

class08:Machine Learning Mini Project

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Running Code

When you click the **Render** button a document will be generated that includes both content and the output of embedded code. You can embed code like this:

```
1 + 1
```

```
[1] 2
```

You can add options to executable code like this

```
[1] 4
```

The `echo: false` option disables the printing of code (only output is displayed).

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
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		

Q. How many patient samples are in this dataset? There are 569 patient samples.

```
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 there 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)
```

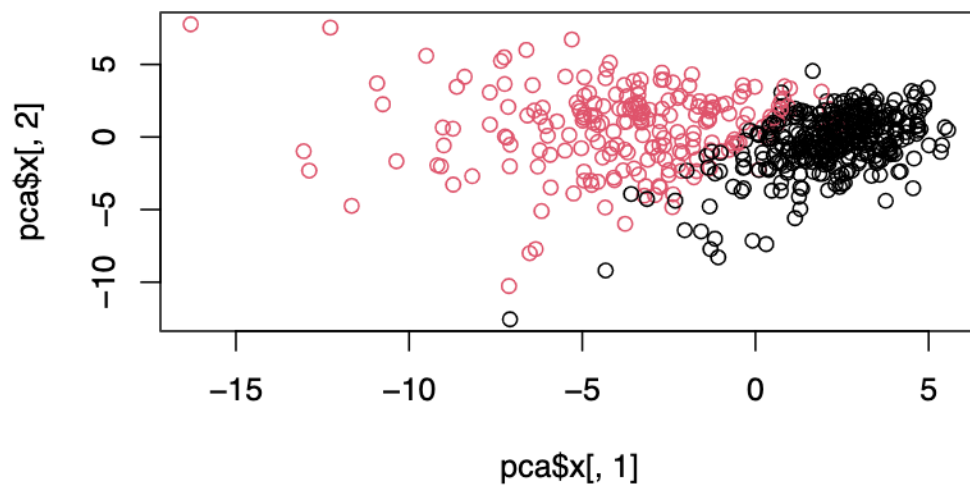
```
$names
```

```
[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)
```

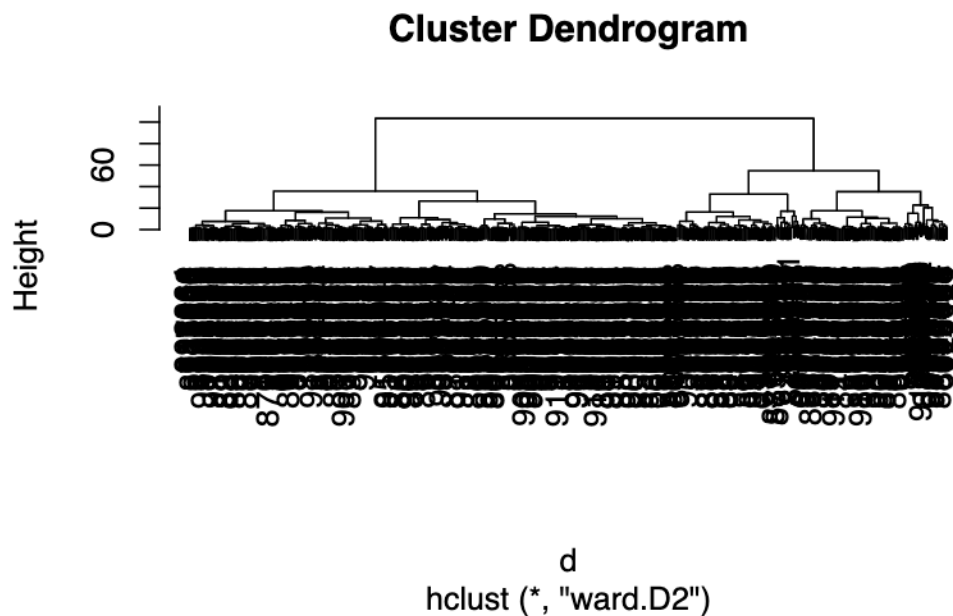
```
$names
[1] "sdev"      "rotation" "center"    "scale"     "x"

$class
[1] "prcomp"
```

Combine PCA results with clustering

We can use our new PCA variables (i.e. the scores along the PCs contained in `t 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)
```



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 group?


```
table(diagnosis)
```

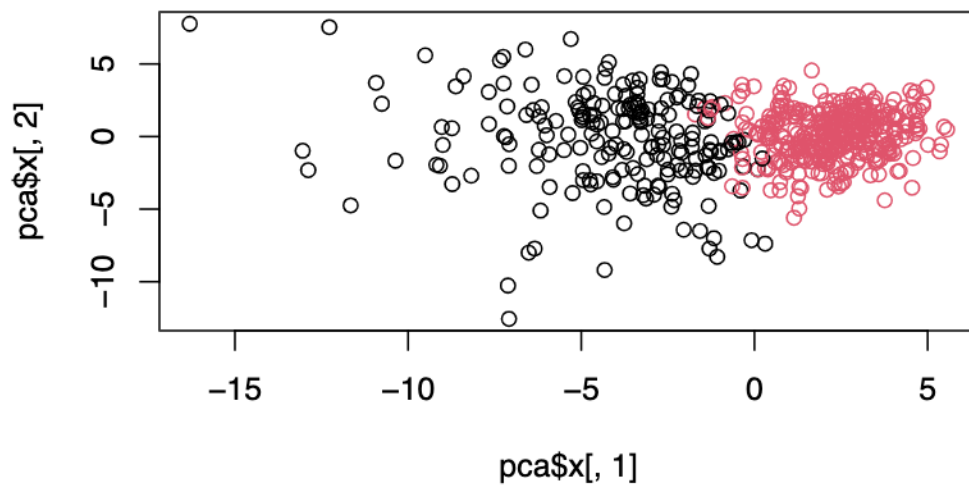
```
diagnosis
  B    M
357 212
```

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

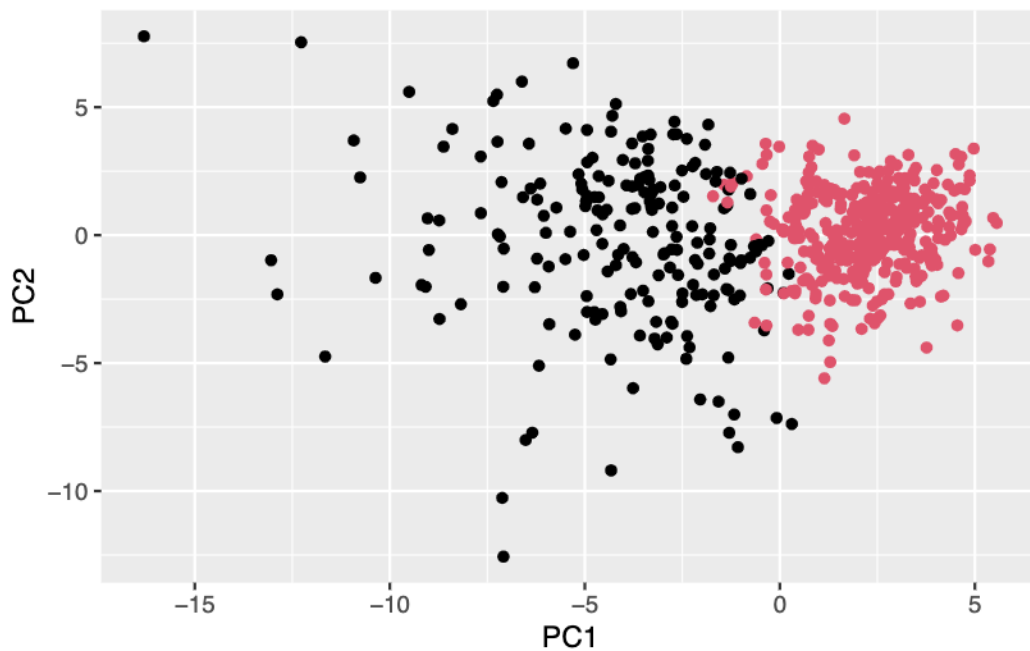
```
      grps
diagnosis 1  2
  B    24 333
  M   179  33
```

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

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



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



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

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

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

Specificity= $TP / (TP + FN)$

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

```
[1] 0.8443396
```

Sensitivity= $TN / (TN + FN)$

333/(333+33)

[1] 0.9098361