

# Class 8 Mini Project

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Preparing the data

```
fna.data <- "WisconsinCancer.csv"
wisc.df <- read.csv(fna.data, row.names = 1)
View(wisc.df)
```

Omit the first column and move it to a diagnosis vector

```
wisc.data <- wisc.df[,-1]
diagnosis <- as.factor(wisc.df$diagnosis)
```

## Exploratory Data Analysis

```
View(wisc.data)
dim(wisc.data)
```

```
[1] 569 30
```

**Question 1: How many observations are in this dataset?**

569 Rows so 569 Observations

## Question 2: How many of the observations have a malignant diagnosis?

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

```
[1] 212
```

212 of the observations have a malignant diagnosis

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

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

```
[1] 10
```

10 variables/features in the data set are suffixed with `_mean`

## Principal Component Analysis

Performing PCA

```
#Check column means and standard deviation  
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

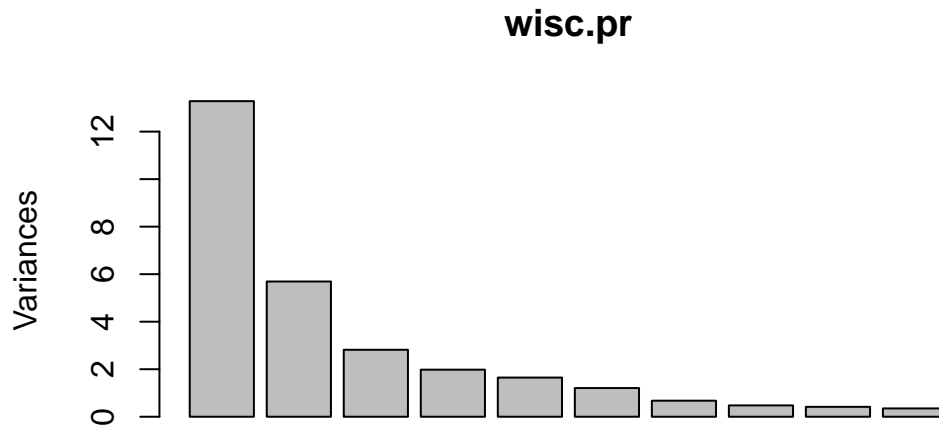
```
#Perform PCA on wisc.data
wisc.pr <- prcomp( wisc.data, scale = TRUE )
```

```
#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					

```
plot(wisc.pr)
```



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

From my results, the proportion of the original variance by the PC1 is 0.4427

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

3 -> PC1, PC2, and PC3

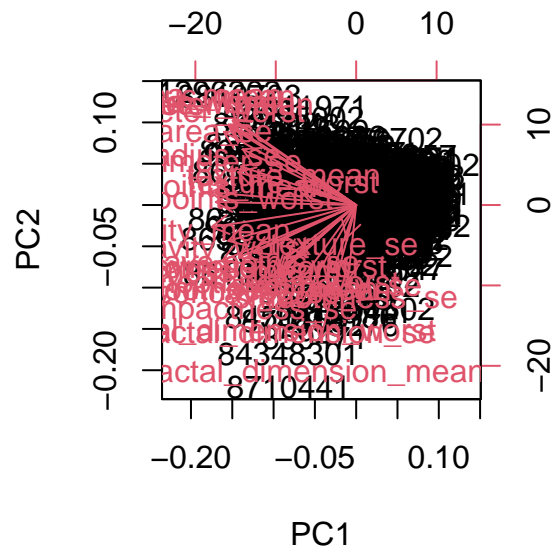
**Question 6: How many principal components (PCs) are required to describe at least 90% of the original variance in this data?**

7 -> PC1, PC2, PC3, PC4, PC5, PC6, PC7

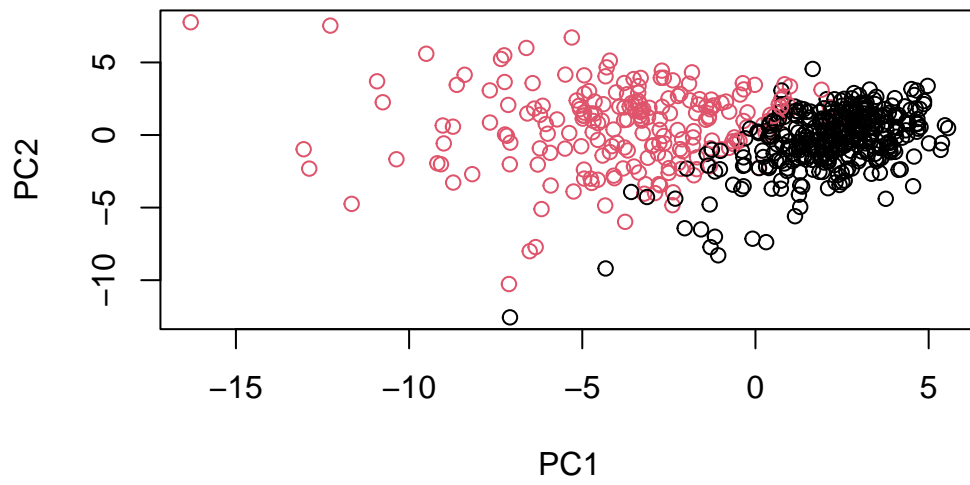
**Question 7: What stands out to you about this plot? Is it easy or difficult to understand? Why?**

What stands out to me about this plot is that each point on the plot is labeled by the row name which makes it really hard to distinguish the difference between points as the names just overlap onto each other causing a huge black uneven circle on the plot.

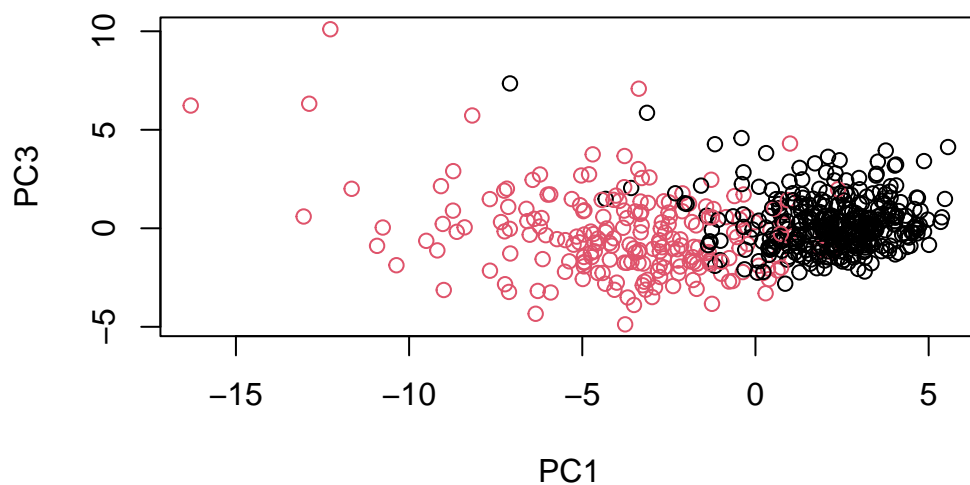
```
biplot(wisc.pr)
```



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



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



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

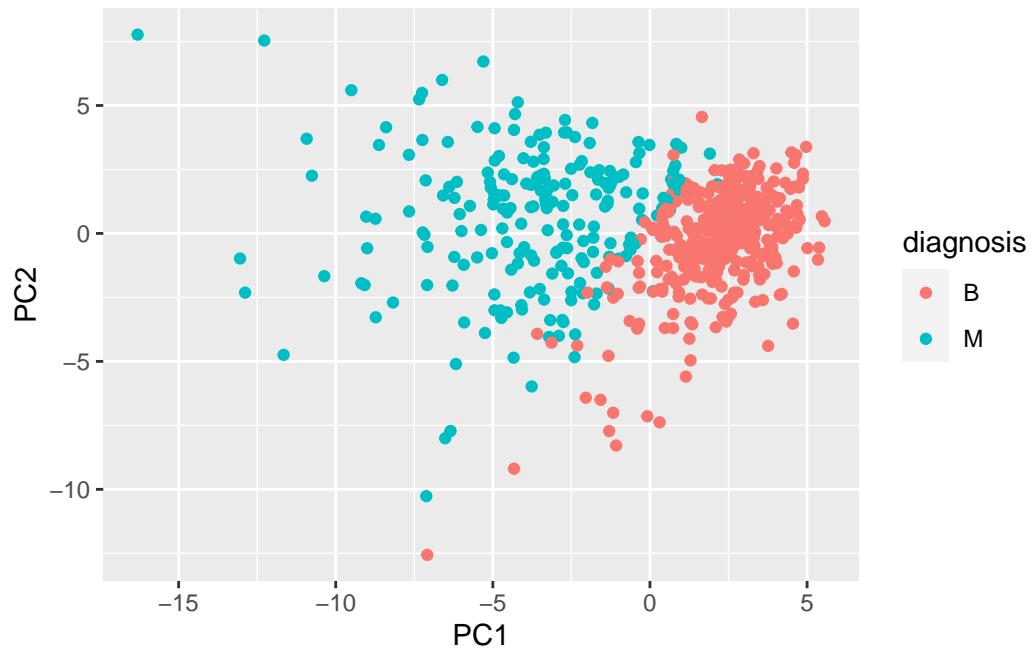
The first plot between PC1 & PC2 has a more observant separation while the second plot between PC1 & PC3 has more data points overlapping

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

# Load the ggplot 2 package
library(ggplot2)

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





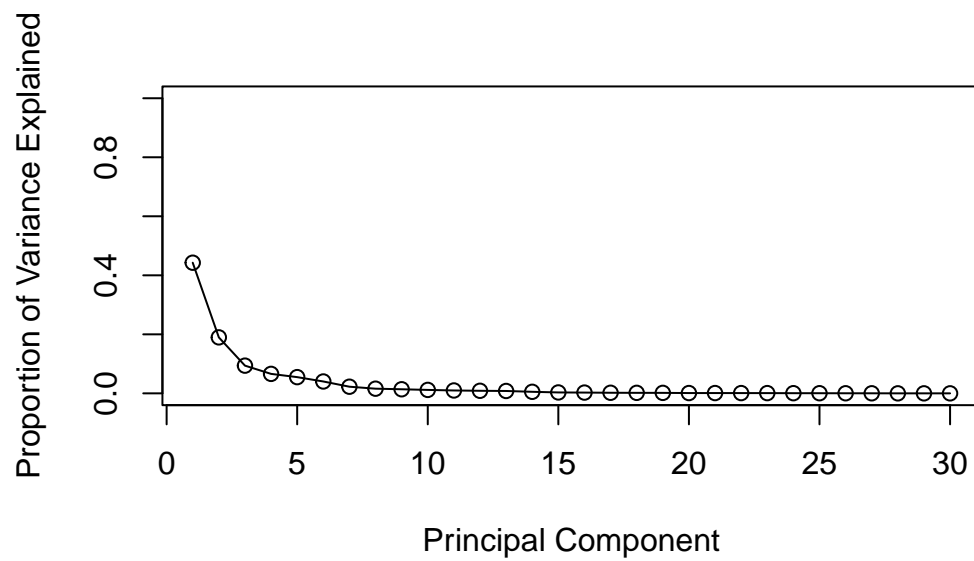
#### Variance Explained

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

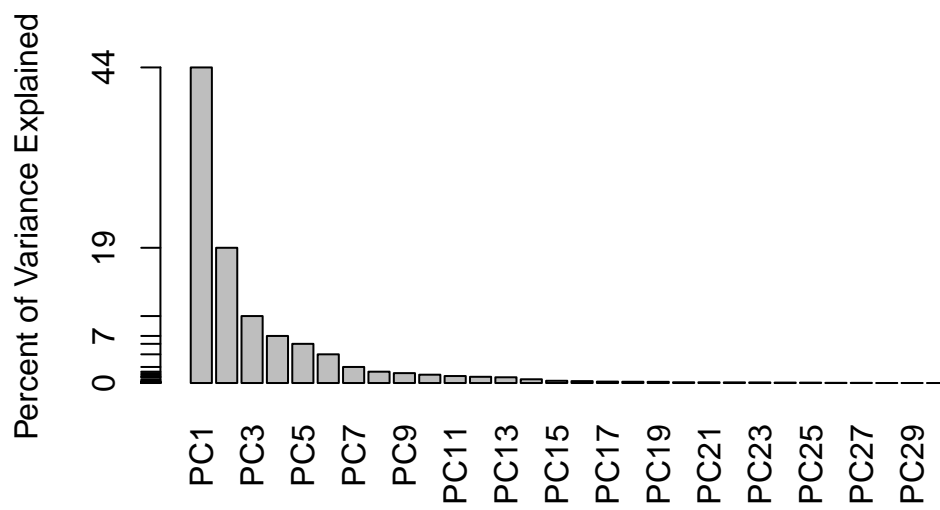
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
#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")
```



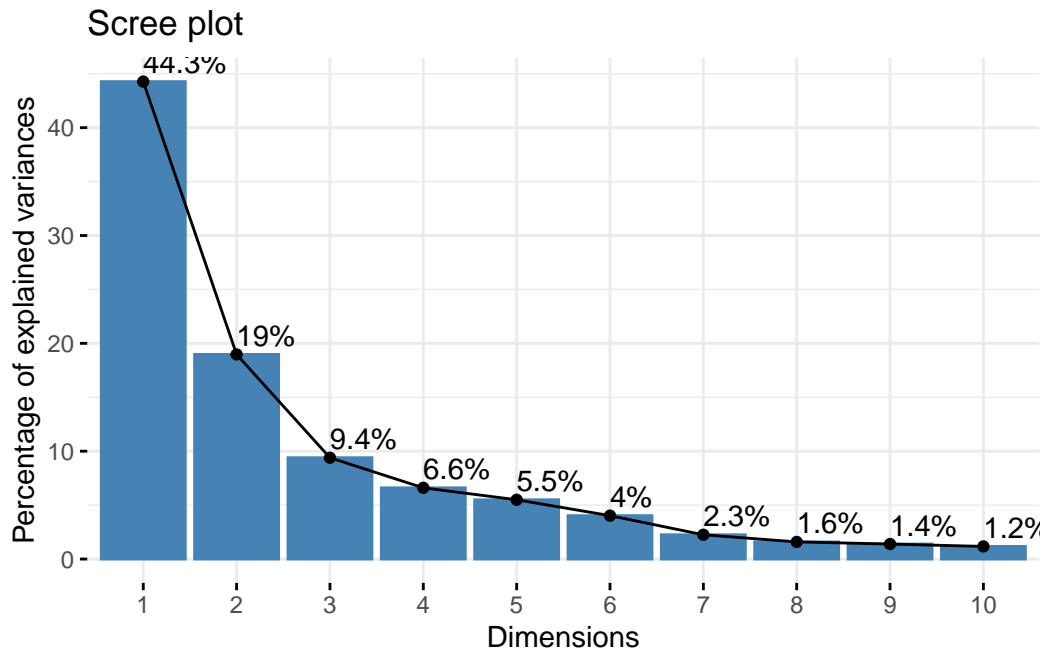
```
#Alternative scree plot of the same data, note data driven y-axis
barplot(pve, ylab = "Percent of Variance Explained",
        names.arg=paste0("PC", 1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100)
```



```
##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)
```



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

The minimum number of PC to explain 80% of the variance of the data is 5 (PC1-5)

## Hierarchical Clustering

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

## Combining Methods

Clustering on PCA Results

**Question 15: How well does the newly created model with four clusters separate out the two diagnoses?**

It separates out the two diagnoses fairly well as the newly created model with four clusters is more easily to observe

**Question 16: 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.**

In terms of separating the diagnoses, the k-means and hierarchical clustering models I created don't do that well compared to the newest models I've created

**Question 17: Which of your analysis procedures resulted in a clustering model with the best specificity? How about sensitivity?**

The analysis procedure which resulted in the best specificity is the hierarchical clustering model. The one with the best sensitivity is the PCA analysis

**Question 18: Which of these new patients should we prioritize for follow up based on your results?**

Patient 2 “‘