

# Class 8 Mini-Project: Unsupervised Learning

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## Importing the Data

Here we analyze data from the University of Wisconsin Medical Center on Breast Cancer FNA.

*#Step 1: Download the Data Set*

*#Step 2: Place the file in the project folder*

*# Step 3: Complete the following code to input the data and store as wisc.df*  
`wisc.df <- read.csv("WisconsinCancer.csv", row.names=1)`

*# Step 4 (optional): Check the file*  
`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
```

The first column, the diagnosis, is not necessary for our analysis. With that in mind, we will make a new data frame that omits this column.

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

Question 1: How many observations are in this dataset?

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

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

Question 2: How many of the observations have a malignant diagnosis (i.e. how many Ms and Bs are there)?

```
#Number of malignant diagnoses
sum(wisc.df$diagnosis == "M")
```

```
## [1] 212
```

```
sum(wisc.df$diagnosis == "B")
```

```
## [1] 357
```

Is there another way, easier, way to answer Question 2?

```
#Create a table of the relevant metrics
table(wisc.df$diagnosis)
```

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

Question 3: How many variables/features in the data are suffixed with `_mean`?

```
#We can use the grep() function, that searches a given data frame for a specified term, in this case the
#We can then use the length() function to arrive at a total
length(grep("_mean", colnames(wisc.df)))
```

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

It will also be helpful to create a “diagnosis” variable for later, made from the diagnosis column of the “wisc.df” data frame. We can store it a factor (using `as.factor()`) and use it to plot with later.

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

```
##      [1] 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
##    [38] B M M M M M M M M M B B B B B M M B M M B B B B M B M M B B B B M 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 M B M M B B M B B M B B B M B B
##  [149] 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 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 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 B M M M B B B B B B B B B B M 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
##  [408] B M B B B B B M B B M B B B B B B B B B B B B M B M M B M B B B B M B B
##  [445] M B M B B M B M B B B B B B B M M B B B B B M B B B B B B B B B M B
##  [482] B B B B B M B M B B M B B B B M M B M M B M 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
##  [556] B B B B B B M M M M M M B
## Levels: B M
```

# Principle Component Analysis

The main function in base R for PCA is “prcomp()”. There is an important optional argument called “scale” in this function.

Before we scale, we should check the data to determine if this step is necessary

```
# 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
```

The first line does the principle component analysis (while scaling the data), the second line shows a summary

```
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
```

Question 4: From your results, what proportion of the original variance is captured by the first principal components (PC1)?

44.27%

Question 5: How many principal components (PCs) are required to describe at least 70% of the original variance in the data?

3 PCs

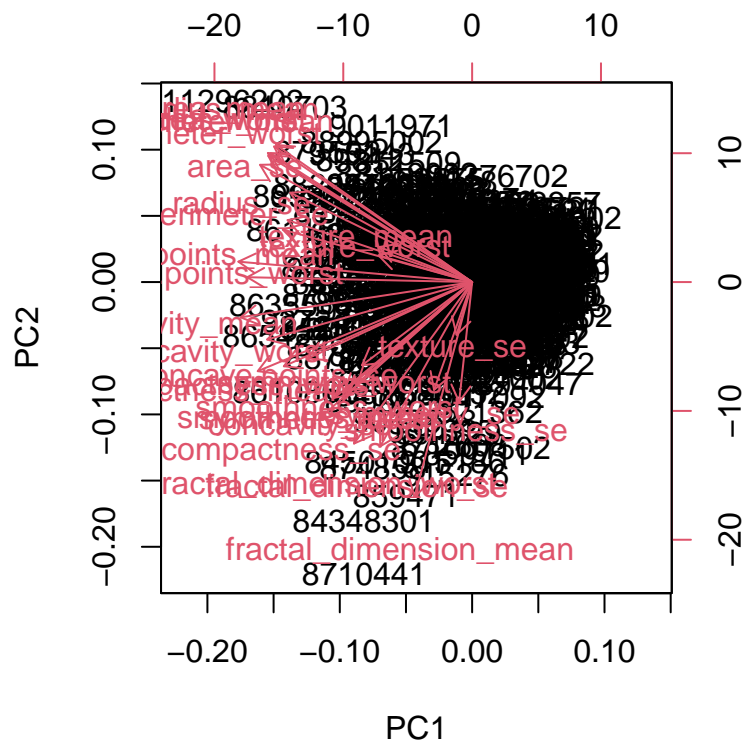
Question 6: How many principal components (PCs) are required to describe at least 90% of the original variance in the data?

7 PCs

The main result of these types of methods is called a PCA plot (a.k.a. score plot. ordination plot)

Question 7: Make a biplot of the PC data

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



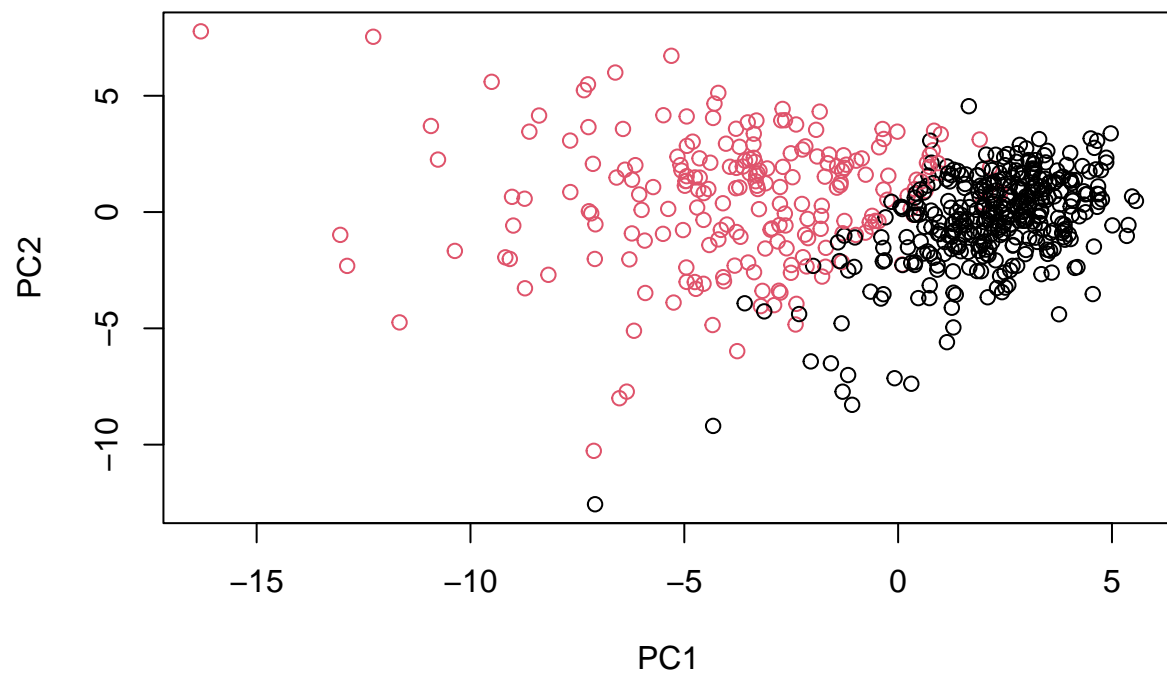
*#This is a really bad, messy plot*

A summary of the “x” for wisc.pr

```
#wisc.pr$x
```

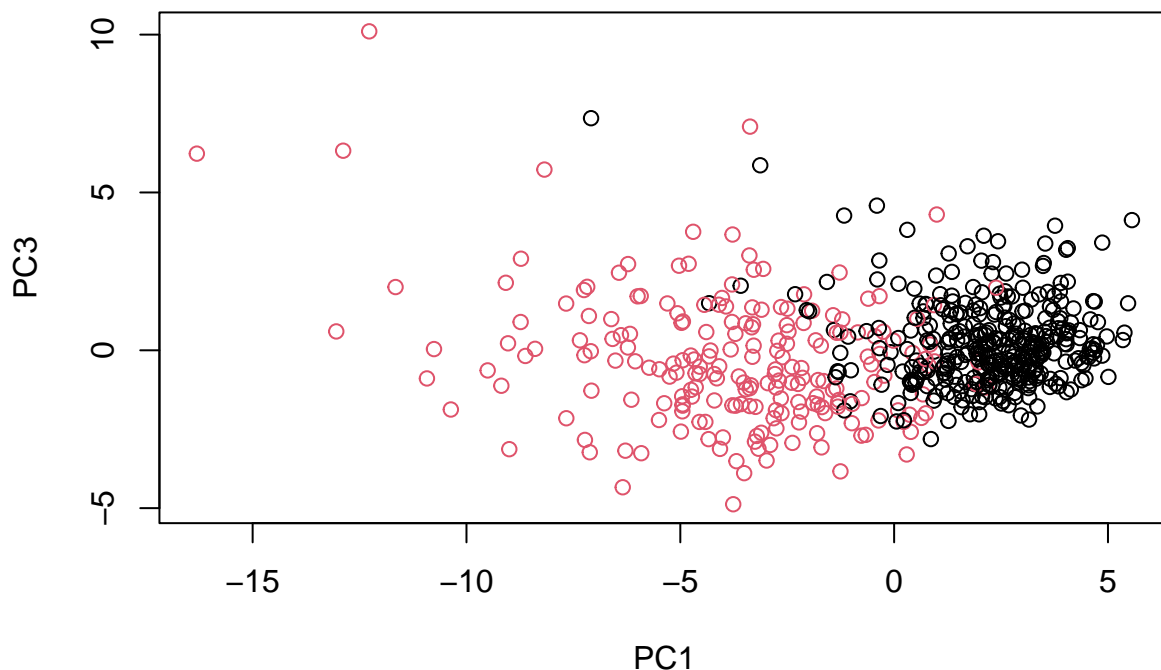
We will now plot PC1 vs. PC2 x values

```
#We can use a simple plot to see how the two compare
plot(wisc.pr$x[,1:2], col = diagnosis)
```



Question 8: Generate a similar plot for principal components 1 and 3. What do you notice about these plots?

```
plot(wisc.pr$x[,c(1,3)], col = diagnosis)
```



This graph has greater overlap between the two groups, as less of the variance can be explained by PC1 + PC3 than PC1 + PC2.

```
#Rotations of the data for PC1
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



Question 9: 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`?

-0.26085376

Question 10: What is the minimum number of principal components required to explain 80% of the variance of the data?

5 PCs

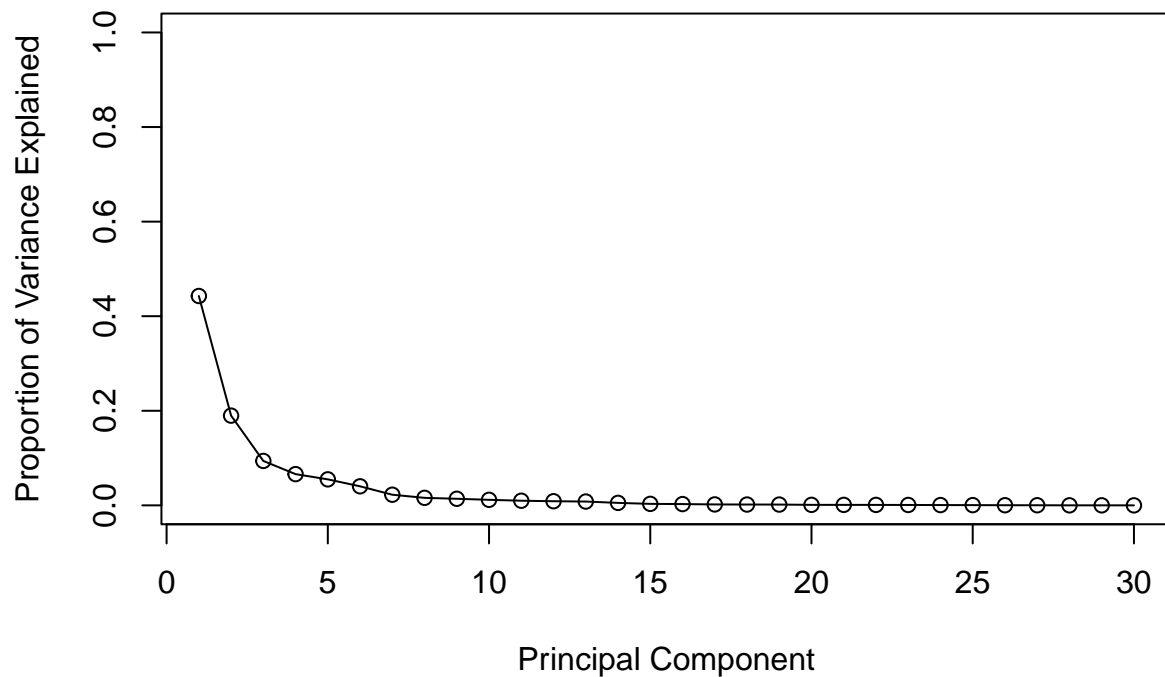
These plots describe the percentage of variance that can be explained by each PC

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

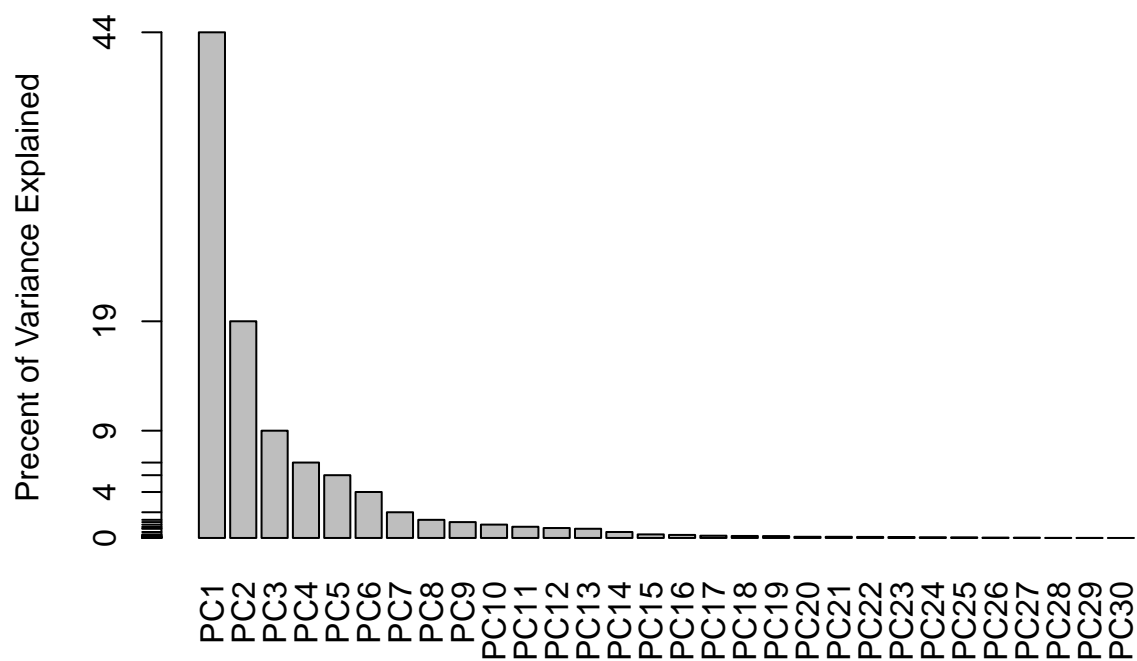
```
## [1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
# 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 = "Percent of Variance Explained",
        names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```

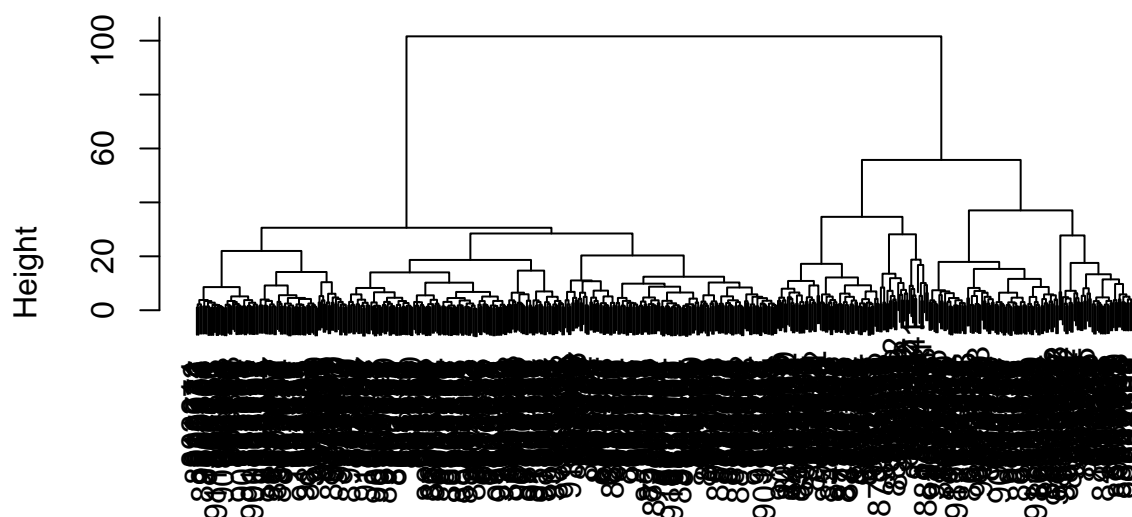


```
#We can create an even more descriptive graph
#library(ggplot2)
#install.packages("factoextra")
#library(factoextra)
#fviz_eig(wisc.pr, addlabels = TRUE)
```

## Hierarchical clustering of raw data is not very helpful

```
#Using the minimum number of principal components required to describe at least 90% of the variability
wisc.pr.hclust <- hclust(dist(wisc.pr$x[,1:7]), method = "ward.D2")
plot(wisc.pr.hclust)
```

## Cluster Dendrogram



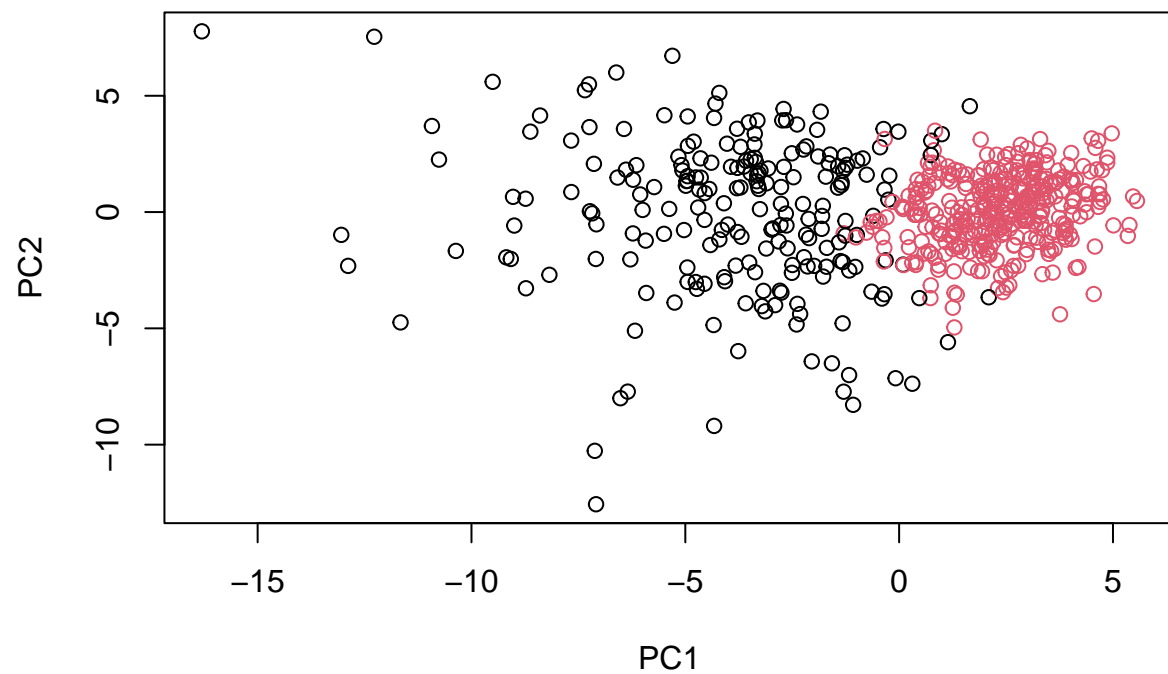
```
dist(wisc.pr$x[, 1:7])  
hclust (*, "ward.D2")
```

It looks as though the data divides into two groups, which could map onto the “benign” and “malignant” categories. Let’s find out. Using the `cutree()` function, we can sort the clusters into two membership groups.

```
#We can first ask how many data points are in each of the two groups  
grps <- cutree(wisc.pr.hclust, k=2)  
table(grps)
```

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

```
#We can plot PC1 vs. PC2 again, coloring by grps to see how it compares to coloring by diagnosis  
plot(wisc.pr$x[,1:2], col = grps)
```



*#Next, we can use our diagnosis factor to see how many of each diagnosis are in each of these two groups*  
`table(grps, diagnosis)`

```
##      diagnosis
## grps   B    M
##   1  28 188
##   2 329  24
```