Class 8: PCA mini project

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Today we will do a complete analysis of some breast cancer biology data, but first let's revisit the main PCA function in R `precomp()` and see what `scale=TRUE/FALSE` does.

```
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
```

Find the mean value per column of this dataset?

```
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
```

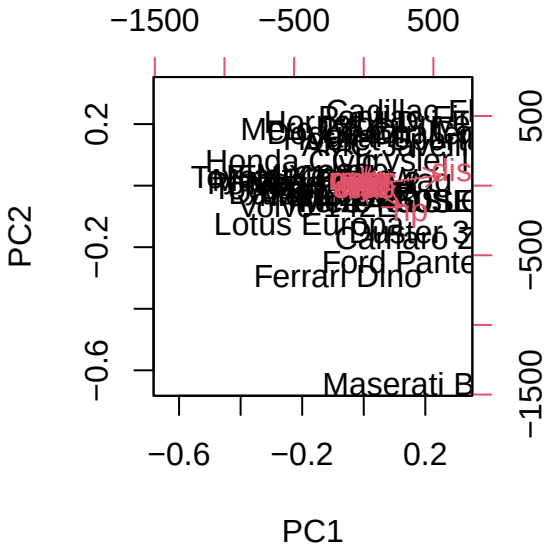
```
apply(mtcars, 2, sd)
```

```
       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
```

It is clear "disp" and "hp" have the highest means values and the highest standard deviation here. They will likely dominate any analysis I do on this dataset. Let's see

```
pc.noscale <- prcomp(mtcars, scale = FALSE)
pc.scale <- prcomp(mtcars, scale = TRUE)
```

```
biplot(pc.noscale)
```



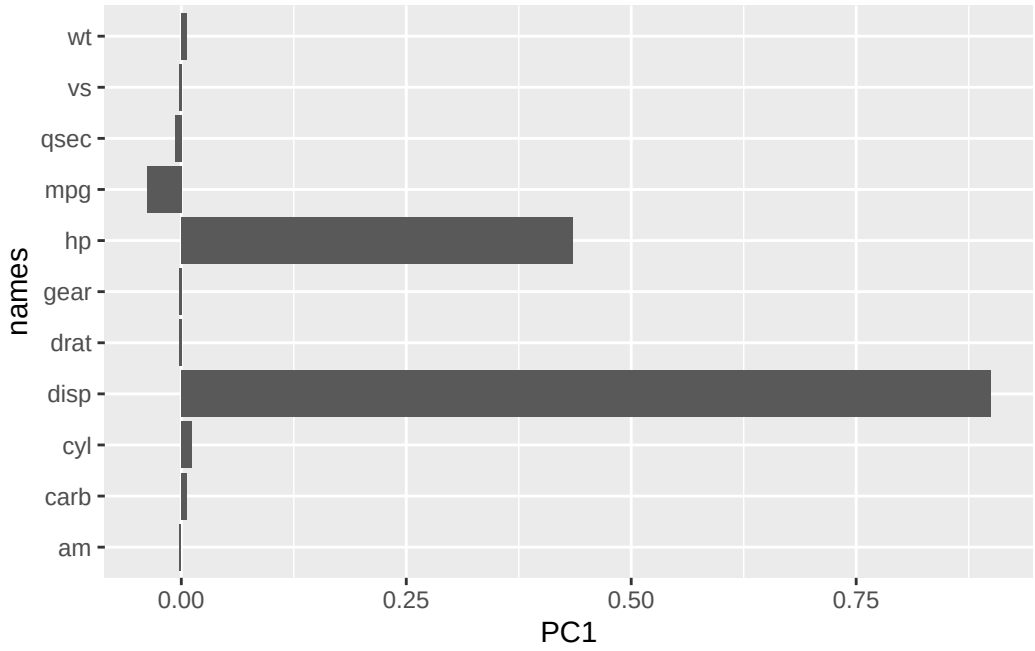

```
pc.noscale$rotation[,1]
```

```
         mpg          cyl         disp           hp         drat           wt
-0.038118199  0.012035150  0.899568146  0.434784387 -0.002660077  0.006239405
        qsec           vs           am         gear         carb
-0.006671270 -0.002729474 -0.001962644 -0.002604768  0.005766010
```

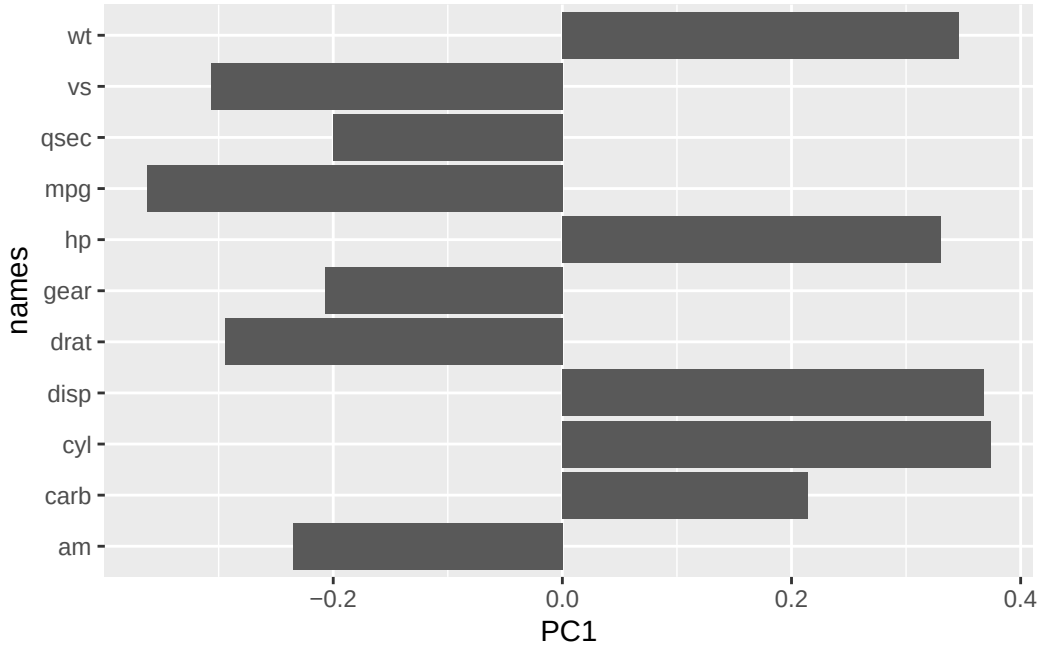
plot the loadings

```
library(ggplot2)

r1 <- as.data.frame(pc.noscale$rotation)
r1$names <- rownames(pc.noscale$rotation)
```

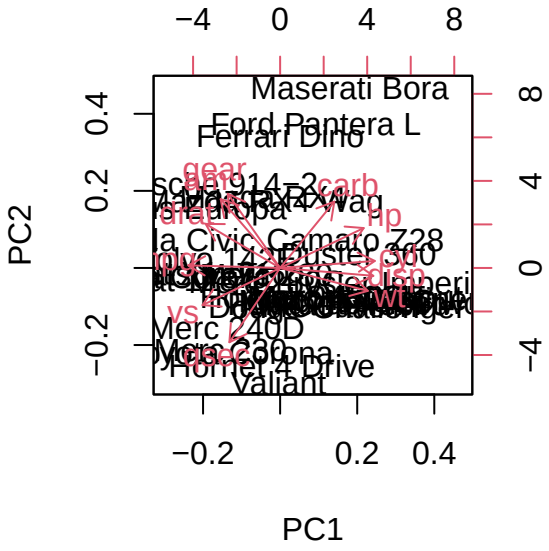
```
ggplot(r1) +
  aes(PC1, names) +
  geom_col()
```




```
r2 <- as.data.frame(pc.scale$rotation)
r2$names <- rownames(pc.scale$rotation)

ggplot(r2) +
  aes(PC1, names) +
  geom_col()
```




```
biplot(pc.scale)
```



Take-home: Generally we always want to set `scale=TRUE` when we do this type

of analysis to avoid our analysis being dominated by individual variables with the largest variance just due to their unit of measurement.

FNA breast cancer data

Load the data into R.

```
wisc.df <- read.csv("WisconsinCancer (1).csv", 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
```

Q1. How many observations are in this dataset?

Ans. There are 569 observations in this dataset.

```
nrow(wisc.df)
```

```
[1] 569
```

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

Ans. There are 212 malignant diagnosis in this dataset.

```
sum(wisc.df$diagnosis == "M")
```

```
[1] 212
```

The `table()` function is super useful here

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

```
  B   M
357 212
```

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

Ans. There are 10 variables/features in the data that are suffixed with _mean.

```
ncol(wisc.df)
```

```
[1] 31
```

```
colnames(wisc.df)
```

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

A useful function for this is `grep()` function

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

```
[1] 10
```

Before we go any further, we need to exclude the diagnosis column from any future analysis - this tells us whether a sample to cancer or non-cancer.

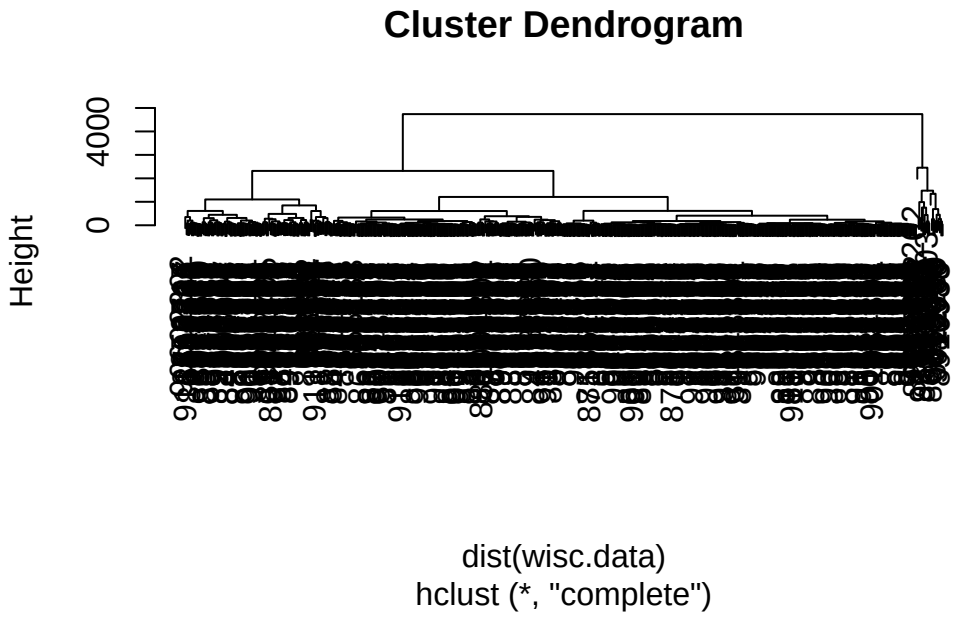
```
diagnosis <- as.factor(wisc.df$diagnosis)
head(diagnosis)
```

```
[1] M M M M M M
Levels: B M
```

```
wisc.data <- wisc.df[,-1]
```

Lets see if we can cluster the `wisc.data` to find some structure in the dataset.

```
hc <- hclust( dist(wisc.data))
plot(hc)
```



Principal Component Analysis (PCA)

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

Ans. The first principal component (PC1) captures 0.4427 (44.27%) of the original variance.

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

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

Ans. There needs to be 3 principal components to describe at least 70% of the original variance in the data.

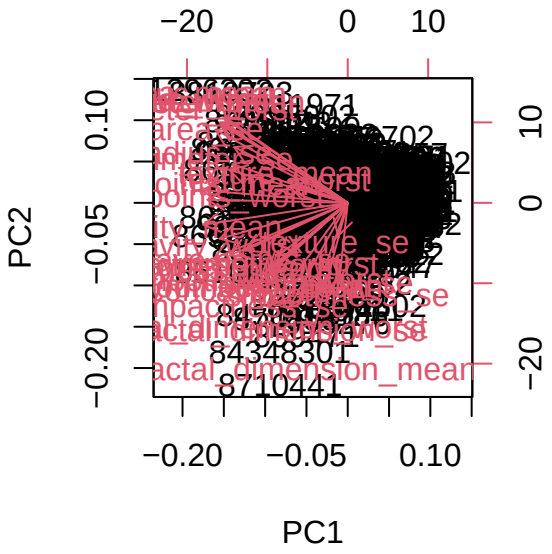
Q6. How many principal components (PCs) are required to describe at least 90% of the original variance in the data?

Ans. There needs to be 9 principal components to describe at least 90% of the original variance in the data.

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

Ans. The biplot is very messy and difficult to understand because all the ID for the patients are clustered too close together. This causes the graph to be hard to interpet and doesn't really give us any information.

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



This biplot sucks! We need to build our own PCA score plot of PC1 vs PC2

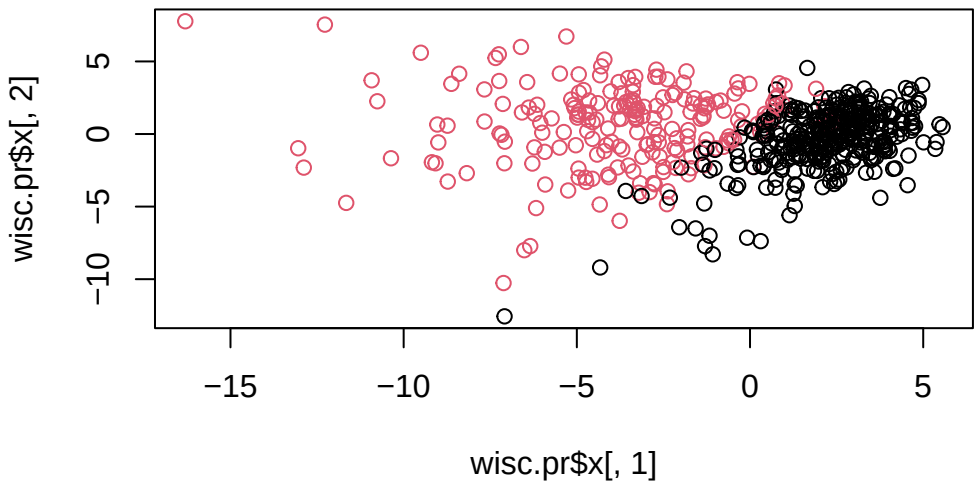
```
head(wisc.pr$x)
```

```
               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 of PC1 vs PC2 the first two columns

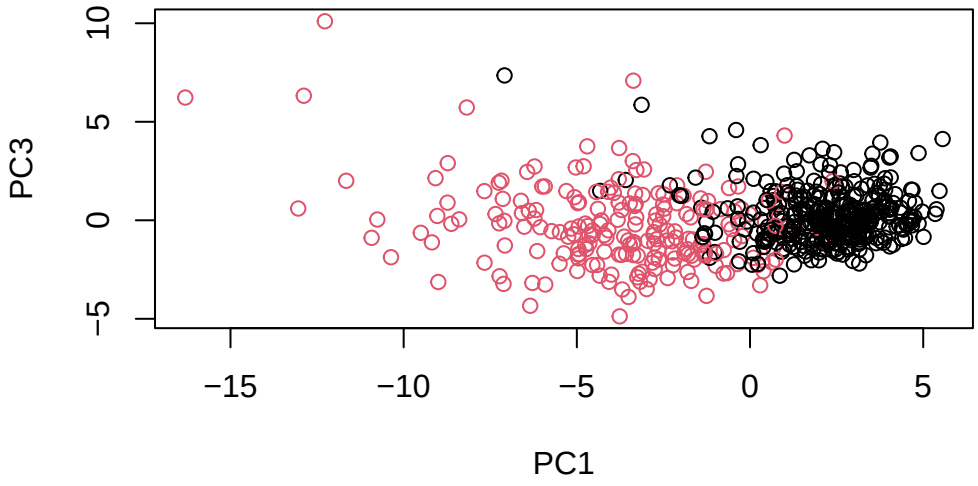
```
plot(wisc.pr$x[,1], wisc.pr$x[,2], col=diagnosis)
```



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

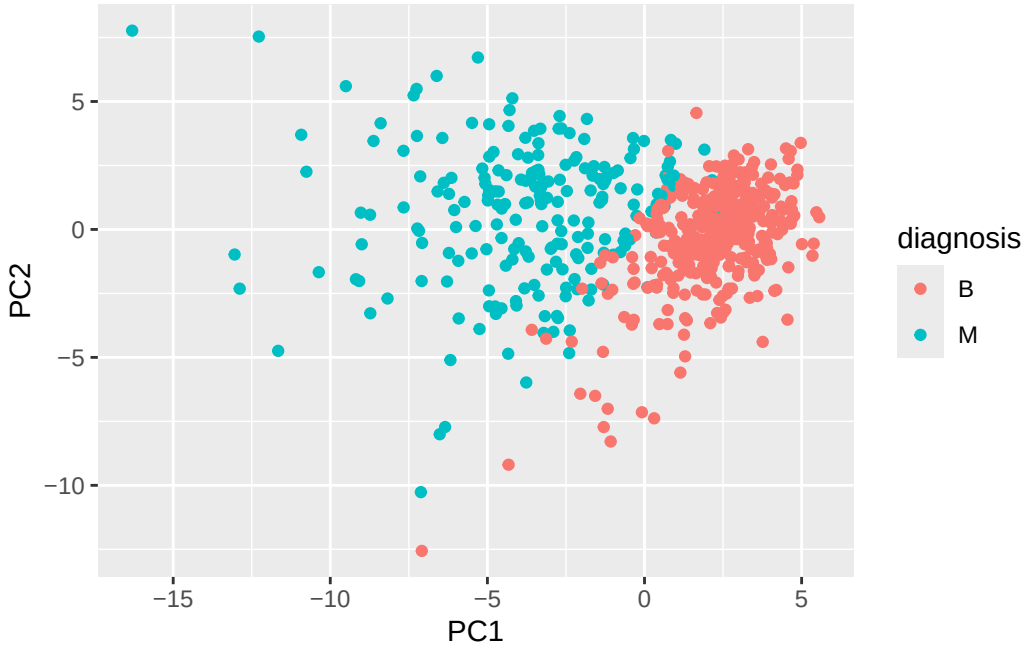
Ans. I noticed that there are still two distinct clusters being showed on the graph, but it is not as distinct compared to PC1 vs PC2 graph.

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



Make a ggplot version of this score plot.

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

ggplot(pc)+
  aes(x=PC1, y=PC2, col=diagnosis) +
  geom_point()
```



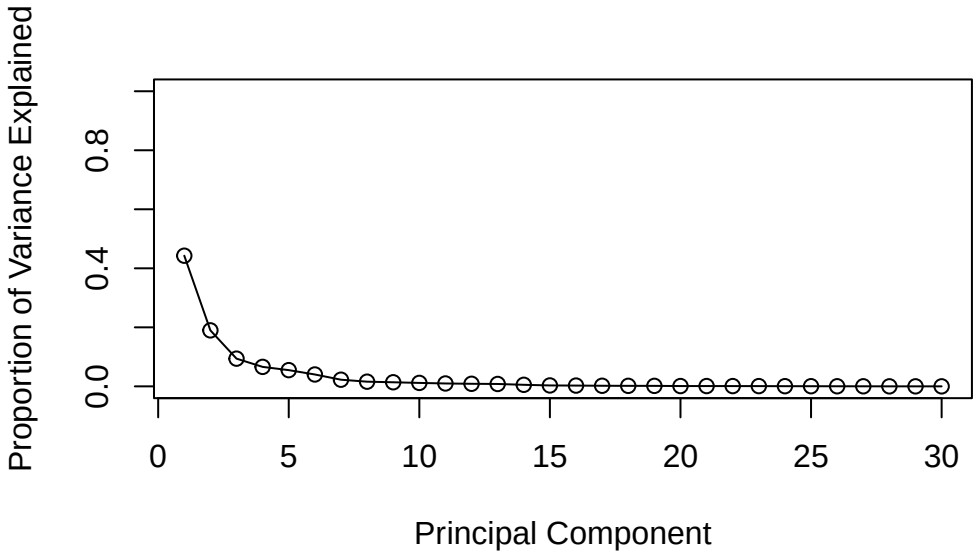
Variance explained

We will first calculate the variance

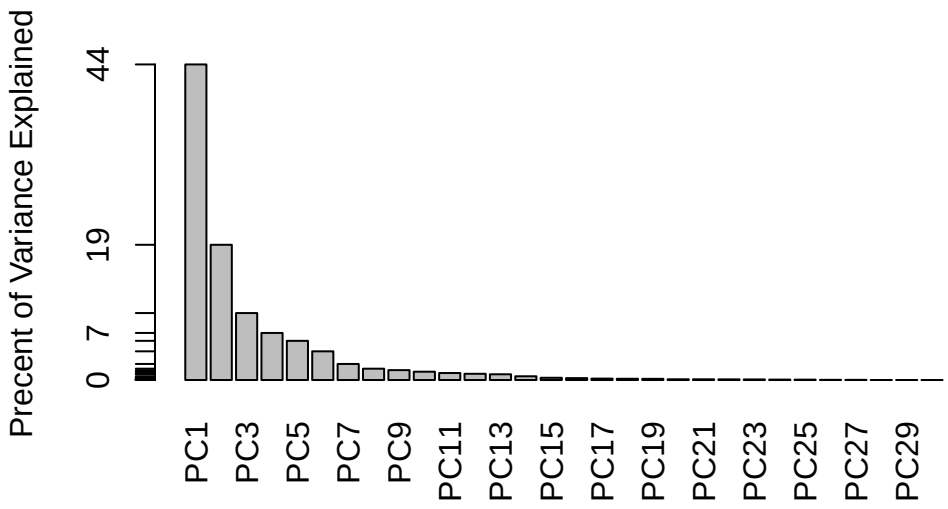
```
# Calculate variance of each component
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

```
[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 )
```

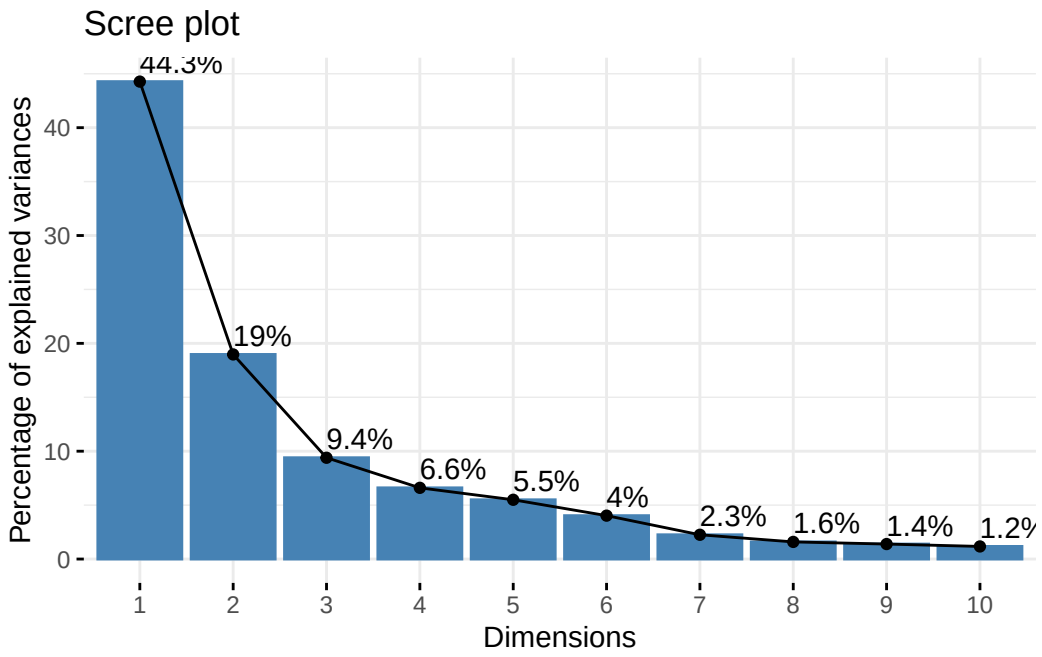


Optional Cran packages:

```
## 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?

Ans. The component of the loading vector for the feature concave.points_mean is -0.2608538.

```
wisc.pr$rotation["concave.points_mean",1]
```

```
[1] -0.2608538
```

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

Ans. The minimum number of principal components required to explain 80% of the variance of the data is 5 (PC1, PC2, PC3, PC4, & PC5).

Hierarchical clustering

First thing I need to do is scale the data.

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

Then I need to calculate the distance.

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

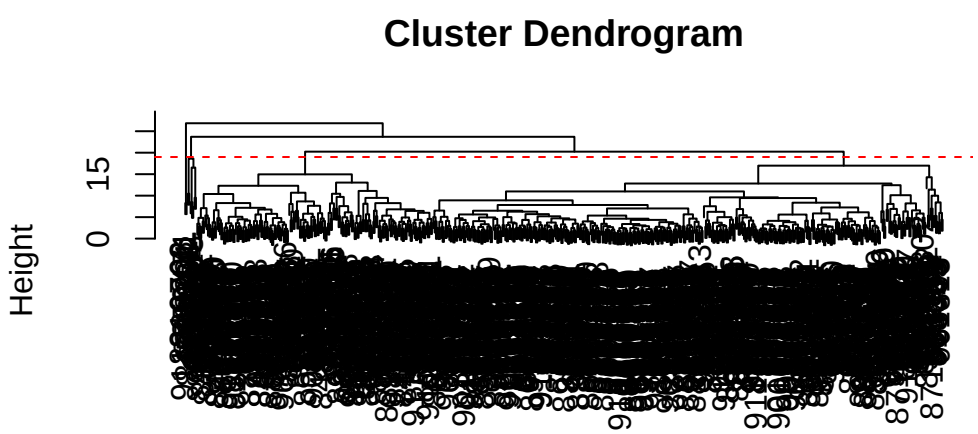
Finally, I need to create a hierarchical clustering model with complete linkage

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

```
Call:
hclust(d = data.dist, method = "complete")

Cluster method   : complete
Distance         : euclidean
Number of objects: 569
```

> Q11. Using the plot() and abline() functions, what is the height at which the clustering model has 4 clusters?
>
> Ans. The clustering model has 4 clusters at a height of 19.

```
plot(wisc.hclust)
abline(h=19, col="red", lty=2)
```



Selecting numbers of cluster

Cut the tree in order to get 4 clusters and use table to compare the data.

```
wisc.hclust.clusters <- cutree(wisc.hclust, h=19)
table(wisc.hclust.clusters, diagnosis)
```

```
                    diagnosis
wisc.hclust.clusters   B   M
                   1  12 165
                   2   2   5
                   3 343  40
                   4   0   2
```

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

Ans. I can't find a better cluster vs diagnoses by cutting the tree into a different number of clusters between 2 and 10. If I have more than 4 clusters, the malignant and benign are more spread out. If I have less than 4 clusters, the malignant and benign are in the same cluster.

```
wisc.hclust.clusters.7 <- cutree(wisc.hclust, h=16)
table(wisc.hclust.clusters.7, diagnosis)
```

```
                     diagnosis
wisc.hclust.clusters.7   B   M
                     1  12 165
                     2   0   3
                     3 331  39
                     4   2   0
                     5  12   1
                     6   0   2
                     7   0   2
```

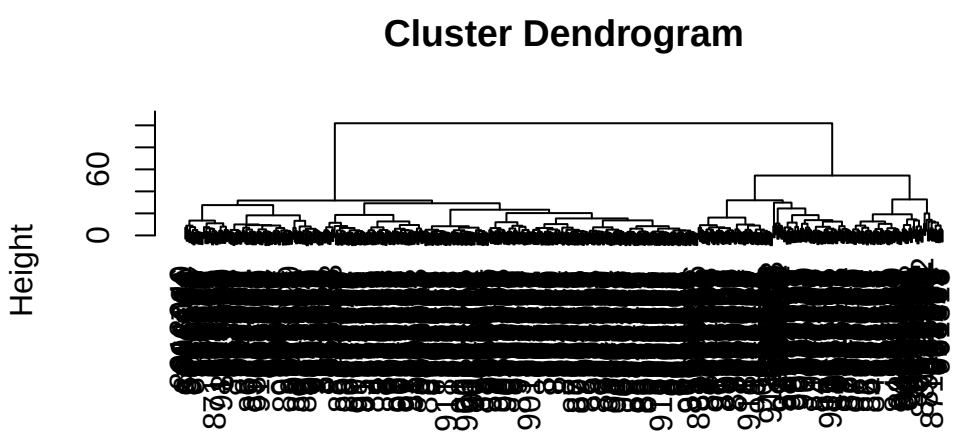
```
wisc.hclust.clusters.3 <- cutree(wisc.hclust, h=21)
table(wisc.hclust.clusters.3, diagnosis)
```

```
                     diagnosis
wisc.hclust.clusters.3   B   M
                     1 355 205
                     2   2   5
                     3   0   2
```

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

Ans. My favorite result for the same data.dist dataset is ward.D2 because the data is easier to see. I also like that they centered the dendrogram in the middle compared to the "complete" with the top of the data being closer to the left.

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



K-means clustering

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

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

```
   diagnosis
      B   M
  1 356  82
  2   1 130
```

```
table(wisc.hclust.clusters, wisc.km$cluster)
```

```
wisc.hclust.clusters   1   2
                   1  68 109
                   2   5   2
                   3 365  18
                   4   0   2
```

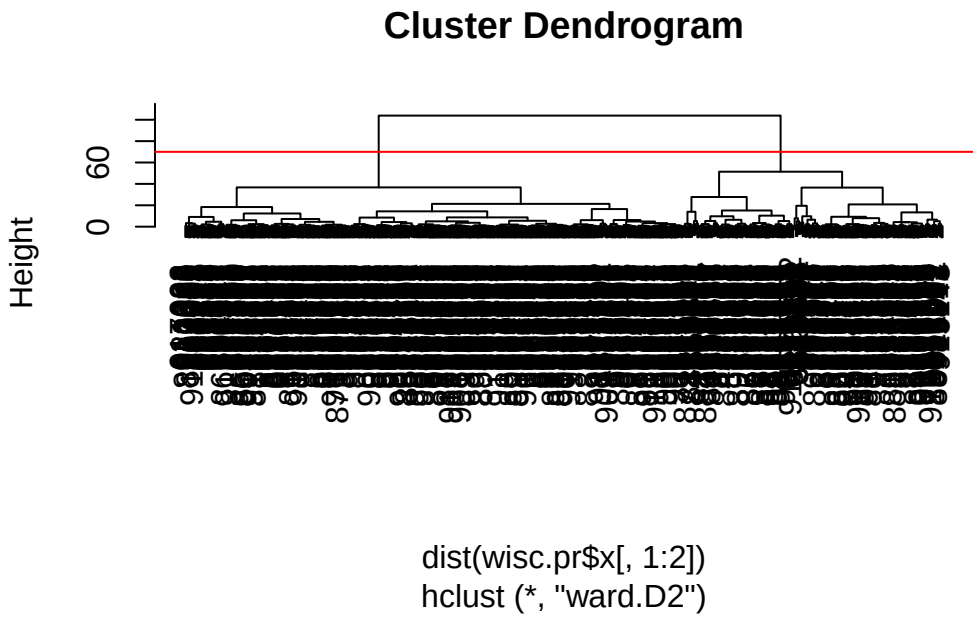
Q14. How well does k-means separate the two diagnoses? How does it compare to your hclust results?

Ans. K-means separate the two diagnoses decently, but it doesn't separate them perfectly. Each cluster still contain both of the diagnosis, but cluster 1 has a better ratio of separation compared to cluster 2. The hclust results separates them into 4 cluster, with two clusters containing majority of the data (Cluster 1 and 3). Hclust seaprates the two dianoses decently, but it doesn't separate them perfectly too. Cluster 1 has almost ~60% benign and ~40% malignant which is poor separation, but cluster 2 has ~5% benign and 95% malignant which is a pretty good separation.

Combining methods

Clustering in PC space

```
hc <- hclust(dist(wisc.pr$x[,1:2]), method = "ward.D2")

plot(hc)
abline(h=70, col="red")
```



Cluster membership vector

```
groups <- cutree(hc, h=70)
table(groups)
```

```
groups
  1   2
195 374
```

```
table(diagnosis)
```

```
diagnosis
  B   M
357 212
```

Cross-table to see how my clustering groups correspond to the expert diagnosis vector of M and B values

```
table(groups, diagnosis)
```

```
      diagnosis
groups   B   M
     1  18 177
     2 339  35
```

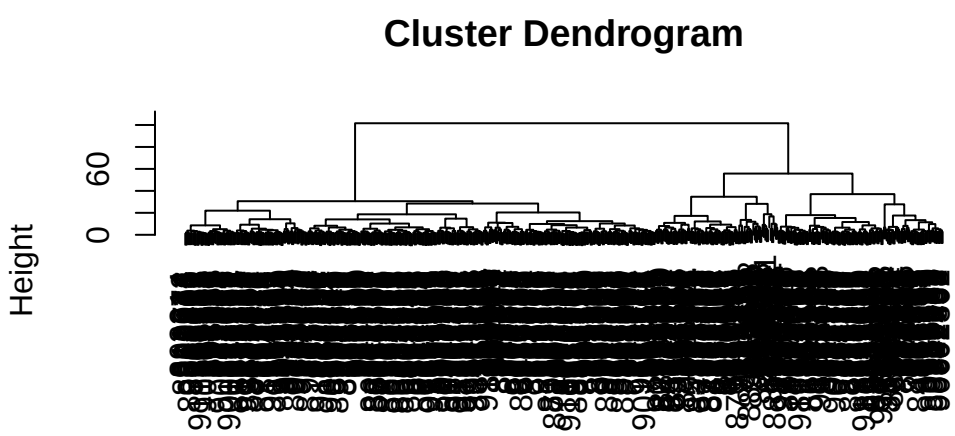
Positive => cancer M Negative => non-cancer B

True = cluster/group 1 False = group 2

True Positive = 177 False Positive = 35 True Negative = 18 False Negative = 339

Create a dendrogram with 7 principal components

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

plot(wisc.pr.hclust)
```




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

```
grps
  1   2
216 353
```

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

```
    diagnosis
grps   B   M
   1  28 188
   2 329  24
```

```
## Use the distance along the first 7 PCs for clustering i.e. wisc.pr$x[, 1:7]
wisc.pr.hclust <- hclust(dist(wisc.pr$x[,1:7]), method="ward.D2")
wisc.pr.hclust.clusters <- cutree(wisc.pr.hclust, k=2)
```

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

Ans. The newly created model contains 2 clusters which is similar to the four clusters (cluster 1 and 3). Therefore, there isn't much of a difference and they both similarlly separate our the two diagnosis.

```
# Compare to actual diagnoses
table(wisc.pr.hclust.clusters, diagnosis)
```

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

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.

Ans. I think the k-mean clustering models did a good job separating malignant and benign in cluster 1, but did a poorer job at separating the diagnosis in cluster 2.

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

```
   diagnosis
      B   M
  1 356  82
  2   1 130
```

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

```
                    diagnosis
wisc.hclust.clusters   B   M
                   1  12 165
                   2   2   5
                   3 343  40
                   4   0   2
```

Sensitivity/Specificity

Sensitivity is the ability to correctly diagnose patients with the condition. I would divide true positive by true positive plus false negative. (TP/(TP+FN)) Specificity is the ability to correctly reject any patients with the benign condition. In order to do that, I would divide true negative by true negative plus false positive. (TN/(TN+FP)).

> Q17. Which of your analysis procedures resulted in a clustering model with the best specificity? How about sensitivity?
>
> Ans. The clustering model with the best specificity and sensitivity is the PCA clustering. They had a higher sensitivity and specificity value compared to kmeans.

Calculations: Positive => cancer M Negative => non-cancer B

True = group 1 False = group 2

True Positive = 130 False Positive = 82 True Negative = 1 False Negative = 356

Kmeans sensitivity:(TP/(TP+FN)) = (130/(130+356)) = 0.2675 Kmeans specificity:(TN/(TN+FP)) = (1/(1+82)) = 0.0120

Positive => cancer M Negative => non-cancer B

True = group 1 False = group 2

True Positive = 188 False Positive = 24 True Negative = 28 False Negative = 329

PCA clustering sensitivity:(TP/(TP+FN)) = (188/(188+329)) = 0.3636 PCA clustering specificity:(TN/(TN+FP)) = (28/(28+24)) = 0.5385

#Prediction

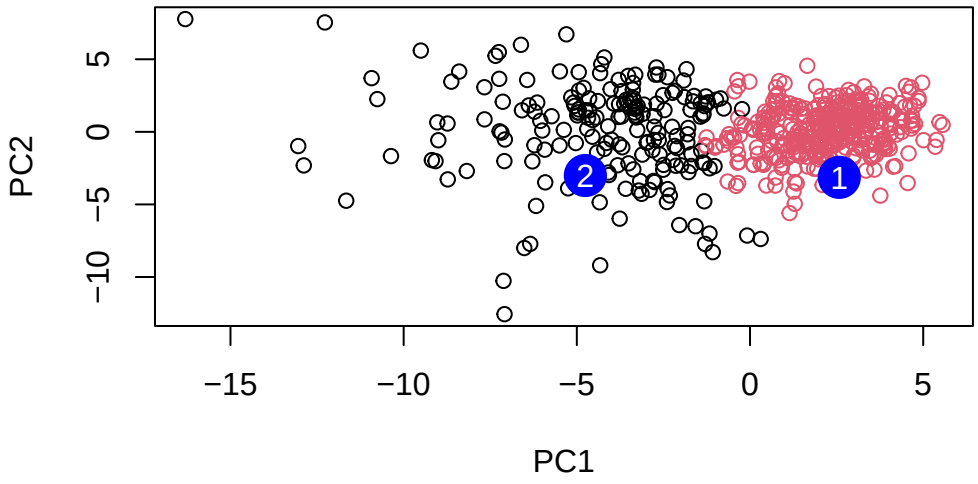
We can use our PCA results (wisc.pr) to make predictions on new unseen data.

```
#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
```

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

Ans. Based on the results, We should prioritize patient 2 because they are likely to have the malignant (cancerous) condition based on their sample.