

Class08-MiniProject

Jessica A15647602

Side note:

```
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

Let's look at the mean value of every column:

```
apply(mtcars, 2, mean)
```

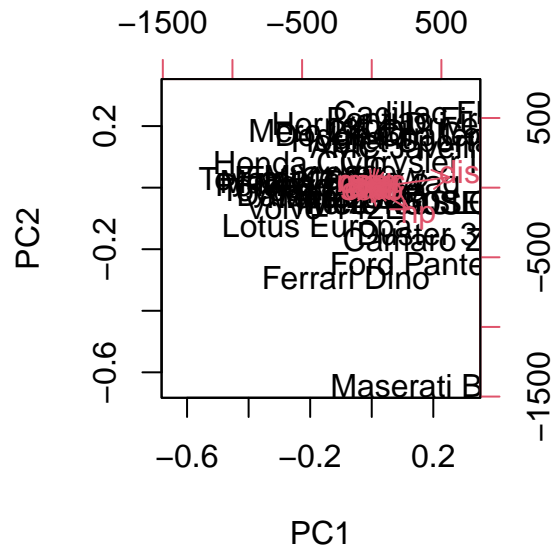
mpg	cyl	disp	hp	drat	wt	qsec
20.090625	6.187500	230.721875	146.687500	3.596563	3.217250	17.848750
vs	am	gear	carb			
0.437500	0.406250	3.687500	2.812500			

Find the sd

```
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	

```
pca <- prcomp(mtcars)
biplot(pca)
```



Let's try scaling the data:

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

	mpg	cyl	dis	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

What is the mean of each dimension/column in mtscale?

```
round(apply(mtscale, 2, mean), 3)
```

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

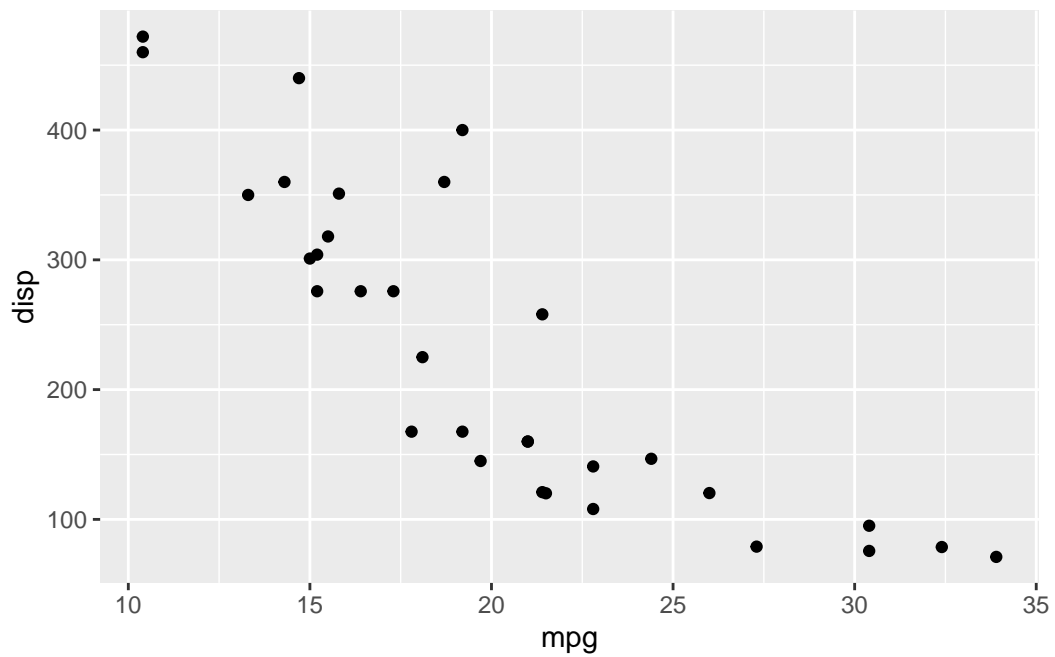
```
round(apply(mtscale, 2, sd), 3)
```

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

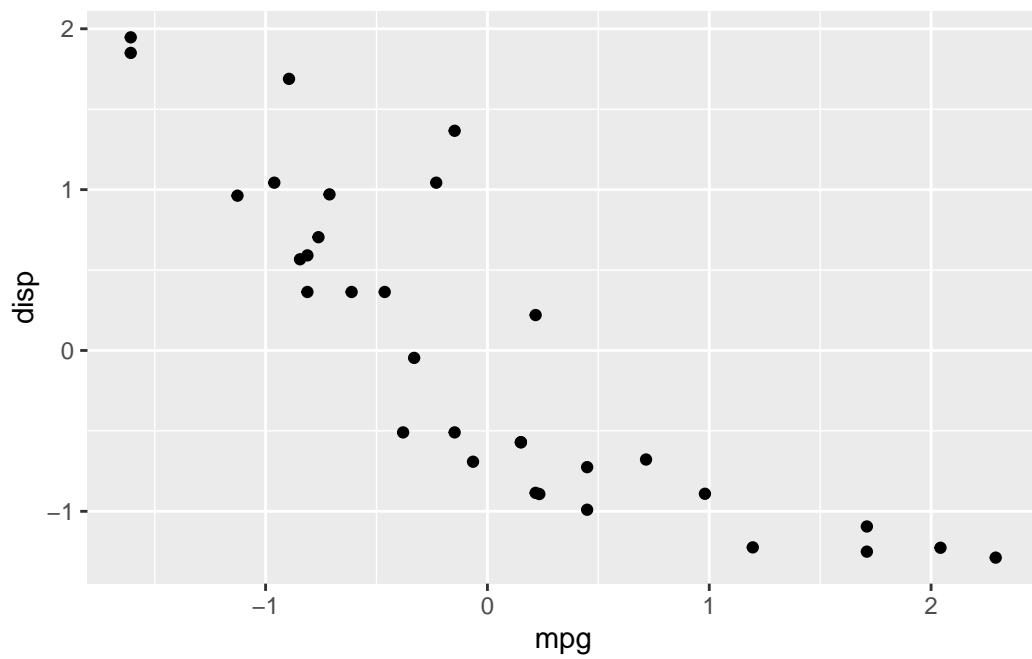
Let's plot mpg vs disp for both mtcars and after the scaled data in mtscale

```
library(ggplot2)

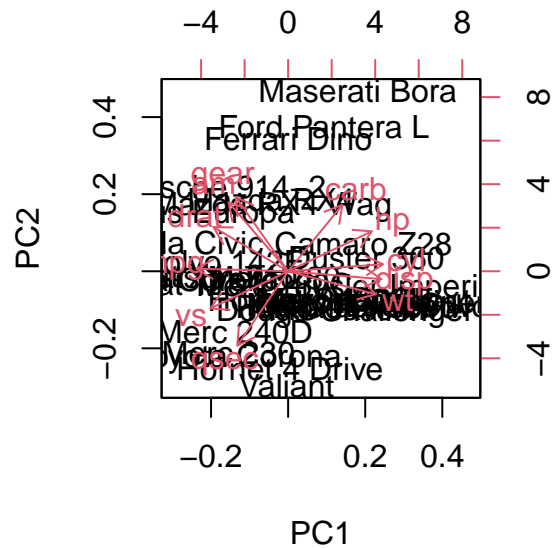
ggplot(mtcars) +
  aes(mpg, disp) +
  geom_point()
```



```
ggplot(mtscale) +  
  aes(mpg, disp) +  
  geom_point()
```



```
pca2 <- prcomp(mtscale)
biplot(pca2)
```



##Breast Cancer FNA Data

```
library(readr)
# 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)

#view
#View(wisc.df)

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

# Create diagnosis vector for later
diagnosis <- factor(wisc.df$diagnosis)
```

```
dim(wisc.data)
```

```
[1] 569 30
```

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

```
[1] 569
```

```
table(diagnosis)
```

```
diagnosis  
  B    M  
357 212
```

```
colnames(wisc.data)
```

```
[1] "radius_mean"      "texture_mean"  
[3] "perimeter_mean"   "area_mean"  
[5] "smoothness_mean"  "compactness_mean"  
[7] "concavity_mean"   "concave.points_mean"  
[9] "symmetry_mean"    "fractal_dimension_mean"  
[11] "radius_se"        "texture_se"  
[13] "perimeter_se"     "area_se"  
[15] "smoothness_se"    "compactness_se"  
[17] "concavity_se"     "concave.points_se"  
[19] "symmetry_se"      "fractal_dimension_se"  
[21] "radius_worst"     "texture_worst"  
[23] "perimeter_worst"  "area_worst"  
[25] "smoothness_worst" "compactness_worst"  
[27] "concavity_worst"  "concave.points_worst"  
[29] "symmetry_worst"   "fractal_dimension_worst"
```

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

```
[1] 10
```

Q1. How many observations are in this dataset? A. There are 569 observations.

Q2. How many of the observations have a malignant diagnosis? A. There are 212 observations with malignant diagnosis.

Q3. How many variables/features in the data are suffixed with `_mean`? A. There are 10 features with `_mean`.

##Principal Component Analysis (PCA)

```
# Check column means and standard deviations
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

We want to scale our data before PCA by setting `scale = true`

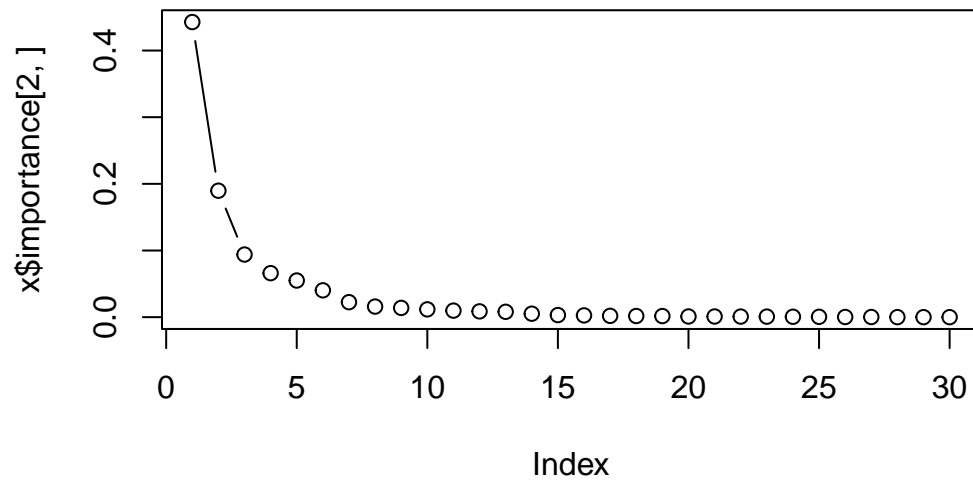
```
# Perform PCA on wisc.data
wisc.pr <- prcomp(wisc.data, scale = TRUE)
```

```
# Look at Variance of each PCa
summary(wisc.pr)
```

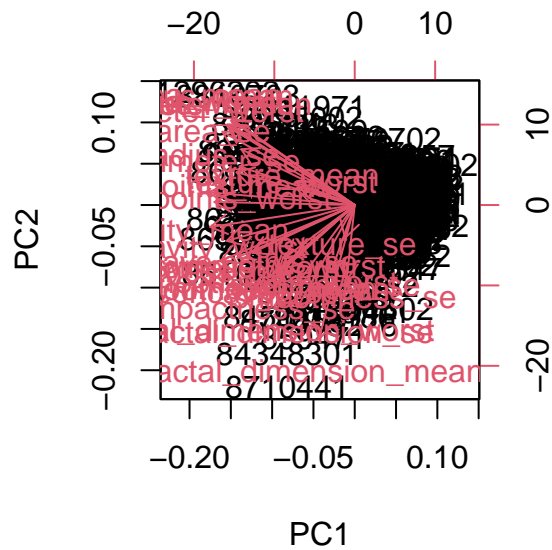
Importance of components:

	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					


```
x <- summary(wisc.pr)
plot(x$importance[2,], typ = "b")
```



```
#Generate PCA plot
biplot(wisc.pr)
```



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

```
$names
```

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

```
$class
```

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

Q4. From your results, what proportion of the original variance is captured by the first principal components (PC1)? A. For PC1, the proportion of variance = 0.4427 ~ 44.27%

Q5. How many principal components (PCs) are required to describe at least 70% of the original variance in the data? A. PC3

Q6. How many principal components (PCs) are required to describe at least 90% of the original variance in the data? A. PC7

Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why? A. The plot is very messy and difficult to understand. The ID values of the patients are labelled and are very large so they cover the entire plot. There is a lot of wording throughout the plot, making it hard to interpret.

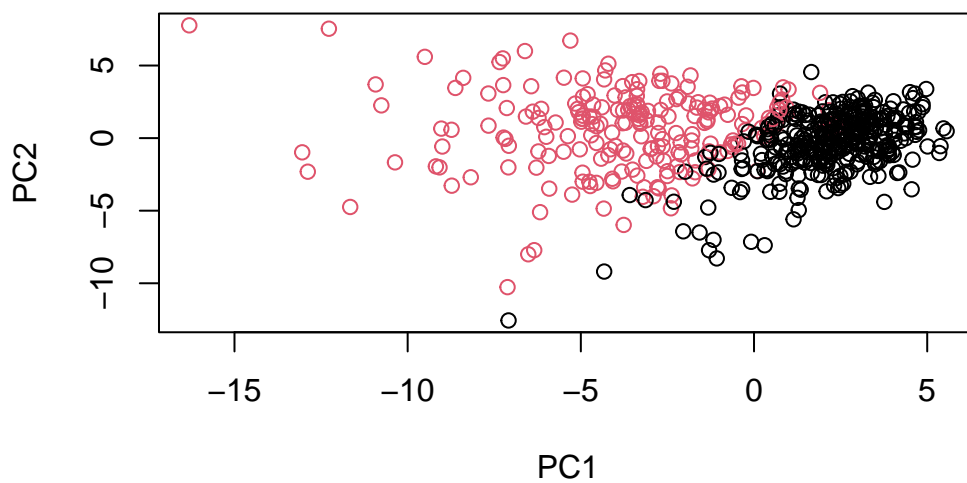
```
head(wisc.pr$x)
```

	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
```

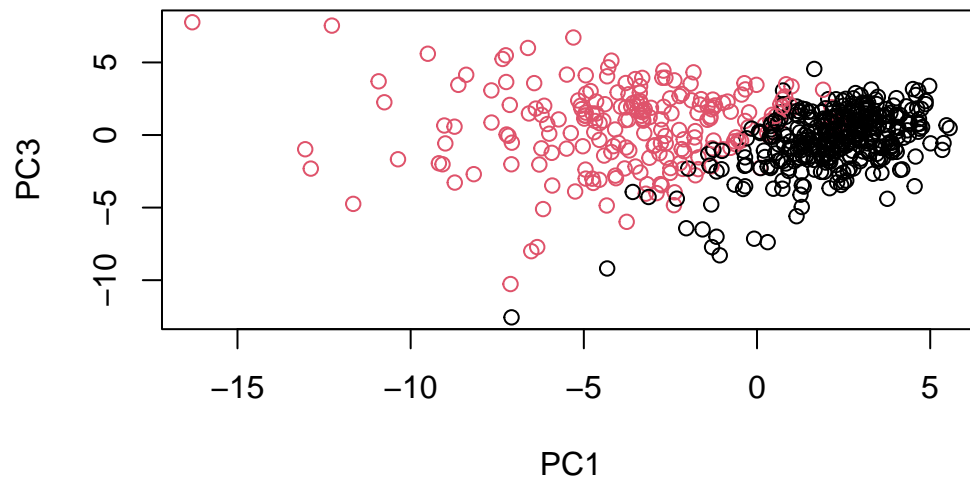
My main PCR result figure

```
# Scatter plot observations by components 1 and 2
plot(wisc.pr$x, 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[, 1:3], col = diagnosis,
     xlab = "PC1", ylab = "PC3")
```

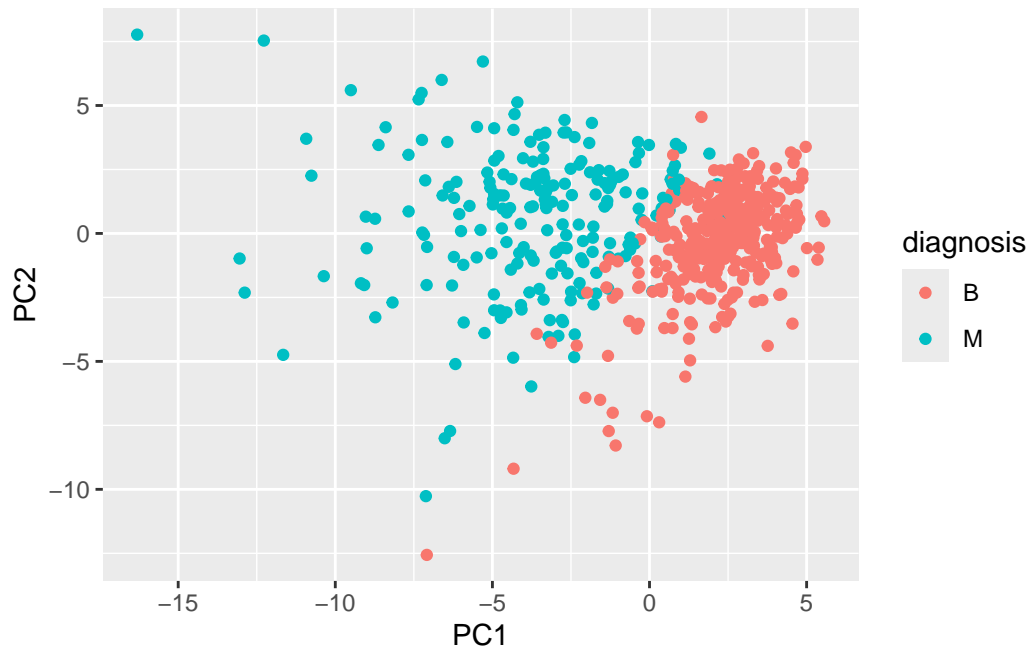


##ggplot

```
# 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()
```



##Variance Explained

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

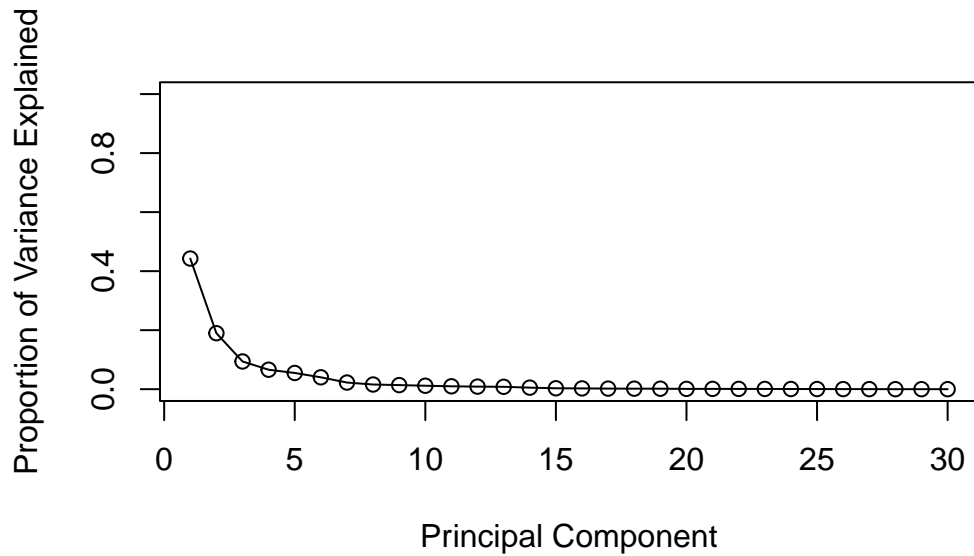
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
#total variance explained of all principal components
Total_val <- sum(pr.var)

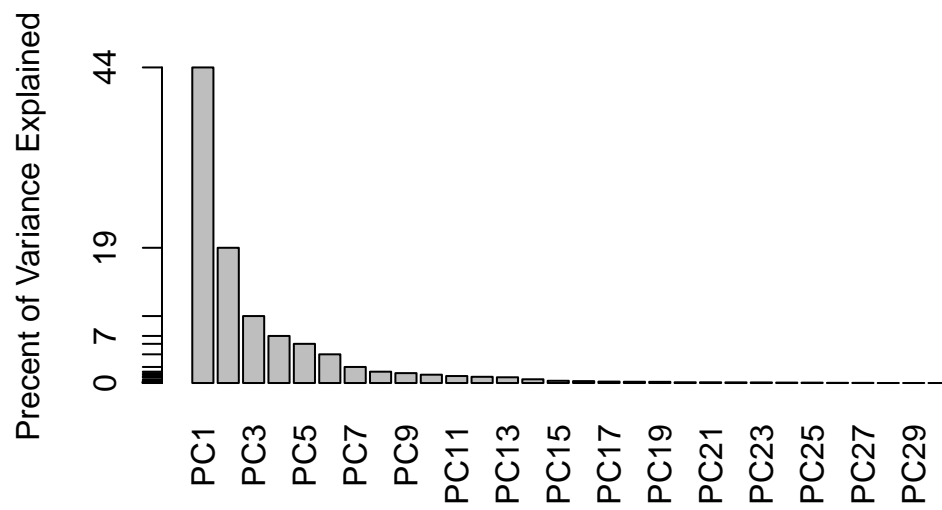
# Variance explained by each principal component: pve
pve <- pr.var/Total_val
pve
```

```
[1] 4.427203e-01 1.897118e-01 9.393163e-02 6.602135e-02 5.495768e-02
[6] 4.024522e-02 2.250734e-02 1.588724e-02 1.389649e-02 1.168978e-02
[11] 9.797190e-03 8.705379e-03 8.045250e-03 5.233657e-03 3.137832e-03
[16] 2.662093e-03 1.979968e-03 1.753959e-03 1.649253e-03 1.038647e-03
[21] 9.990965e-04 9.146468e-04 8.113613e-04 6.018336e-04 5.160424e-04
[26] 2.725880e-04 2.300155e-04 5.297793e-05 2.496010e-05 4.434827e-06
```

```
# Plot variance explained for each principal component
plot(pve, xlab = "Principal Component",
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```



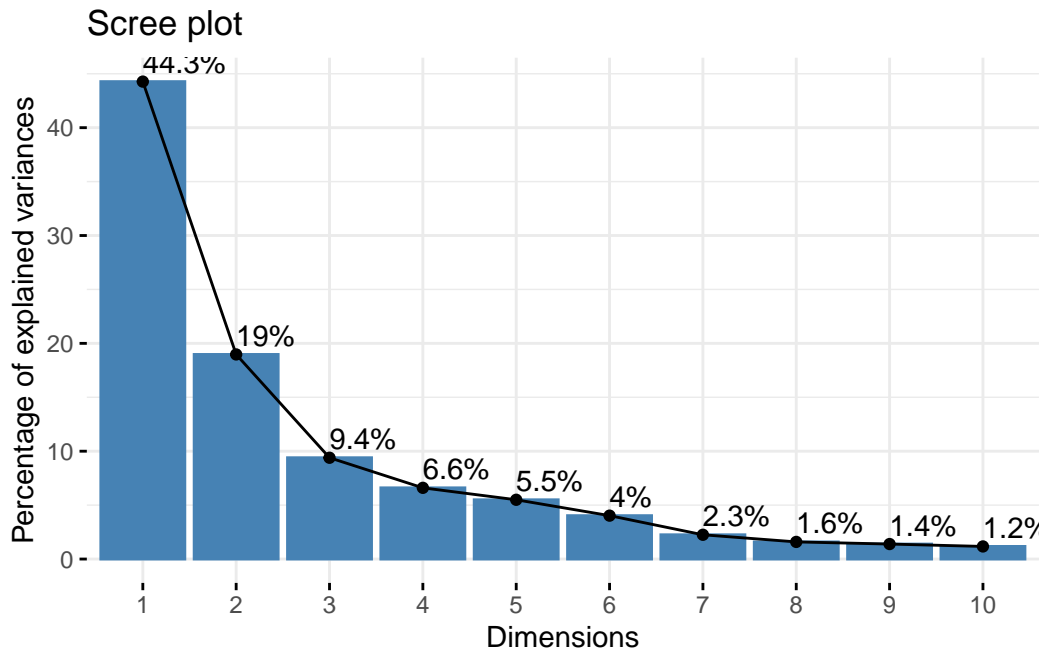
```
# Alternative scree plot of the same data, note data driven y-axis
barplot(pve, ylab = "Precent of Variance Explained",
        names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```



```
## 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)
```

##Communicating PCA results

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. A. `concave.points_mean` = -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

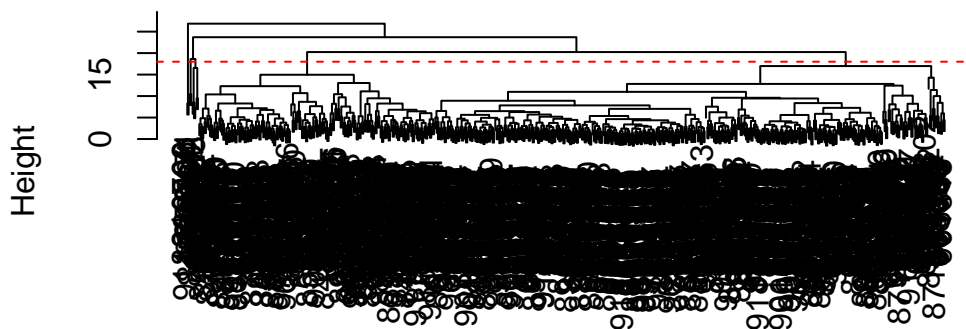
texture_worst	perimeter_worst	area_worst
-0.10446933	-0.23663968	-0.22487053
smoothness_worst	compactness_worst	concavity_worst
-0.12795256	-0.21009588	-0.22876753
concave.points_worst	symmetry_worst	fractal_dimension_worst
-0.25088597	-0.12290456	-0.13178394

Hierarchical clustering

Q10. Using the plot() and abline() functions, what is the height at which the clustering model has 4 clusters? A. Height is around 18-19

```
# 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")
plot(wisc.hclust)
abline(h = 18 , col="red", lty=2)
```

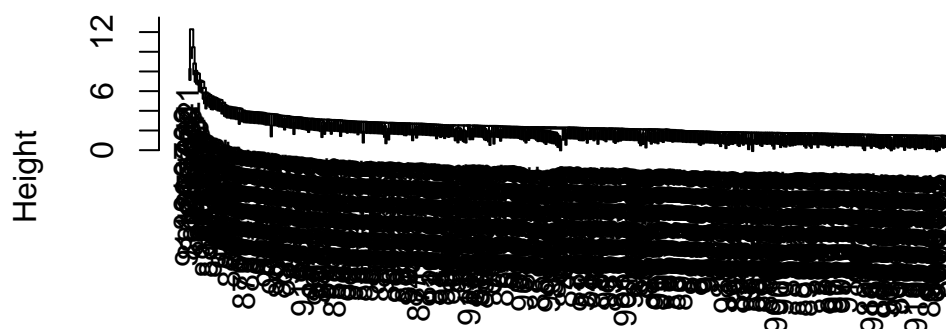
Cluster Dendrogram



data.dist
hclust (*, "complete")

```
wisc.hclust <- hclust(data.dist, method = "single")
plot(wisc.hclust)
abline(h = 18 , col="red", lty=2)
```

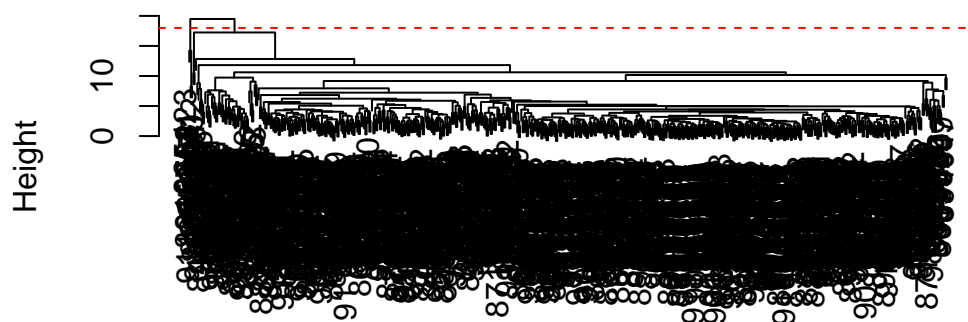
Cluster Dendrogram



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

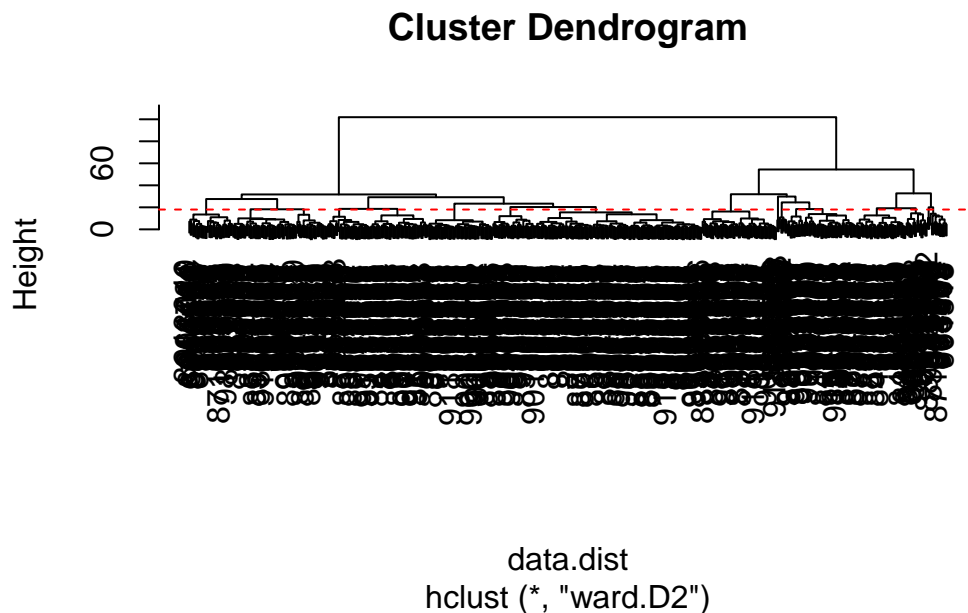
```
wisc.hclust <- hclust(data.dist, method = "average")  
plot(wisc.hclust)  
abline(h = 18 , col="red", lty=2)
```

Cluster Dendrogram



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

```
wisc.hclust <- hclust(data.dist, method = "ward.D2")
plot(wisc.hclust)
abline(h = 18 , col="red", lty=2)
```



Q12. Which method gives your favorite results for the same data.dist dataset?
Explain your reasoning. A. I liked the “ward.D2” plot, it was the cleanest.

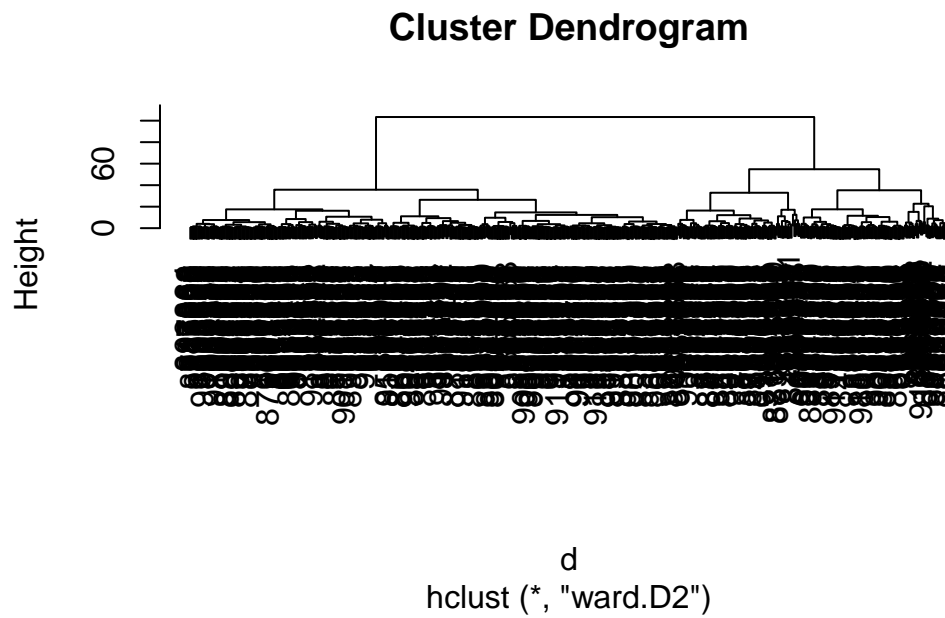
##Combining Methods

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

	diagnosis	
wisc.hclust.clusters	B	M
1	0	115
2	6	48
3	337	48
4	14	1

##Cluster in PC Space

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



```
d <- dist(wisc.pr$x[,1:4])
hc <- hclust(d, method ="ward.D2")
plot(hc)
```

Cluster Dendrogram



d
hclust (*, "ward.D2")

Cut this tree to yield 2 clusters

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

```
grps
  1  2
171 398
```

Compare to my expert M and B diagnosis

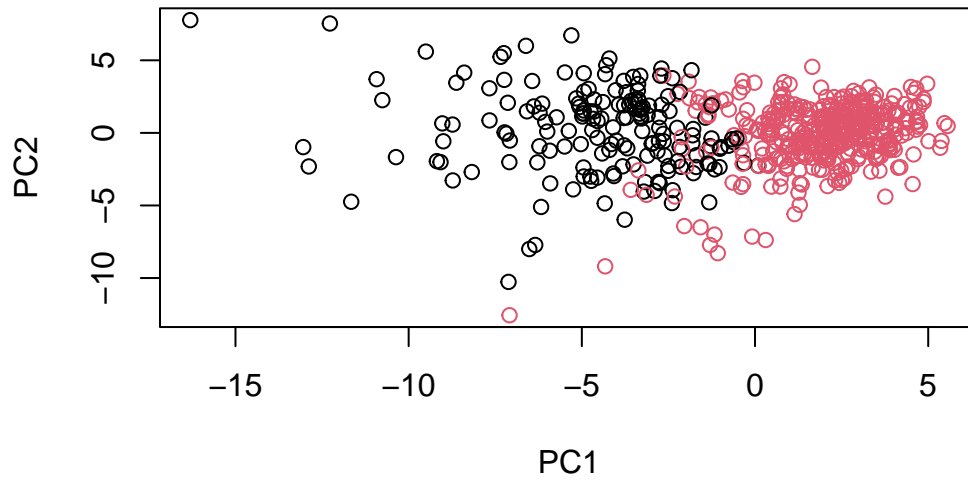
```
table(diagnosis)
```

```
diagnosis
  B  M
357 212
```

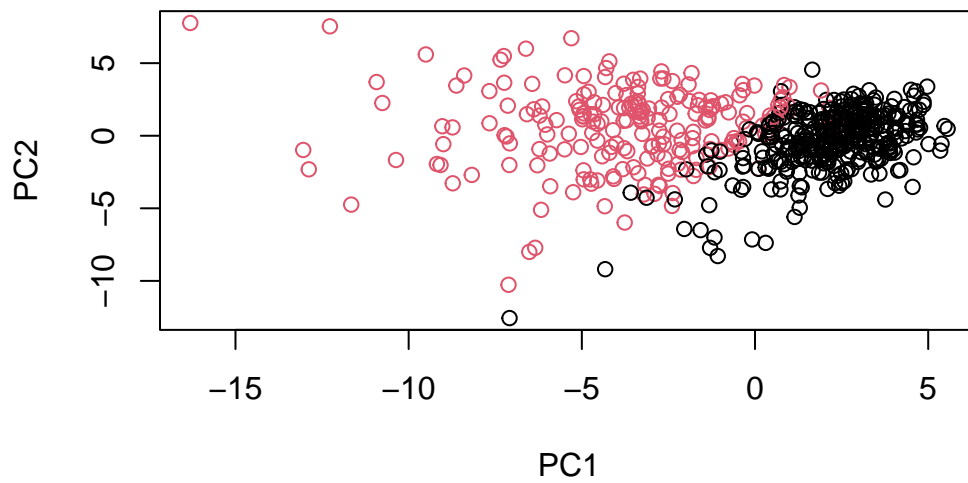
```
table(diagnosis, grps)
```

```
      grps
diagnosis  1  2
  B      6 351
  M     165  47
```

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



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



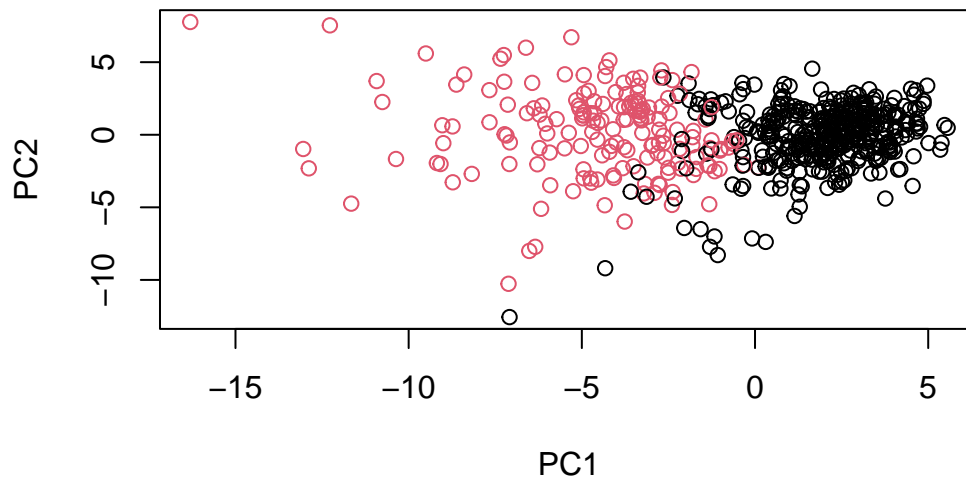
```
g <- as.factor(grps)
levels(g)
```

```
[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)
```



““