

Class09

```
fna.data <- "WisconsinCancer.csv"
wisc.df <- read.csv(fna.data, row.names=1)
wisc.data <- wisc.df[,-1]
diagnosis <- factor(wisc.df$diagnosis)
diagnosis
```

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

Q1. How many observations are in this dataset?

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

```
[1] 569
```

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

```
table(diagnosis)
```

```
diagnosis
  B    M
357 212
```

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

```
[1] 0
```

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

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

```
[1] 1 2 3 4 5 6 7 8 9 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

```
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					

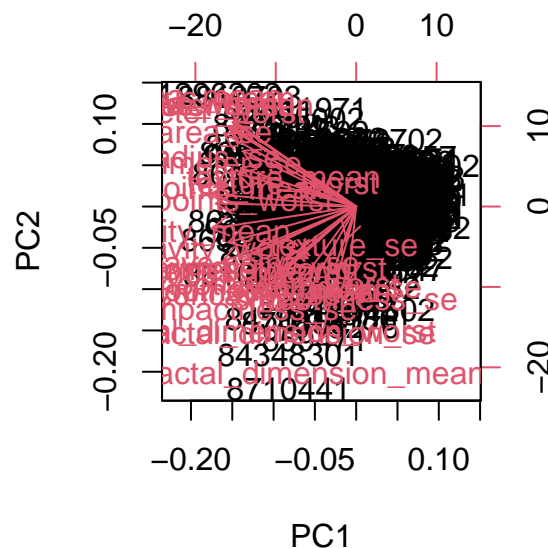
Q4. From your results, what proportion of the original variance is captured by the first principal components (PC1)? .4427

Q5. How many principal components (PCs) are required to describe at least 70% of the original variance in the data? 3! PC1,2 and 3

Q6. How many principal components (PCs) are required to describe at least 90% of the original variance in the data? 7!

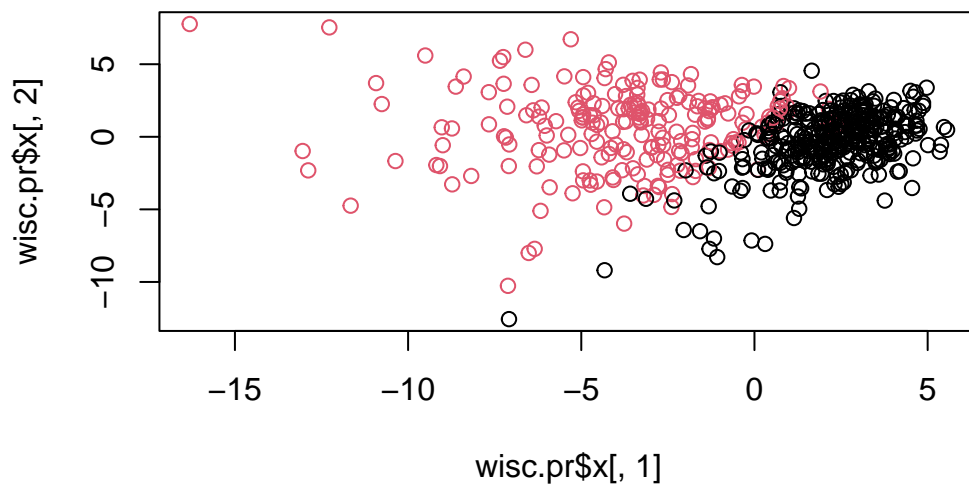
Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why?

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



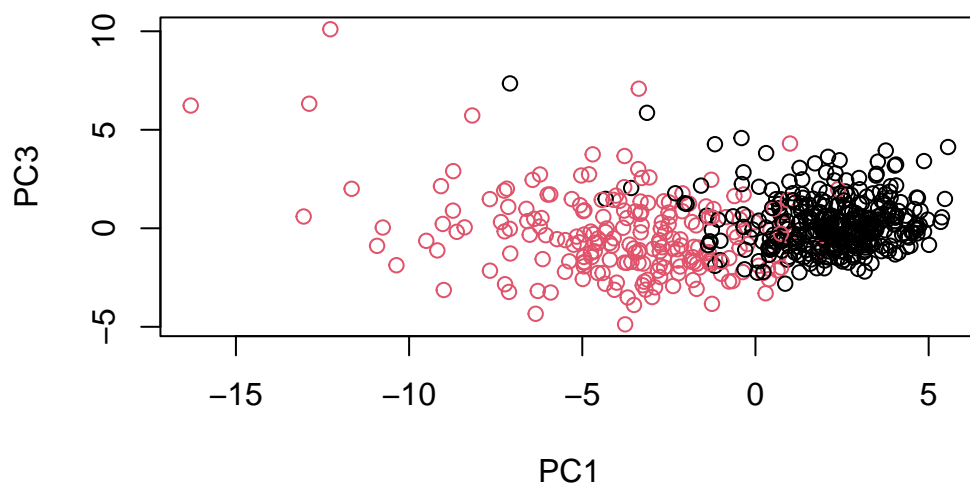
I can't see the points because of all the text labels!

```
# Scatter plot observations by components 1 and 2
plot(wisc.pr$x[,1], wisc.pr$x[,2], col = diagnosis)
```



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

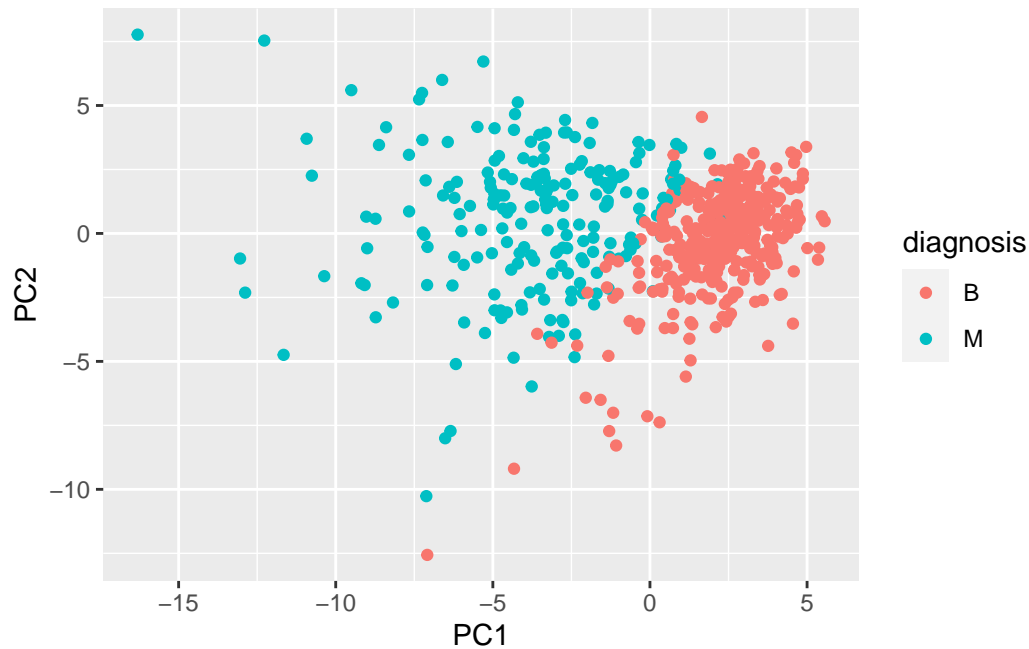
```
# Repeat for components 1 and 3
plot(wisc.pr$x[,1], wisc.pr$x[,3], col = diagnosis, xlab = "PC1", ylab = "PC3")
```



```
# 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)
```

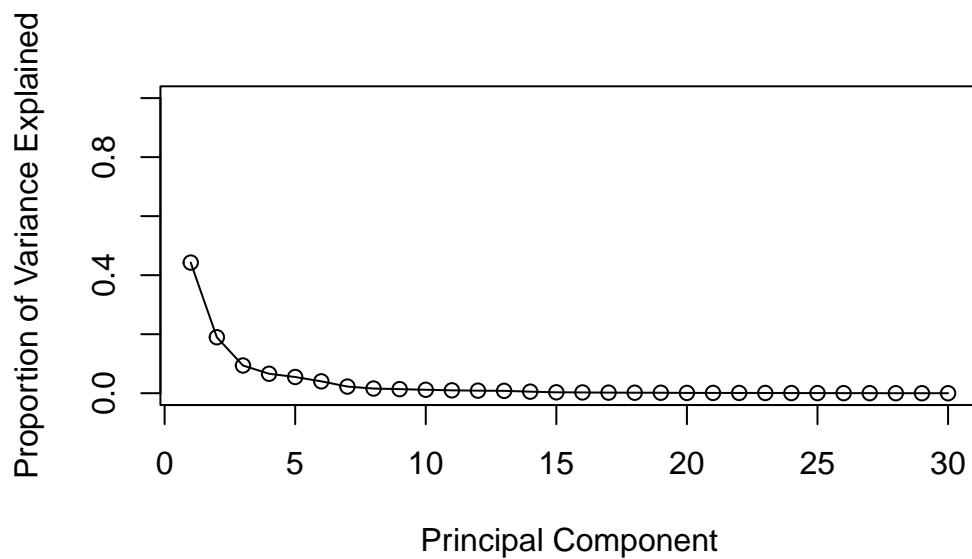
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
#which(pcvar>= .9)

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

```
[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
```

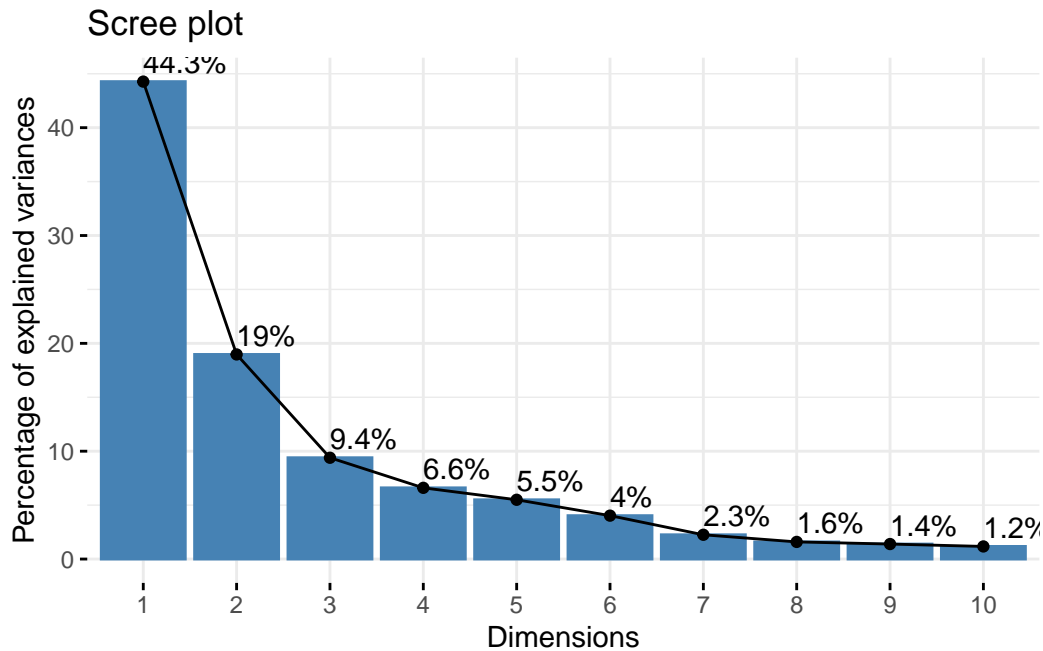
```
# Plot variance explained for each principal component
plot(pve, xlab = "Principal Component",
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```



```
## 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$rotation[,1]`) for the feature `concave.points_mean`? This tells us how much this original feature contributes to the first PC.

```
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

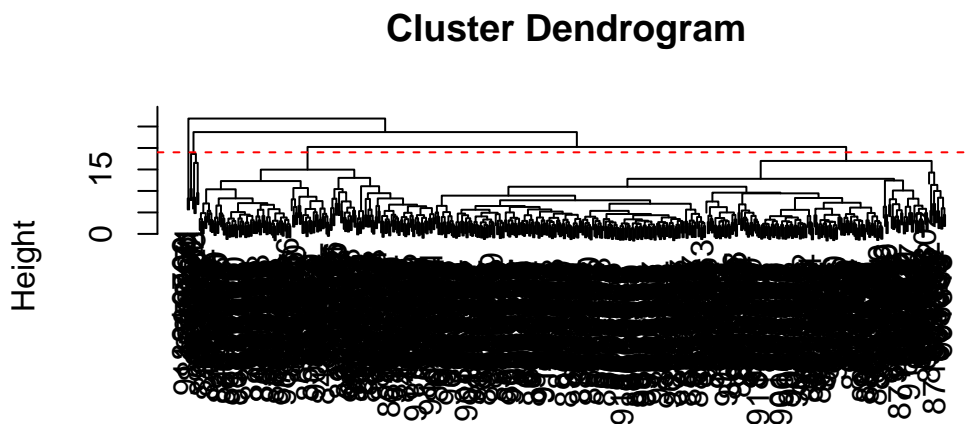
Negative value of concave points negatively contributes to PC1 on the left of the x-axis

Section 3

```
# 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")
```

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

```
plot(wisc.hclust)
abline(h=19, col="red", lty=2)
```



```
data.dist
hclust (*, "complete")
```

```
wisc.hclust.clusters <- cutree(wisc.hclust,h=19)
table(wisc.hclust.clusters, diagnosis)
```

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

Q11. OPTIONAL: Can you find a better cluster vs diagnoses match by cutting into a different number of clusters between 2 and 10? How do you judge the quality of your result in each case?

```
wisc.hclust.clusters <- cutree(wisc.hclust,h=18)
table(wisc.hclust.clusters, diagnosis)
```

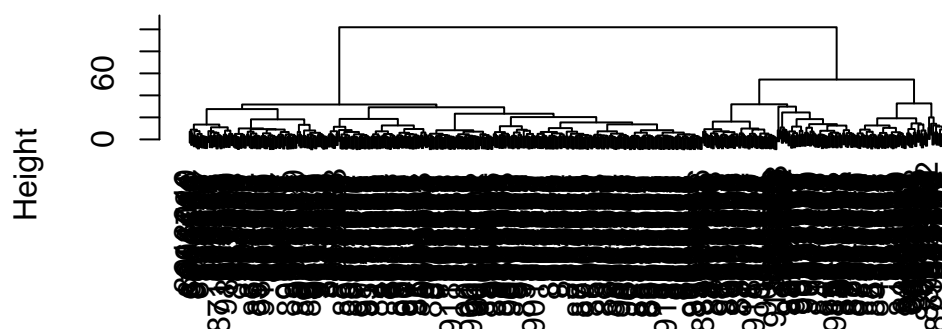
	diagnosis		
wisc.hclust.clusters	B	M	
1	12	165	
2	0	5	
3	343	40	
4	2	0	
5	0	2	

I think the way we did the clustering is best

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

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

Cluster Dendrogram



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

```
wisc.hclust.clusters <- cutree(wisc.hclust, h=55)
table(wisc.hclust.clusters, diagnosis)
```

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

ward.D2 looks the best as far as clustering benign and malignant cases in different clusters

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

```
grps
 1  2
184 385
```

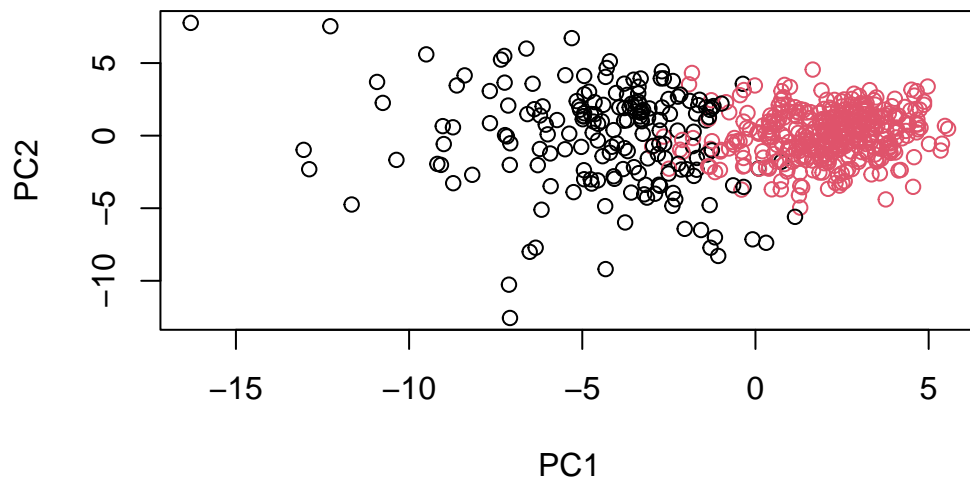
```
table(grps, diagnosis)
```

```

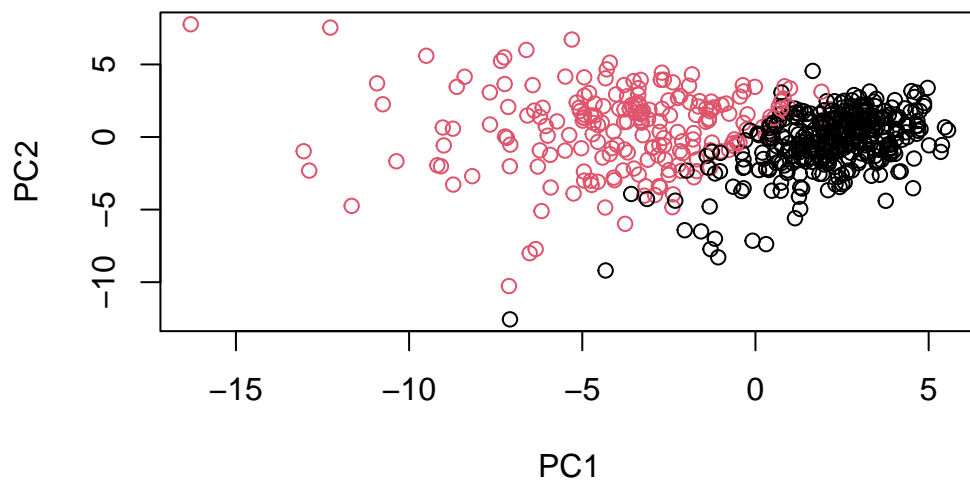
diagnosis
grps  B  M
1    20 164
2    337 48

```

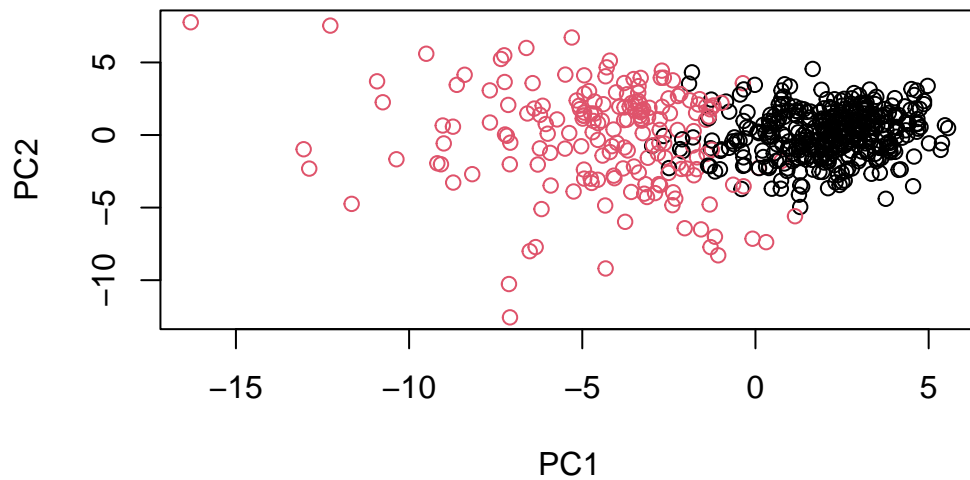
```
plot(wisc.pr$x[,1:2], col=grps)
```



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



```
##turn our groups into a factor and reorder the levels so cluster 2 comes first and thus g  
g <- as.factor(grps)  
g <- relevel(g,2)  
plot(wisc.pr$x[,1:2], col=g)
```



```
#install.packages("rgl")
library(rgl)
plot3d(wisc.pr$x[,1:3], xlab="PC 1", ylab="PC 2", zlab="PC 3", cex=1.5, size=1, type="s",

## Use the distance along the first 7 PCs for clustering i.e. wisc.pr$x[, 1:7]
dist <- dist(wisc.pr$x[, 1:7])
wisc.pr.hclust <- hclust(dist, method="ward.D2")
wisc.pr.hclust.clusters2 <- cutree(wisc.pr.hclust, k=2)
wisc.pr.hclust.clusters4 <- cutree(wisc.pr.hclust, k=4)
```

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

```
# Compare to actual diagnoses
table(wisc.pr.hclust.clusters2, diagnosis)
```

```
          diagnosis
wisc.pr.hclust.clusters2  B  M
1          28 188
2          329  24
```

```
table(wisc.pr.hclust.clusters4, diagnosis)
```

	diagnosis	
wisc.pr.hclust.clusters4	B	M
1	0	45
2	2	77
3	26	66
4	329	24

2 clusters looks 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.

```
table(wisc.pr.hclust.clusters2, diagnosis)
```

	diagnosis	
wisc.pr.hclust.clusters2	B	M
1	28	188
2	329	24

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

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

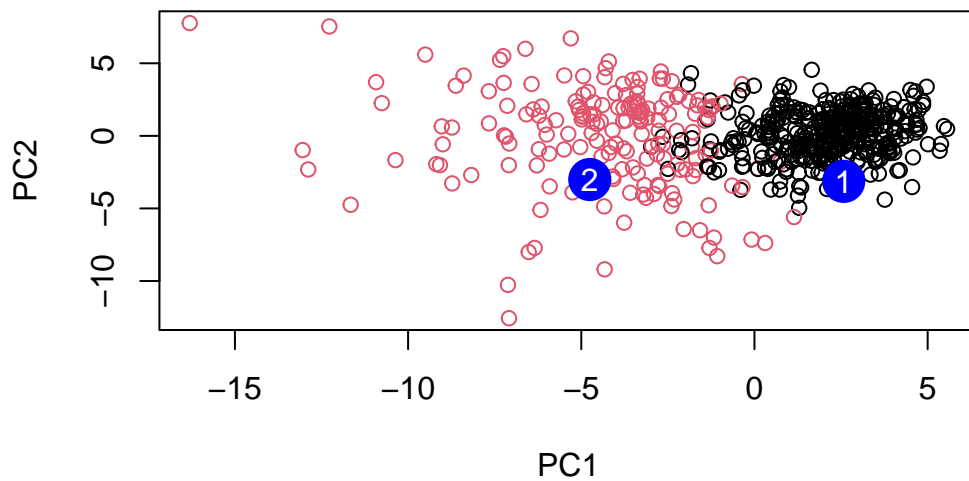
```
# 90% success with the 2 clusters- best one i think
```

Q16. Which of these new patients should we prioritize for follow up based on your results?

```
url <- "https://tinyurl.com/new-samples-CSV"
new <- read.csv(url)
npc <- predict(wisc.pr, newdata=new)
npc
```


	PC1	PC2	PC3	PC4	PC5	PC6	PC7
[1,]	2.576616	-3.135913	1.3990492	-0.7631950	2.781648	-0.8150185	-0.3959098
[2,]	-4.754928	-3.009033	-0.1660946	-0.6052952	-1.140698	-1.2189945	0.8193031
	PC8	PC9	PC10	PC11	PC12	PC13	PC14
[1,]	-0.2307350	0.1029569	-0.9272861	0.3411457	0.375921	0.1610764	1.187882
[2,]	-0.3307423	0.5281896	-0.4855301	0.7173233	-1.185917	0.5893856	0.303029
	PC15	PC16	PC17	PC18	PC19	PC20	
[1,]	0.3216974	-0.1743616	-0.07875393	-0.11207028	-0.08802955	-0.2495216	
[2,]	0.1299153	0.1448061	-0.40509706	0.06565549	0.25591230	-0.4289500	
	PC21	PC22	PC23	PC24	PC25	PC26	
[1,]	0.1228233	0.09358453	0.08347651	0.1223396	0.02124121	0.078884581	
[2,]	-0.1224776	0.01732146	0.06316631	-0.2338618	-0.20755948	-0.009833238	
	PC27	PC28	PC29	PC30			
[1,]	0.220199544	-0.02946023	-0.015620933	0.005269029			
[2,]	-0.001134152	0.09638361	0.002795349	-0.019015820			

```
plot(wisc.pr$x[,1:2], col=g)
points(npc[,1], npc[,2], col="blue", pch=16, cex=3)
text(npc[,1], npc[,2], c(1,2), col="white")
```



lets prioritize patient 2