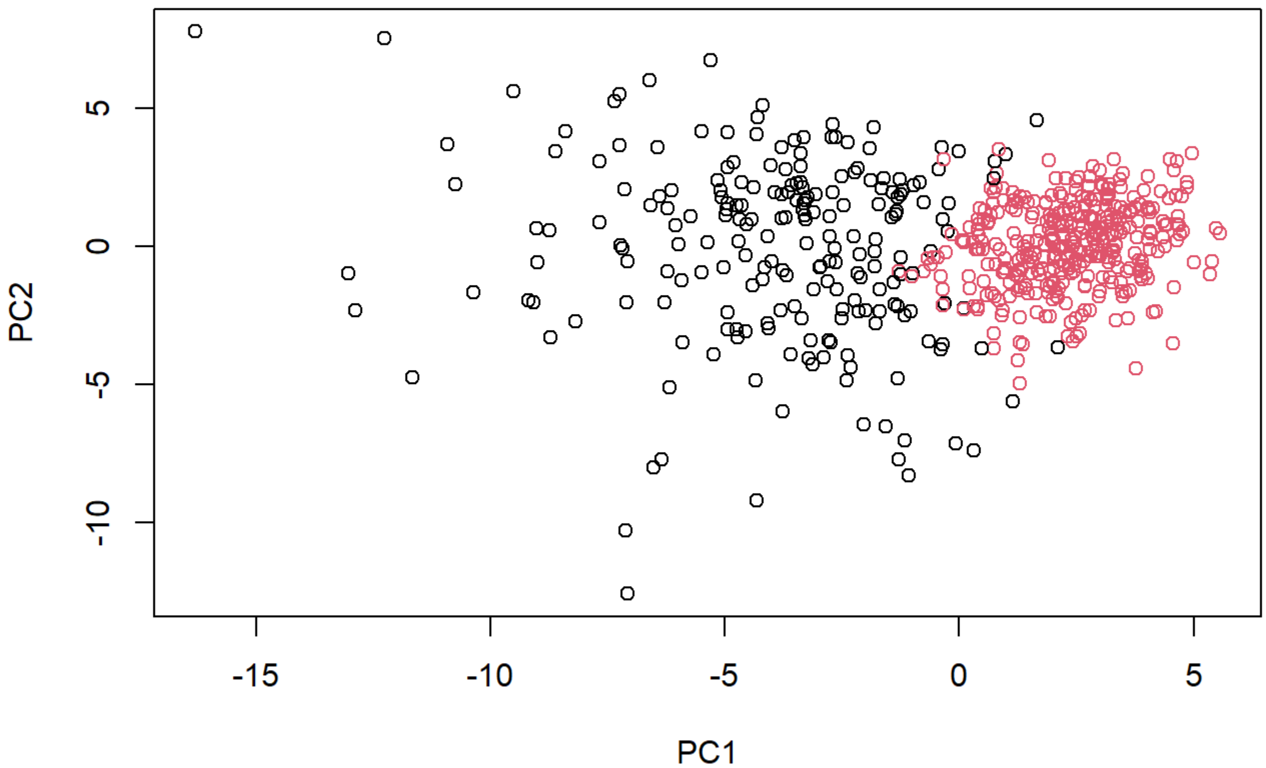

```
#Determining whether two main clusters indicate malignant and benign diagnoses
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

```
## grps
##   1   2
## 216 353
```

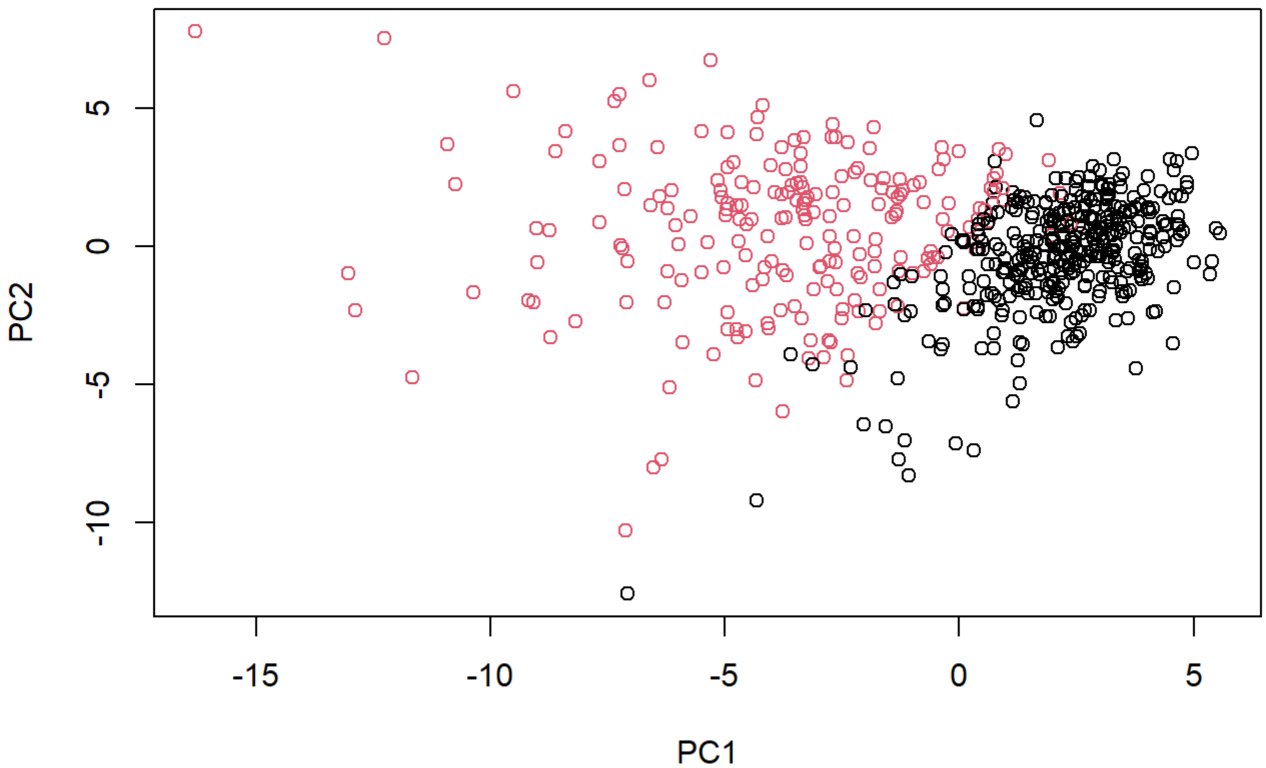
```
table(grps, diagnosis)
```

```
##     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)
```




```
# Use distance along first 7 PCs for clustering
wisc.pr.hclust <- hclust(dist(wisc.pr$x[,1:7]), method="ward.D2")
wisc.pr.hclust.clusters <- cutree(wisc.pr.hclust, k=2)
# Comparing to actual diagnosis
table(wisc.pr.hclust.clusters, diagnosis)
```

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

```
# [Q15] How well does the newly created model with four clusters separate out the two diagnoses?
# The new model separates the two diagnosis well as a majority of each diagnosis is separated in
to one of the clusters

# [Q16] How well do the k-means and hierarchical clustering models you created in previous secti
ons (i.e. before PCA) do in terms of separating the 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
```

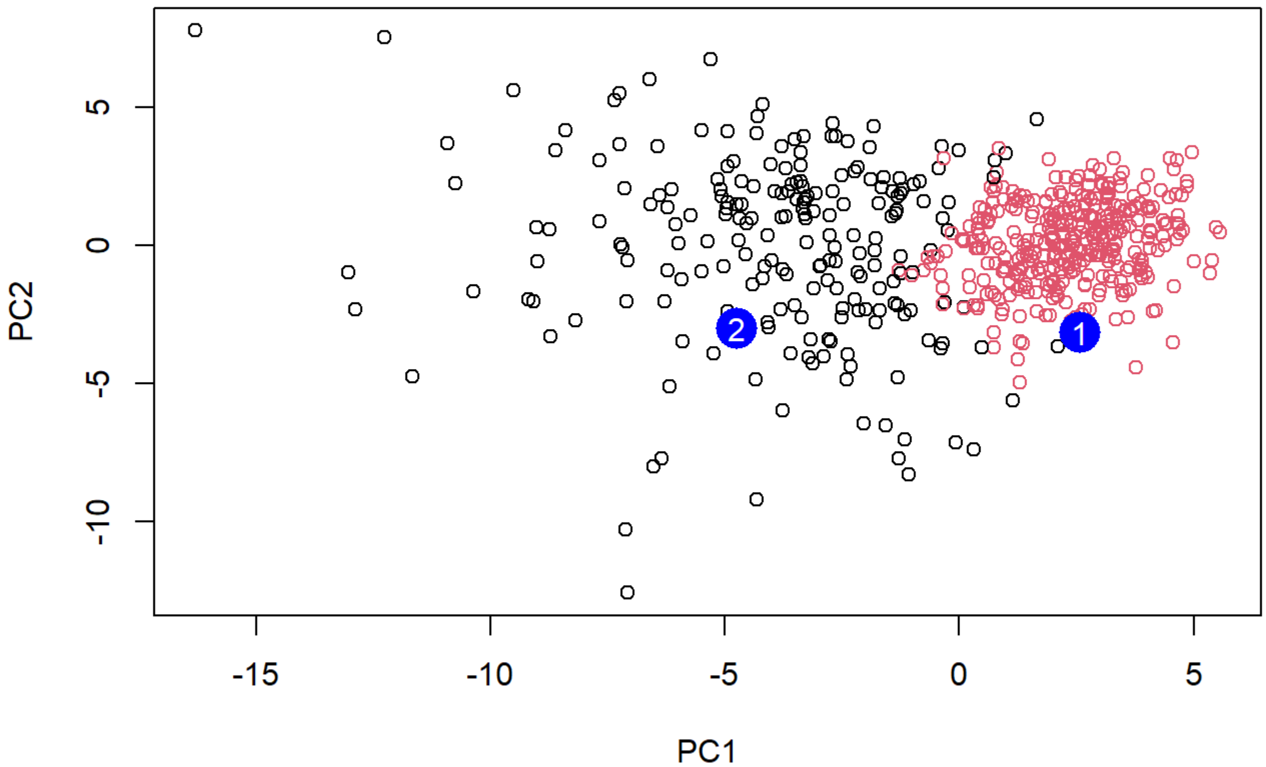
```
# Both clustering models created separate the diagnosis into separate clusters very well.
```

```
# 6) Sensitivity/Specificity

# Sensitivity: test's ability to correctly detect ill patients with condition; TP/(TP+FN)
# Specificity: test's ability to correctly reject healthy patients w/o condition; TN/(TN+FN)


# [Q17] Which of your analysis procedures resulted in a clustering model with the best specifici
ty? How about sensitivity?
# The k-means clustering method has the best specificity, while the combined clustering method u
sing ward.D2 and hierarchical clustering had the best sensitivity.
```

```
# 7) Prediction

# Use predict() to project new cancer cell data onto previous PCA model
#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 new data onto previous PCA model
plot(wisc.pr$x[,1:2], col=grps)
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 2 should be prioritized since patient 1 is likely to be a true negative and therefore
 have a benign tumor.
```