

# Class 8: Breast Cancer Analysis

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## Background

The goal of today’s mini-project is to explore a complete analysis using the unsupervised learning techniques covered in the last class. We will extend what we learned by combining PCA as a preprocessing step to clustering using data that consist of measurements of cell nuclei of human breast masses.

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

The data is available as a CSV from class website:

```
wisc.df <- read.csv("WisconsinCancer (2).csv", row.names=1)
```

Make sure we do not include sample id or diagnosis columns in the data that we analyze below.

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

```
[1] 569 30
```

## Exploratory data analysis

Q1. How many observations are in this dataset?

There are 569 observations/samples/patients in the data set. I used nrow(wisc.data) to find that number.

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

There are 212; see code below (two ways to determine)

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

```
[1] 212
```

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

B	M
357	212

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

There are 10; see code below

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

[1] 10

Easier to read:

```
n <- colnames(wisc.data)
inds <- grep("_mean", n)
length(inds)
```

[1] 10

## Principal Component Analysis

The main function in Base R for PCA is called `prcomp()`. An optional argument `scale` should nearly always be switched to `scale=TRUE` for this function.

```
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 principal components (PC1)?

The answer is 0.4427203, see code below

```

pr.var <- wisc.pr$sdev^2
pr.var / sum(pr.var)

```

```

[1] 4.427203e-01 1.897118e-01 9.393163e-02 6.602135e-02 5.495768e-02
[6] 4.024522e-02 2.250734e-02 1.588724e-02 1.389649e-02 1.168978e-02
[11] 9.797190e-03 8.705379e-03 8.045250e-03 5.233657e-03 3.137832e-03
[16] 2.662093e-03 1.979968e-03 1.753959e-03 1.649253e-03 1.038647e-03
[21] 9.990965e-04 9.146468e-04 8.113613e-04 6.018336e-04 5.160424e-04
[26] 2.725880e-04 2.300155e-04 5.297793e-05 2.496010e-05 4.434827e-06

```

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

A: Three PCs are required (PC1-3). See summary below.

```
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

```

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

A: Seven PCs are required (PC1-7). See summary below.

```
summary(wisc.pr)
```

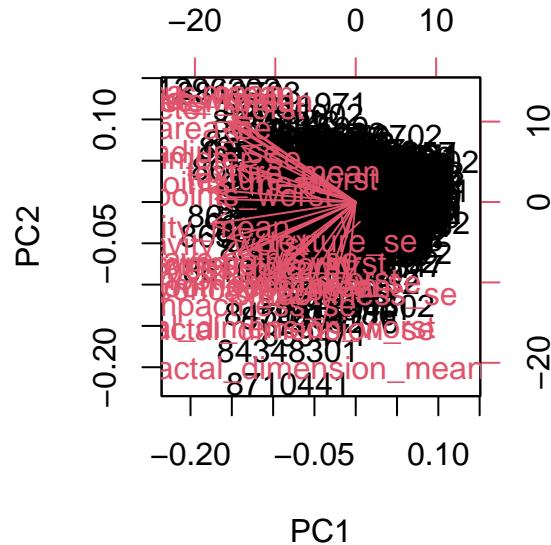
Importance of components:

	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					

## Interpreting PCA results

Create a biplot of the wisc.pr using the `biplot()` function.

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

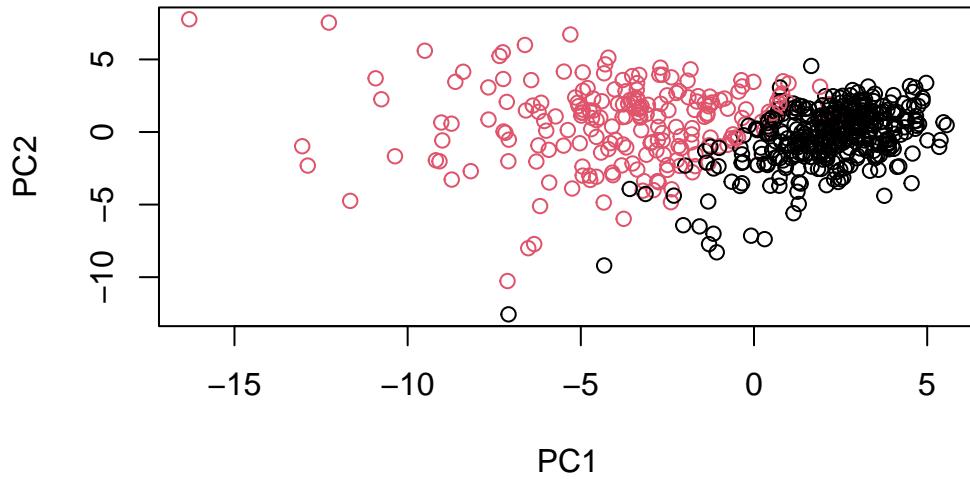


Q7. What stands out to you about this plot? Is it easy or difficult to understand?  
Why?

A: The plot is very cluttered with lots of overlap between labels, making it almost impossible to interpret the PCA result.

### Scatter plot observations by components 1 and 2

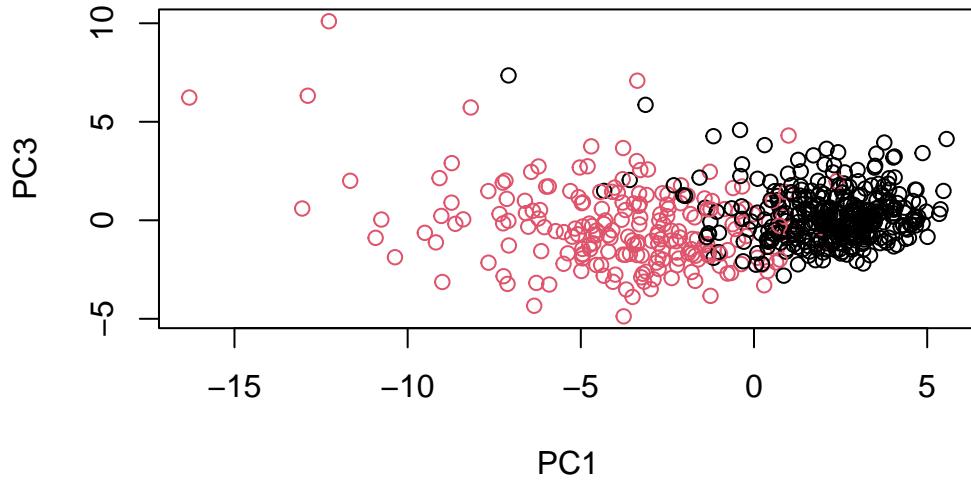
```
plot( wisc.pr$x[,1], wisc.pr$x[,2] , col = diagnosis ,
      xlab = "PC1", ylab = "PC2")
```



Q8. Generate a similar plot for principal components 1 and 3. What do you notice about these plots?

A: I notice the first plot (PC1 and 2) has less overlap between clusters (i.e. it has a cleaner cut). See plot for PC1 and 3 below.

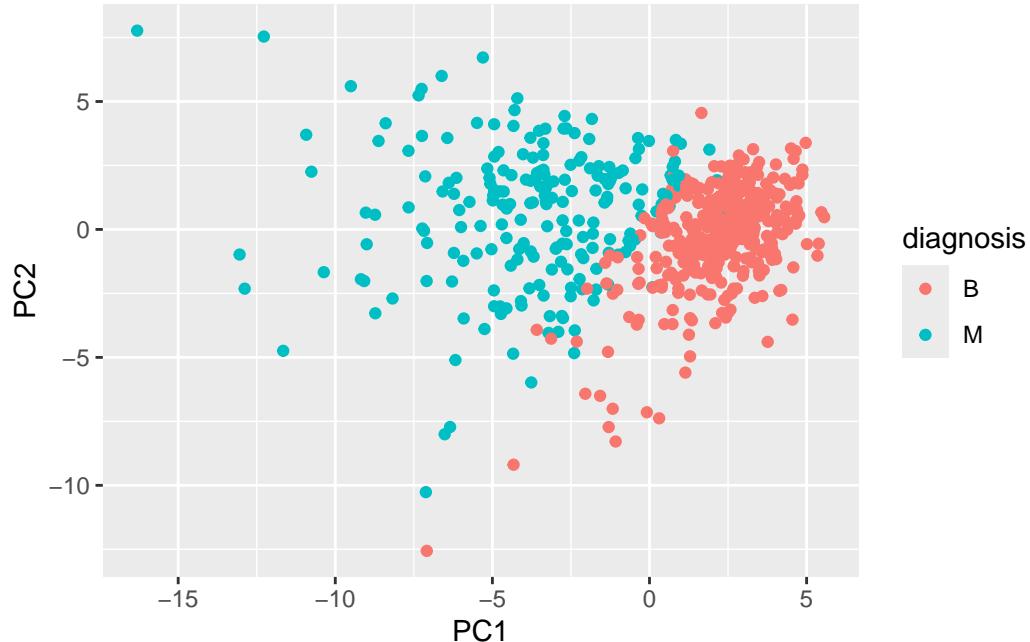
```
# Repeat for components 1 and 3
plot( wisc.pr$x[,1], wisc.pr$x[,3] , col = diagnosis ,
      xlab = "PC1", ylab = "PC3")
```



Let's make our main result figure - the “PC plot” or “score plot”, “ordination plot”...

```
library(ggplot2)

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



## Variance Explained

Calculate variance of each component

```
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

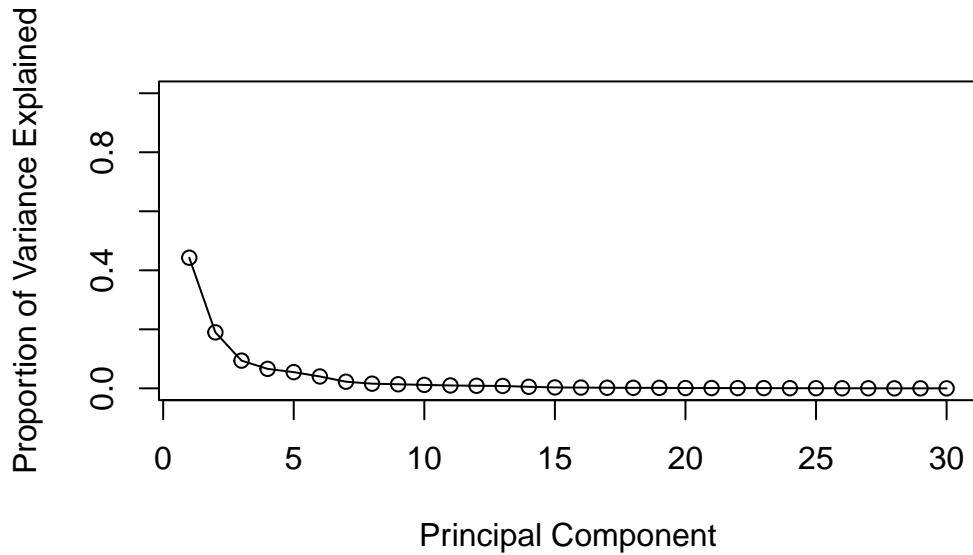
```
[1] 13.281608 5.691355 2.817949 1.980640 1.648731 1.207357
```

Variance explained by each principal component: pve

```
pve <- pr.var / sum(pr.var)
```

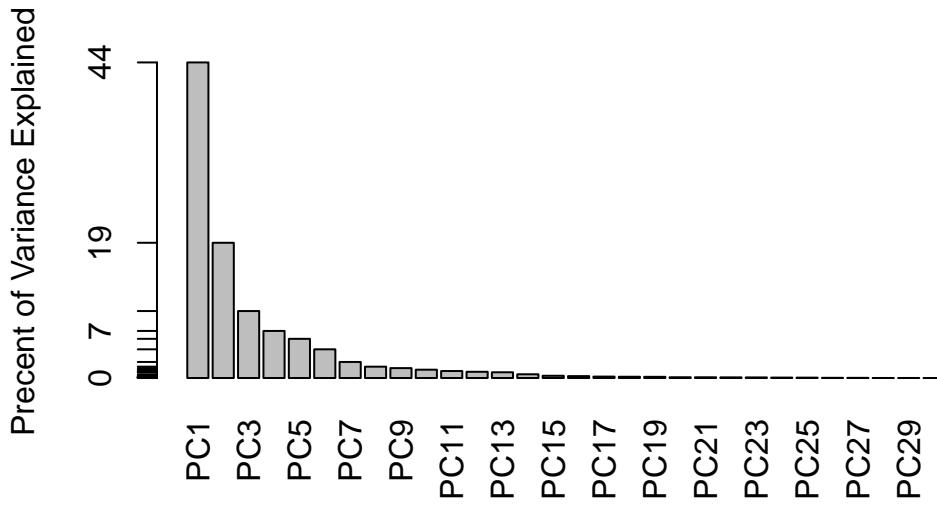
Plot variance explained for each principal component

```
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 )
```



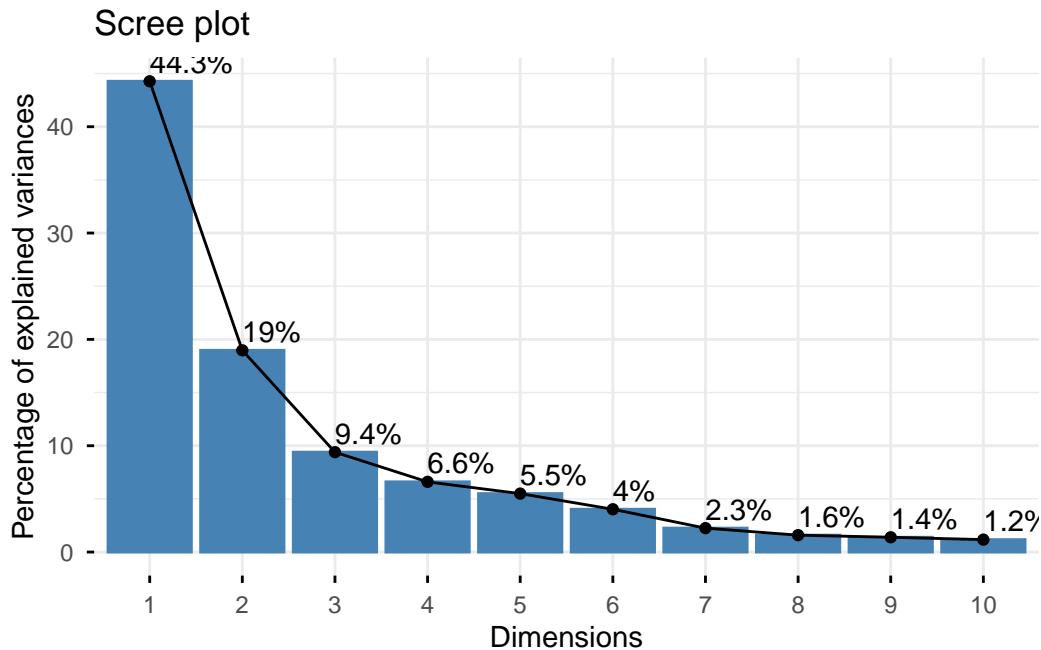
ggplot based graph

```
library(factoextra)
```

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

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

```
Warning in geom_bar(stat = "identity", fill = barfill, color = barcolor, :  
Ignoring empty aesthetic: `width`.
```



## Communicating PCA Results

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`? This tells us how much this original feature contributes to the first PC.

A: Using the code below, the loading vector is -0.26085376

```
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

## Hierarchical Clustering

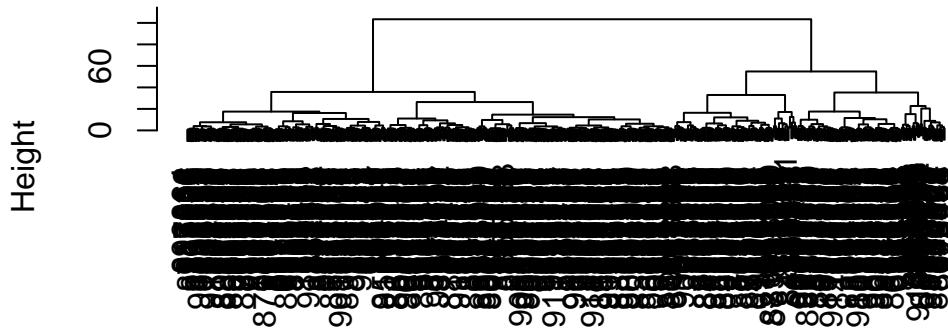
```
apply(scale(wisc.data), 2, sd)
```

radius_mean	texture_mean	perimeter_mean
1	1	1
area_mean	smoothness_mean	compactness_mean
1	1	1
concavity_mean	concave.points_mean	symmetry_mean
1	1	1
fractal_dimension_mean	radius_se	texture_se
1	1	1
perimeter_se	area_se	smoothness_se
1	1	1
compactness_se	concavity_se	concave.points_se
1	1	1
symmetry_se	fractal_dimension_se	radius_worst
1	1	1
texture_worst	perimeter_worst	area_worst
1	1	1
smoothness_worst	compactness_worst	concavity_worst
1	1	1
concave.points_worst	symmetry_worst	fractal_dimension_worst
1	1	1

## Combining PCA and clustering

```
d <- dist( wisc.pr$x[,1:3] )
wisc.pr.hclust <- hclust(d, method="ward.D2")
plot(wisc.pr.hclust)
```

## Cluster Dendrogram



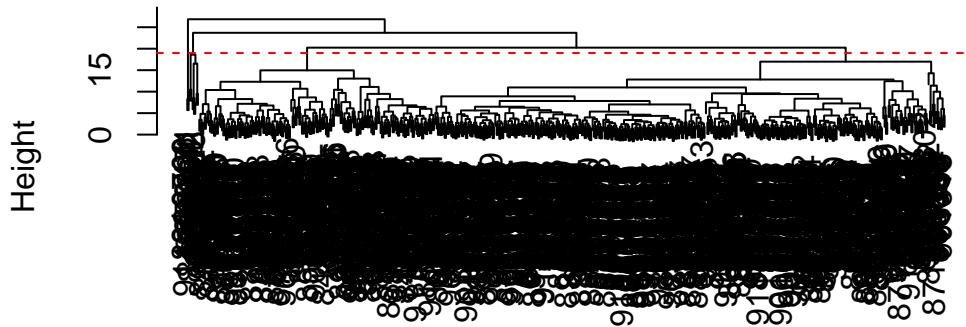
d  
hclust (\*, "ward.D2")

Q10. Using the plot() and abline() functions, what is the height at which the clustering model has 4 clusters?

A: According to the plot below, **19** is the height at which the clustering model has 4 clusters.

```
data.scaled <- scale(wisc.data)
data.dist <- dist(data.scaled)
wisc.hclust <- hclust(data.dist, method="complete")
plot(wisc.hclust)
abline(h=19, col='red', lty=2)
```

## Cluster Dendrogram



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

grps	B	M
1	24	179
2	333	33

TP: 179 FP: 24

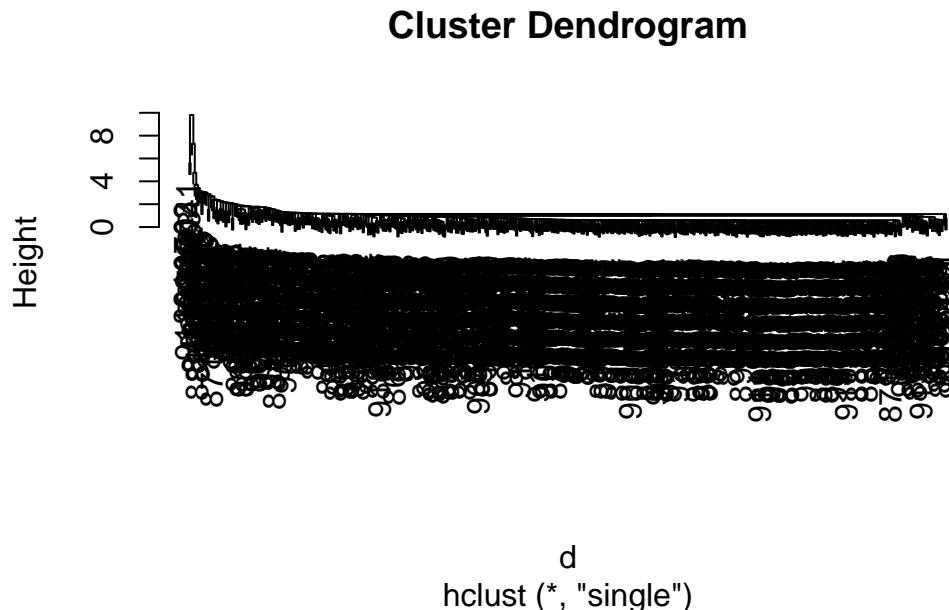
Sensitivity: TP/(TP+FN)

### Using Different Methods (“single”)

Q12. Which method gives your favorite results for the same data.dist dataset?  
Explain your reasoning.

A: My favorite method is “ward.D2” because it generates a plot that allows for use of abline() to find where the clustering model has 4 clusters.

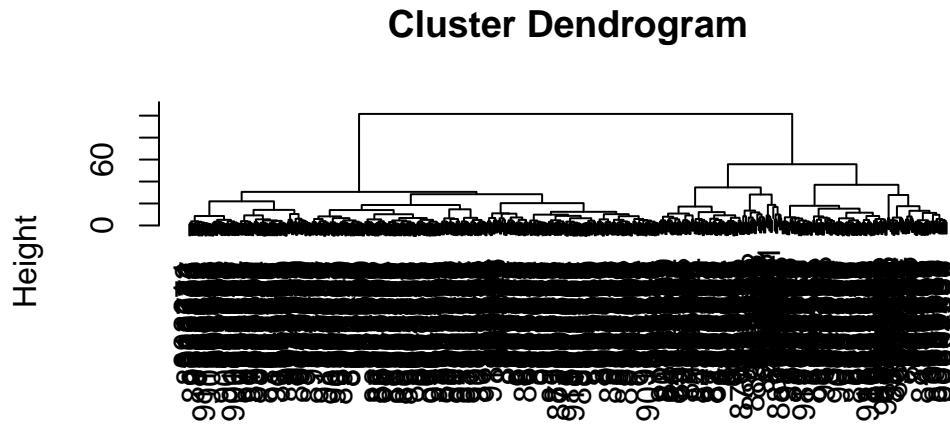
```
d <- dist( wisc.pr$x[,1:3] )  
wisc.pr.hclust <- hclust(d, method="single")  
plot(wisc.pr.hclust)
```



## Combining Methods

Clustering on PCA results

```
wisc.pr.hclust <- hclust(dist(wisc.pr$x[, 1:7]), method = "ward.D2")
plot(wisc.pr.hclust)
```



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

Determine if these two clusters are malignant and benign

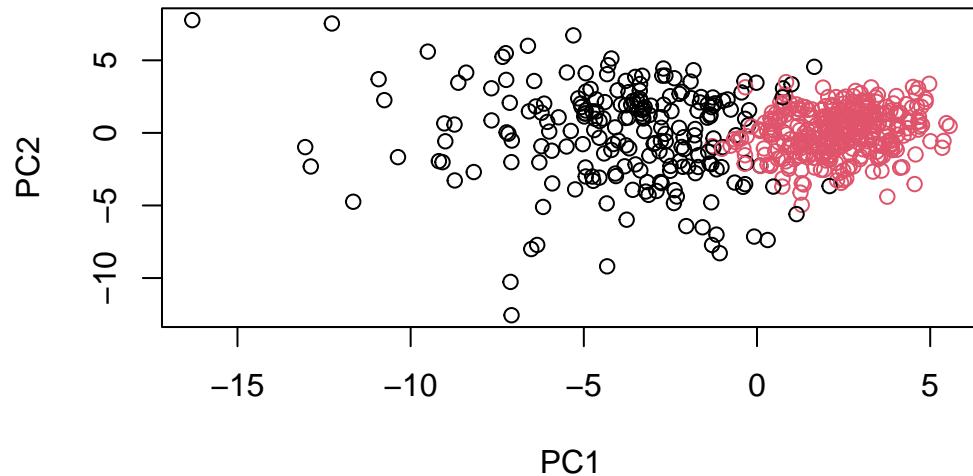
```
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

```
grps
 1   2
216 353
```

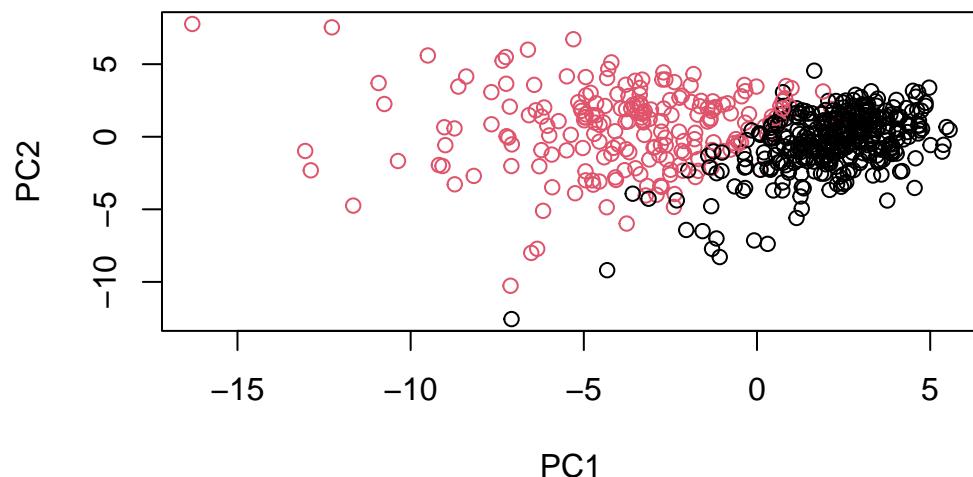
```
table(grps, diagnosis)
```

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)
```



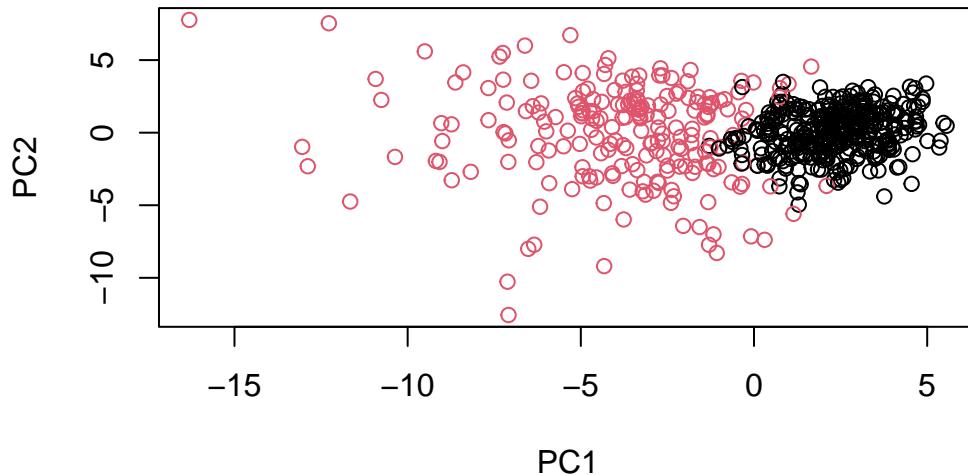
```
g <- as.factor(grps)
levels(g)
```

```
[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)
```



**Use the distance along the first 7 PCs for clustering i.e. wisc.pr\$x[, 1:7]**

```
wisc.pr.hclust <- hclust(dist(wisc.pr$x[, 1:7]), method="ward.D2")
```

Cut this hierarchical clustering model into 2 clusters and assign the results to wisc.pr.hclust.clusters.

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

Using `table()`, compare the results from your new hierarchical clustering model with the actual diagnoses.

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

wisc.pr.hclust.clusters	diagnosis	
	B	M
1	0	45
2	2	77
3	26	66
4	329	24

Q13. How well does the newly created model with four clusters separate out the two diagnoses?

A: It does so much better.

Q14. How well do the 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.

A: They are much better.