

Class 8: PCA Mini Project

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It is important to consider scaling your data before analysis such as PCA.

For example:

```
head(mtcars)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	1

```
colMeans(mtcars)
```

mpg	cyl	disp	hp	drat	wt	qsec
20.090625	6.187500	230.721875	146.687500	3.596563	3.217250	17.848750
vs	am	gear	carb			
0.437500	0.406250	3.687500	2.812500			

```
apply(mtcars,2,sd)
```

mpg	cyl	disp	hp	drat	wt
6.0269481	1.7859216	123.9386938	68.5628685	0.5346787	0.9784574
qsec	vs	am	gear	carb	
1.7869432	0.5040161	0.4989909	0.7378041	1.6152000	

```
x <- scale(mtcars)
head(x)
```

	mpg	cyl	disp	hp	drat
Mazda RX4	0.1508848	-0.1049878	-0.57061982	-0.5350928	0.5675137
Mazda RX4 Wag	0.1508848	-0.1049878	-0.57061982	-0.5350928	0.5675137
Datsun 710	0.4495434	-1.2248578	-0.99018209	-0.7830405	0.4739996
Hornet 4 Drive	0.2172534	-0.1049878	0.22009369	-0.5350928	-0.9661175
Hornet Sportabout	-0.2307345	1.0148821	1.04308123	0.4129422	-0.8351978
Valiant	-0.3302874	-0.1049878	-0.04616698	-0.6080186	-1.5646078

	wt	qsec	vs	am	gear
Mazda RX4	-0.610399567	-0.7771651	-0.8680278	1.1899014	0.4235542
Mazda RX4 Wag	-0.349785269	-0.4637808	-0.8680278	1.1899014	0.4235542
Datsun 710	-0.917004624	0.4260068	1.1160357	1.1899014	0.4235542
Hornet 4 Drive	-0.002299538	0.8904872	1.1160357	-0.8141431	-0.9318192
Hornet Sportabout	0.227654255	-0.4637808	-0.8680278	-0.8141431	-0.9318192
Valiant	0.248094592	1.3269868	1.1160357	-0.8141431	-0.9318192

	carb
Mazda RX4	0.7352031
Mazda RX4 Wag	0.7352031
Datsun 710	-1.1221521
Hornet 4 Drive	-1.1221521
Hornet Sportabout	-0.5030337
Valiant	-1.1221521

```
round(colMeans(x),2)
```

mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
0	0	0	0	0	0	0	0	0	0	0

```
apply(x,2,sd)
```

mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
1	1	1	1	1	1	1	1	1	1	1

Load 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	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

```
prcomp
```

```
function (x, ...)
UseMethod("prcomp")
<bytecode: 0x120c95188>
<environment: namespace:stats>
```

Remove this first `diagnosis` column from the data set as I don't want to pass this to PCA etc. It is essentially the expert "answer" that we will compare our analysis results to.

```
wisc.data <- wisc.df[,-1]
dim(wisc.data)
```

```
[1] 569 30
```

```
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		

```
diagnosis <- wisc.df[,1]
table(diagnosis)
```

```
diagnosis
  B   M
357 212
```

Q1. How many observations are in this dataset?

569 observations

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

212 Malignant

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

10 variables in the data are suffixed with __mean.

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

```
[1] 10
```

##Principal Component Analysis

```
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=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					

See what is in our PCA result object:

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

```
$names
```

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

```
$class
```

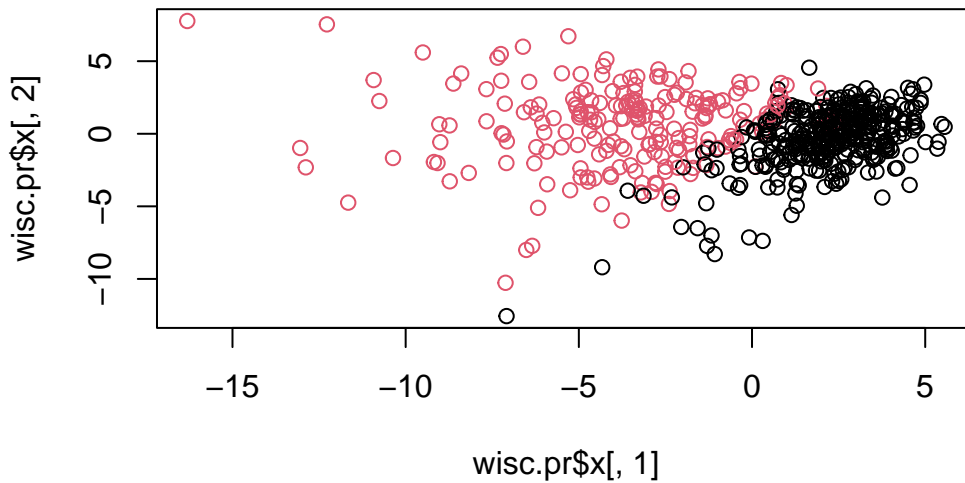
```
[1] "prcomp"
```

```
head(wisc.pr$x)
```


	PC1	PC2	PC3	PC4	PC5	PC6
842302	-9.184755	-1.946870	-1.1221788	3.6305364	1.1940595	1.41018364
842517	-2.385703	3.764859	-0.5288274	1.1172808	-0.6212284	0.02863116
84300903	-5.728855	1.074229	-0.5512625	0.9112808	0.1769302	0.54097615
84348301	-7.116691	-10.266556	-3.2299475	0.1524129	2.9582754	3.05073750
84358402	-3.931842	1.946359	1.3885450	2.9380542	-0.5462667	-1.22541641
843786	-2.378155	-3.946456	-2.9322967	0.9402096	1.0551135	-0.45064213
	PC7	PC8	PC9	PC10	PC11	PC12
842302	2.15747152	0.39805698	-0.15698023	-0.8766305	-0.2627243	-0.8582593
842517	0.01334635	-0.24077660	-0.71127897	1.1060218	-0.8124048	0.1577838
84300903	-0.66757908	-0.09728813	0.02404449	0.4538760	0.6050715	0.1242777
84348301	1.42865363	-1.05863376	-1.40420412	-1.1159933	1.1505012	1.0104267
84358402	-0.93538950	-0.63581661	-0.26357355	0.3773724	-0.6507870	-0.1104183
843786	0.49001396	0.16529843	-0.13335576	-0.5299649	-0.1096698	0.0813699
	PC13	PC14	PC15	PC16	PC17	
842302	0.10329677	-0.690196797	0.601264078	0.74446075	-0.26523740	
842517	-0.94269981	-0.652900844	-0.008966977	-0.64823831	-0.01719707	
84300903	-0.41026561	0.016665095	-0.482994760	0.32482472	0.19075064	
84348301	-0.93245070	-0.486988399	0.168699395	0.05132509	0.48220960	
84358402	0.38760691	-0.538706543	-0.310046684	-0.15247165	0.13302526	
843786	-0.02625135	0.003133944	-0.178447576	-0.01270566	0.19671335	
	PC18	PC19	PC20	PC21	PC22	
842302	-0.54907956	0.1336499	0.34526111	0.096430045	-0.06878939	
842517	0.31801756	-0.2473470	-0.11403274	-0.077259494	0.09449530	
84300903	-0.08789759	-0.3922812	-0.20435242	0.310793246	0.06025601	
84348301	-0.03584323	-0.0267241	-0.46432511	0.433811661	0.20308706	
84358402	-0.01869779	0.4610302	0.06543782	-0.116442469	0.01763433	
843786	-0.29727706	-0.1297265	-0.07117453	-0.002400178	0.10108043	
	PC23	PC24	PC25	PC26	PC27	
842302	0.08444429	0.175102213	0.150887294	-0.201326305	-0.25236294	
842517	-0.21752666	-0.011280193	0.170360355	-0.041092627	0.18111081	
84300903	-0.07422581	-0.102671419	-0.171007656	0.004731249	0.04952586	
84348301	-0.12399554	-0.153294780	-0.077427574	-0.274982822	0.18330078	
84358402	0.13933105	0.005327110	-0.003059371	0.039219780	0.03213957	
843786	0.03344819	-0.002837749	-0.122282765	-0.030272333	-0.08438081	
	PC28	PC29	PC30			
842302	-0.0338846387	0.045607590	0.0471277407			
842517	0.0325955021	-0.005682424	0.0018662342			
84300903	0.0469844833	0.003143131	-0.0007498749			
84348301	0.0424469831	-0.069233868	0.0199198881			
84358402	-0.0347556386	0.005033481	-0.0211951203			
843786	0.0007296587	-0.019703996	-0.0034564331			

Main “PC score plot”, “PC1 vs PC2 plot”:

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



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

0.4427

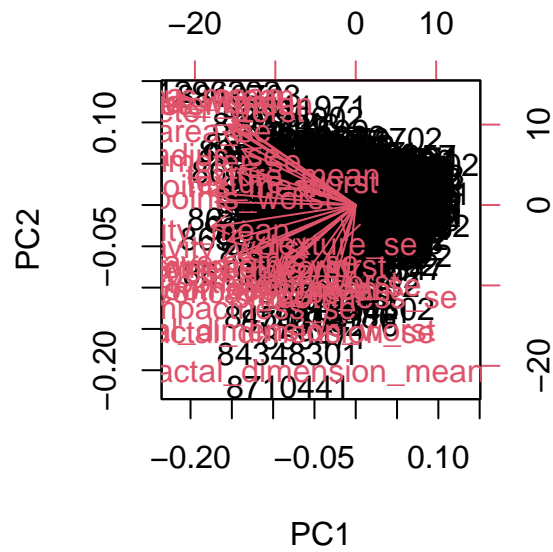
Q5. How many principal components (PCs) are required to describe at least 70% of the original variance in the data?

3 PCs to describe at least 70% of the original variance in the original variance in the data.

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

7 PCs to describe at least 70% of the original variance in the original variance in the data.

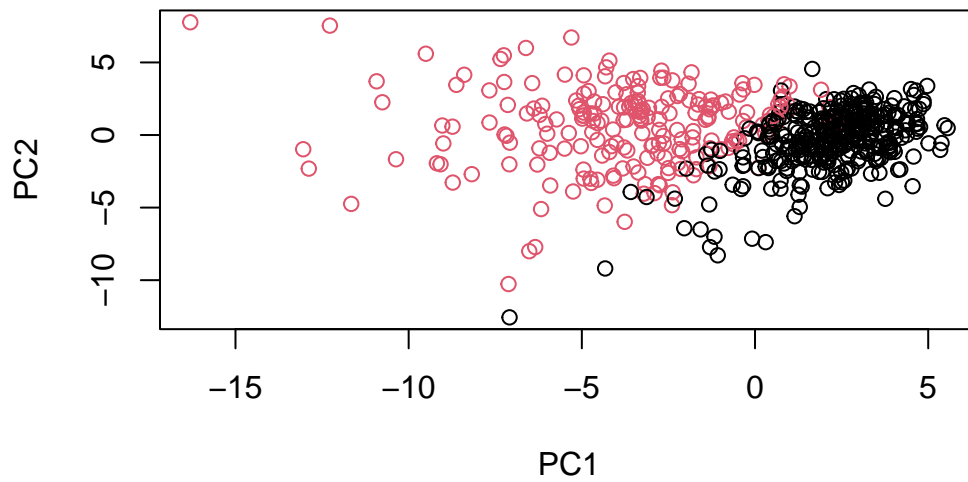
```
biplot(wisc.pr)
```



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

The plot is too crowded,very difficult to understand.

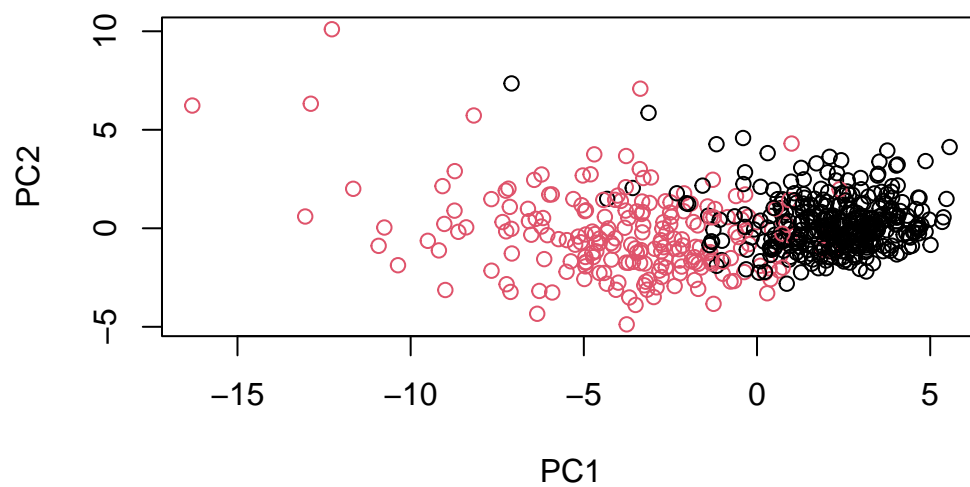
```
plot( wisc.pr$x[,1],wisc.pr$x[,2] , col = as.factor(diagnosis) ,
      xlab = "PC1", ylab = "PC2")
```



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

The clusters are less distinctive compared to PC1 vs PC2 plot.

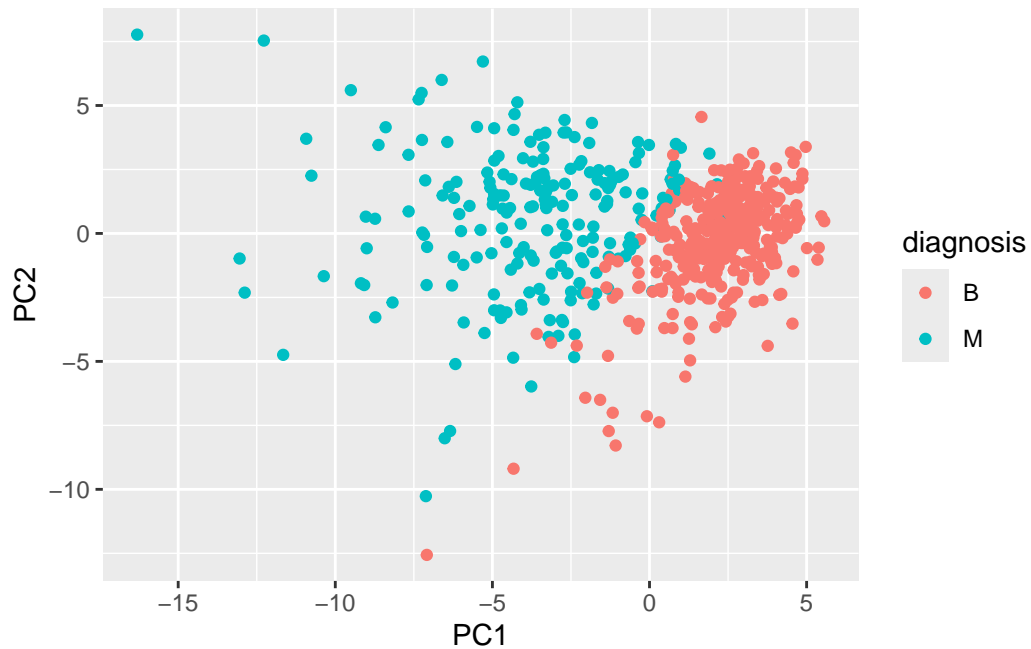
```
plot( wisc.pr$x[,1],wisc.pr$x[,3] , col = as.factor(diagnosis) ,  
      xlab = "PC1", ylab = "PC2")
```



```
# 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()
```

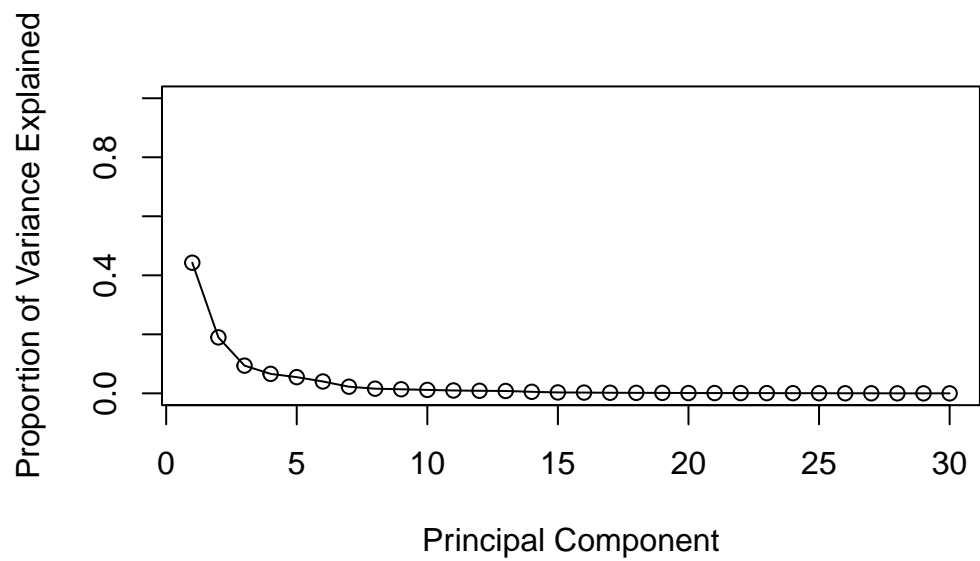


```
# Calculate variance of each component
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

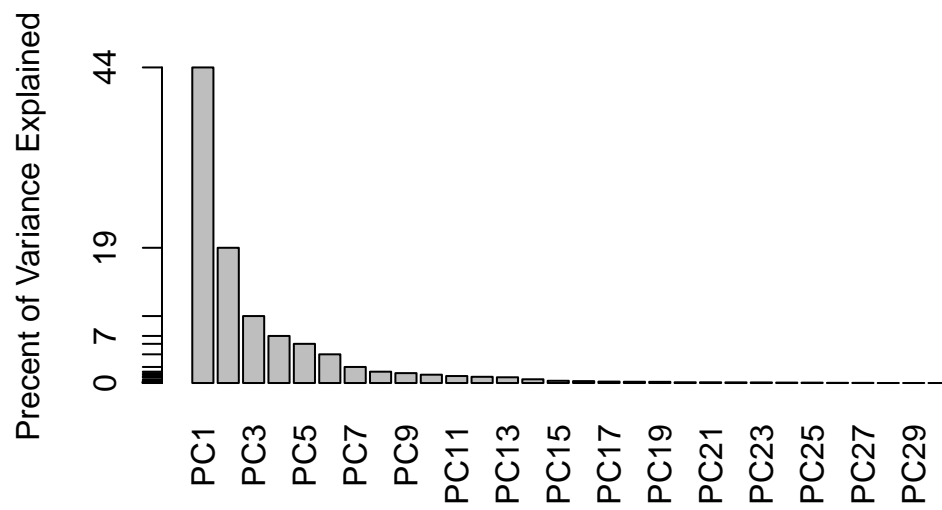
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
# 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")
```



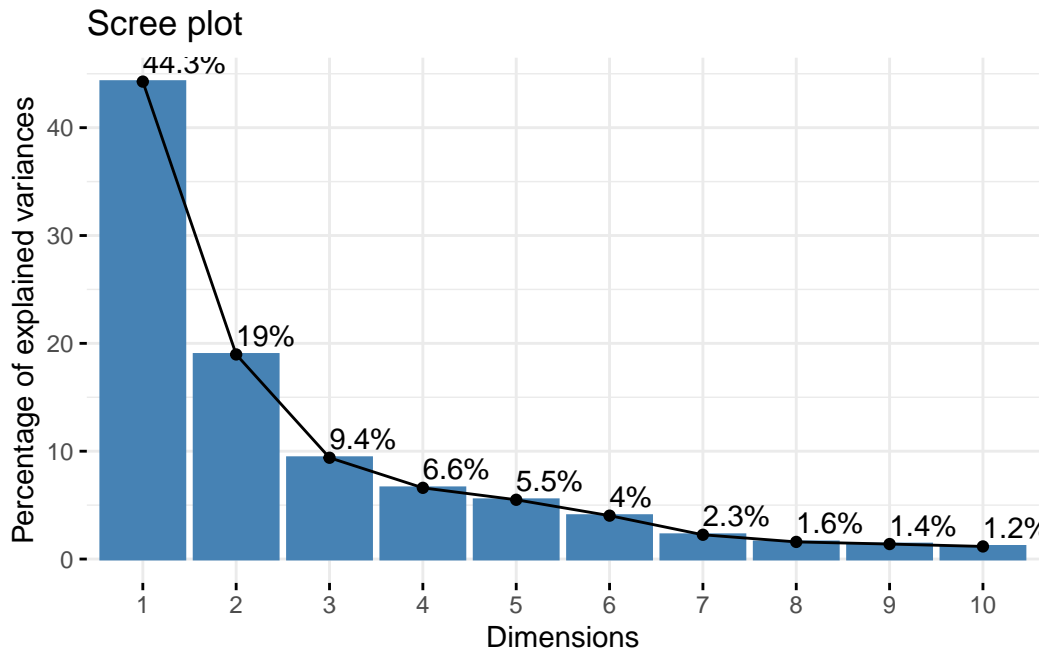
```
# Alternative scree plot of the same data, note data driven y-axis
barplot(pve, ylab = "Precent of Variance Explained",
        names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```



```
## ggplot based graph
#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`?

`concave.points_mean`: -0.26085376

```
wisc.pr$rotation[,1]
```

<code>radius_mean</code>	<code>texture_mean</code>	<code>perimeter_mean</code>
-0.21890244	-0.10372458	-0.22753729
<code>area_mean</code>	<code>smoothness_mean</code>	<code>compactness_mean</code>
-0.22099499	-0.14258969	-0.23928535
<code>concavity_mean</code>	<code>concave.points_mean</code>	<code>symmetry_mean</code>
-0.25840048	-0.26085376	-0.13816696
<code>fractal_dimension_mean</code>	<code>radius_se</code>	<code>texture_se</code>
-0.06436335	-0.20597878	-0.01742803
<code>perimeter_se</code>	<code>area_se</code>	<code>smoothness_se</code>
-0.21132592	-0.20286964	-0.01453145
<code>compactness_se</code>	<code>concavity_se</code>	<code>concave.points_se</code>
-0.17039345	-0.15358979	-0.18341740
<code>symmetry_se</code>	<code>fractal_dimension_se</code>	<code>radius_worst</code>
-0.04249842	-0.10256832	-0.22799663
<code>texture_worst</code>	<code>perimeter_worst</code>	<code>area_worst</code>
-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

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

5 PCs

Hierarchical clustering

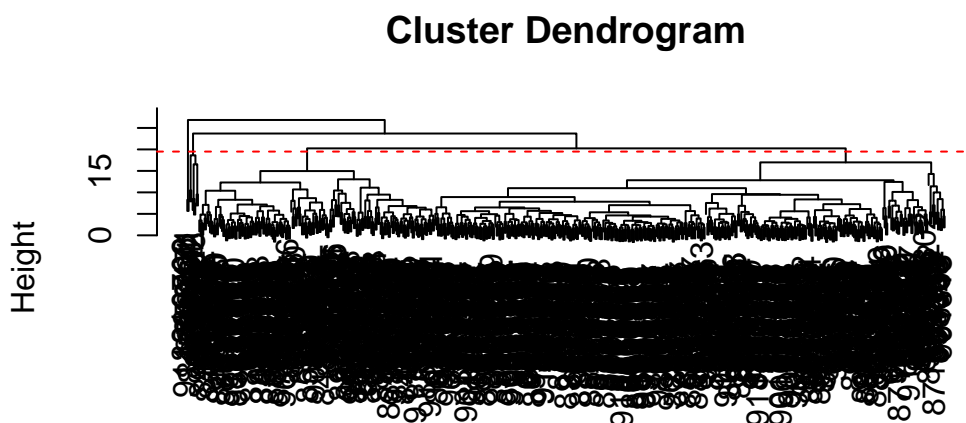
```
# Scale the wisc.data data using the "scale()" function
data.scaled <- scale(wisc.data)
```

```
data.dist <- dist(data.scaled)
```

```
wisc.hclust <- hclust(data.dist, method="complete")
```

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

```
plot(wisc.hclust)
abline(h=19.5, col="red", lty=2)
```



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

```
wisc.hclust.clusters <- cutree(wisc.hclust,k=4)
wisc.hclust.clusters <- cutree(wisc.hclust,k=2)
```

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

	diagnosis	
wisc.hclust.clusters	B	M
1	357	210
2	0	2

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

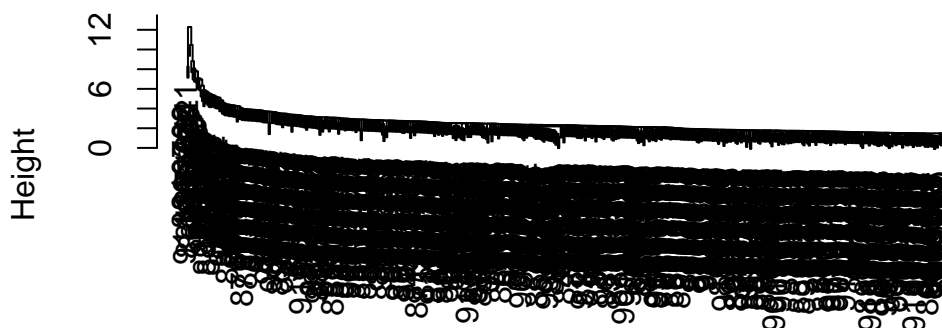
2 clusters

Q13. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning.

ward.D2 gives a clean dendrogram and the table() of ward.D2 has a reasonable distribution of M and B, where one group is composed mainly by M and the other group mainly by B.

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

Cluster Dendrogram



```
wisc.hclust.clusters.single <- cutree(wisc.hclust.single,k=2)
table(wisc.hclust.clusters.single, diagnosis)
```

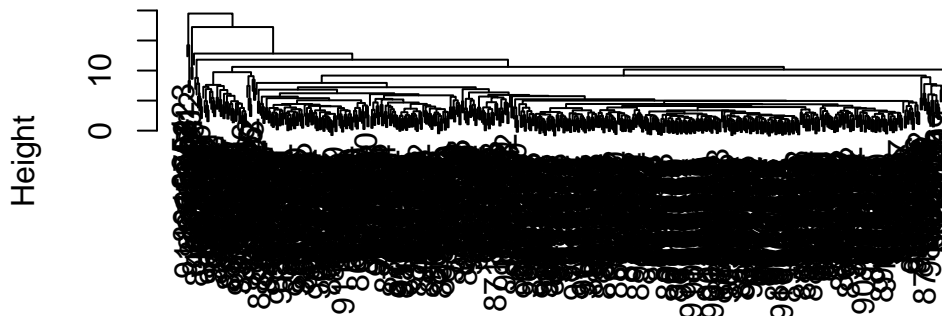
```

              diagnosis
wisc.hclust.clusters.single  B  M
1 357 210
2   0   2

```

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

Cluster Dendrogram



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

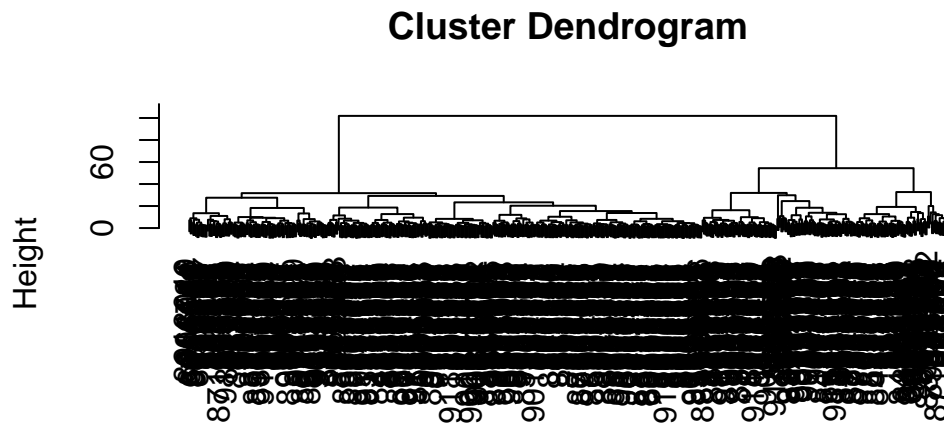
```
wisc.hclust.clusters.average <- cutree(wisc.hclust.average,k=2)
table(wisc.hclust.clusters.average, diagnosis)
```

```

              diagnosis
wisc.hclust.clusters.average  B  M
1 357 209
2   0   3

```

```
wisc.hclust.wardd2<- hclust(data.dist, method="ward.D2")
plot(wisc.hclust.wardd2)
```



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

```
wisc.hclust.clusters.wardd2 <- cutree(wisc.hclust.wardd2,k=2)
table(wisc.hclust.clusters.wardd2, diagnosis)
```

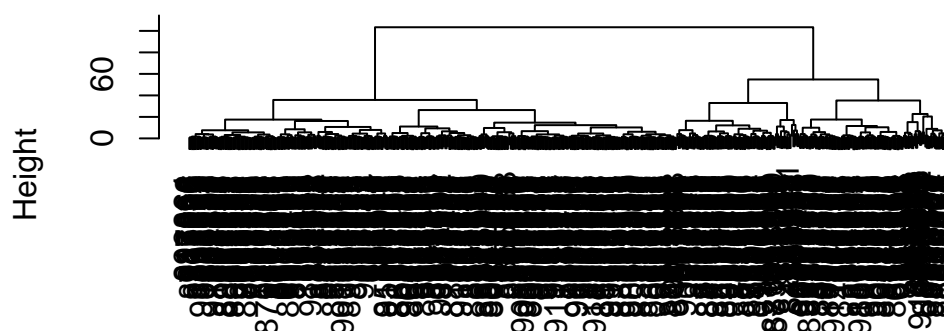
	diagnosis	
wisc.hclust.clusters.wardd2	B	M
1	20	164
2	337	48

Combine PCA and clustering

Our PCA results were in wisc.pr\$x

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

Cluster Dendrogram



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

Cut tree into two groups:

```
grps <- cutree(hc, k=2)
table(grps)
```

```
grps
  1   2
203 366
```

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

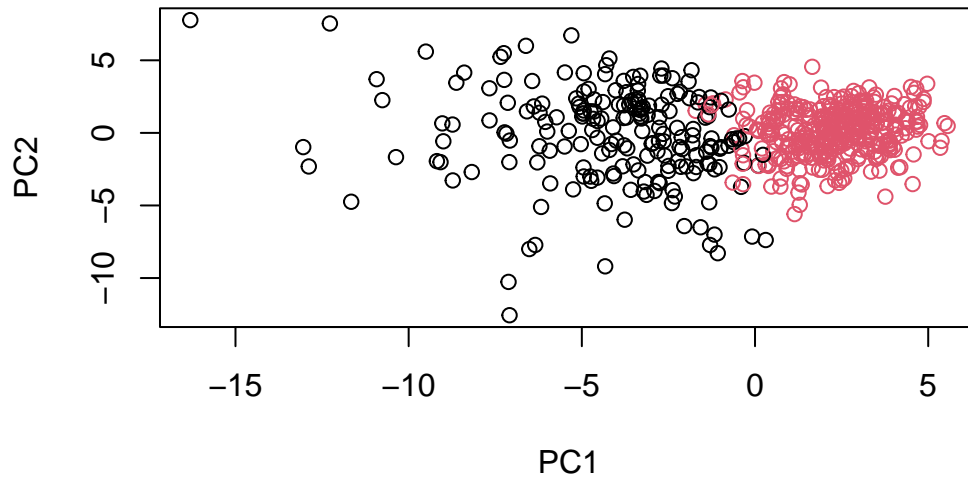
The new combined model does a great job at separating the two diagnoses with one group mainly composed of B and the other of M.

Compare my clustering result(my `grps`) to the expert `diagnosis`

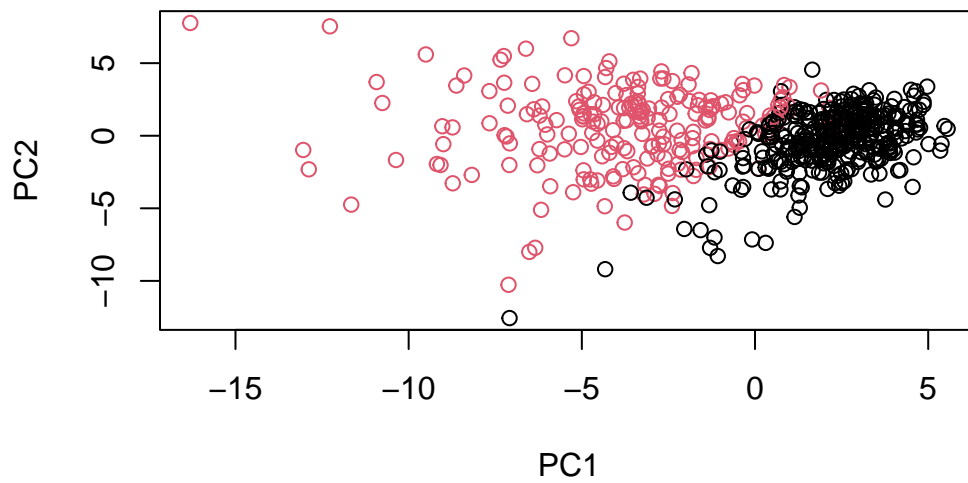
```
table(diagnosis,grps)
```

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

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



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



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.

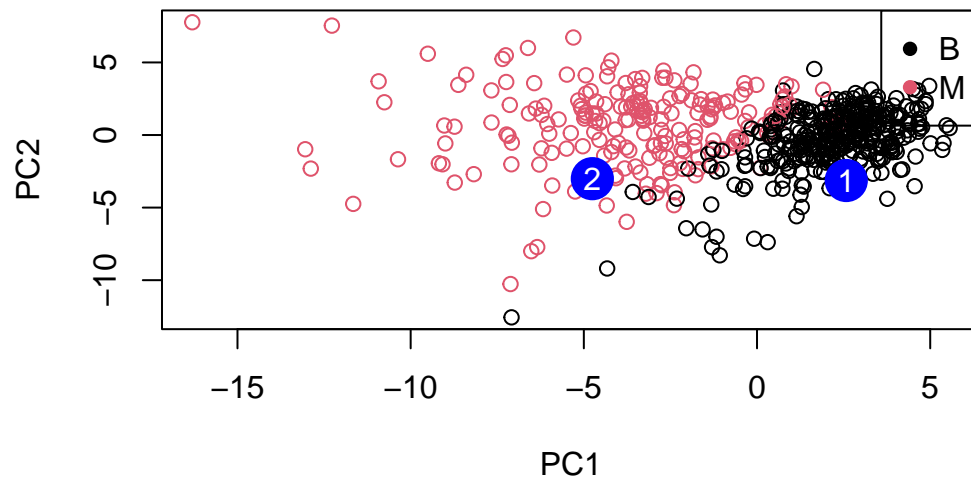
The `hclust` plot with `ward.D2` works as good as the plot we got for combining PCA and clustering, but `single` & `average` & `complete` does not effectively separate the data into two groups.

##Prediction

```
#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=as.factor(diagnosis))
points(npc[,1], npc[,2], col="blue", pch=16, cex=3)
text(npc[,1], npc[,2], c(1,2), col="white")
legend("topright", legend = levels(as.factor(diagnosis)), col = 1:2, pch = 16)
```

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

Patient 2 should be prioritized for a follow up.