

# Class 8 Breast Cancer Analysis Mini Project

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## Background

The goal of this mini-project is to explore a complete analysis using the unsupervised learning techniques covered in class.

The data itself comes from the Wisconsin Breast Cancer Diagnostic Data Set first reported by K. P. Benne and O. L. Mangasarian: “Robust Linear Programming Discrimination of Two Linearly Inseparable Sets”.

Values in this data set describe characteristics of the cell nuclei present in digitized images of a fine needle aspiration (FNA) of a breast mass.

## Data import

Data was downloaded from the class website as a CSV file

```
wisc.df <- read.csv("WisconsinCancer.csv", 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
842517	0.1812		0.05667	0.5435	0.7339
84300903	0.2069		0.05999	0.7456	0.7869
84348301	0.2597		0.09744	0.4956	1.1560
84358402	0.1809		0.05883	0.7572	0.7813
843786	0.2087		0.07613	0.3345	0.8902
	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 “diagnosis” is the expert opinion on the sample (i.e. FNA)

```
wisc.df$diagnosis
```

```
[1] "M" "M"
[19] "M" "B" "B" "B" "M" "M"
[37] "M" "B" "M" "M" "M" "M" "M" "M" "M" "M" "M" "B" "M" "B" "B" "B" "B" "B" "B" "M"
[55] "M" "B" "M" "M" "B" "B" "B" "B" "M" "B" "M" "M" "B" "B" "B" "B" "B" "B" "B" "M" "B"
[73] "M" "M" "B" "M" "B" "M" "B" "B" "B" "M" "B" "M" "B" "M" "B" "M" "M" "M" "B" "B" "B"
[91] "B" "M" "B" "B" "M" "M" "B" "B" "B" "M" "B" "M" "B" "B" "B" "B" "M" "B" "B" "B" "B"
[109] "M" "B" "B" "B" "B" "B" "B" "B" "B" "M" "M" "M" "B" "M" "B" "B" "B" "M" "M" "B" "B" "B"
[127] "M" "M" "B" "M" "B" "M" "M" "B" "M" "M" "B" "B" "M" "B" "B" "B" "B" "M" "B" "B" "B" "B"
[145] "B" "B" "M" "B" "M" "B" "B" "B" "B" "B" "B" "M"
[163] "M" "B" "M" "B" "B" "M" "M" "B" "B" "B" "M" "M" "B" "B" "B" "B" "B" "M" "B" "B" "B"
[181] "M" "M" "M" "B" "M" "B" "M" "B" "B" "B" "M" "B" "B" "M" "M" "M" "B" "M" "M" "B" "M" "M"
[199] "M" "M" "B" "M" "M" "M" "B" "M" "B" "M" "B" "M" "B" "B" "M" "B" "M" "M" "M" "M" "M" "M"
[217] "B" "B" "M" "M" "B" "B" "B" "M" "B" "B" "B" "B" "B" "B" "B" "B" "M" "M" "B" "B" "B" "M"
[235] "B" "B" "M" "M" "B" "M" "B" "B" "B" "B" "B" "M" "B" "B" "B" "B" "B" "B" "B" "B" "M" "B"
[253] "M" "B" "B" "B" "B" "B" "B"
[271] "B" "B" "M" "B" "M" "B" "B" "M" "B" "B" "B" "M" "B" "M" "B" "M" "B" "B" "B" "B" "B" "B"
[289] "B" "M" "B" "B" "M" "B" "M" "B" "M" "B" "B" "B" "B"
[307] "B" "M" "B" "B" "B" "B" "M" "B" "M"
[325] "B" "B" "B" "B" "M" "M" "M" "B" "B" "B" "B" "B" "B" "M" "B" "M" "B" "M" "B" "M" "B" "B"
[343] "B" "M" "B" "B" "B" "B" "B" "B" "B" "B" "B" "M" "M" "M" "B" "B" "B" "B" "B" "B" "B" "B"
[361] "B" "B" "B" "B" "B" "M" "M" "B" "M" "M" "M" "B" "M" "B" "M" "B" "M" "B" "B" "B" "B" "B" "B"
[379] "B" "M" "B" "B" "B" "B" "B" "B" "M" "B" "B" "B" "B" "B" "M" "B" "B" "M" "B" "M" "B" "B" "B"
[397] "B" "B" "B" "B" "M" "B" "M" "B" "B" "B" "B" "B" "B" "B"
[415] "M" "B" "B" "M" "B" "M" "B"
```

```
[433] "M" "M" "B" "M" "B" "B" "B" "B" "B" "M" "B" "B" "M" "B" "M" "B" "B" "M"  
[451] "B" "M" "B" "B" "B" "B" "B" "B" "B" "M" "M" "B" "B" "B" "B" "B" "B"  
[469] "M" "B" "B" "B" "B" "B" "B" "B" "B" "B" "M" "B" "B" "B" "B" "B" "B"  
[487] "B" "M" "B" "M" "B" "B" "M" "B" "B" "B" "B" "B" "M" "M" "B" "M" "B" "M"  
[505] "B" "B" "B" "B" "B" "M" "B" "B" "M" "B" "M" "B" "M" "B" "B" "B" "B" "M"  
[523] "B" "M" "B" "M" "M" "B" "B"  
[541] "B"  
[559] "B" "B" "B" "B" "M" "M" "M" "M" "M" "M" "M" "B"
```

Remove the diagnosis from the data for subsequent analysis

```
wisc.data <- wisc.df[,-1]  
dim(wisc.data)
```

```
[1] 569 30
```

Store the diagnosis as a vector to use later when we compare our results to those from experts in the field

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

Q1. How many observations are in this dataset?

There are 569 observations/patients in the data set

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

```
table(wisc.df$diagnosis)
```

B	M
357	212

212 of the observations have a malignant diagnosis

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

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

```
[1] 10
```

There are 10 variables in the data suffixed with \_mean

## Principal Component Analysis

The `prcomp` function to do PCA has `scale=False` default. In general we nearly always want to set this to TRUE so our analysis is dominated by columns/variables in our dataset that have high standard deviation and mean when compared to others for instance because of differences in scale

```
wisc.pr <- prcomp(wisc.data, scale = TRUE )
summary(wisc.pr)
```

Importance of components:

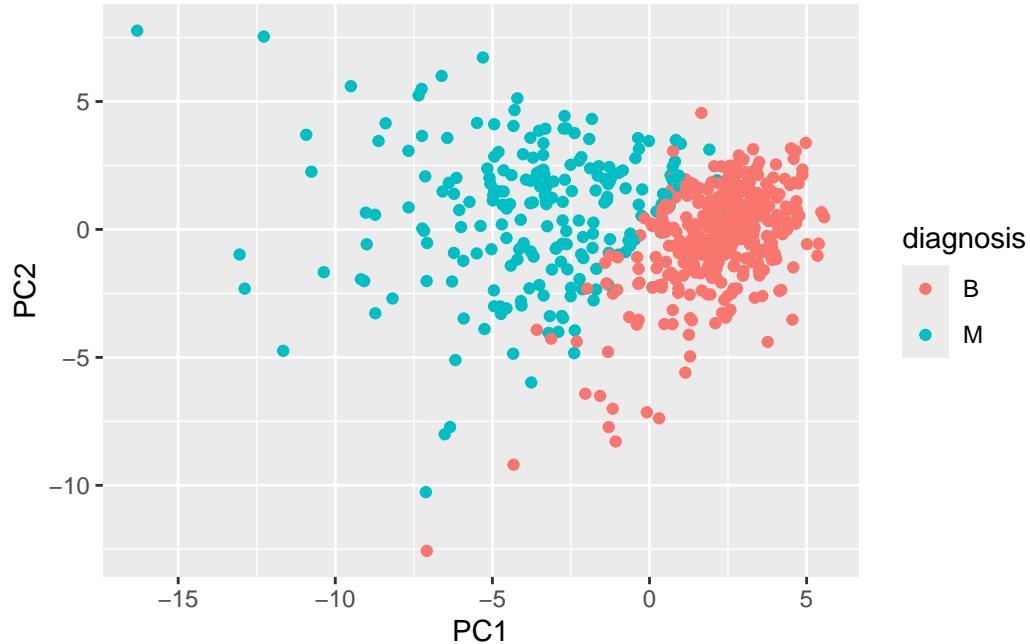
	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Standard deviation	3.6444	2.3857	1.67867	1.40735	1.28403	1.09880	0.82172
Proportion of Variance	0.4427	0.1897	0.09393	0.06602	0.05496	0.04025	0.02251
Cumulative Proportion	0.4427	0.6324	0.72636	0.79239	0.84734	0.88759	0.91010
	PC8	PC9	PC10	PC11	PC12	PC13	PC14
Standard deviation	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					

The main PC result figure is called a “score plot” or “PC plot” or “ordination plot”

```
library(ggplot2)
```

```
Warning: package 'ggplot2' was built under R version 4.4.3
```

```
ggplot(wisc.pr$x) +
  aes(PC1, PC2, col=diagnosis) +
  geom_point()
```



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

44.27% of the original variance is captured by PC1

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

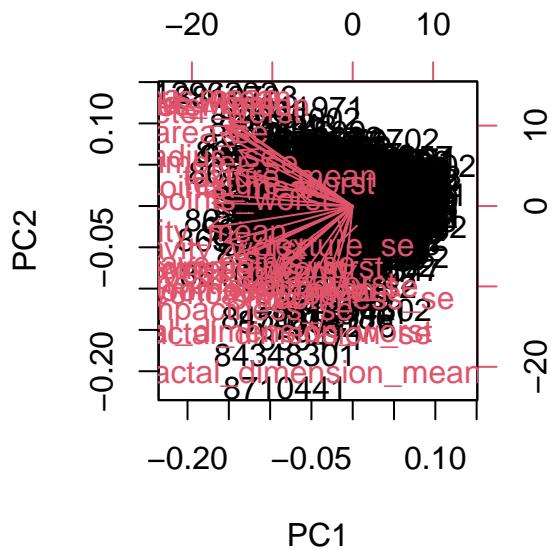
You need 3 PCs to describe at least 70% of the original variance

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

You need at least 7 PCs to describe at least 90% of the original variance

### Interpreting PCA results

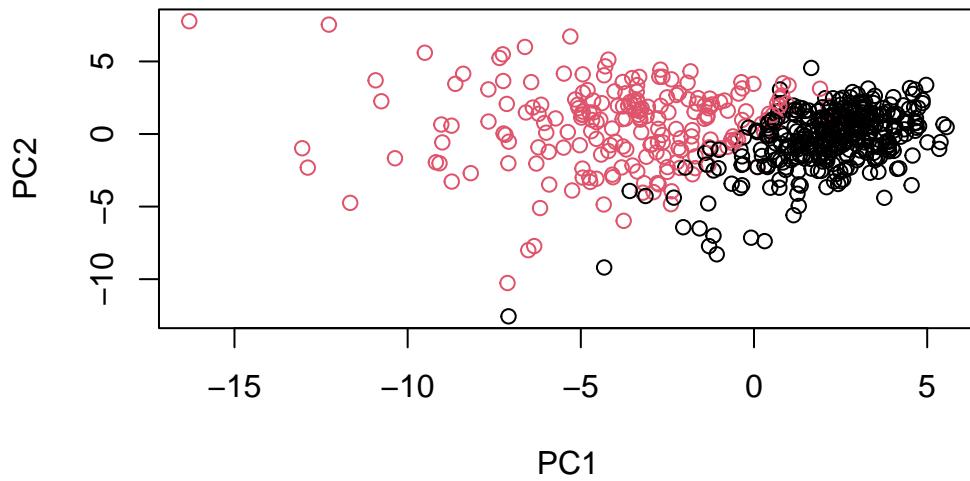
```
biplot(wisc.pr)
```



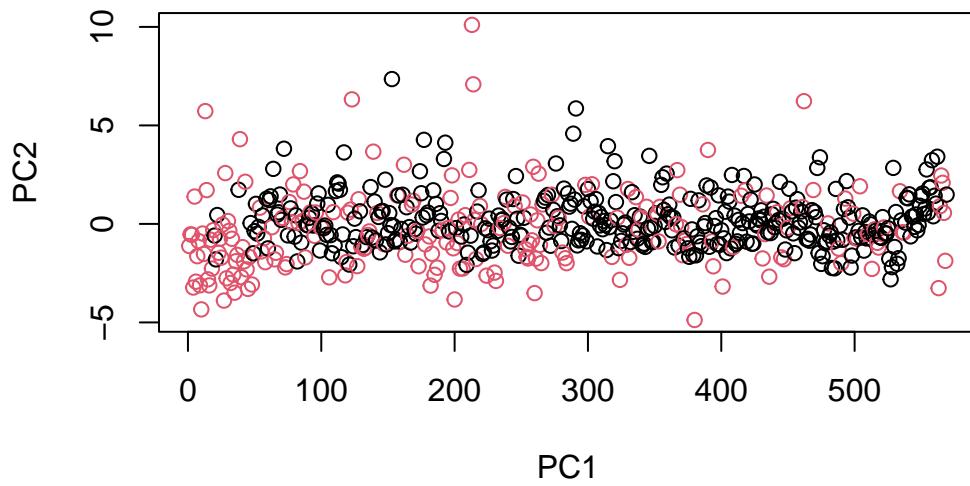
Q7. What stands out to you about this plot? Is it easy or difficult to understand?  
Why?

The data is all clustered together with all the text overlapping each other. The graph is hard to understand because of this.

```
plot( wisc.pr$x, col = diagnosis ,
      xlab = "PC1", ylab = "PC2")
```



```
plot( wisc.pr$x[,3], col = diagnosis ,  
      xlab = "PC1", ylab = "PC2")
```



## PCA Screen -plot

A plot of how much variance each PC captures. We can get this from `wisc.pr$sdev` or from the output of `summary(wisc.pr)`

```
##var.tbl  
  
##var <- var.tbl$importance[2,]  
##cum.var <- var.tbl$importance[3,]  
  
##plot(var, typ ="b", ylab = "Percent Variance Captured",  
##      xlab ="PC Number")
```

```
##plot(cum.var, typ ="b", ylab = "Percent Variance Captured",  
##      xlab ="PC Number")
```

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`?

```
wisc.pr$rotation["concave.points_mean", "PC1"]
```

```
[1] -0.2608538
```

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

You need at least 5 PCs to explain 80% of the variance

## Hierachial Clustering

Just clustering the original data is not very informative or helpful

```
data.scaled <- scale(wisc.data)
data.dist <- dist(data.scaled)
##wisc.hclust <- hclust(data.dist,)

##table(cutree(wisc.hclust, k=4))

##table(cutree(wisc.hclust, diagnosis))
```

## Combining Methods (Clustering and PCA)

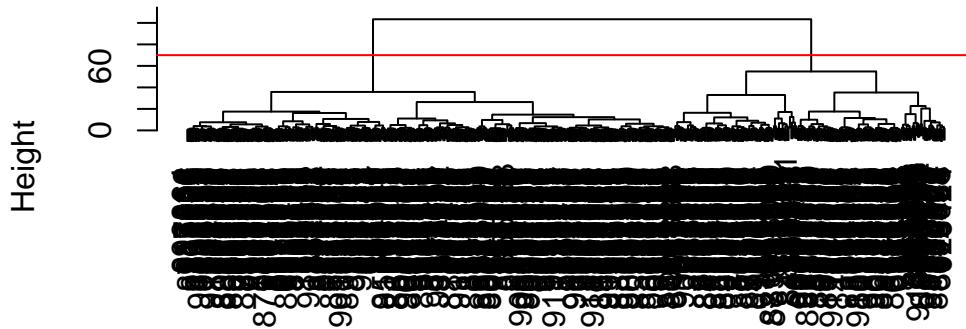
Clustering the orginal data was not very effectvive. The PCA results looked promising. Here we combine these methods by clustering from our PCA results. In other words ‘clustering in PC space’

```
## Take the first 3 PCs
dist.pc<- dist(wisc.pr$x[,1:3])
wisc.pr.hclust <-hclust(dist.pc, method = "ward.D2")
```

View the tree

```
plot(wisc.pr.hclust)
abline(h=70, col ="red")
```

## Cluster Dendrogram



```
dist.pc  
hclust (*, "ward.D2")
```

To get our clustering membership vector (i.e. our main clustering results) we “cut” the tree at a desired height or to yield a desired height or to yield a destied number of “k” groups

```
grps <- cutree(wisc.pr.hclust, h=70)  
table(grps)
```

grps  
1 2  
203 366

How does this clustering grp compare to the expert

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

grps	B	M
1	24	179
2	333	33

Sensitivity is  $TP/(TP+FN)$  Specificity is  $TN/(TN + FN)$

## **7. Prediction**

We can use our PCA model for prediction with new input patient samples