Class 8: PCA Mini Project

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Today we will do a complete analysis of some breast cancer biopsy data but first let's revisit the main PCA function in R `prcomp()` 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 data set?

```
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 
```

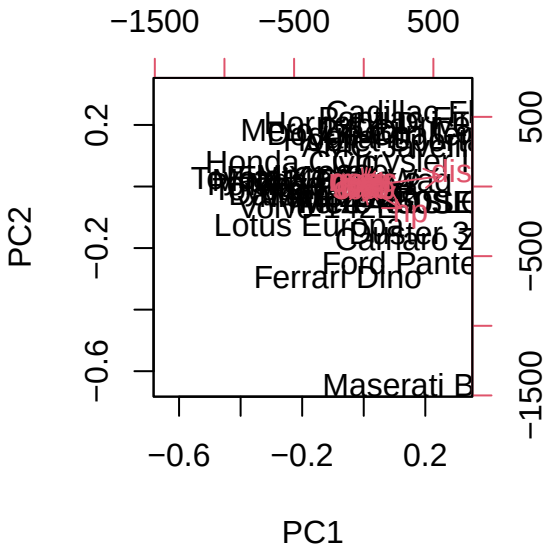
```
apply(mtcars, 2, sd)
```

```
       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 that "disp" and "hp" have the highest mean values and standard deviation. They will likely dominate any analysis I do on this data set. Let's see:

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

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



Rotation tells us how much each is contributing to the PCs.

```
pc.noscale$rotation
```

```
              PC1          PC2          PC3          PC4          PC5
mpg  -0.038118199  0.009184847  0.982070847  0.047634784 -0.08832843
cyl   0.012035150 -0.003372487 -0.063483942 -0.227991962  0.23872590
disp  0.899568146  0.435372320  0.031442656 -0.005086826 -0.01073597
hp    0.434784387 -0.899307303  0.025093049  0.035715638  0.01655194
drat -0.002660077 -0.003900205  0.039724928 -0.057129357 -0.13332765
wt    0.006239405  0.004861023 -0.084910258  0.127962867 -0.24354296
qsec -0.006671270  0.025011743 -0.071670457  0.886472188 -0.21416101
vs   -0.002729474  0.002198425  0.004203328  0.177123945 -0.01688851
am   -0.001962644 -0.005793760  0.054806391 -0.135658793 -0.06270200
```

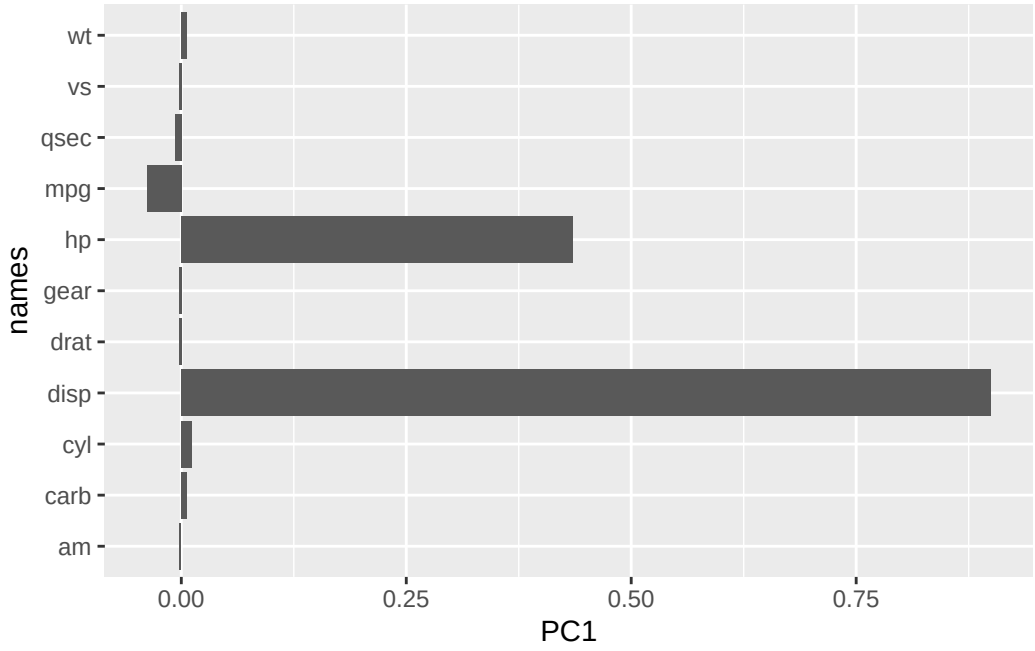
```
gear -0.002604768 -0.011272462  0.048524372 -0.129913811 -0.27616440
carb  0.005766010 -0.027779208 -0.102897231 -0.268931427 -0.85520810
              PC6          PC7           PC8          PC9          PC10
mpg  -0.143790084 -0.039239174 -2.271040e-02 -0.002790139  0.030630361
cyl  -0.793818050  0.425011021  1.890403e-01  0.042677206  0.131718534
disp  0.007424138  0.000582398  5.841464e-04  0.003532713 -0.005399132
hp    0.001653685 -0.002212538 -4.748087e-06 -0.003734085  0.001862554
drat  0.227229260  0.034847411  9.385817e-01 -0.014131110  0.184102094
wt   -0.127142296 -0.186558915 -1.561907e-01 -0.390600261  0.829886844
qsec -0.189564973  0.254844548  1.028515e-01 -0.095914479 -0.204240658
vs    0.102619063 -0.080788938  2.132903e-03  0.684043835  0.303060724
am    0.205217266  0.200858874  2.273255e-02 -0.572372433 -0.162808201
gear  0.334971103  0.801625551 -2.174878e-01  0.156118559  0.203540645
carb -0.283788381 -0.165474186 -3.972219e-03  0.127583043 -0.239954748
              PC11
mpg   0.0158569365
cyl  -0.1454453628
disp -0.0009420262
hp    0.0021526102
drat  0.0973818815
wt    0.0198581635
qsec -0.0110677880
vs   -0.6256900918
am   -0.7331658036
gear  0.1909325849
carb -0.0557957968
```

Plot the loadings

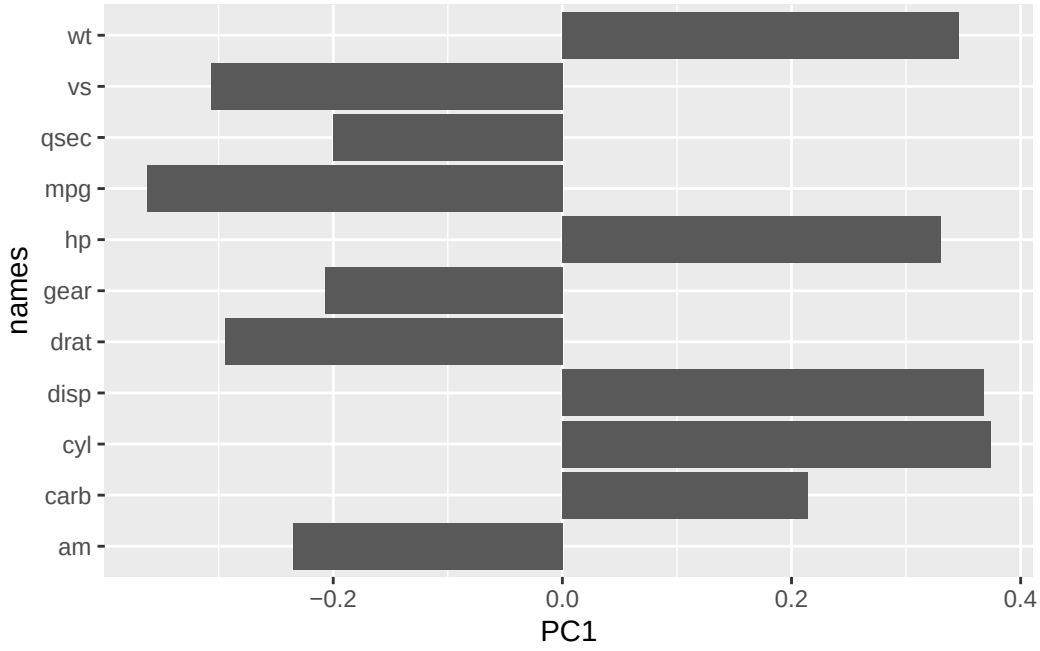
```
library(ggplot2)
```

```
Warning: package 'ggplot2' was built under R version 4.3.3
```

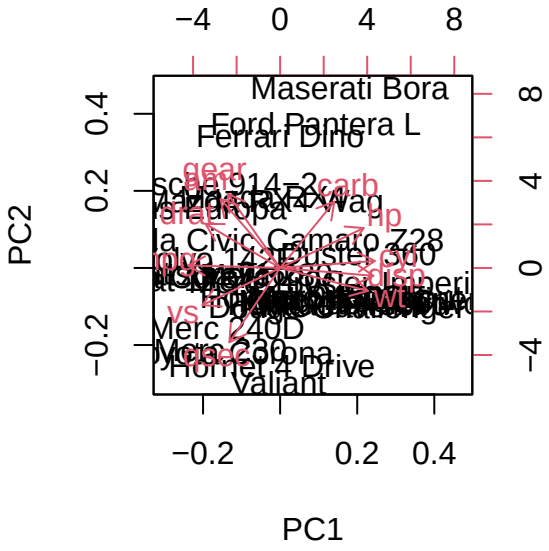
```
r1 <- as.data.frame(pc.noscale$rotation)
r1$names <- rownames(pc.noscale$rotation)

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 you always want to set `scale=TRUE` (this scales the sd in

columns to 1) 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. We saved this csv into our project folder for this project.

```
wisc.df <- read.csv("WisconsinCancer.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? (how many individuals?)

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

```
[1] 569
```

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

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

```
[1] 212
```

The `table()` function is super useful here is will tabulate everything in the column we specify. In this case it will give us both "M" and "B."

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

```
  B   M
357 212
```

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

The number of columns:

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

```
[1] 31
```

The names of columns:

```
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()`. It prints out the number of the column that features our "_mean." Adding `length()` will tell us how many there are.

```
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.

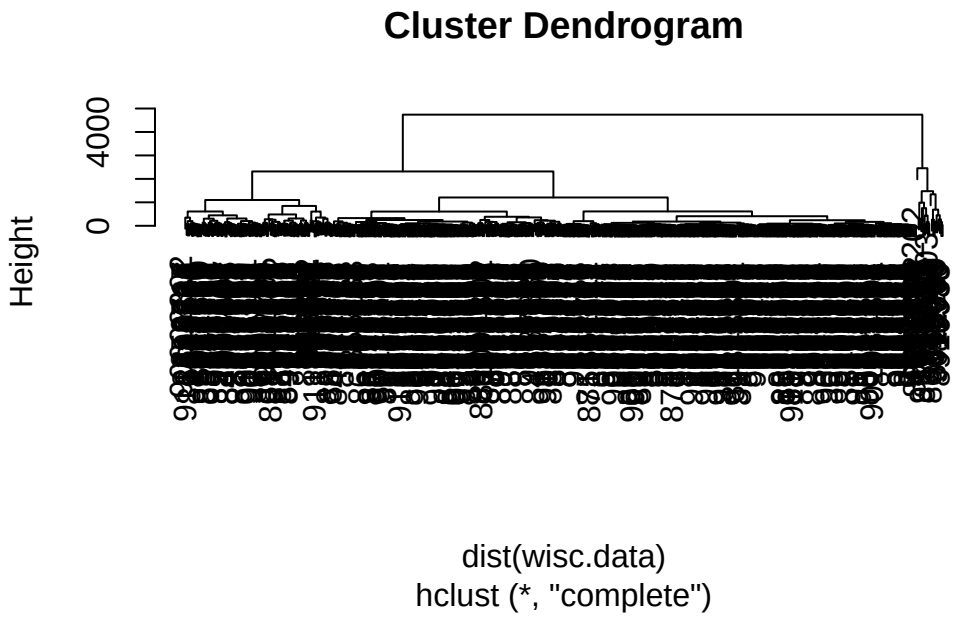
```
diagnosis <- as.factor(wisc.df$diagnosis)
head(diagnosis)
```

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

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

Let's see if we can cluster with `wisc.data` to find some structure.

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



Principal Component Analysis (PCA)

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

```
Importance of components:
                          PC1    PC2     PC3     PC4     PC5     PC6     PC7
Standard deviation     3.6444 2.3857 1.67867 1.40735 1.28403 1.09880 0.82172
Proportion of Variance 0.4427 0.1897 0.09393 0.06602 0.05496 0.04025 0.02251
Cumulative Proportion  0.4427 0.6324 0.72636 0.79239 0.84734 0.88759 0.91010
                           PC8    PC9    PC10   PC11    PC12    PC13    PC14
Standard deviation     0.69037 0.6457 0.59219 0.5421 0.51104 0.49128 0.39624
Proportion of Variance 0.01589 0.0139 0.01169 0.0098 0.00871 0.00805 0.00523
Cumulative Proportion  0.92598 0.9399 0.95157 0.9614 0.97007 0.97812 0.98335
                          PC15    PC16    PC17    PC18    PC19    PC20   PC21
Standard deviation     0.30681 0.28260 0.24372 0.22939 0.22244 0.17652 0.1731
Proportion of Variance 0.00314 0.00266 0.00198 0.00175 0.00165 0.00104 0.0010
Cumulative Proportion  0.98649 0.98915 0.99113 0.99288 0.99453 0.99557 0.9966
                          PC22    PC23   PC24    PC25    PC26    PC27    PC28
Standard deviation     0.16565 0.15602 0.1344 0.12442 0.09043 0.08307 0.03987
Proportion of Variance 0.00091 0.00081 0.0006 0.00052 0.00027 0.00023 0.00005
Cumulative Proportion  0.99749 0.99830 0.9989 0.99942 0.99969 0.99992 0.99997
                          PC29    PC30
Standard deviation     0.02736 0.01153
Proportion of Variance 0.00002 0.00000
Cumulative Proportion  1.00000 1.00000
```

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

44% is captured by PC1.

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

3 principal components are required.

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

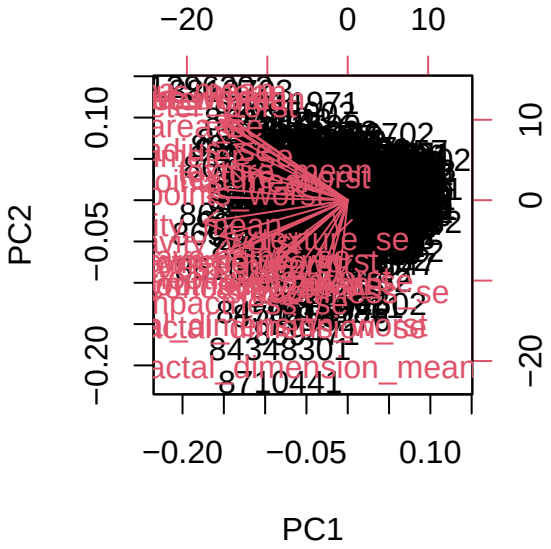
7 principal components are required.

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

This plot is hard to visualize and separate individual components, and is difficult to understand because of this. The use of row names makes it difficult to visualize.

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

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



Our own and better plot:

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

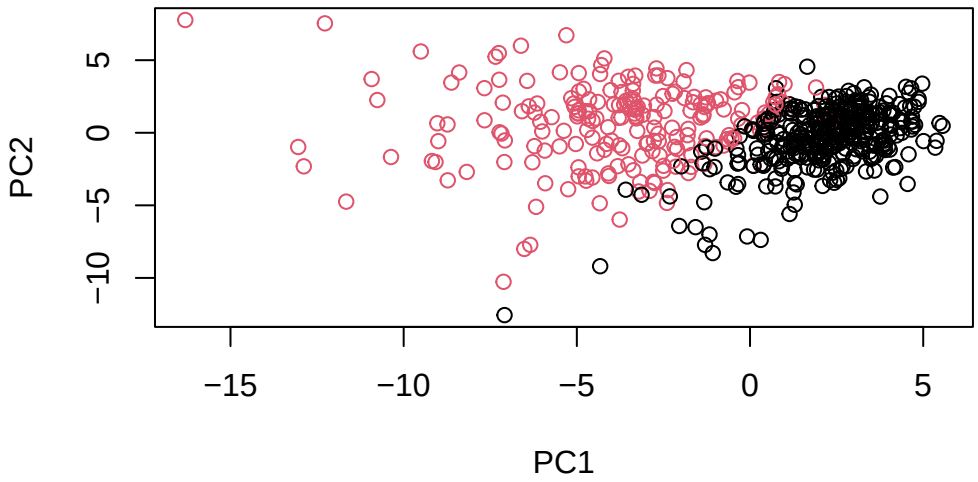
```
$names
[1] "sdev"     "rotation" "center"   "scale"    "x"

$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 of PC1 vs PC2 the first two columns. Each point represents an individual sample.

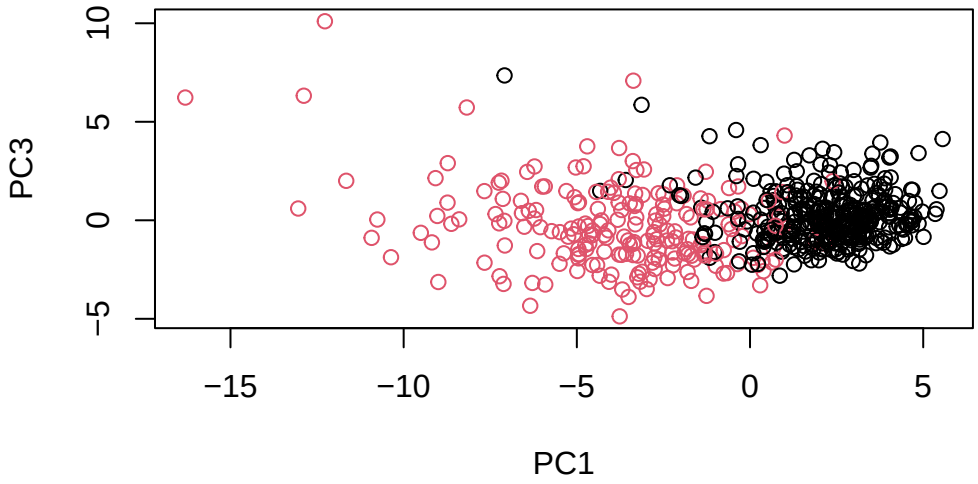
```
plot(wisc.pr$x[,1], wisc.pr$x[,2], xlab="PC1", ylab="PC2", col=diagnosis)
```



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

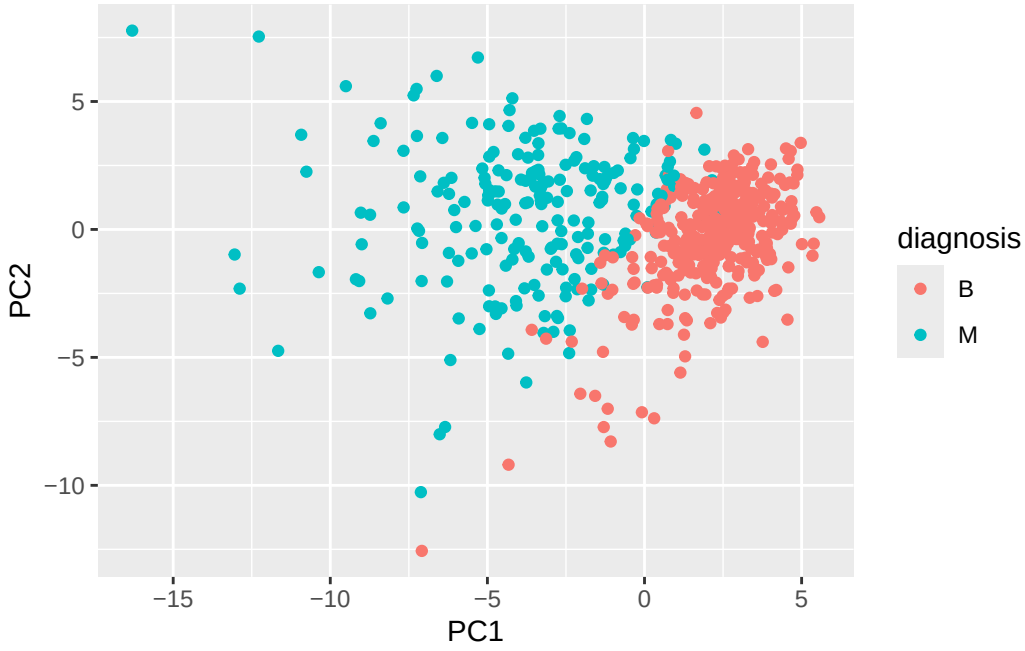
The values for PC3 are lower than that of PC2, so the points are more negative on the graph, since PC2 explains more variance than PC3.

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



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()
```



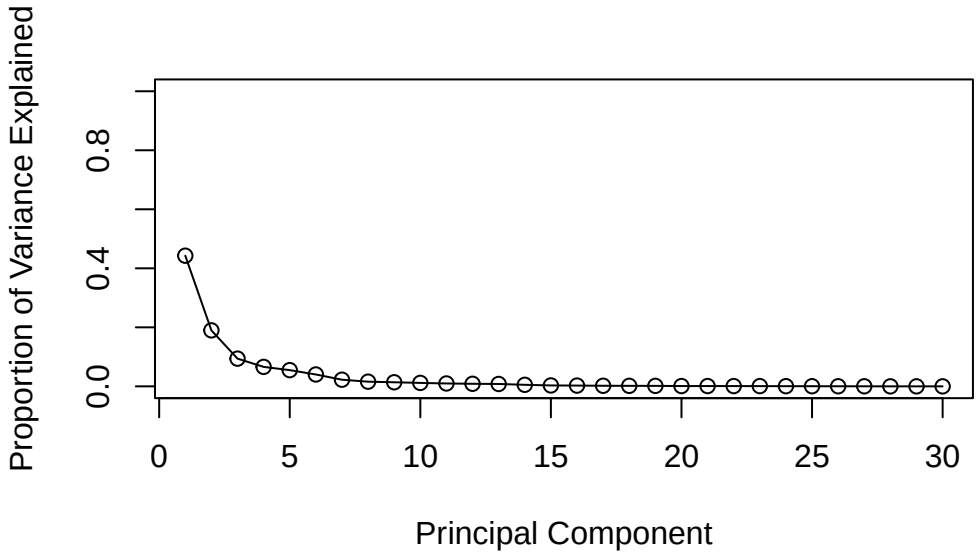
Variance:

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

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

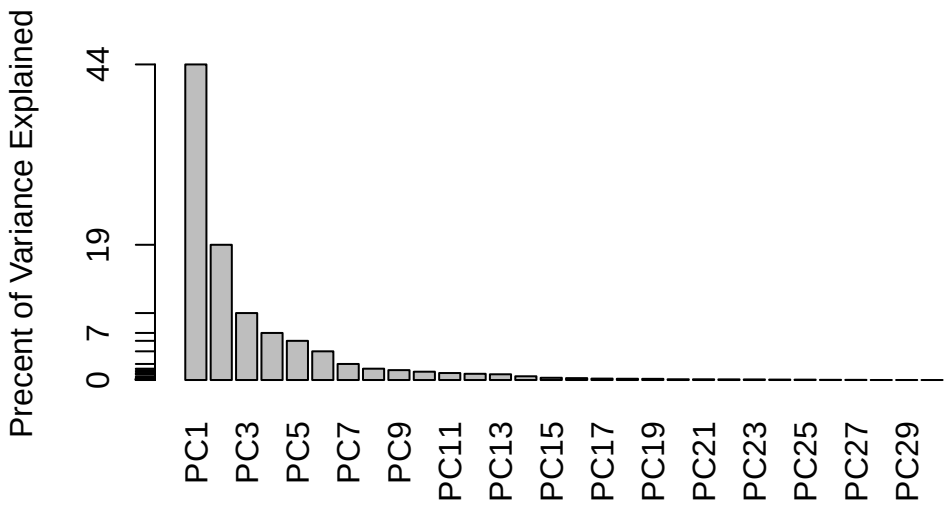
Scree plot:

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

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



Alternative scree plot:

```
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 )
```

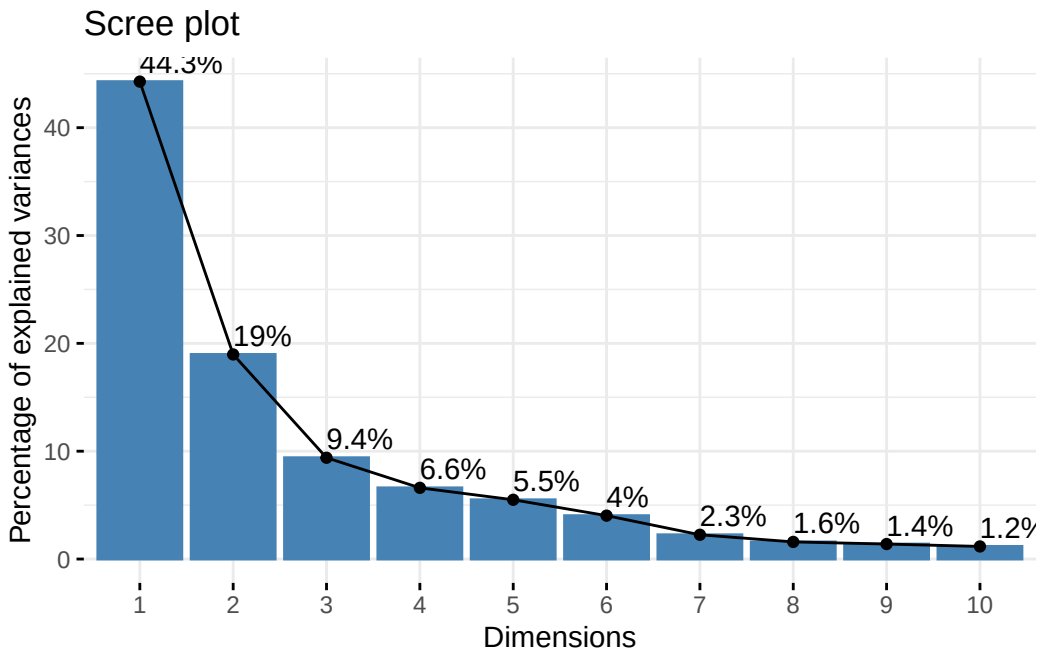



```
library(factoextra)
```

```
Warning: package 'factoextra' was built under R version 4.3.3
```

```
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?

$rotation shows how the original variables contribute to PCs (how they weigh)

```
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?

About 4-5 principal components. PC4 covers 79% while PC5 covers 84%.

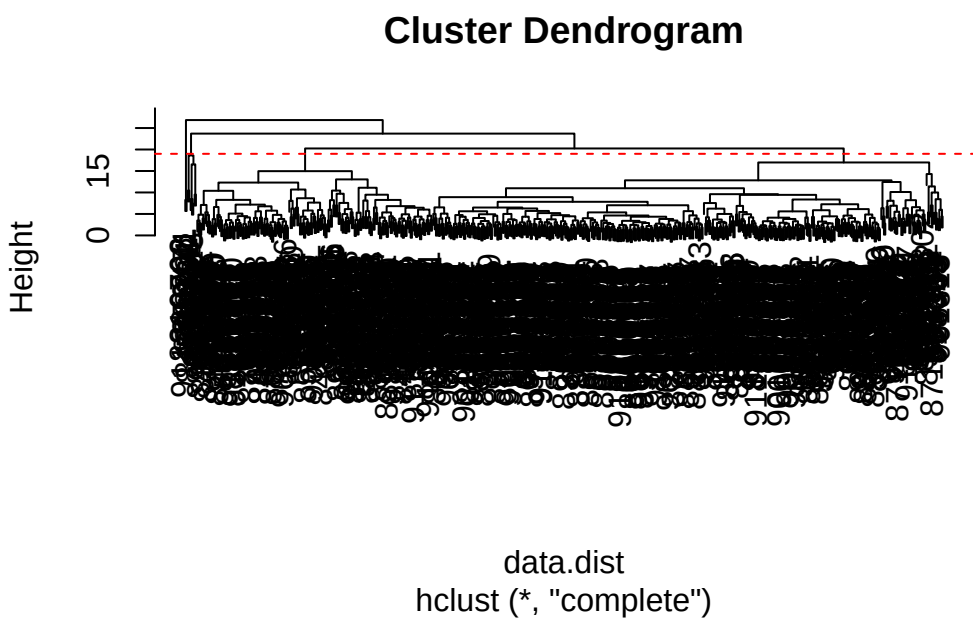
```
data.scaled <- scale(wisc.data)
```

```
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, col="red", lty=2)
```




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

```
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?

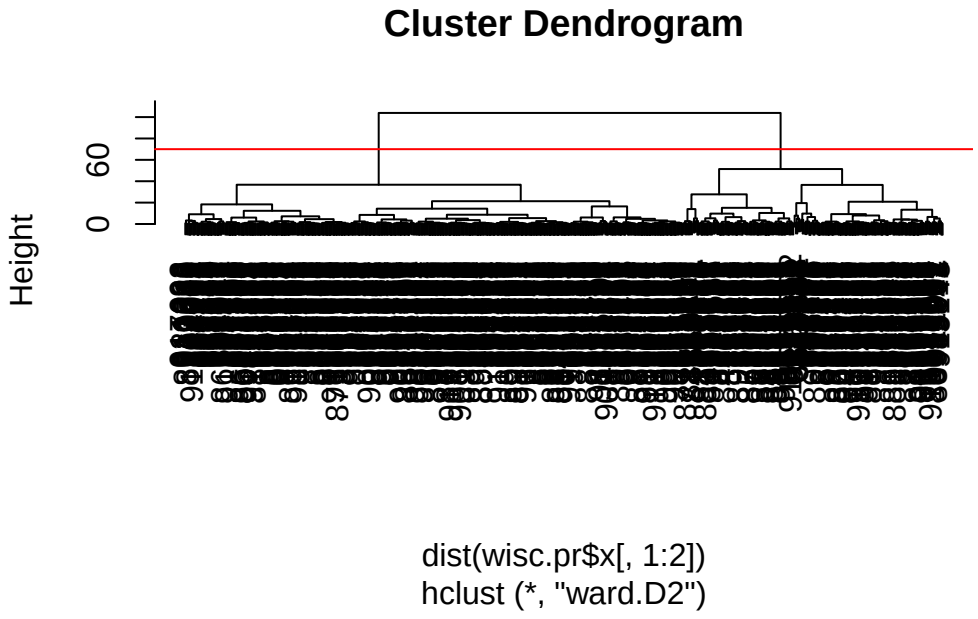
At smaller clusters (e.g. 2) there is no differentiation between B and M. It appears that most points are associated with cluster 1. As you cut more clusters B still corresponds strongly with 3 while M does with 1. Additionally, you get more samples that "stray" away from either cluster 1 or 3 and into other clusters. 4 seems to maintain these associates the most.

Clustering in PC space

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

I think "ward.D2" provides a clearer image of the result we want. "Single" honestly produces a giant mess, and the others appear to be similar to ward.D2, but don't produce a clearer, distinct separation of clusters along one axis.

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

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




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

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

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

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

K-means doesn't do the best job separate the two diagnoses, we see a lot of malignant associated with both cluster1 and 2. I think hclust is more accurate.

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

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

Cluster membership vector

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

```
grps
  1   2
195 374
```

```
table(diagnosis)
```

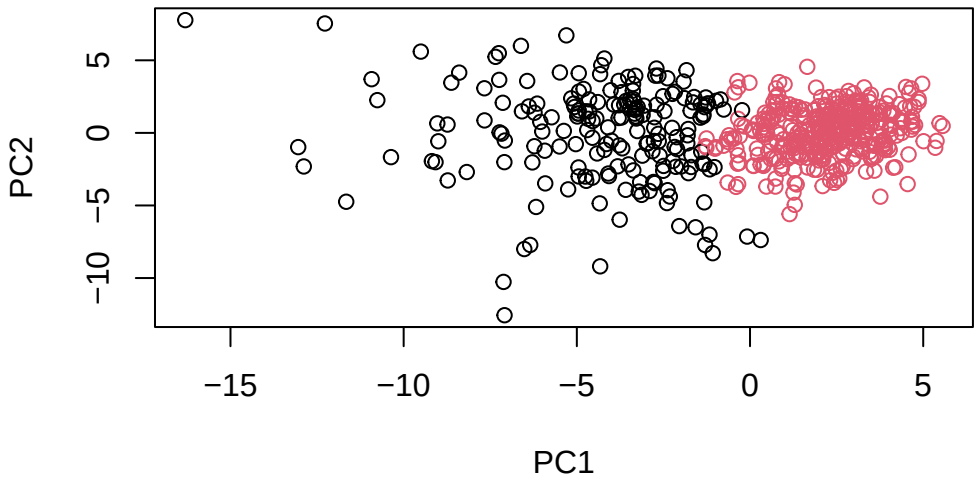
```
diagnosis
  B   M
357 212
```

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

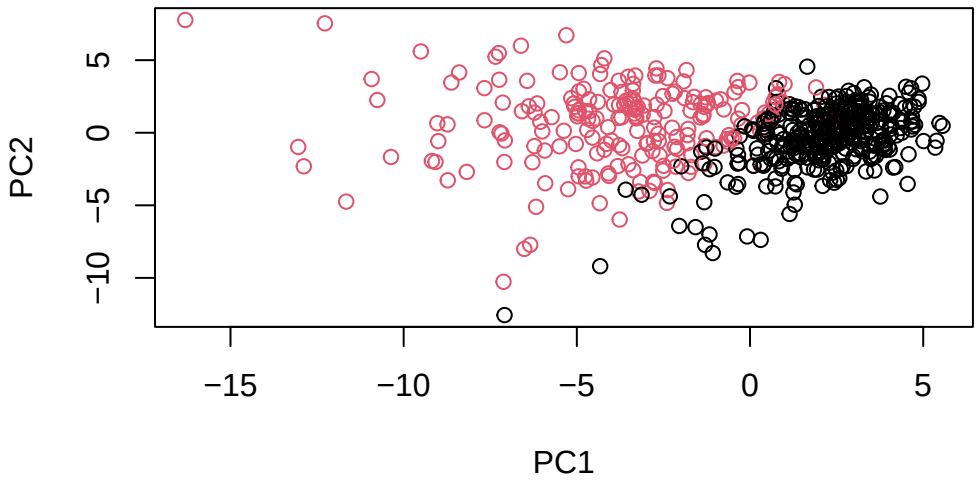
```
table(grps, diagnosis)
```

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

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




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



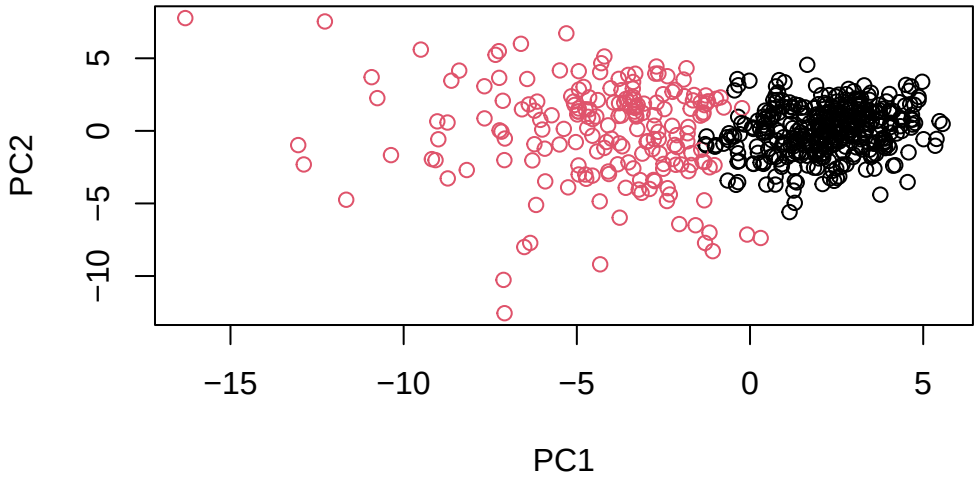
```
g <- as.factor(grps)
levels(g)
```

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

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

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

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




```
library(rgl)
```

```
Warning: package 'rgl' was built under R version 4.3.3
```

```
plot3d(wisc.pr$x[,1:3], xlab="PC 1", ylab="PC 2", zlab="PC 3", cex=1.5, size=1, type="s", col
```

```
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?

The new model separates the two diagnosis well, but not as well as when we first created the model. There are still a good chunk of B that correspond to cluster1.

```
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.

The other methods arent as accurate as PCA. They do a good job separating points into clusters, but since you have to specify the cluster yourself some points could be associated with an incorrect cluster.

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

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

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

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

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

PCA has a better specifity and sensitivity.

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

True => cluster/grp 1 False => grp 2

True Positive: 177 (grp1 M) False Positive: 18 True Negative: 339 False Negative: 35

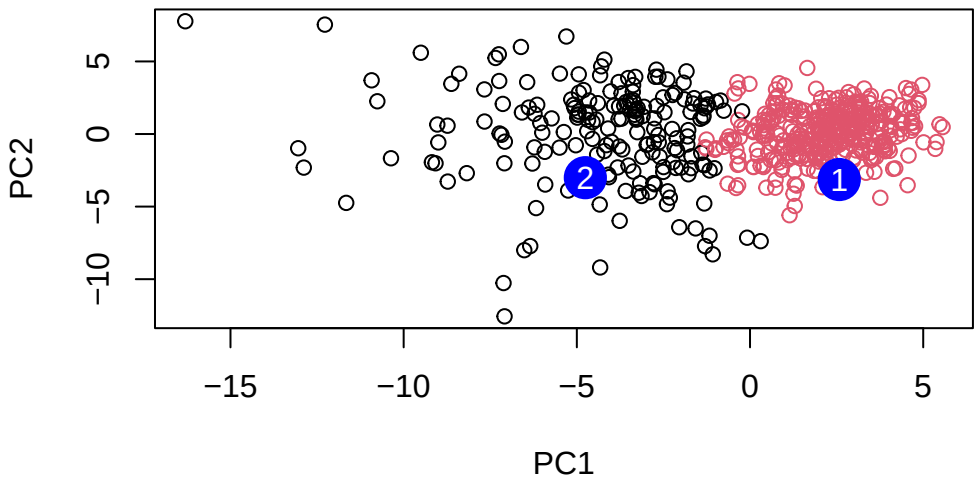
We want to minimize false positive/negatives and optimize true.

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

```
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=grps)
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?

Pt1 should be prioritized, as their sample is clustered with patients in group 1, indicating that their sample is malignant.