

Class 8: Mini Project

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Breast Cancer Project

Today we are going to explore some data from the University of Wisconsin Cancer Center on Breast biopsy data.

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

	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		

Q. How many patient samples are in this dataset?

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

```
[1] 569
```

There are 569 patients in this dataset.

Q. How many cancer (M) and non cancer (B) samples are there?

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

```
B    M  
357 212
```

Save the diagnosis for later use as a reference to compare how well we do with PCA etc.

```
diagnosis <- as.factor(wisc.data$diagnosis)  
#diagnosis
```

Now exclude the diagnosis column from the data.

```
wisc <- wisc.data[,-1]
```

Q. How many “dimensions”, “variables”, “columns”, are in this dataset?

```
ncol(wisc)
```

```
[1] 30
```

Principal Component Analysis (PCA)

To perform PCA in R we can use the `prcomp()` function. It takes as input a numeric dataset and optional `scale=FALSE/TRUE` argument.

We generally always want to set `scale=TRUE` but let's make sure by checking if the mean and standard deviation values are different across these 30 columns.

```
round(colMeans(wisc))
```

radius_mean	texture_mean	perimeter_mean
14	19	92
area_mean	smoothness_mean	compactness_mean
655	0	0
concavity_mean	concave.points_mean	symmetry_mean
0	0	0

fractal_dimension_mean	radius_se	texture_se
0	0	1
perimeter_se	area_se	smoothness_se
3	40	0
compactness_se	concavity_se	concave.points_se
0	0	0
symmetry_se	fractal_dimension_se	radius_worst
0	0	16
texture_worst	perimeter_worst	area_worst
26	107	881
smoothness_worst	compactness_worst	concavity_worst
0	0	0
concave.points_worst	symmetry_worst	fractal_dimension_worst
0	0	0

```
pca <- prcomp(wisc, scale=TRUE)
summary(pca)
```

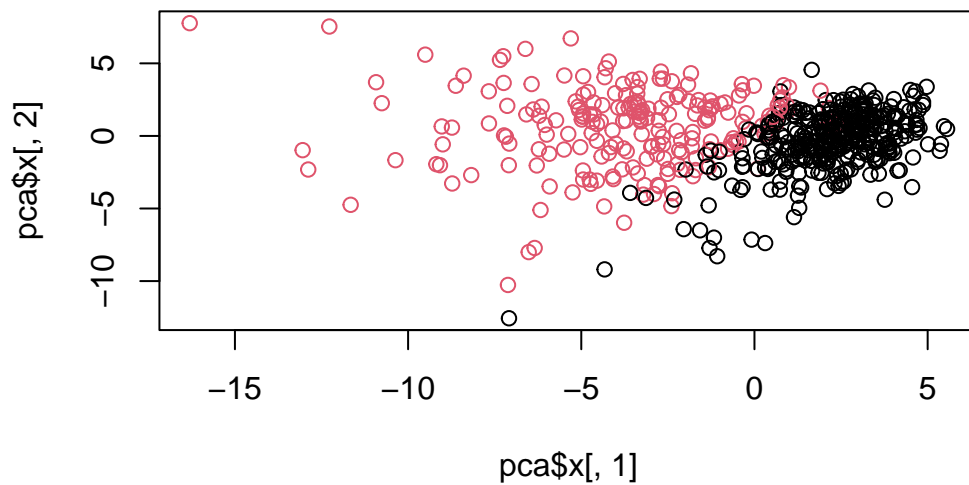
Importance of components:

	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					

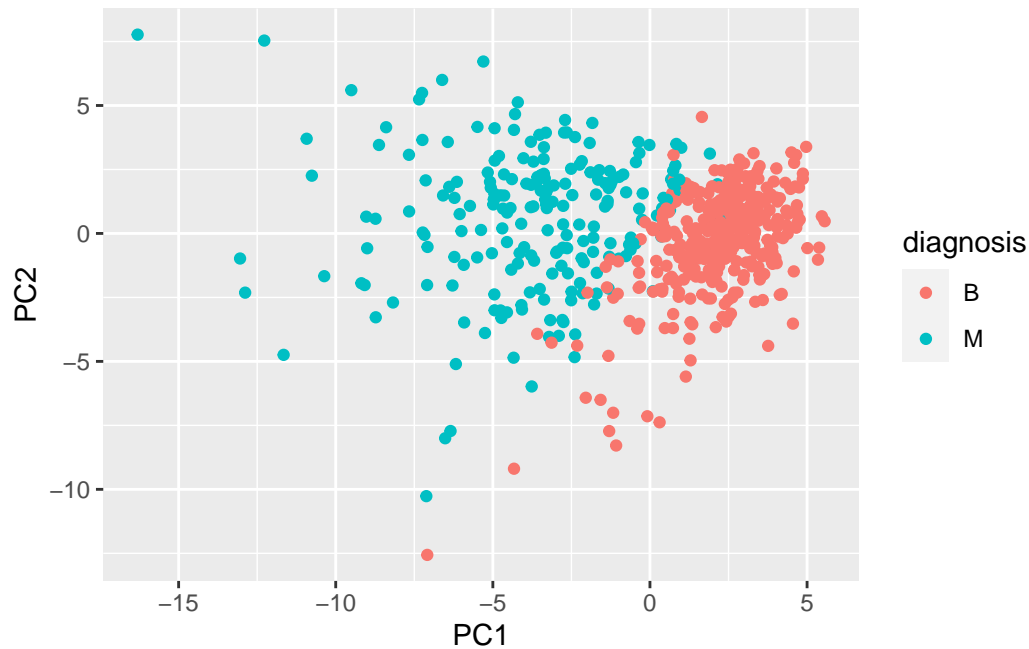
```
attributes(pca)
```

```
$names  
[1] "sdev"      "rotation" "center"    "scale"     "x"  
  
$class  
[1] "prcomp"
```

```
plot(pca$x[,1],pca$x[,2], col=diagnosis)
```



```
library(ggplot2)  
  
x <- as.data.frame(pca$x)  
  
ggplot(x) +  
  aes(PC1, PC2, col = diagnosis) +  
  geom_point()
```



Q. How much variance is captured in the top 3 PCs?

They capture 76% of the total variance.

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.

```
pca$rotation["concave.points_mean",1]
```

```
[1] -0.2608538
```

```
attributes(pca)
```

```
$names
[1] "sdev"      "rotation" "center"    "scale"     "x"

$class
[1] "prcomp"
```

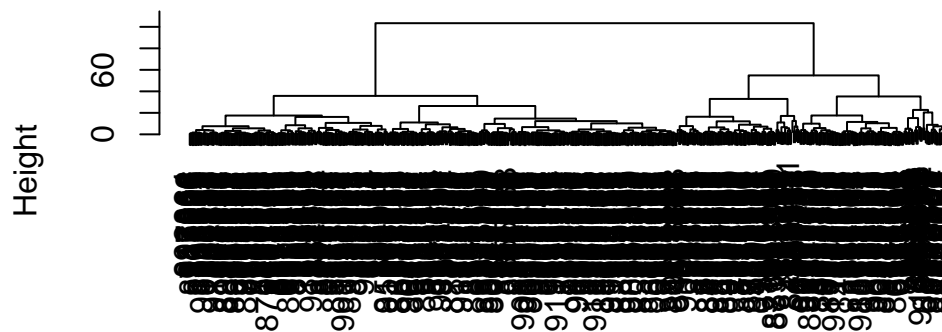
Combine PCA results with clustering.

We can use our new pCA variables (i.e. the scores along the PCs contained in `pca$x`) as input for other methods such as clustering.

```
# Hclust needs a distance matrix as input
d <- dist(pca$x[,1:3])

hc <- hclust(d, method= "ward.D2")
plot(hc)
```

Cluster Dendrogram



d
hclust (*, "ward.D2")

To get our cluster membership vector we can use the `cutree()` function and specify a height (`h`) or number of groups (`k`).

```
grps <- cutree(hc, h=80)
table(grps)
```

```
grps
 1  2
203 366
```

I want to find out how many diagnosis “M” and “B” are in each grp?

```
table(diagnosis)
```

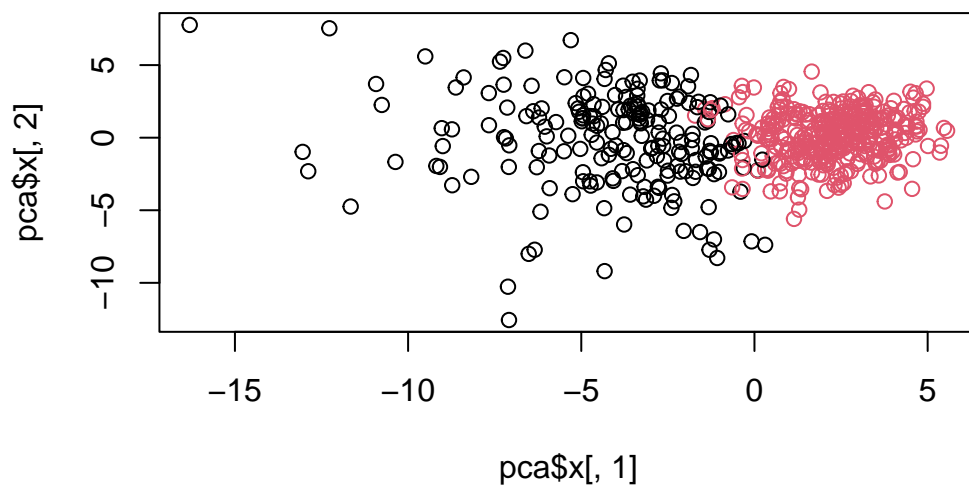
```
diagnosis
  B    M
357 212
```

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

```
      grps
diagnosis 1  2
  B    24 333
  M   179  33
```

We can also plot our results using our clustering vector `grps`.

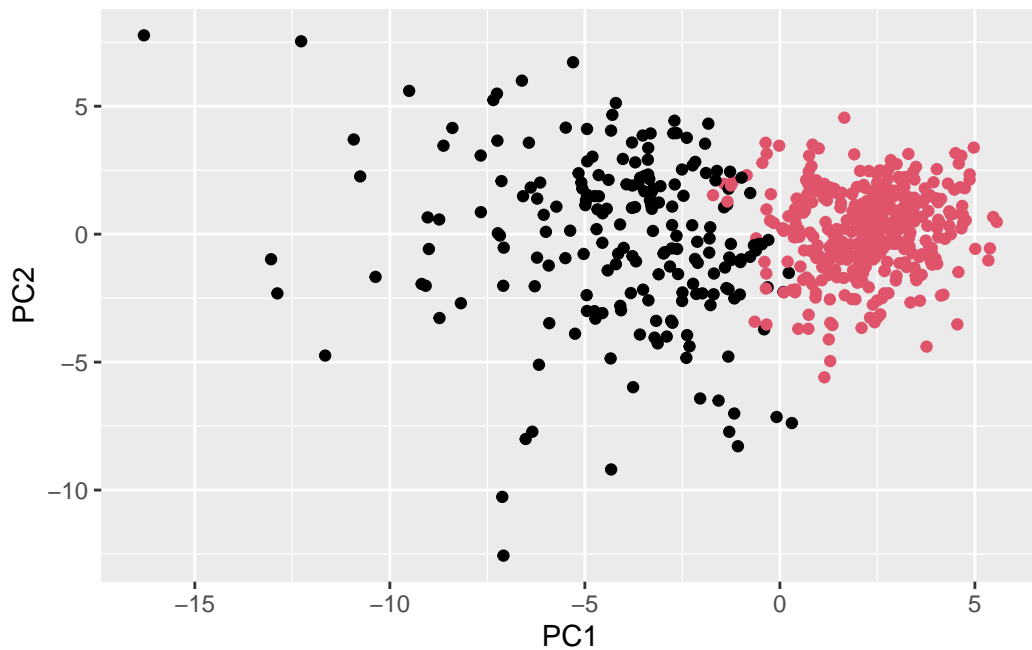
```
plot(pca$x[,1], pca$x[,2], col = grps)
```




```
library(ggplot2)

x <- as.data.frame(pca$x)

ggplot(x) +
  aes(PC1, PC2) +
  geom_point(col = grps)
```



Q15. What is the specificity and sensitivity of our current results?

specificity:

```
24/(24+333)
```

```
[1] 0.06722689
```

sensitivity:

```
179/(179+33)
```

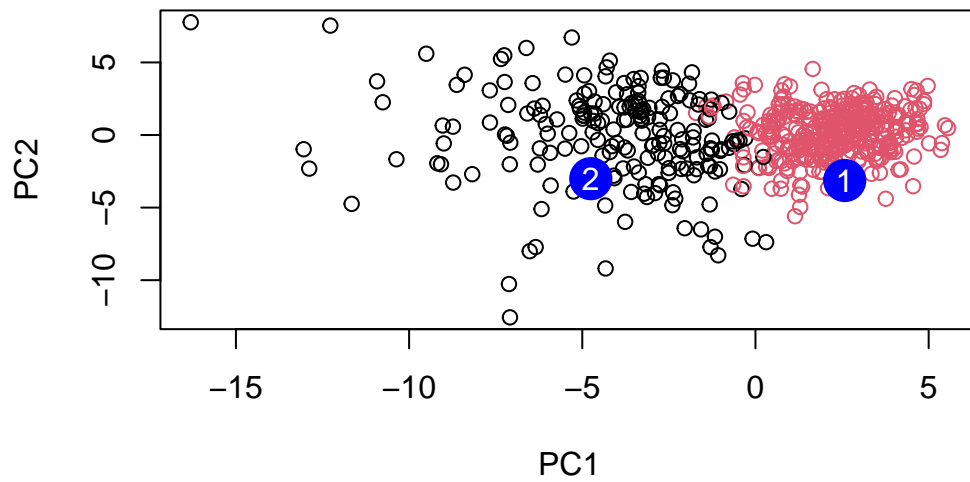
```
[1] 0.8443396
```

Predictions

```
#url <- "new_samples.csv"
url <- "https://tinyurl.com/new-samples-CSV"
new <- read.csv(url)
npc <- predict(pca, 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(pca$x[,1:2], col=grps)
points(npc[,1], npc[,2], col="blue", pch=16, cex=3)
text(npc[,1], npc[,2], c(1,2), col="white")
```



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

We should prioritize patient 2 for a follow up because the results look the most like the malignant results.