

Class 8: PCA Mini Project

Chloe Wong (PID: A16893383)

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

```
fna.data <- "WisconsinCancer.csv"
```

```
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		

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

```
diagnosis
  B   M
357 212
```

Remove this first **diagnosis** column from the dataset 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.

```
#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				

##Exploratory data analysis

Q1. How many observations are in this dataset?

569 observations

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

```
[1] 569
```

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

212 observations have a malignant diagnosis

```
table(diagnosis)
```

```
diagnosis
```

```
  B    M  
357 212
```

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

10 variables

```
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:

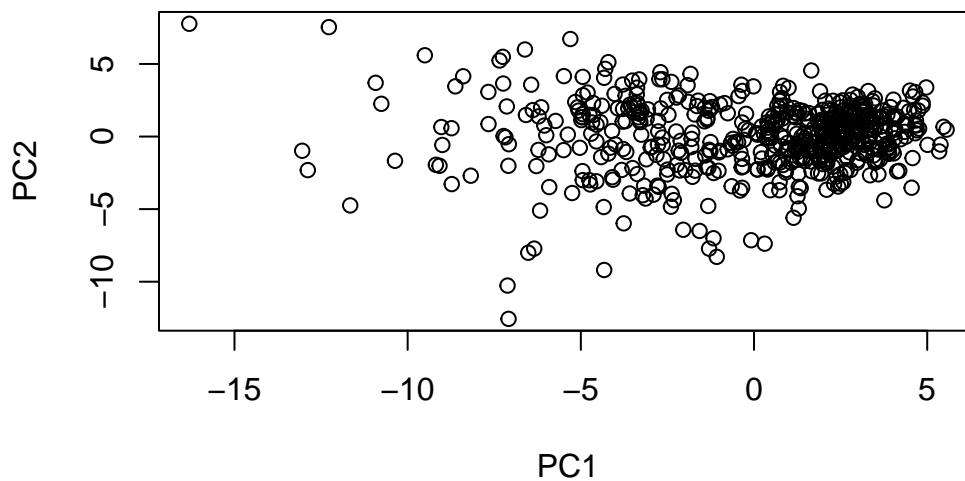
	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Standard deviation	3.6444	2.3857	1.67867	1.40735	1.28403	1.09880	0.82172
Proportion of Variance	0.4427	0.1897	0.09393	0.06602	0.05496	0.04025	0.02251
Cumulative Proportion	0.4427	0.6324	0.72636	0.79239	0.84734	0.88759	0.91010
	PC8	PC9	PC10	PC11	PC12	PC13	PC14
Standard deviation	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					

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

See what is in our PCA results object:

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




```
#plot(wisc.pr$x)
```

```
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

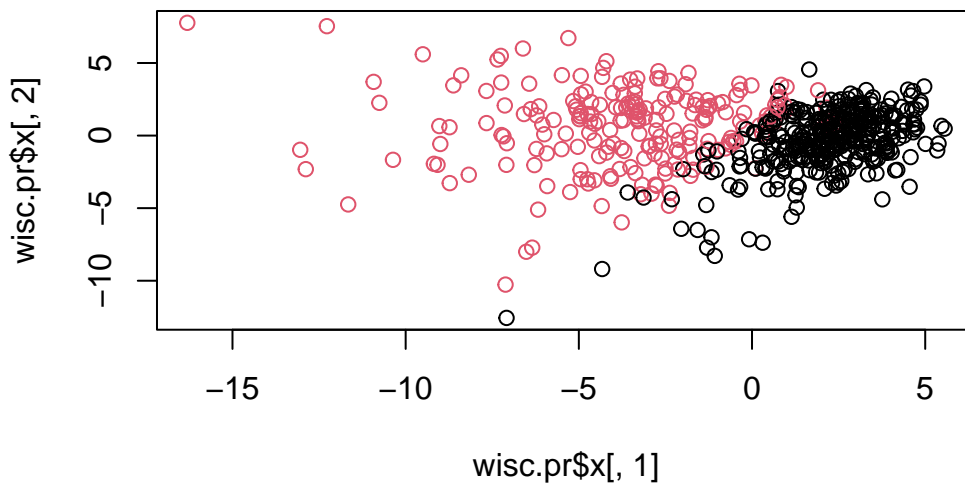
	PC13	PC14	PC15	PC16	PC17
842302	0.10329677	-0.690196797	0.601264078	0.74446075	-0.26523740
842517	-0.94269981	-0.652900844	-0.008966977	-0.64823831	-0.01719707
84300903	-0.41026561	0.016665095	-0.482994760	0.32482472	0.19075064
84348301	-0.93245070	-0.486988399	0.168699395	0.05132509	0.48220960
84358402	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

```
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 or 44.27%

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

3

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

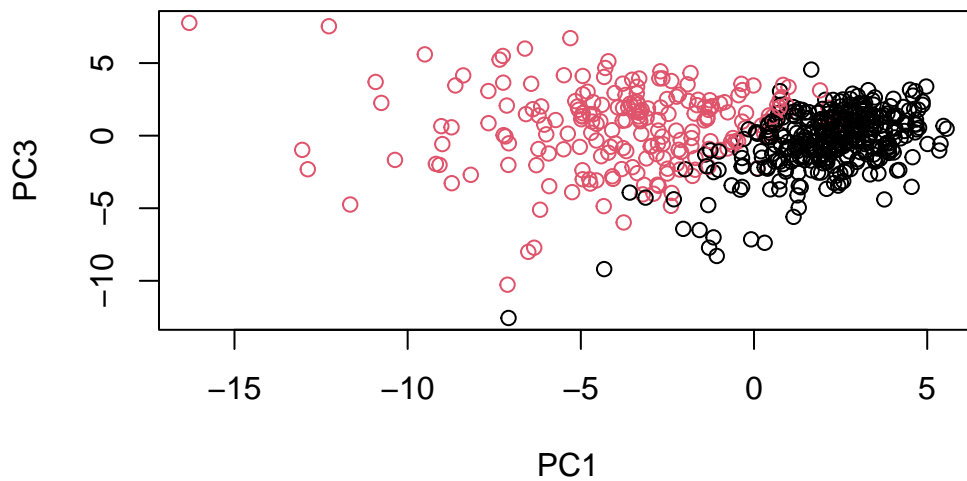
7

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

There are a bunch of words with no points visible with the words also being unreadable. This plot is difficult to understand as you cannot make sense of the PCA result as the plot is unreadable and uninterpretable.

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

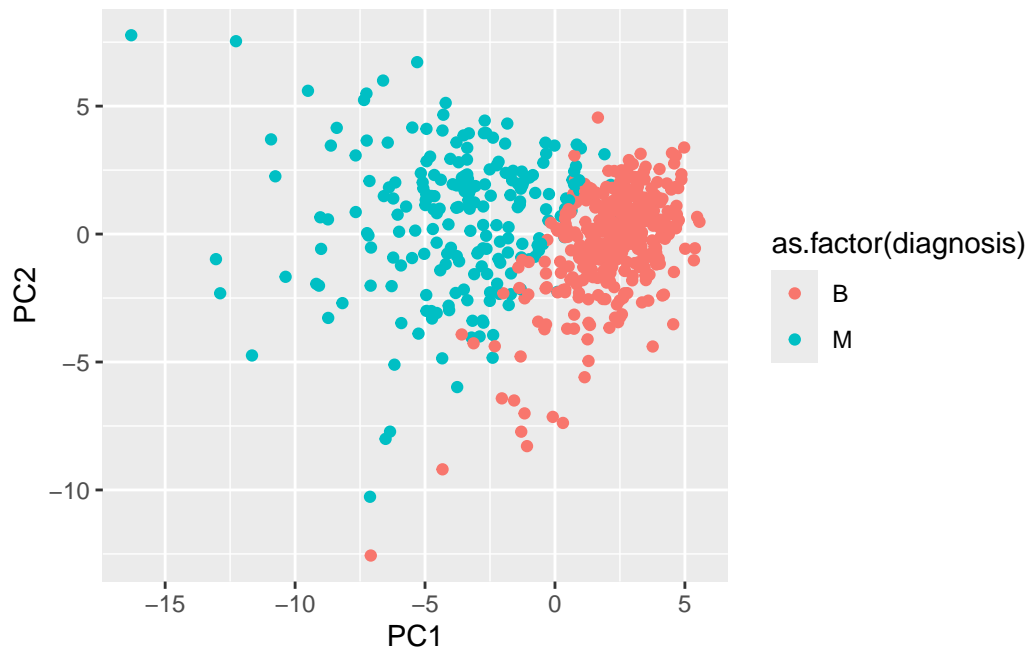
```
plot(wisc.pr$x[, 1:3 ], col = as.factor(diagnosis),  
     xlab = "PC1", ylab = "PC3")
```



```
df <- as.data.frame(wisc.pr$x)
df$diagnosis <- diagnosis

library(ggplot2)

ggplot(df) +
  aes(PC1, PC2, col=as.factor(diagnosis)) +
  geom_point()
```

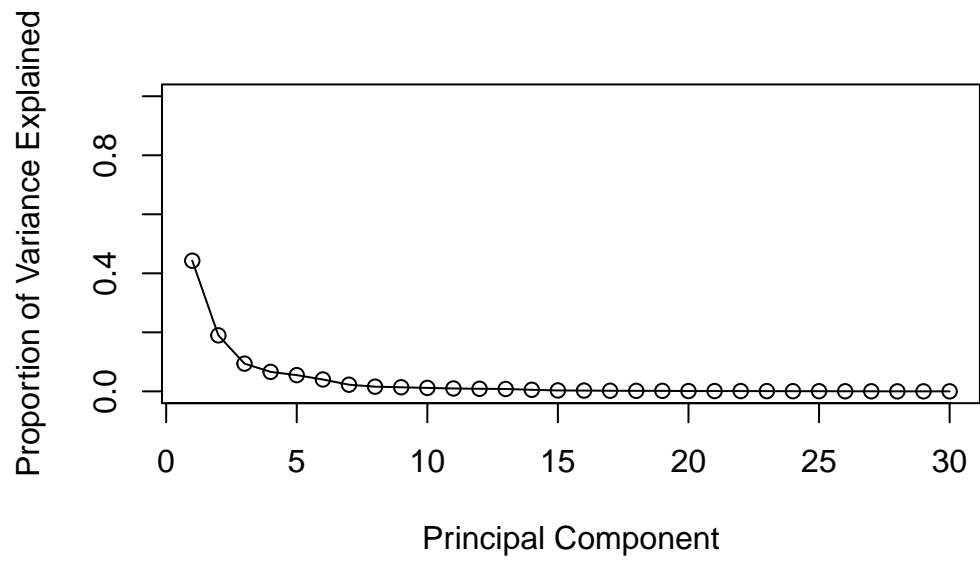


```
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

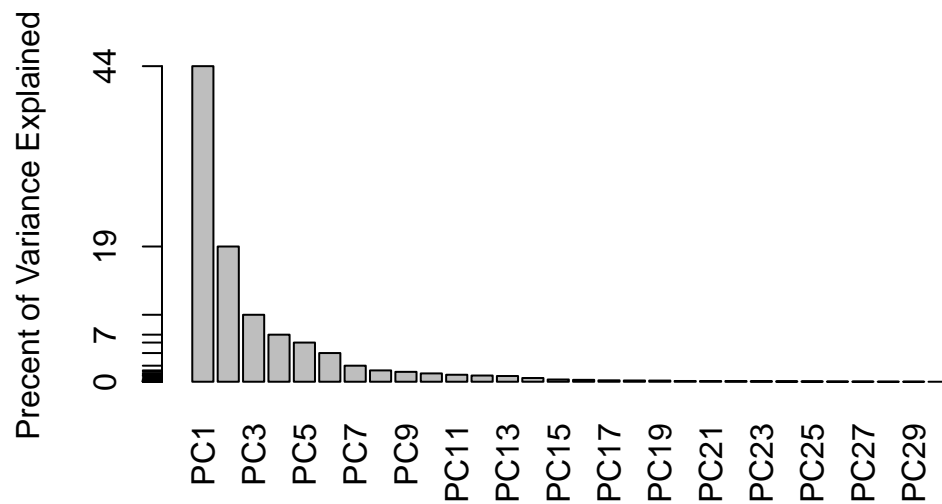
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
pve <- pr.var / sum(pr.var)

plot(pve, xlab = "Principal Component",
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```



```
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 )
```



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` contributes to component of the loading vector by -0.26085376.

```
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

```
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					

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

The minimum number of principal components required to explain 80% of the variance of the data 5.

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

The clustering model has 4 clusters at height = 32.

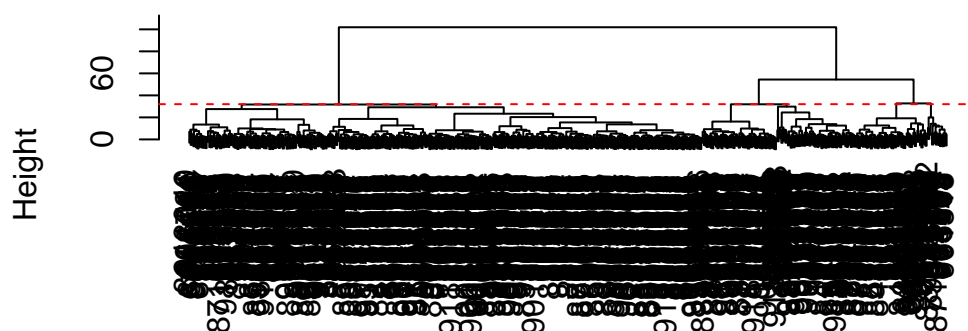
```
data.scaled <- scale(wisc.data)

data.dist <- dist(data.scaled)

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

```
plot(wisc.hclust)
abline(h=32, col="red", lty=2)
```

Cluster Dendrogram



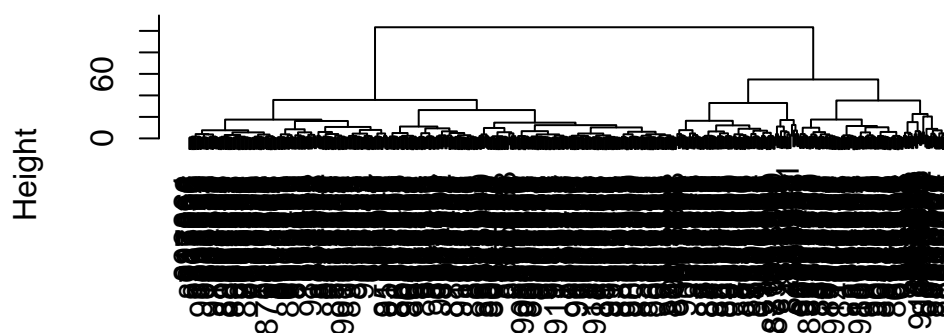
```
data.dist  
hclust (*, "ward.D2")
```

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

No there is not a better cluster vs diagnoses match by cutting into a different number of clusters between 2 and 10.

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


Cluster Dendrogram



d
hclust (*, "ward.D2")

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

```
      diagnosis
wisc.hclust.clusters  B  M
1      24 179
2     333  33
```

```
wisc.hclust.clusters <- cutree(hc, k=3)
table(wisc.hclust.clusters, diagnosis)
```

```
      diagnosis
wisc.hclust.clusters  B  M
1         0 111
2      24  68
3     333  33
```

```
wisc.hclust.clusters <- cutree(hc, k=4)
table(wisc.hclust.clusters, diagnosis)
```

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

```
wisc.hclust.clusters <- cutree(hc, k=5)
table(wisc.hclust.clusters, diagnosis)
```

	diagnosis		
wisc.hclust.clusters	B	M	
1	0	33	
2	0	78	
3	24	68	
4	184	32	
5	149	1	

```
wisc.hclust.clusters <- cutree(hc, k=6)
table(wisc.hclust.clusters, diagnosis)
```

	diagnosis		
wisc.hclust.clusters	B	M	
1	0	33	
2	0	78	
3	13	5	
4	11	63	
5	184	32	
6	149	1	

```
wisc.hclust.clusters <- cutree(hc, k=7)
table(wisc.hclust.clusters, diagnosis)
```

	diagnosis		
wisc.hclust.clusters	B	M	
1	0	33	
2	0	78	
3	13	5	
4	11	63	
5	39	28	
6	149	1	
7	145	4	

```
wisc.hclust.clusters <- cutree(hc, k=8)
table(wisc.hclust.clusters, diagnosis)
```

	diagnosis	
wisc.hclust.clusters	B	M
1	0	14
2	0	78
3	13	5
4	11	63
5	39	28
6	149	1
7	145	4
8	0	19

```
wisc.hclust.clusters <- cutree(hc, k=9)
table(wisc.hclust.clusters, diagnosis)
```

	diagnosis	
wisc.hclust.clusters	B	M
1	0	14
2	0	78
3	13	5
4	11	63
5	39	28
6	149	1
7	145	4
8	0	17
9	0	2

```
wisc.hclust.clusters <- cutree(hc, k=10)
table(wisc.hclust.clusters, diagnosis)
```

	diagnosis	
wisc.hclust.clusters	B	M
1	0	14
2	0	47
3	13	5
4	0	31
5	11	63
6	39	28

7	149	1
8	145	4
9	0	17
10	0	2

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

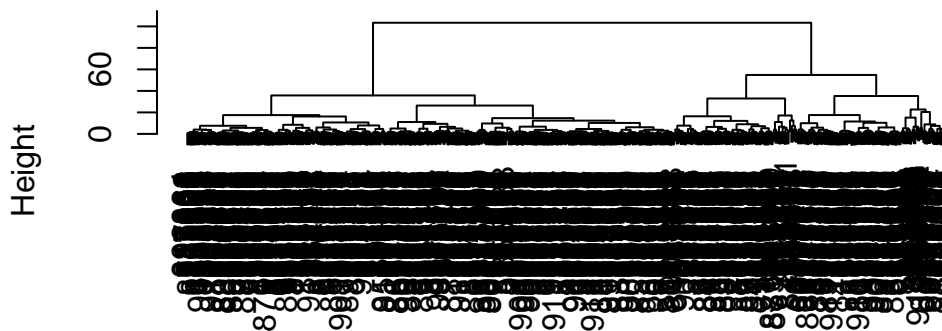
The method that gives me my favorite results for the same data.dist dataset is the PCA scatter plots. This is simply because I personally feel as though they are easier to read and interpret. The color coding makes it easy on the eye with the points being clearly visible while the hierarchical cluster is personally harder for me to distinguish different clusters and various points in the dataset.

##Combine PCA and clustering

Our PCA results were in `wisc.pr$x`

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

Cluster Dendrogram

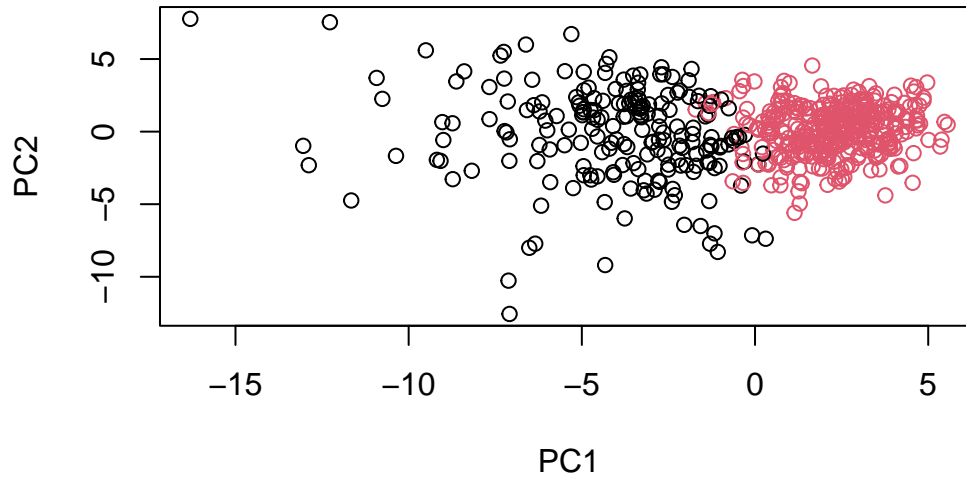


d
hclust (*, "ward.D2")

Cut tree into two groups/branches/clusters...

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

```
plot(wisc.pr$x, col=grps)
```



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

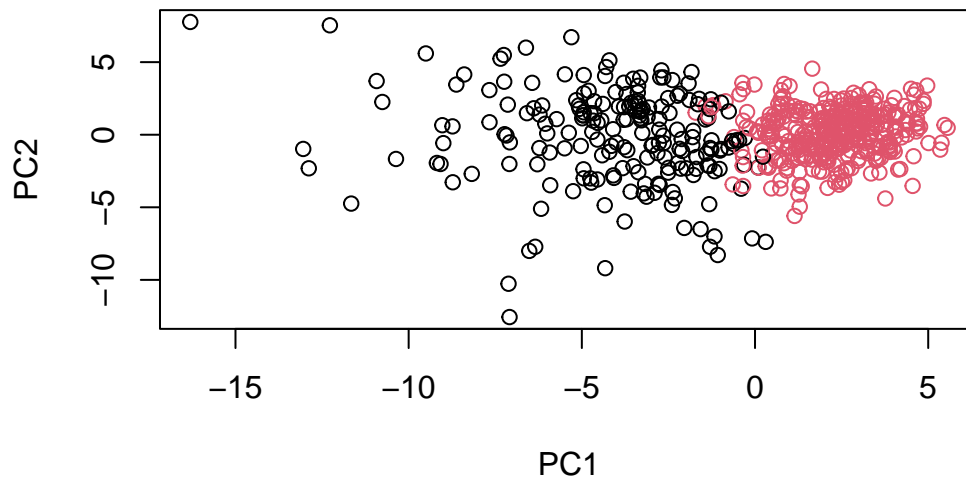
```
table(grps)
```

```
grps
  1  2
203 366
```

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

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

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



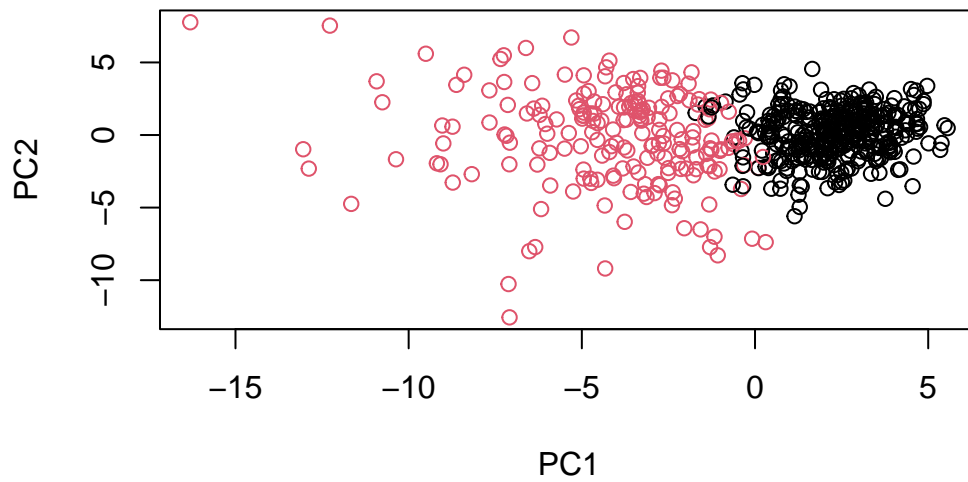
```
g <- as.factor(grps)
levels(g)
```

```
[1] "1" "2"
```

```
g <- relevel(g,2)
levels(g)
```

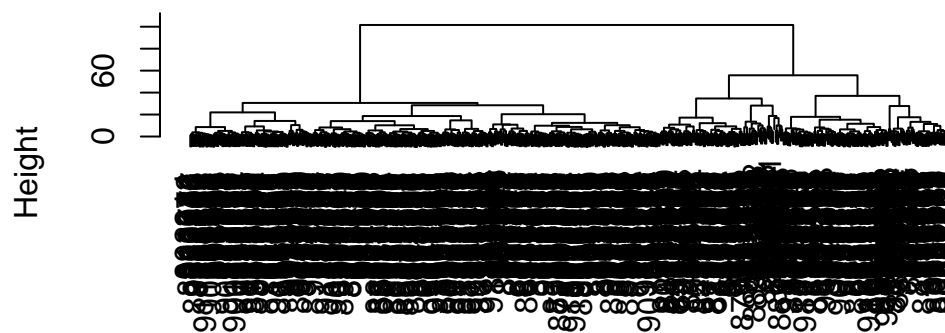
```
[1] "2" "1"
```

```
# Plot using our re-ordered factor
plot(wisc.pr$x[,1:2], col=g)
```



```
data.dist <- dist(wisc.pr$x[,1:7])
wisc.pr.hclust <- hclust(data.dist, method="ward.D2")
plot(wisc.pr.hclust)
```

Cluster Dendrogram



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

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

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

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

The newly created model with four clusters separates out the two diagnoses decently, but things to improve on include the number of outliers present. However, you are able to visibly see a distinct separation with the four clusters present.

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 k-means and hierarchical clustering model also do fairly well in terms of separating the diagnoses. However, my only critique is that with the clustering model, it is visually harder to see distinctions between the clusters and the data appears to be more widespread.

```
wisc.km <- kmeans(scale(wisc.data), centers=2, nstart=20)
```

```
table(wisc.km$cluster, diagnosis)
```

```
      diagnosis
      B   M
1     14 175
2    343  37
```

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

```
      diagnosis
wisc.hclust.clusters  B   M
1         0  14
2         0  47
3        13   5
4         0  31
```

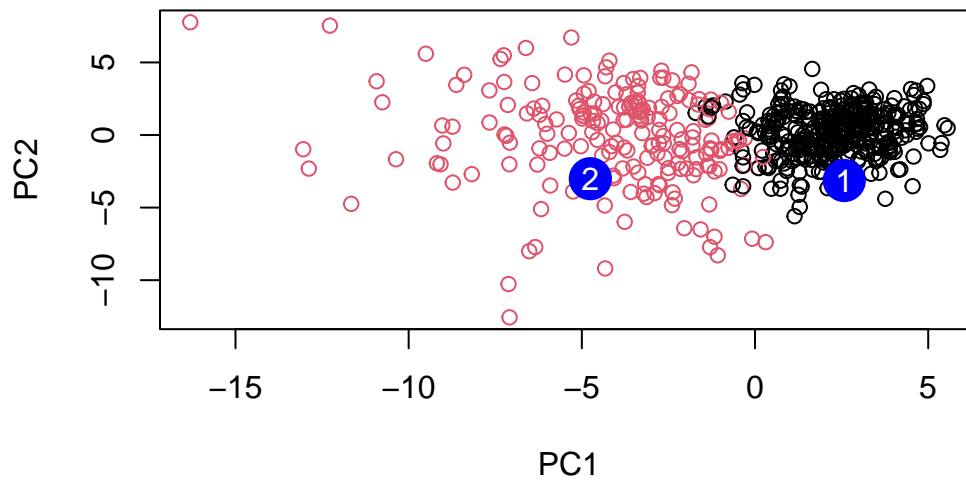

5	11	63
6	39	28
7	149	1
8	145	4
9	0	17
10	0	2

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=g)
points(npc[,1], npc[,2], col="blue", pch=16, cex=3)
text(npc[,1], npc[,2], c(1,2), col="white")
```



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

Patient 1 should be prioritized for follow up based on my results as in the graph, the clustering of malignant is seen mainly near patient 1.

```
sessionInfo()
```

```
R version 4.4.1 (2024-06-14 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows 10 x64 (build 19045)
```

```
Matrix products: default
```

```
locale:
[1] LC_COLLATE=English_United States.utf8
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8
```

```
time zone: America/Los_Angeles
```

tzcode source: internal

attached base packages:

[1] stats graphics grDevices utils datasets methods base

other attached packages:

[1] ggplot2_3.5.1

loaded via a namespace (and not attached):

[1] vctrs_0.6.5	cli_3.6.3	knitr_1.48	rlang_1.1.4
[5] xfun_0.48	generics_0.1.3	jsonlite_1.8.9	labeling_0.4.3
[9] glue_1.8.0	colorspace_2.1-1	htmltools_0.5.8.1	scales_1.3.0
[13] fansi_1.0.6	rmarkdown_2.28	grid_4.4.1	evaluate_1.0.1
[17] munsell_0.5.1	tibble_3.2.1	fastmap_1.2.0	yaml_2.3.10
[21] lifecycle_1.0.4	compiler_4.4.1	dplyr_1.1.4	pkgconfig_2.0.3
[25] farver_2.1.2	digest_0.6.37	R6_2.5.1	tidyselect_1.2.1
[29] utf8_1.2.4	pillar_1.9.0	magrittr_2.0.3	withr_3.0.1
[33] tools_4.4.1	gtable_0.3.5		