Class9

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10/27/2021

```
wisc.data <- wisc.df[,-1]
```

```
diagnosis <- factor(wisc.df$diagnosis)
```

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

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

```
# Q2. How many of the observations have a malignant diagnosis?
summary(diagnosis)
```

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

```
#Q3. How many variables/features in the data are suffixed with mean?
library(stringr)
cn<-colnames(wisc.data, do.NULL = TRUE, prefix = "col")
sum(str_count(cn, "_mean"))
```

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

```
# 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
```

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

#Insect results with summary
summary(wisc.pr)
```

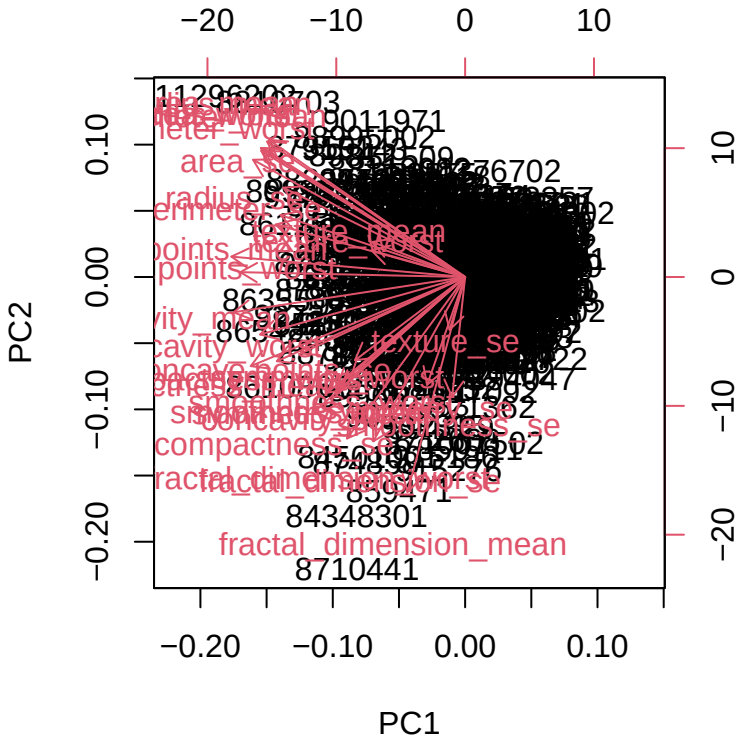
```
## Importance of components:
##                           PC1    PC2     PC3     PC4     PC5     PC6     PC7
## Standard deviation     3.6444 2.3857 1.67867 1.40735 1.28403 1.09880 0.82172
## Proportion of Variance 0.4427 0.1897 0.09393 0.06602 0.05496 0.04025 0.02251
## Cumulative Proportion  0.4427 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 com

##44.27% is the variance in the PC1 component
```

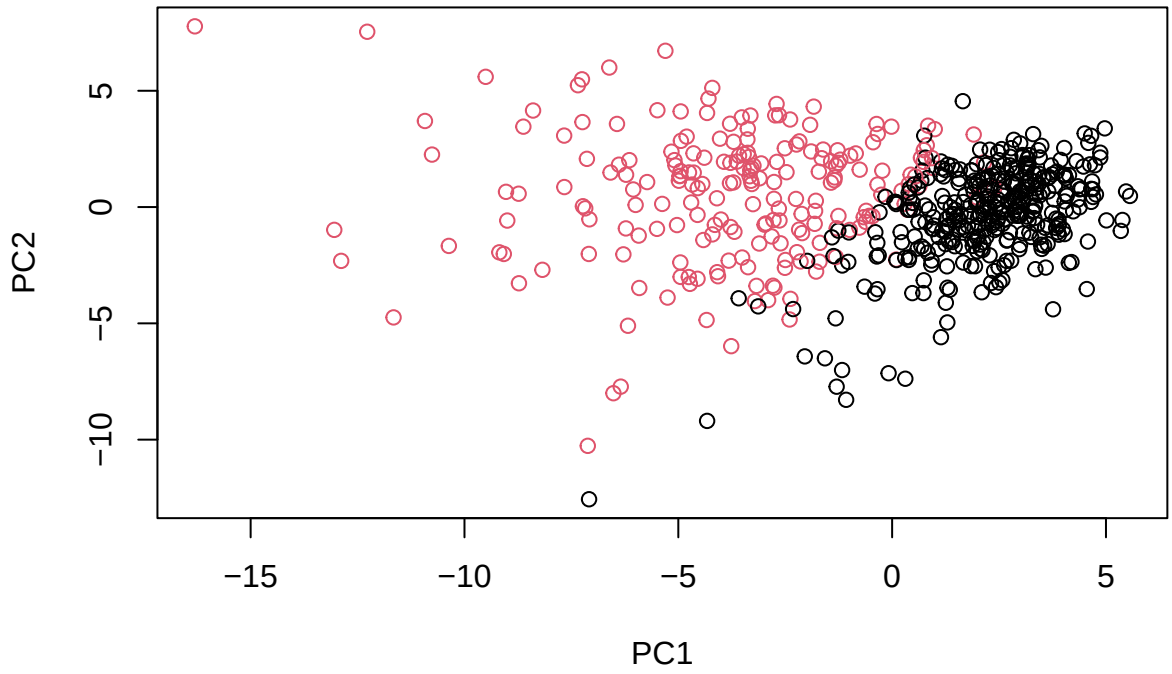
```
#Q5. How many principal components (PCs) are required to describe at least 70% of the original variance

#At least 3 PCs 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

#At least 7 PCs are required to describe at least 90% of the original variance in the data
```

```
#Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why?
biplot(wisc.pr)
```

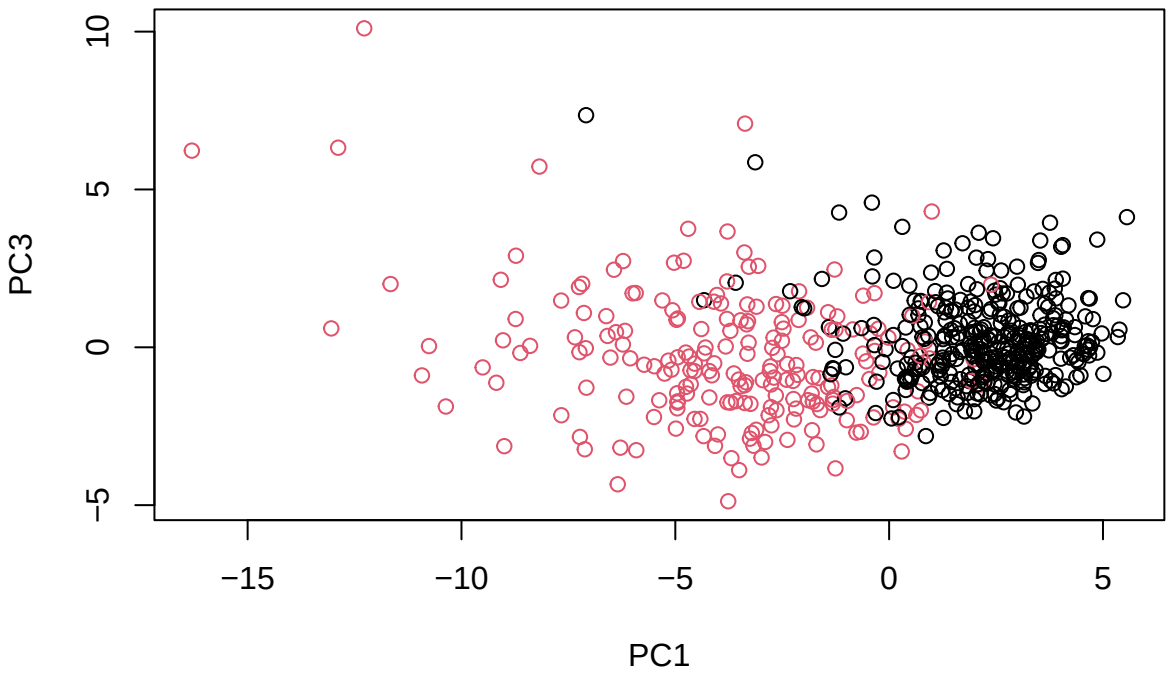



```
#The graph is hard to visualize with numbers and letters while if the data just showed dots or points i
```

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

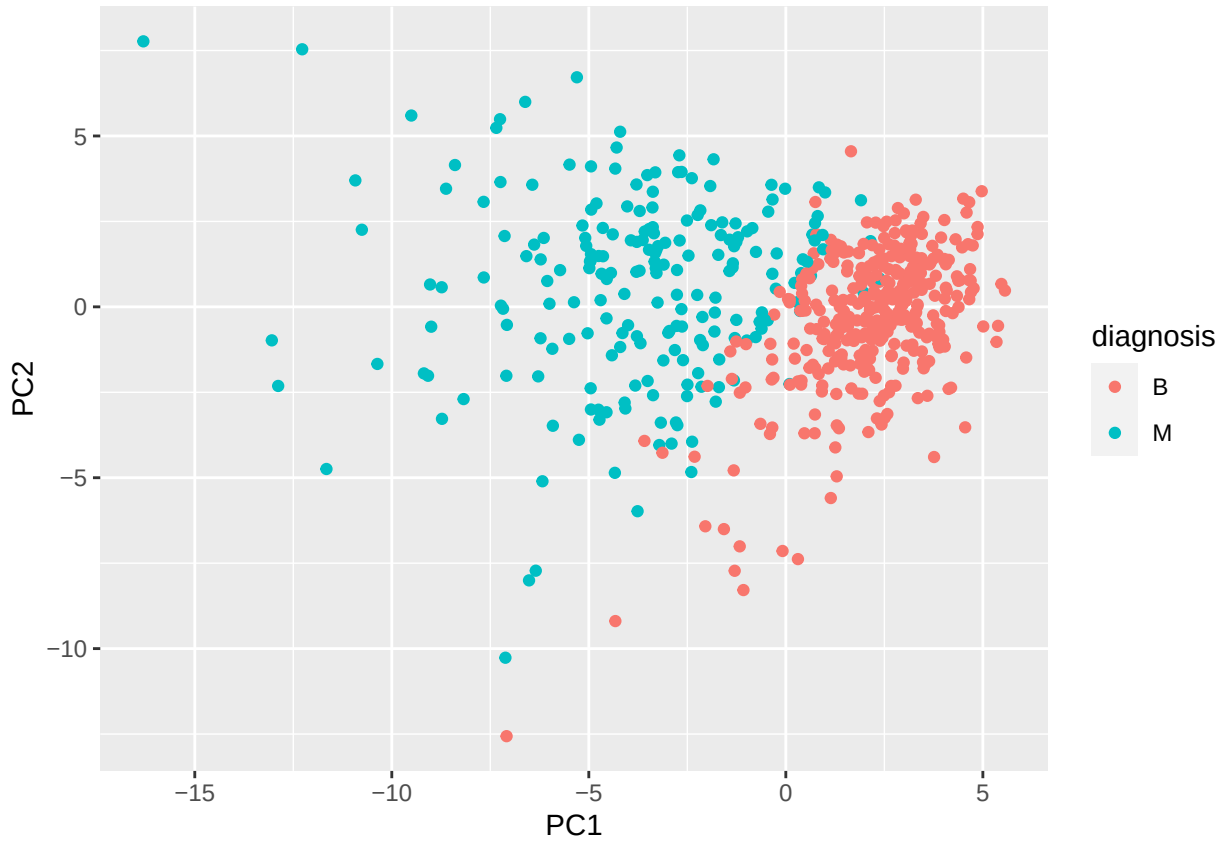



```
#Q8. Generate a similar plot for principal components 1 and 3. What do you notice about these plots?
plot(wisc.pr$x [,-2] , col = diagnosis ,
     xlab = "PC1", ylab = "PC3")
```




```
#This plot data sets moved down compared to the plot above. "Because principal component 2 explains mor
```

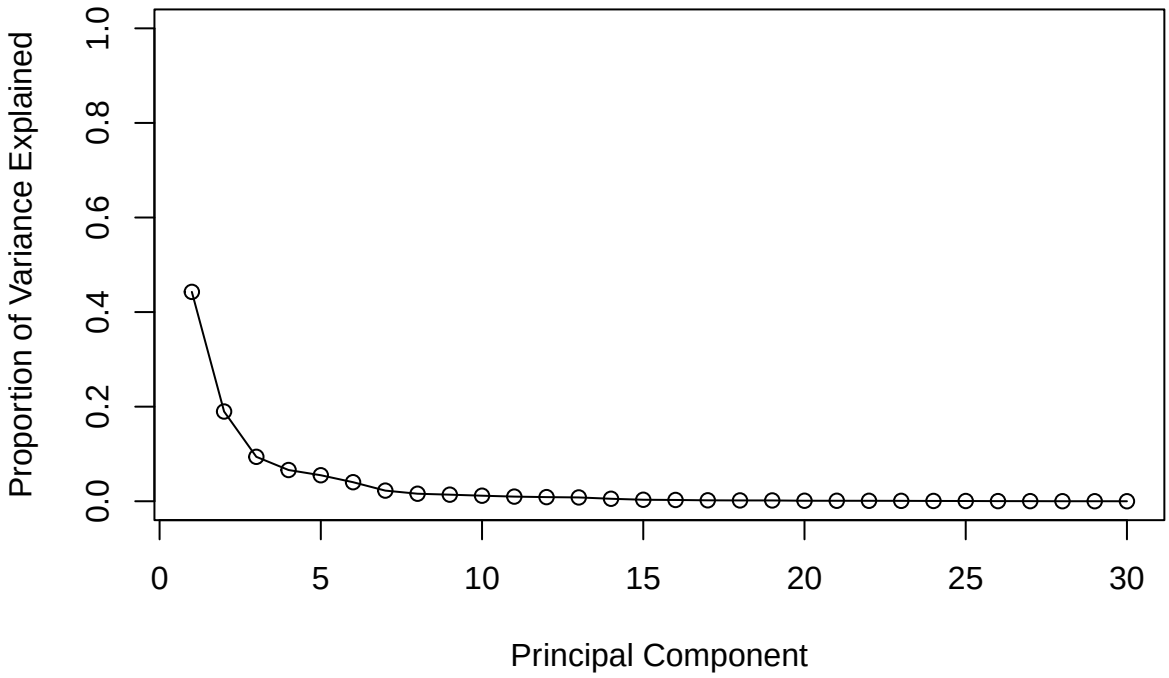
```
# Create a data.frame for ggplot
df <- as.data.frame(wisc.pr$x)
df$diagnosis <- diagnosis

# Load the ggplot2 package
library(ggplot2)

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



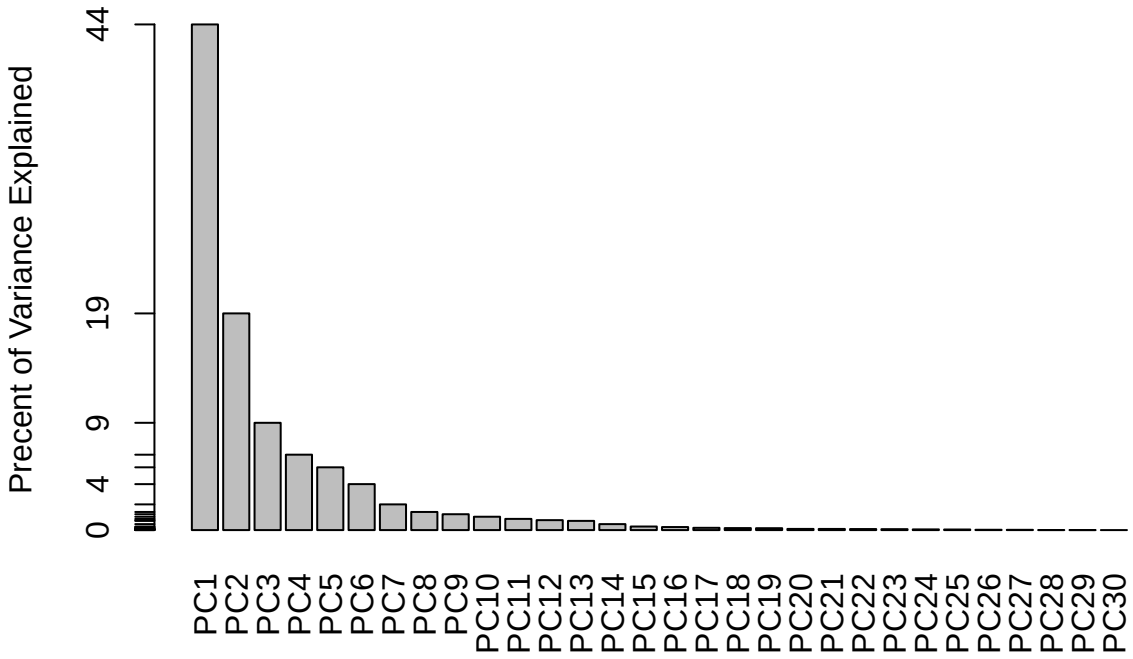

```
# Calculate variance of each component
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

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

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

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



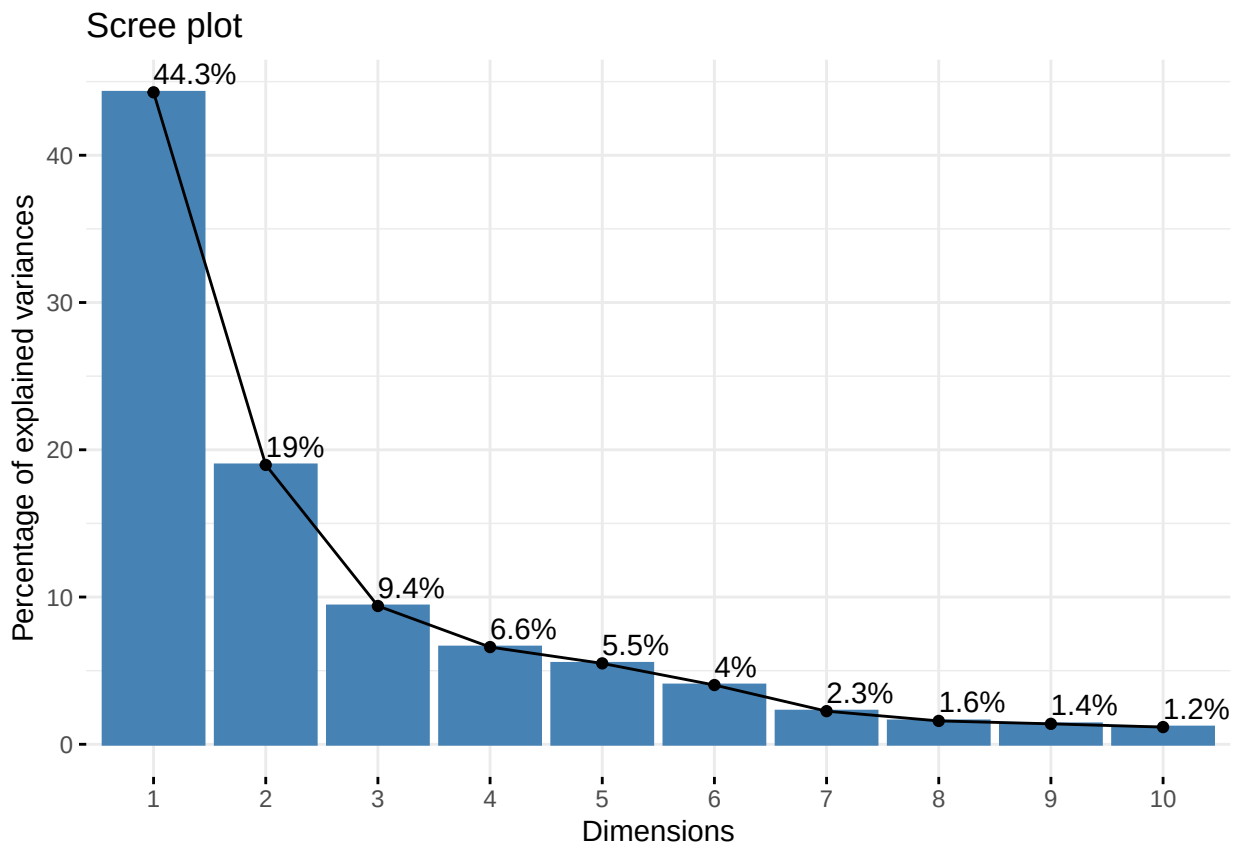

```
# Alternative scree plot of the same data, note data driven y-axis
barplot(pve, ylab = "Precent of Variance Explained",
     names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```




```
## 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. wisc.pr$rota

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

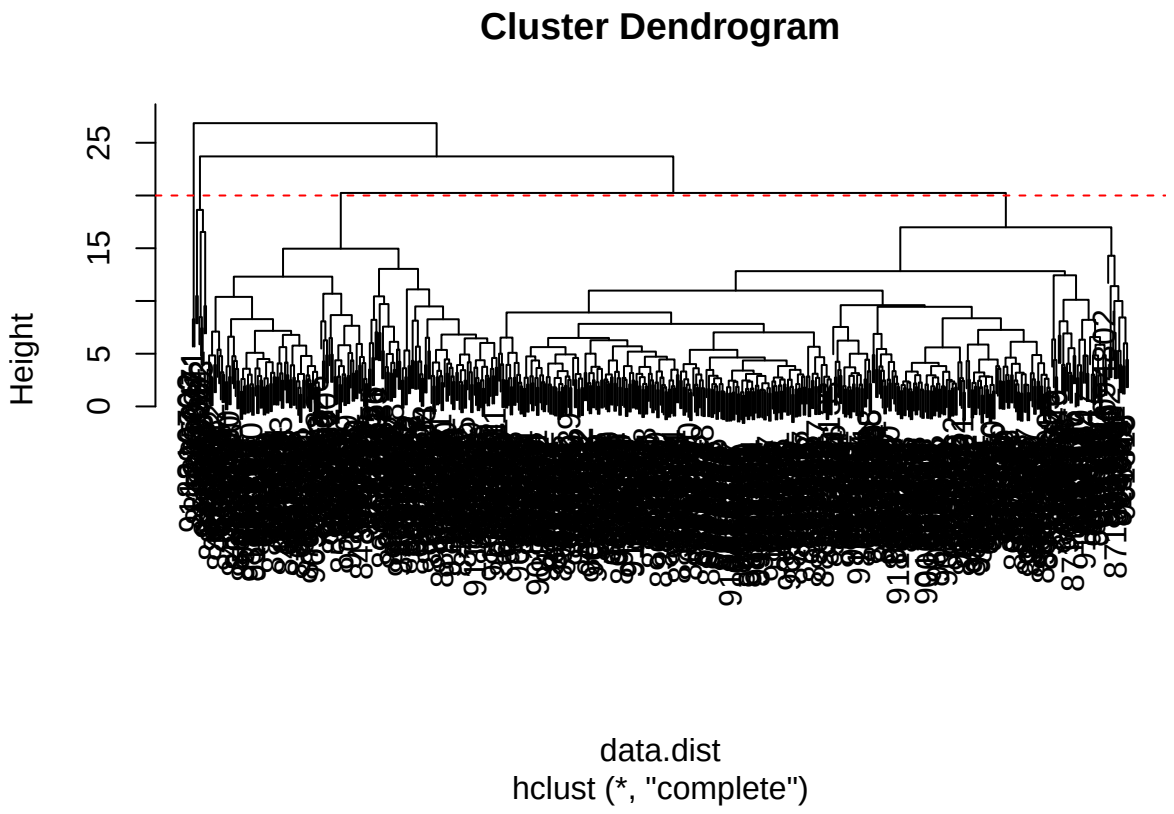
```
##             radius_mean            texture_mean          perimeter_mean
##              -0.21890244              -0.10372458              -0.22753729
##               area_mean         smoothness_mean        compactness_mean
##              -0.22099499              -0.14258969              -0.23928535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

```
##Output: -0.26085376

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

#The minimum number of PCs required to explain 80% of the variance of the data is 5.
```

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

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

```
#Q11. Using the plot() and abline() functions, what is the height at which the clustering model has 4 c
plot(wisc.hclust)
abline(wisc.hclust,h=20, col="red", lty=2)
```




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

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

```
#Q12. Can you find a better cluster vs diagnoses match by cutting into a different number of clusters b

wisc.hclust.clusters2 <- cutree(wisc.hclust, k = 2)
wisc.hclust.clusters3 <- cutree(wisc.hclust, k = 5)
wisc.hclust.clusters4 <- cutree(wisc.hclust, k = 10)
table(wisc.hclust.clusters2, wisc.hclust.clusters3, wisc.hclust.clusters4)
```

```
## , , wisc.hclust.clusters4 = 1
##
##                      wisc.hclust.clusters3
## wisc.hclust.clusters2   1   2   3   4   5
##                     1  98   0   0   0   0
##                     2   0   0   0   0   0
##
## , , wisc.hclust.clusters4 = 2
##
##                      wisc.hclust.clusters3
## wisc.hclust.clusters2   1   2   3   4   5
##                     1  59   0   0   0   0
##                     2   0   0   0   0   0
##
## , , wisc.hclust.clusters4 = 3
##
##                      wisc.hclust.clusters3
## wisc.hclust.clusters2   1   2   3   4   5
##                     1   0   3   0   0   0
##                     2   0   0   0   0   0
##
## , , wisc.hclust.clusters4 = 4
##
##                      wisc.hclust.clusters3
## wisc.hclust.clusters2   1   2   3   4   5
##                     1   0   0 370   0   0
##                     2   0   0   0   0   0
##
## , , wisc.hclust.clusters4 = 5
##
##                      wisc.hclust.clusters3
## wisc.hclust.clusters2   1   2   3   4   5
##                     1  20   0   0   0   0
##                     2   0   0   0   0   0
##
## , , wisc.hclust.clusters4 = 6
##
##                      wisc.hclust.clusters3
## wisc.hclust.clusters2   1   2   3   4   5
##                     1   0   0   0   2   0
##                     2   0   0   0   0   0
##
## , , wisc.hclust.clusters4 = 7
##
##                      wisc.hclust.clusters3
## wisc.hclust.clusters2   1   2   3   4   5
```

```
##                     1   0   0  12   0   0
##                     2   0   0   0   0   0
##
## , , wisc.hclust.clusters4 = 8
##
##                      wisc.hclust.clusters3
## wisc.hclust.clusters2   1   2   3   4   5
##                     1   0   2   0   0   0
##                     2   0   0   0   0   0
##
## , , wisc.hclust.clusters4 = 9
##
##                      wisc.hclust.clusters3
## wisc.hclust.clusters2   1   2   3   4   5
##                     1   0   0   0   0   0
##                     2   0   0   0   0   2
##
## , , wisc.hclust.clusters4 = 10
##
##                      wisc.hclust.clusters3
## wisc.hclust.clusters2   1   2   3   4   5
##                     1   0   0   1   0   0
##                     2   0   0   0   0   0
```

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

hclust(dist(data.scaled), method = "ward.D2")
```

```
##
## Call:
## hclust(d = dist(data.scaled), method = "ward.D2")
##
## Cluster method   : ward.D2
## Distance         : euclidean
## Number of objects: 569
```

```
##
```

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

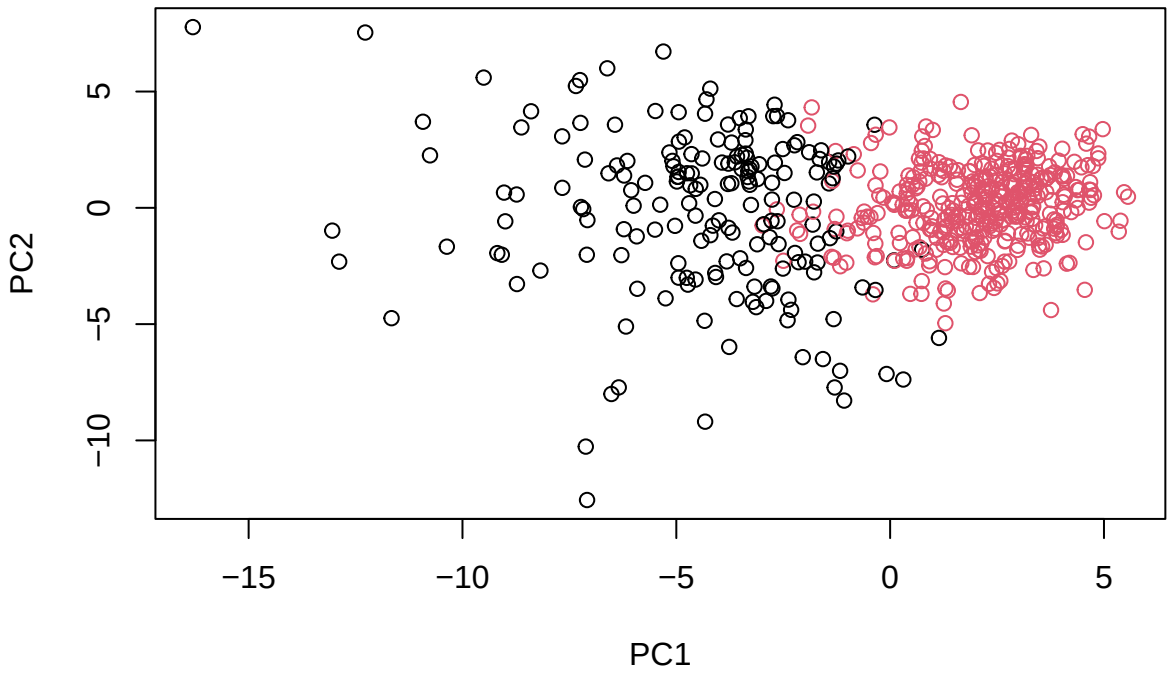
```
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

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

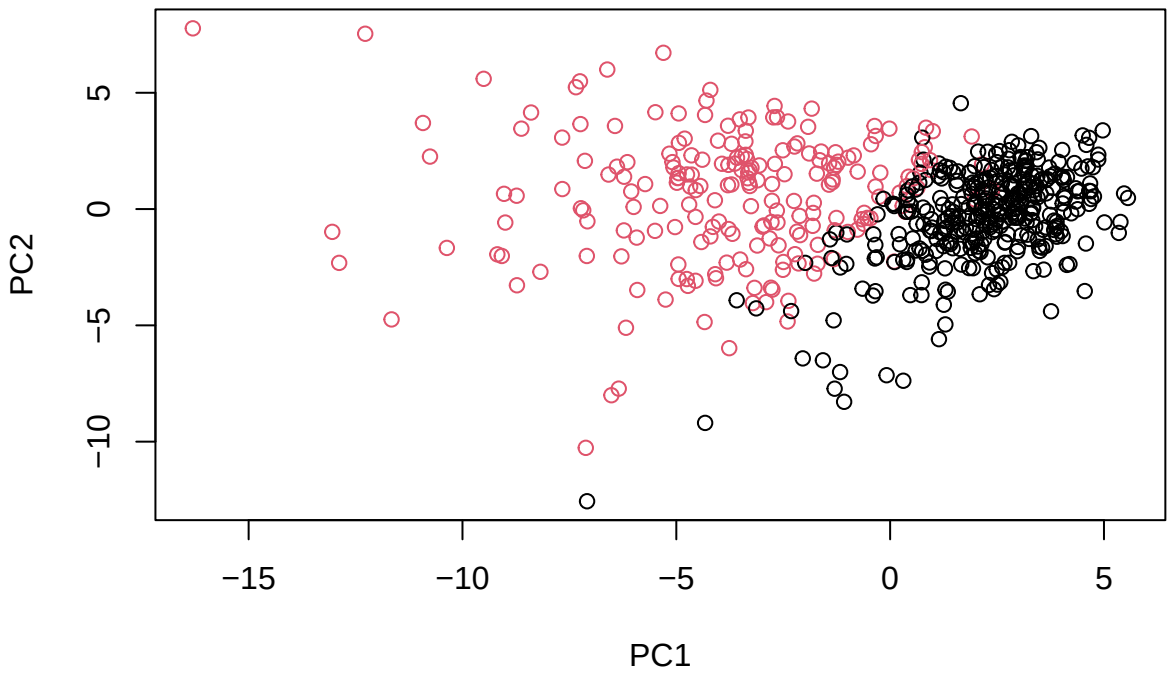
```
table(grps, diagnosis)
```

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

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




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



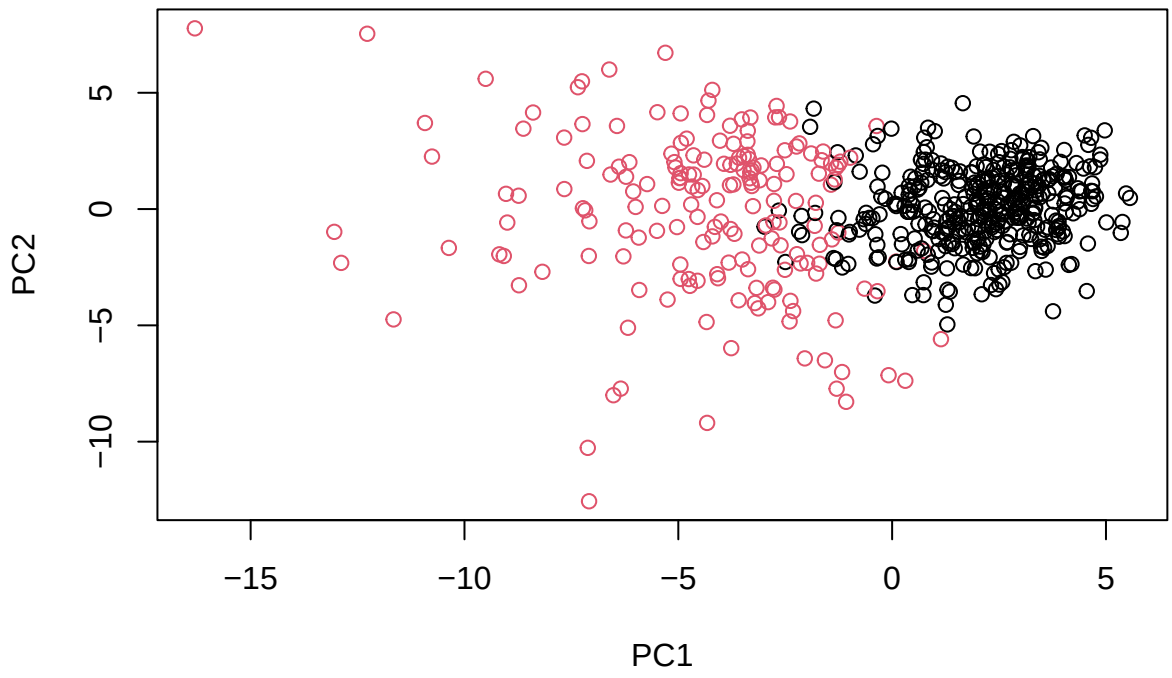

```
g <- as.factor(grps)
levels(g)
```

```
## [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)
```




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

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

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

```
##Q16. How well do the k-means and hierarchical clustering models you created in previous sections (i.e

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

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