

# Class 08

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##Mini Project: Unsupervised Learning with PCA and Clustering

Before we get stuck into project work we will have a quick look at

Read the data from lab 7:

```
url2 <- "https://tinyurl.com/expression-CSV"
rna.data <- read.csv(url2, row.names =1)
head(rna.data)
```

	wt1	wt2	wt3	wt4	wt5	ko1	ko2	ko3	ko4	ko5
gene1	439	458	408	429	420	90	88	86	90	93
gene2	219	200	204	210	187	427	423	434	433	426
gene3	1006	989	1030	1017	973	252	237	238	226	210
gene4	783	792	829	856	760	849	856	835	885	894
gene5	181	249	204	244	225	277	305	272	270	279
gene6	460	502	491	491	493	612	594	577	618	638

Q. How many genes are in this data set?

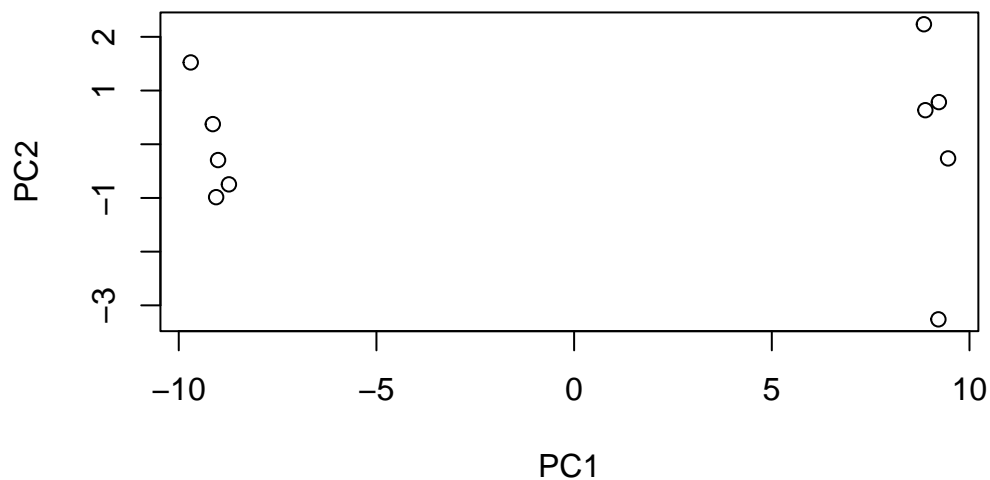
```
nrow(rna.data)
```

```
[1] 100
```

100 rows

##Run PCA

```
pca <- prcomp(t(rna.data), scale = TRUE)
plot(pca$x[,1], pca$x[,2], xlab="PC1", ylab="PC2")
```



```
summary(pca)
```

Importance of components:

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Standard deviation	9.6237	1.5198	1.05787	1.05203	0.88062	0.82545	0.80111
Proportion of Variance	0.9262	0.0231	0.01119	0.01107	0.00775	0.00681	0.00642
Cumulative Proportion	0.9262	0.9493	0.96045	0.97152	0.97928	0.98609	0.99251

	PC8	PC9	PC10
Standard deviation	0.62065	0.60342	3.457e-15
Proportion of Variance	0.00385	0.00364	0.000e+00
Cumulative Proportion	0.99636	1.00000	1.000e+00

```
pca$x
```

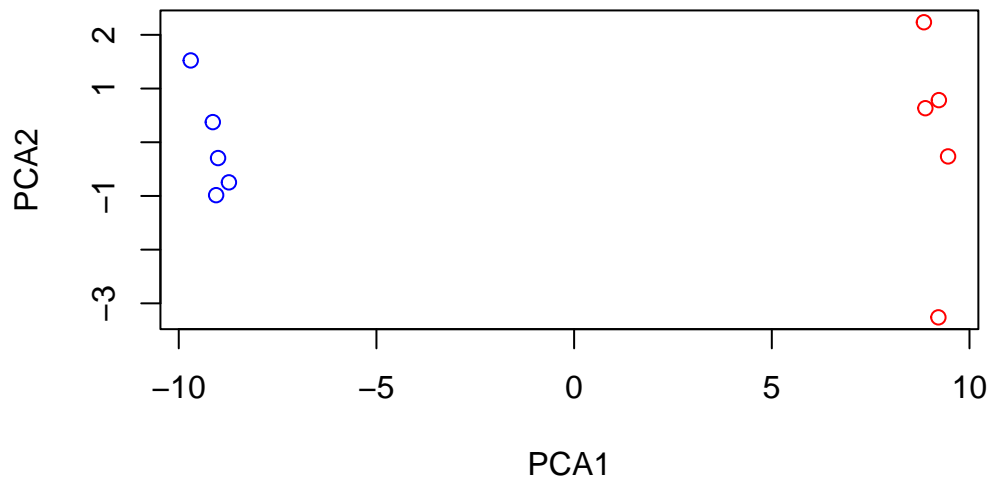
	PC1	PC2	PC3	PC4	PC5	PC6
wt1	-9.697374	1.5233313	-0.2753567	0.7322391	-0.6749398	1.1823860
wt2	-9.138950	0.3748504	1.0867958	-1.9461655	0.7571209	-0.4369228
wt3	-9.054263	-0.9855163	0.4152966	1.4166028	0.5835918	0.6937236
wt4	-8.731483	-0.7468371	0.5875748	0.2268129	-1.5404775	-1.2723618
wt5	-9.006312	-0.2945307	-1.8498101	-0.4303812	0.8666124	-0.2496025

ko1	8.846999	2.2345475	-0.1462750	-1.1544333	-0.6947862	0.7128021
ko2	9.213885	-3.2607503	0.2287292	-0.7658122	-0.4922849	0.9170241
ko3	9.458412	-0.2636283	-1.5778183	0.2433549	0.3654124	-0.5837724
ko4	8.883412	0.6339701	1.5205064	0.7760158	1.2158376	-0.1446094
ko5	9.225673	0.7845635	0.0103574	0.9017667	-0.3860869	-0.8186668
	PC7	PC8	PC9	PC10		
wt1	-0.24446614	1.03519396	0.07010231	3.073930e-15		
wt2	-0.03275370	0.26622249	0.72780448	1.963707e-15		
wt3	-0.03578383	-1.05851494	0.52979799	2.893519e-15		
wt4	-0.52795595	-0.20995085	-0.50325679	2.872702e-15		
wt5	0.83227047	-0.05891489	-0.81258430	1.693090e-15		
ko1	-0.07864392	-0.94652648	-0.24613776	4.052314e-15		
ko2	0.30945771	0.33231138	-0.08786782	3.268219e-15		
ko3	-1.43723425	0.14495188	0.56617746	2.636780e-15		
ko4	-0.35073859	0.30381920	-0.87353886	3.615164e-15		
ko5	1.56584821	0.19140827	0.62950330	3.379241e-15		

```
#We have 5 WT and 5 KO samples
mycols <- c(rep("blue", 5), rep("red", 5))
mycols
```

```
[1] "blue" "blue" "blue" "blue" "blue" "red" "red" "red" "red" "red"
```

```
plot(pca$x[,1], pca$x[,2], xlab="PCA1", ylab="PCA2", col= mycols)
```



I could examine which genes contribute most to this first PC

```
head(sort(abs(pca$rotation[,1]), decreasing = T))
```

gene100	gene66	gene45	gene68	gene98	gene60
0.1038708	0.1038455	0.1038402	0.1038395	0.1038372	0.1038055

#Analysis of Breast Cancer FNA (Fine Needle Aspirations) Data

The data itself comes from the Wisconsin Breast Cancer Diagnostic Data Set.

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.

First, we need to read the data:

```
# Save your input data file into your Project directory
fna.data <- "WisconsinCancer.csv"

# Complete the following code to input the data and store as wisc.df
wisc.df <- read.csv(fna.data, 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		

Note that the first column here `wisc.df$diagnosis` is a pathologist provided expert diagnosis

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

Now I want to make sure I remove that column from my dataset for analysis

```
# We can use -1 here to remove the first column
wisc.data <- wisc.df[,-1]
head(wisc.data)
```

	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean
842302	17.99	10.38	122.80	1001.0	0.11840
842517	20.57	17.77	132.90	1326.0	0.08474
84300903	19.69	21.25	130.00	1203.0	0.10960
84348301	11.42	20.38	77.58	386.1	0.14250
84358402	20.29	14.34	135.10	1297.0	0.10030
843786	12.45	15.70	82.57	477.1	0.12780
	compactness_mean	concavity_mean	concave.points_mean	symmetry_mean	
842302	0.27760	0.3001		0.14710	0.2419
842517	0.07864	0.0869		0.07017	0.1812
84300903	0.15990	0.1974		0.12790	0.2069
84348301	0.28390	0.2414		0.10520	0.2597
84358402	0.13280	0.1980		0.10430	0.1809
843786	0.17000	0.1578		0.08089	0.2087
	fractal_dimension_mean	radius_se	texture_se	perimeter_se	area_se
842302		0.07871	1.0950	0.9053	8.589 153.40
842517		0.05667	0.5435	0.7339	3.398 74.08
84300903		0.05999	0.7456	0.7869	4.585 94.03

84348301	0.09744	0.4956	1.1560	3.445	27.23
84358402	0.05883	0.7572	0.7813	5.438	94.44
843786	0.07613	0.3345	0.8902	2.217	27.19
	smoothness_se	compactness_se	concavity_se	concave.points_se	
842302	0.006399	0.04904	0.05373	0.01587	
842517	0.005225	0.01308	0.01860	0.01340	
84300903	0.006150	0.04006	0.03832	0.02058	
84348301	0.009110	0.07458	0.05661	0.01867	
84358402	0.011490	0.02461	0.05688	0.01885	
843786	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				

Q1. How many observations are in this dataset?

```
length(wisc.data)
```

```
[1] 30
```

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

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

```
  B    M  
357 212
```

212 have malignant diagnosis

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

```
length(grep("__mean", colnames(wisc.data)))
```

```
[1] 10
```

##Principal Component Analysis

Here we will use `'prcomp()'` on the `'wisc.data'` object - the one without the diagnosis column.

First we have to decide whether to use the `'scale=TRUE'` argument when we run `'prcomp()'`.

We can look at the means and sd of each column. If they are similar then we are all good to go. If not we should use `'scale = TRUE'`.

```
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

They are very different so we should scale=TRUE.

```
wisc.pr<- prcomp(wisc.data, scale=T)
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)?

44.27%

Q5. How many principal components (PCs) are required to describe at least 70% of the original variance in the data? 3 PCs capture 72.6% of the original variance.

Q6. How many principal components (PCs) are required to describe at least 90% of the original variance in the data? 7 PCs capture 91.01% of the original variance

##Plotting the PCA results

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

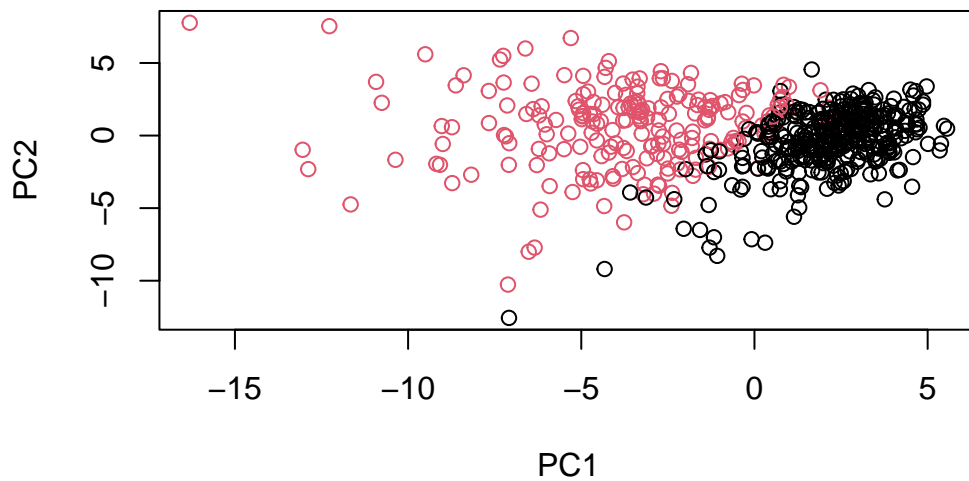
Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why? It is extremely difficult to understand, because every point of data is clustered together and you can't see what you are interpreting.

```
attributes(wisc.pr)
```

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

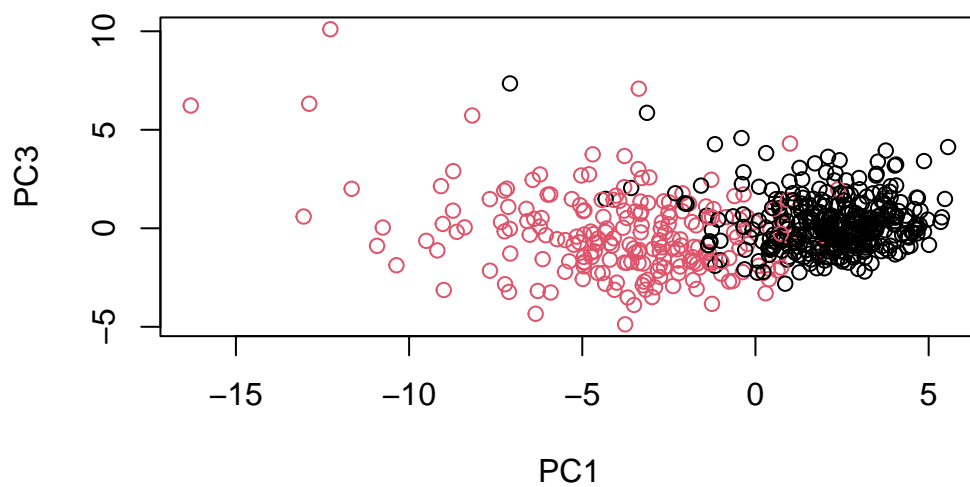
```
$class  
[1] "prcomp"
```

```
#Scatter plot observations by components 1 and 2  
plot(wisc.pr$x[,1], wisc.pr$x[,2], col=diagnosis, xlab="PC1", ylab= "PC2")
```



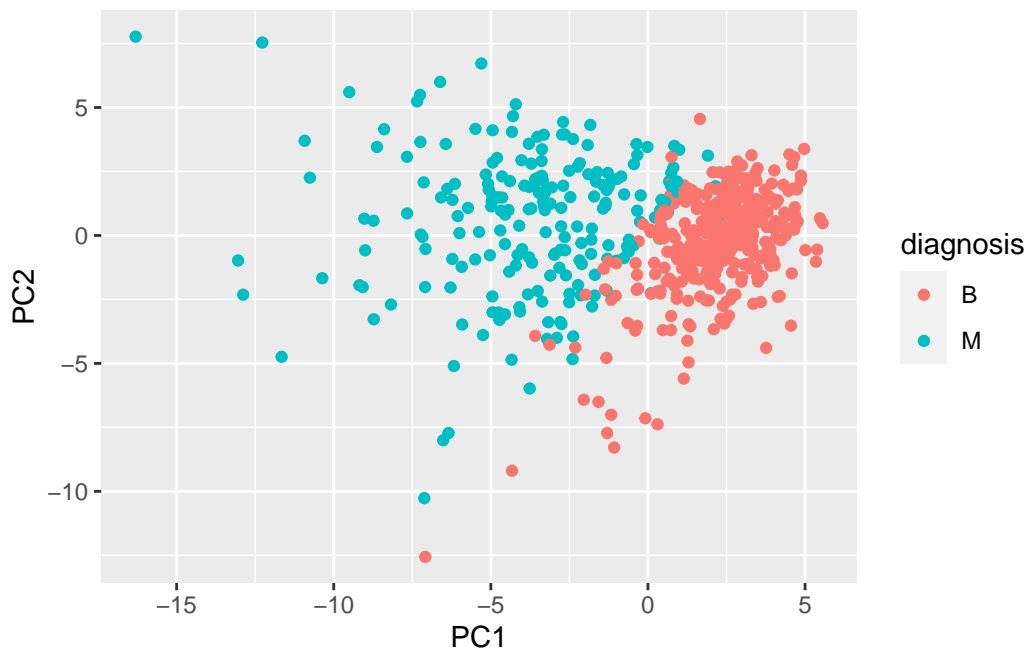
Q8. Generate a similar plot for principal components 1 and 3. What do you notice about these plots?

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



These plots are much easier to interpret and read, and there is much more distinct clustering in these plots than in the `dist.plot` function.

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



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",1]
```

```
[1] -0.2608538
```

-0.2608538 is the component of the loading vector.

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

```
tbl <- summary(wisc.pr)
which(tbl$importance[3,]>0.8)[1]
```

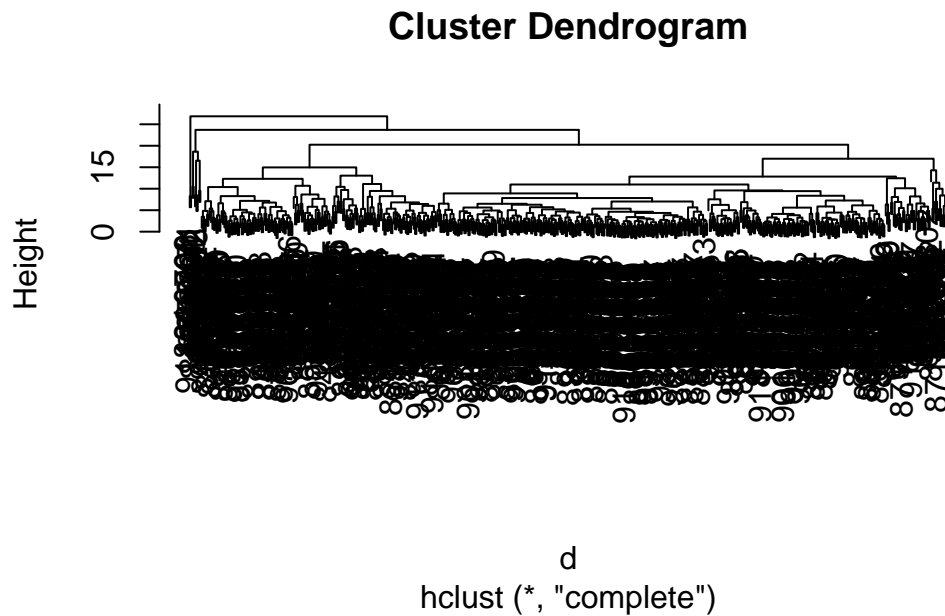
```
PC5
5
```

5 PCs are needed to capture 80% of the variance of the data.

#Hierarchical Clustering

The main function of the Hierarchical clustering is called 'hclust()', it takes a distance matrix as input.

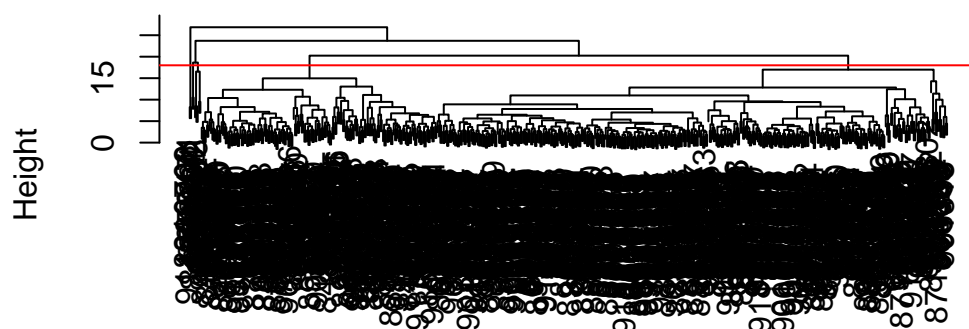
```
d <- dist(scale(wisc.data))
wisc.hclust <- hclust(d)
plot(wisc.hclust)
```



Q11. Using the plot() and abline() functions, what is the height at which the clustering model has 4 clusters?

```
plot(wisc.hclust)
abline(h=18, col="red")
```

## Cluster Dendrogram



d  
hclust (\*, "complete")

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

grps

1	2	3	4	5
177	5	383	2	2

grps

842302	842517	84300903	84348301	84358402	843786	844359	84458202
1	1	1	2	1	1	1	1
844981	84501001	845636	84610002	846226	846381	84667401	84799002
1	2	3	1	1	3	1	1
848406	84862001	849014	8510426	8510653	8510824	8511133	851509
3	1	1	3	3	3	1	1
852552	852631	852763	852781	852973	853201	853401	853612
1	1	1	1	1	3	1	1
85382601	854002	854039	854253	854268	854941	855133	855138
1	1	1	1	1	3	3	1
855167	855563	855625	856106	85638502	857010	85713702	85715

3	1	1	1	1	1	3	1
857155	857156	857343	857373	857374	857392	857438	85759902
3	3	3	3	3	1	3	3
857637	857793	857810	858477	858970	858981	858986	859196
1	1	3	3	3	3	1	3
85922302	859283	859464	859465	859471	859487	859575	859711
1	1	3	3	4	3	1	3
859717	859983	8610175	8610404	8610629	8610637	8610862	8610908
1	1	3	3	3	1	2	3
861103	8611161	8611555	8611792	8612080	8612399	86135501	86135502
3	1	1	1	3	1	3	1
861597	861598	861648	861799	861853	862009	862028	86208
3	1	3	3	3	3	1	1
86211	862261	862485	862548	862717	862722	862965	862980
3	3	3	3	3	3	3	3
862989	863030	863031	863270	86355	864018	864033	86408
3	1	1	3	1	3	3	3
86409	864292	864496	864685	864726	864729	864877	865128
3	3	3	3	3	1	1	3
865137	86517	865423	865432	865468	86561	866083	866203
3	1	2	3	3	3	1	3
866458	866674	866714	8670	86730502	867387	867739	868202
1	1	3	1	1	3	1	3
868223	868682	868826	868871	868999	869104	869218	869224
3	3	1	3	3	3	3	3
869254	869476	869691	86973701	86973702	869931	871001501	871001502
3	3	1	3	3	3	3	3
8710441	87106	8711002	8711003	8711202	8711216	871122	871149
4	3	3	3	1	3	3	3
8711561	8711803	871201	8712064	8712289	8712291	87127	8712729
3	1	1	3	1	3	3	3
8712766	8712853	87139402	87163	87164	871641	871642	872113
1	3	3	3	1	3	3	3
872608	87281702	873357	873586	873592	873593	873701	873843
3	1	3	3	1	1	1	3
873885	874158	874217	874373	874662	874839	874858	875093
1	3	3	3	3	3	2	3
875099	875263	87556202	875878	875938	877159	877486	877500
3	1	1	3	1	3	1	1
877501	877989	878796	87880	87930	879523	879804	879830
3	3	1	1	3	3	3	3
8810158	8810436	881046502	8810528	8810703	881094802	8810955	8810987
1	3	1	3	5	3	1	1



8811523	8811779	8811842	88119002	8812816	8812818	8812844	8812877
3	3	1	1	3	3	3	1
8813129	88143502	88147101	88147102	88147202	881861	881972	88199202
3	3	3	3	3	1	1	3
88203002	88206102	882488	88249602	88299702	883263	883270	88330202
3	1	3	3	1	1	3	1
88350402	883539	883852	88411702	884180	884437	884448	884626
3	3	3	3	1	3	3	3
88466802	884689	884948	88518501	885429	8860702	886226	886452
3	3	1	3	1	3	1	3
88649001	886776	887181	88725602	887549	888264	888570	889403
1	1	1	1	1	3	1	3
889719	88995002	8910251	8910499	8910506	8910720	8910721	8910748
1	1	3	3	3	3	3	3
8910988	8910996	8911163	8911164	8911230	8911670	8911800	8911834
1	3	3	3	3	3	3	3
8912049	8912055	89122	8912280	8912284	8912521	8912909	8913
1	3	1	1	3	3	3	3
8913049	89143601	89143602	8915	891670	891703	891716	891923
3	3	3	3	3	3	3	3
891936	892189	892214	892399	892438	892604	89263202	892657
3	3	3	3	1	3	1	3
89296	893061	89344	89346	893526	893548	893783	89382601
3	3	3	3	3	3	3	3
89382602	893988	894047	894089	894090	894326	894329	894335
3	3	3	3	3	1	3	3
894604	894618	894855	895100	89511501	89511502	89524	895299
3	3	3	1	3	3	3	3
8953902	895633	896839	896864	897132	897137	897374	89742801
1	1	1	1	3	3	3	1
897604	897630	897880	89812	89813	898143	89827	898431
3	1	3	1	3	3	3	1
89864002	898677	898678	89869	898690	899147	899187	899667
3	3	3	3	3	3	3	1
899987	9010018	901011	9010258	9010259	901028	9010333	901034301
1	1	3	3	3	3	3	3
901034302	901041	9010598	9010872	9010877	901088	9011494	9011495
3	3	3	3	3	1	1	3
9011971	9012000	9012315	9012568	9012795	901288	9013005	901303
1	1	1	3	1	1	3	3
901315	9013579	9013594	9013838	901549	901836	90250	90251
3	3	3	1	3	3	3	3
902727	90291	902975	902976	903011	90312	90317302	903483

3	3	3	3	3	1	3	3
903507	903516	903554	903811	90401601	90401602	904302	904357
1	1	3	3	3	3	3	3
90439701	904647	904689	9047	904969	904971	905189	905190
1	3	3	3	3	3	3	3
90524101	905501	905502	905520	905539	905557	905680	905686
1	3	3	3	3	3	3	3
905978	90602302	906024	906290	906539	906564	906616	906878
3	1	3	3	3	1	3	3
907145	907367	907409	90745	90769601	90769602	907914	907915
3	3	3	3	3	3	1	3
908194	908445	908469	908489	908916	909220	909231	909410
1	1	3	1	3	3	3	3
909411	909445	90944601	909777	9110127	9110720	9110732	9110944
3	3	3	3	3	3	1	3
911150	911157302	9111596	9111805	9111843	911201	911202	9112085
3	1	3	1	3	3	3	3
9112366	9112367	9112594	9112712	911296201	911296202	9113156	911320501
3	3	3	3	1	5	3	3
911320502	9113239	9113455	9113514	9113538	911366	9113778	9113816
3	3	3	3	1	1	3	3
911384	9113846	911391	911408	911654	911673	911685	911916
3	3	3	3	3	3	3	1
912193	91227	912519	912558	912600	913063	913102	913505
3	3	3	3	3	3	3	1
913512	913535	91376701	91376702	914062	914101	914102	914333
3	3	3	3	1	3	3	3
914366	914580	914769	91485	914862	91504	91505	915143
1	3	1	1	3	1	3	1
915186	915276	91544001	91544002	915452	915460	91550	915664
3	3	3	3	3	1	3	3
915691	915940	91594602	916221	916799	916838	917062	917080
1	3	3	3	1	1	3	3
917092	91762702	91789	917896	917897	91805	91813701	91813702
3	1	3	3	3	3	1	3
918192	918465	91858	91903901	91903902	91930402	919537	919555
3	3	3	3	3	1	3	1
91979701	919812	921092	921362	921385	921386	921644	922296
3	1	3	3	3	1	3	3
922297	922576	922577	922840	923169	923465	923748	923780
3	3	3	3	3	3	3	3
924084	924342	924632	924934	924964	925236	925277	925291
3	3	3	3	3	3	3	3

925292	925311	925622	926125	926424	926682	926954	927241
3	3	1	1	1	1	3	1
92751							
3							

The height at which the model has 4 clusters is at height 18.

Q12. Can you find a better cluster vs diagnoses match by cutting into a different number of clusters between 2 and 10?

```
better <- cutree(wisc.hclust, h=9)
table(better, diagnosis)
```

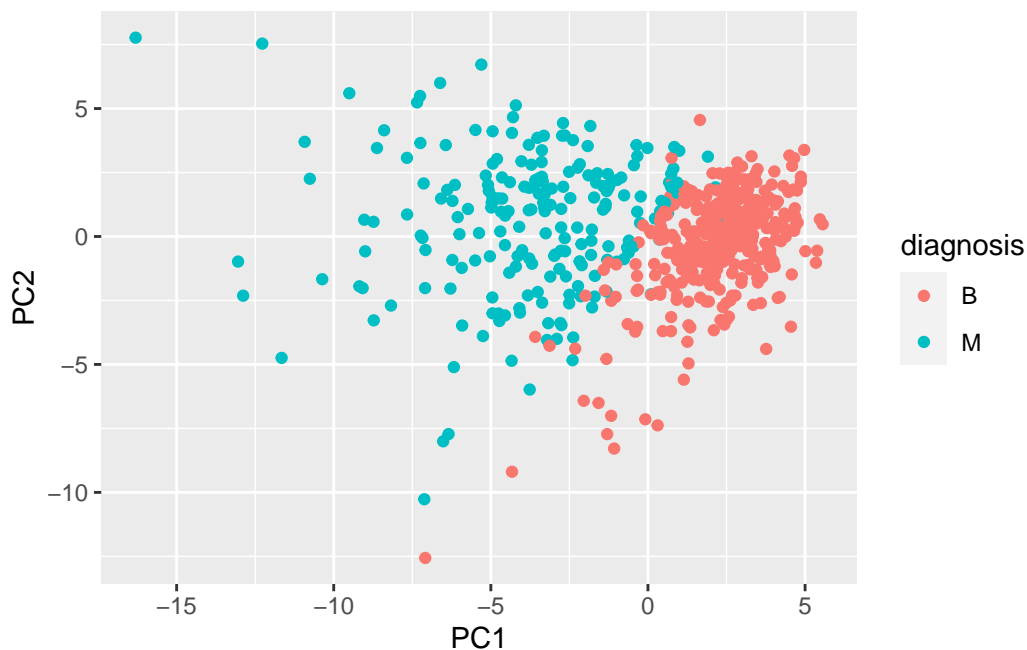
	diagnosis	
better	B	M
1	0	24
2	0	45
3	0	3
4	0	11
5	12	46
6	9	15
7	0	2
8	197	6
9	0	5
10	2	15
11	89	3
12	19	0
13	11	0
14	1	0
15	3	0
16	0	12
17	0	1
18	0	6
19	7	0
20	0	1
21	1	0
22	0	6
23	4	0
24	0	2
25	0	1
26	0	8
27	2	0

Yes, if I cut into 9 I find a better match.

Q13. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning. ward.D2 clusters based on the sum of squared differences within all clusters, versus single and complete cluster based on the minimum/maximum distances. Average clusters based on average data. Hence, if we do single/complete, we may not be grouping our data by its actual similarity. Average will not give any meaningful data.

Come back here later to see how our cluster groups correspond to M or B groups.

```
ggplot(pc) +  
  aes(PC1, PC2, color = diagnosis) +  
  geom_point()
```



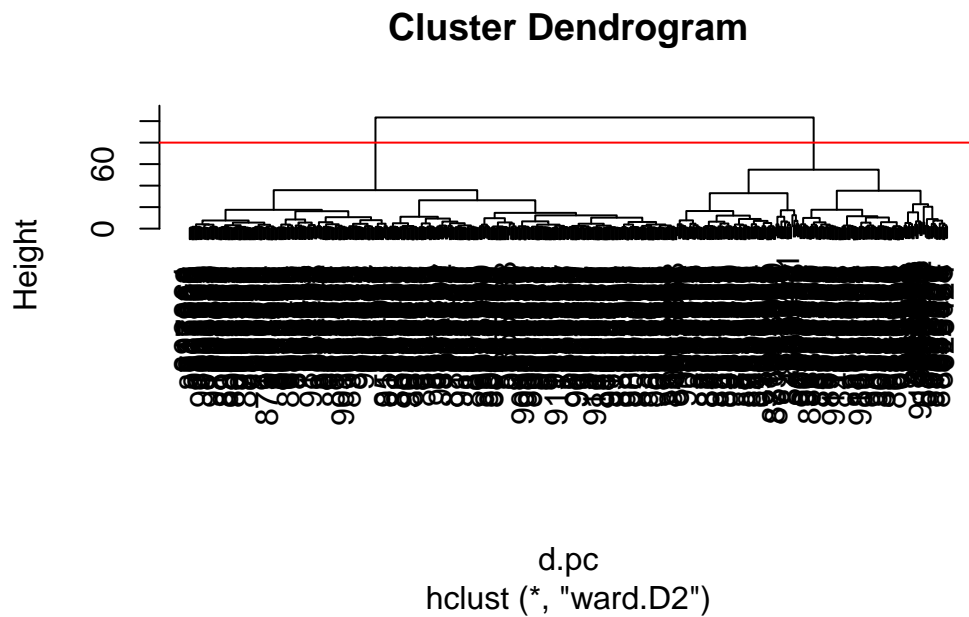
#### ##5. Combining methods

Here we will perform clustering on our PCA results rather than the original data.

In other words we will cluster using 'wisc.pr\$x' - our new better variables or PCs. We can choose as many or as few PCs to use as we'd like. It's your call!

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

```
plot(wisc.pr.hclust)
abline(h=80, col="red")
```



```
grps <- cutree(wisc.pr.hclust, h=80)
table(grps)
```

```
grps
  1  2
203 366
```

We can use 'table()' function to make a cross-table as well as just a count table.

```
table(diagnosis)
```

```
diagnosis
  B  M
357 212
```

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

```

      diagnosis
grps   B    M
1    24 179
2   333   33

```

From these cross-table results, it is indicated that our cluster 1 mostly captures cancer (M) and our cluster 2 mostly captures healthy (B) samples/ individuals.

Q15. How well does the newly created model with four clusters separate out the two diagnoses?

It does very well, and concisely groups the 4 clusters.

Q16. How well do the k-means and 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.

```

wisc.hclust.clusters <- cutree(wisc.pr.hclust, h=35.5)
table(wisc.hclust.clusters, diagnosis)

```

```

      diagnosis
wisc.hclust.clusters  B    M
1         0 111
2        24   68
3       184   32
4       149    1

```

```

wisc.km <- kmeans(wisc.data, centers= 2, nstart= 20)
table(wisc.km$cluster, diagnosis)

```

```

      diagnosis
      B    M
1  356   82
2    1  130

```

Q17. Which of your analysis procedures resulted in a clustering model with the best specificity? How about sensitivity?

```

111/212 #hclust sensitivity

```

```

[1] 0.5235849

```

```
130/212 #kmeans sensitivity
```

```
[1] 0.6132075
```

```
149/357 #hclust specificity
```

```
[1] 0.4173669
```

```
356/357 #kmeans specificity
```

```
[1] 0.9971989
```

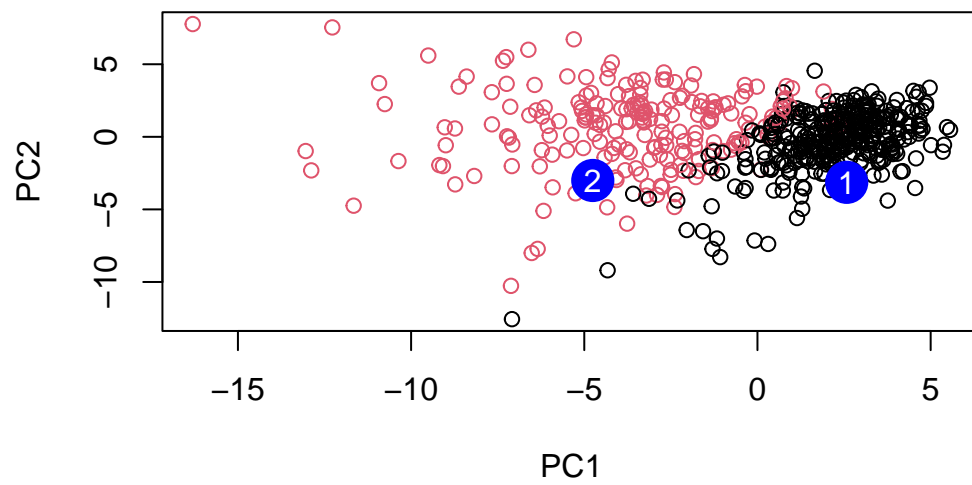
The best sensitivity and specificity was the wisc.kmean.

Q18. Which of these new patients should we prioritize for follow up based on your results?

```
#url <- "new_samples.csv"
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=diagnosis)
points(npc[,1], npc[,2], col="blue", pch=16, cex=3)
text(npc[,1], npc[,2], c(1,2), col="white")
```



Patient 2