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 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 
```

Find the standard deviation per column of this data set.

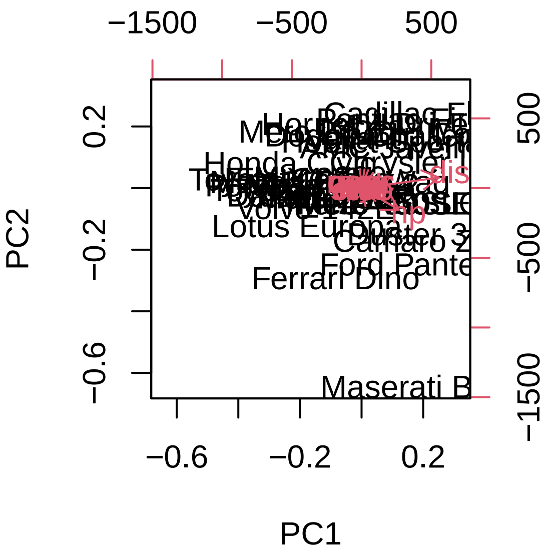
```
apply(mtcars, 2, sd)
```

```
        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 mean values and standard deviation. They will likely dominate any analysis I do on this dataset. Let’s see:

```
pc.noscale <- prcomp(mtcars, scale = F)
pc.scale <- prcomp(mtcars, scale = T)
```

```
# Bi plot of mtcars dataset with no scaling
biplot(pc.noscale)
```

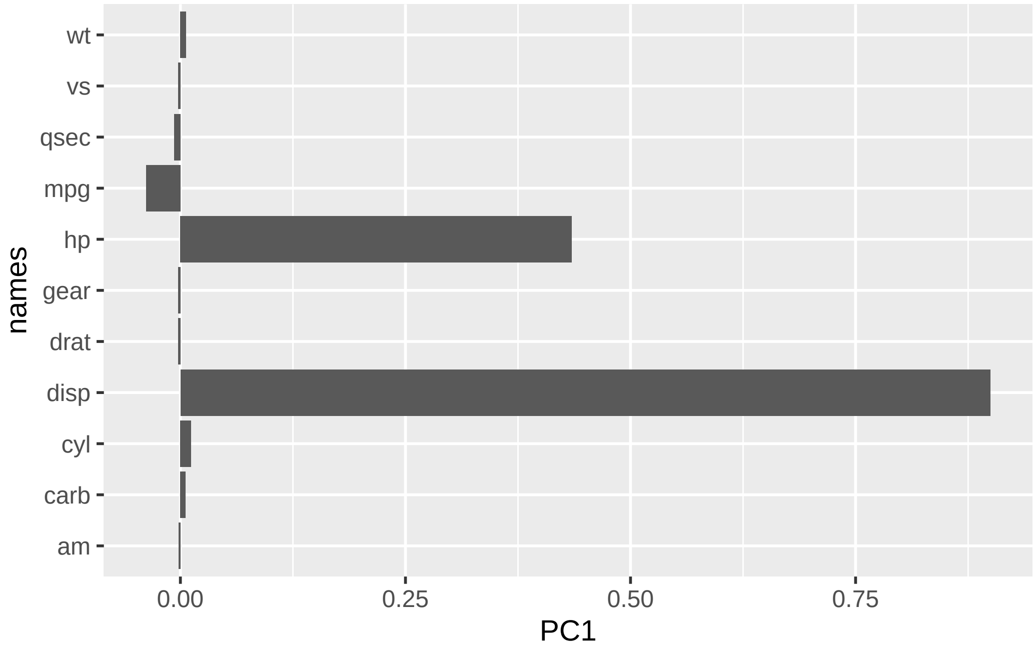


```
# How much each column contributes to the car's position on the plot PC1 vs. PC2
pc.noscale$rotation[ ,1]
```

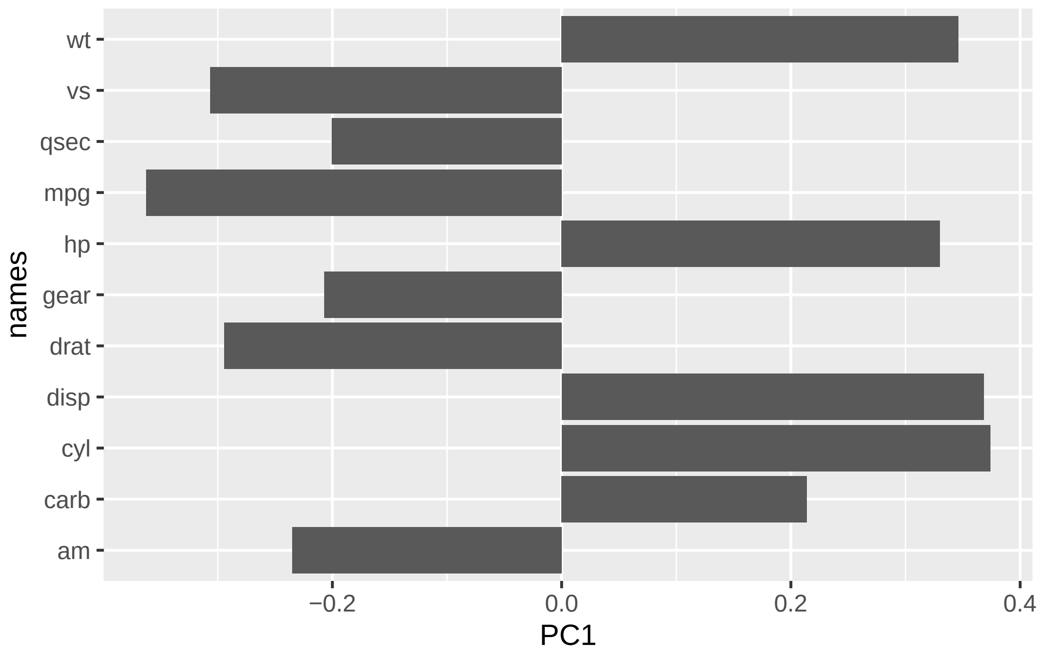
```
         mpg          cyl         disp           hp         drat           wt 
-0.038118199  0.012035150  0.899568146  0.434784387 -0.002660077  0.006239405 
        qsec           vs           am         gear         carb 
-0.006671270 -0.002729474 -0.001962644 -0.002604768  0.005766010 
```

Plot the loadings

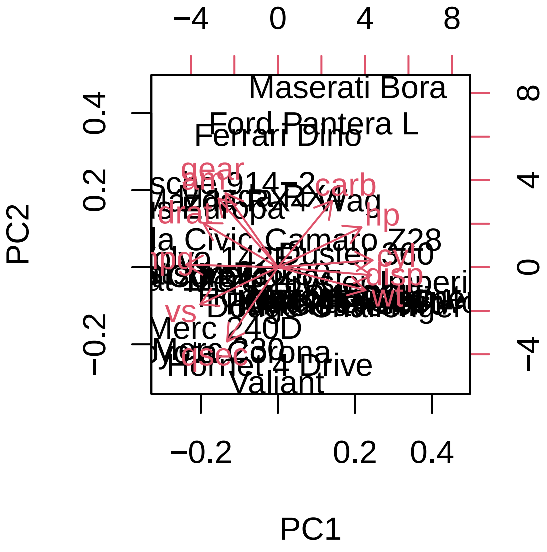
```r
library(ggplot2)

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

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



```r
# ggplot with scaling, gives a fairer distribution
r2 <- as.data.frame(pc.scale$rotation)
r2$names <- rownames(pc.scale$rotation)

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



```r
# Bi plot of mtcars with scaling makes it easier to see patterns and similarities in the cars
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.

```r
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?

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

```
[1] 569
```

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

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

```
[1] 212
```

The `table()` function is useful here as well.

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

```

  B   M 
357 212 
```

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

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

```
[1] 31
```

```r
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()`

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

```
[1] 10
```

Before going any further, we need to exclude the diagnoses column for any future analysis - this tells us whether a sample is cancer or non-cancer.

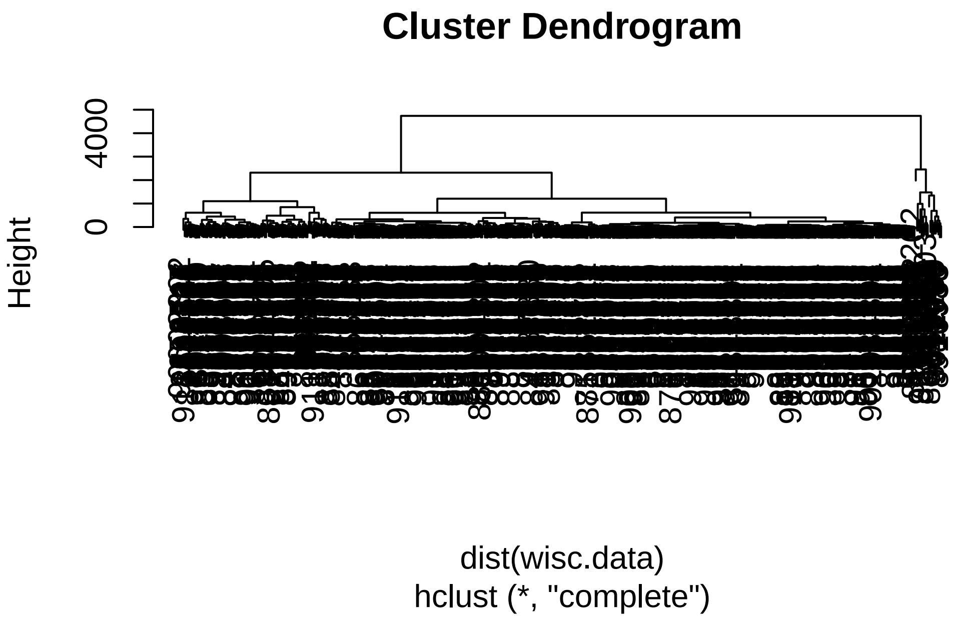
```
diagnosis <- as.factor(wisc.df$diagnosis)
head(diagnosis)
```

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

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

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

```
# The cluster dendrogram for this data is very messy
hc <- hclust( dist(wisc.data))
plot(hc)
```



Principal Component Anaylsis (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)?

Based on the summary, PC1 captures 44% of the original variance.

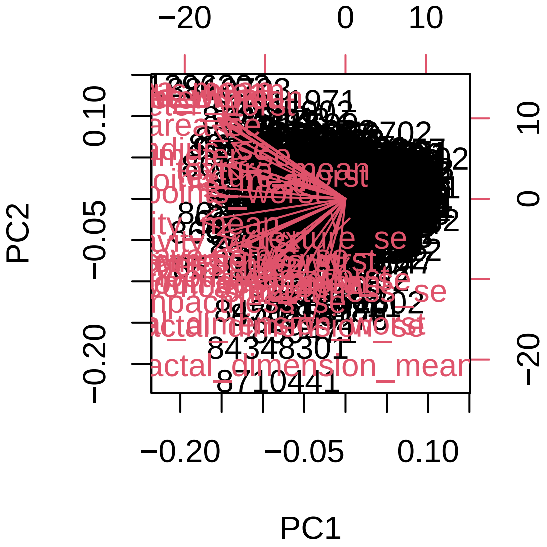
> Q5. How many principal components (PCs) are required to describe at least 70% of the original variance in the data?

The cumulative proportion shows that up to PC3 is required to describe at least 70% of the original variance.

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

The cumulative proportion shows that up to PC6 is required to describe at least 90% of the original variance.

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



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

It is really difficult to understand because it is difficult to see trends when there is a big mess on the plot.

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

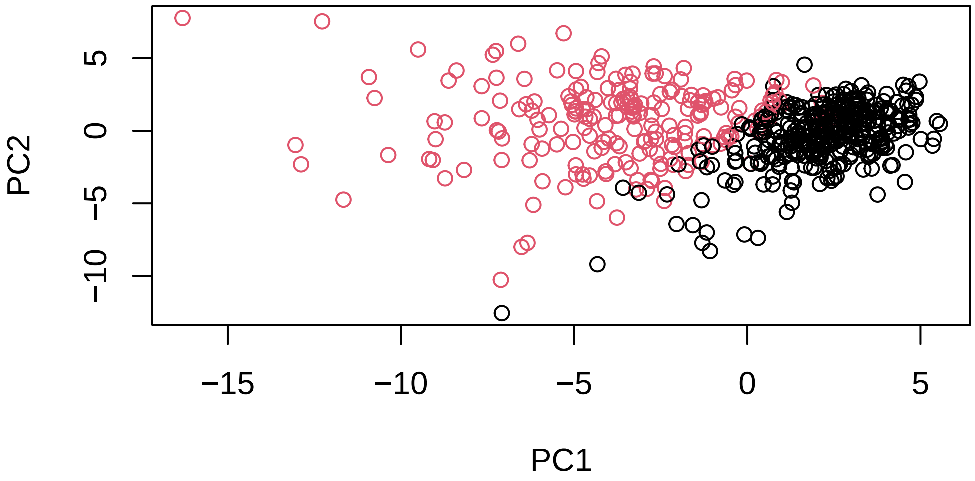
```
head(wisc.pr$x)
```

```
                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
```

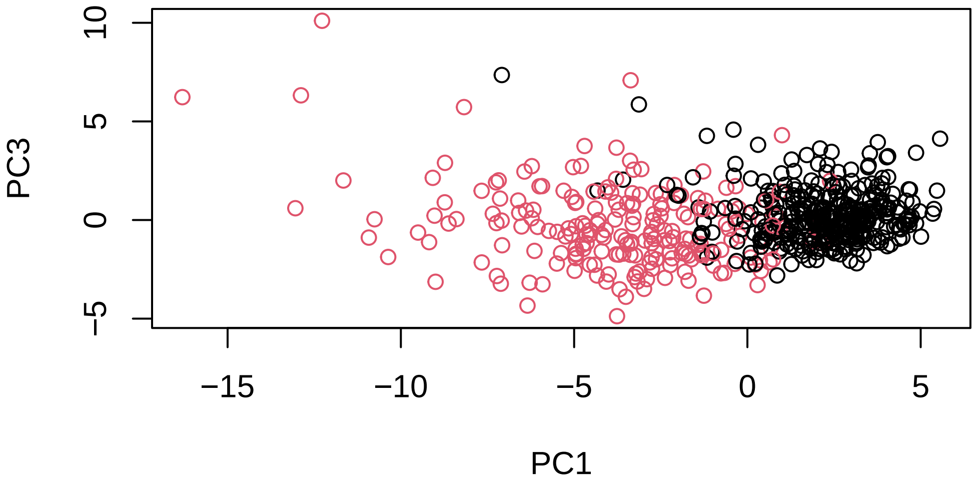
Plot of PC1 vs. PC2, the first two columns

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



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

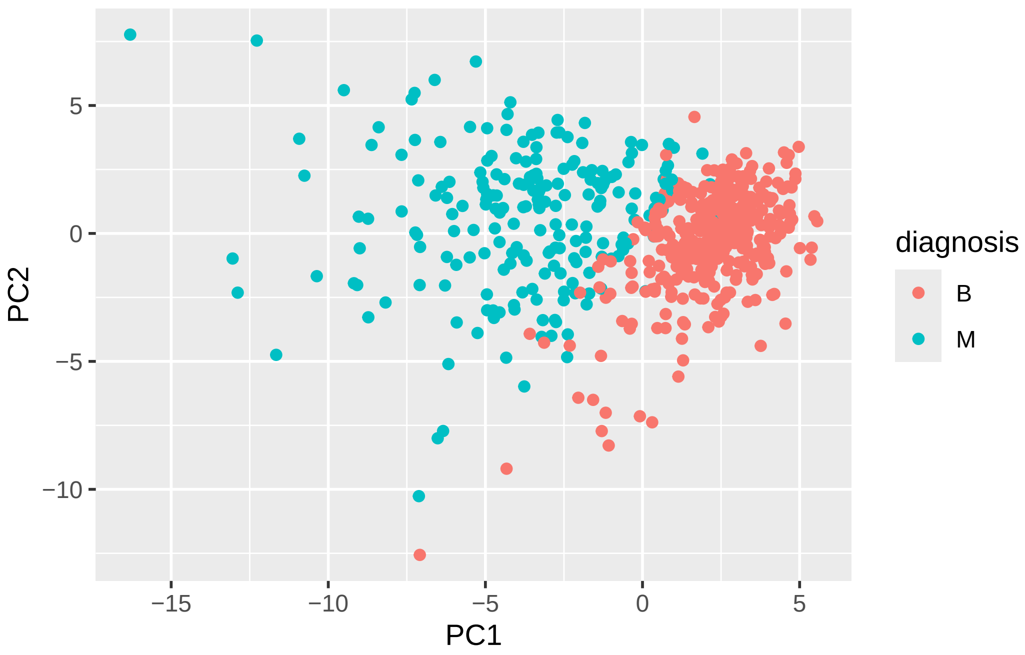
```
plot(wisc.pr$x[,1], wisc.pr$x[,3], col=diagnosis,
     xlab = "PC1", ylab = "PC3")
```



The separation between the two groups are not as clean as the plot vs. PC2, since PC3 represents much less variance in the data. There is some overlap with the red and black points.

Make a ggplot version of this score plot

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

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

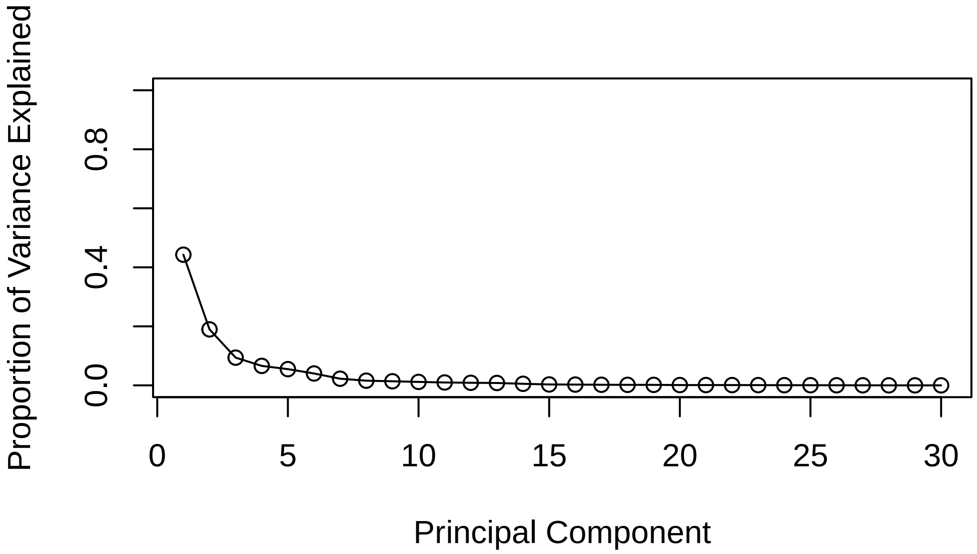


Variance

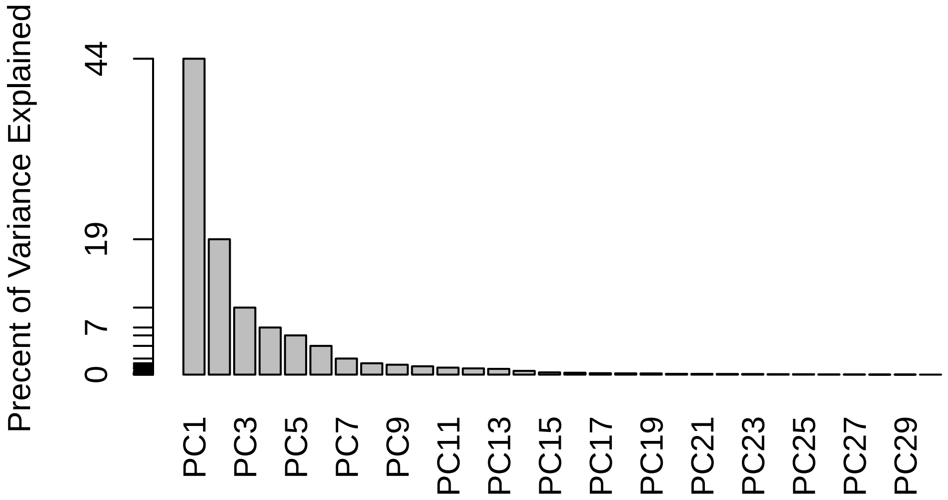
```
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

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

```
# 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")
```



```
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?

```
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?

```
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
```

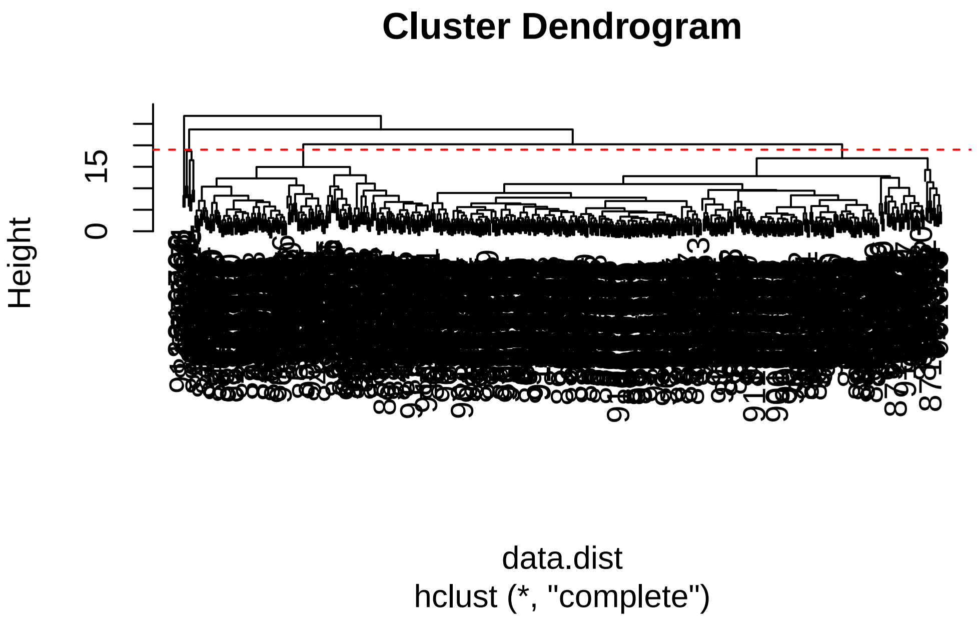
Based on the cumulative proportion, up to PC5 represents at least 80% of the data’s variance.

Hierarchical clustering

```r
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?

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



Selecting number of clusters

```r
wisc.hclust.clusters <- cutree(wisc.hclust, h=19)
# Compare the cluster membership to the actual diagnoses.
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?

```r
table(cutree(wisc.hclust, h=4), diagnosis)
```

```
    diagnosis
      B  M
  1   0  1
  2   0  6
  3   0  7
  4   0  1
  5   0  3
  6   0  4
  7   0  6
  8   0  3
  9   0  1
  10  4  9
  11  0  4
  12  0  1
  13  0  3
  14  0  2
  15  0  3
  16  0  3
  17  0  4
  18 21  0
  19  7  1
  20  7  0
  21  0  1
  22  0  2
  23  0  1
  24  0  5
  25  1  4
  26  0  6
  27  0  2
  28  3  1
  29  5  0
  30  0  1
  31  1  3
```

32	5	2
33	3	1
34	0	1
35	1	8
36	1	4
37	6	0
38	15	0
39	10	0
40	15	0
41	12	0
42	0	3
43	12	0
44	3	0
45	4	0
46	4	0
47	0	2
48	1	0
49	7	0
50	1	0
51	28	0
52	1	0
53	1	0
54	0	1
55	0	1
56	0	1
57	0	1
58	0	3
59	12	0
60	3	0
61	0	9
62	0	4
63	8	2
64	2	0
65	6	0
66	0	2
67	0	1
68	3	0
69	6	0
70	1	0
71	1	0
72	0	2
73	0	1
74	0	1

75	4	0
76	0	3
77	8	0
78	7	1
79	3	1
80	3	1
81	0	1
82	3	0
83	7	0
84	2	0
85	0	1
86	5	0
87	2	0
88	1	0
89	1	1
90	20	0
91	5	0
92	0	1
93	0	2
94	0	2
95	0	1
96	2	0
97	1	0
98	4	0
99	0	2
100	0	2
101	2	0
102	0	5
103	0	1
104	1	0
105	1	0
106	0	2
107	0	2
108	0	1
109	0	1
110	4	0
111	0	2
112	0	1
113	0	1
114	0	1
115	0	1
116	2	0
117	0	3

118	0	4
119	2	0
120	0	1
121	2	0
122	3	0
123	0	3
124	0	1
125	0	1
126	0	1
127	0	1
128	0	2
129	3	0
130	1	0
131	1	0
132	3	0
133	3	1
134	8	0
135	1	0
136	2	0
137	0	1
138	0	1
139	0	1
140	0	1
141	0	2
142	0	1
143	1	0
144	1	0
145	0	1
146	1	0
147	0	1
148	0	2
149	1	0
150	0	1
151	3	0
152	0	1
153	0	1
154	2	0
155	0	1
156	1	0
157	2	0
158	1	0
159	1	0
160	0	1

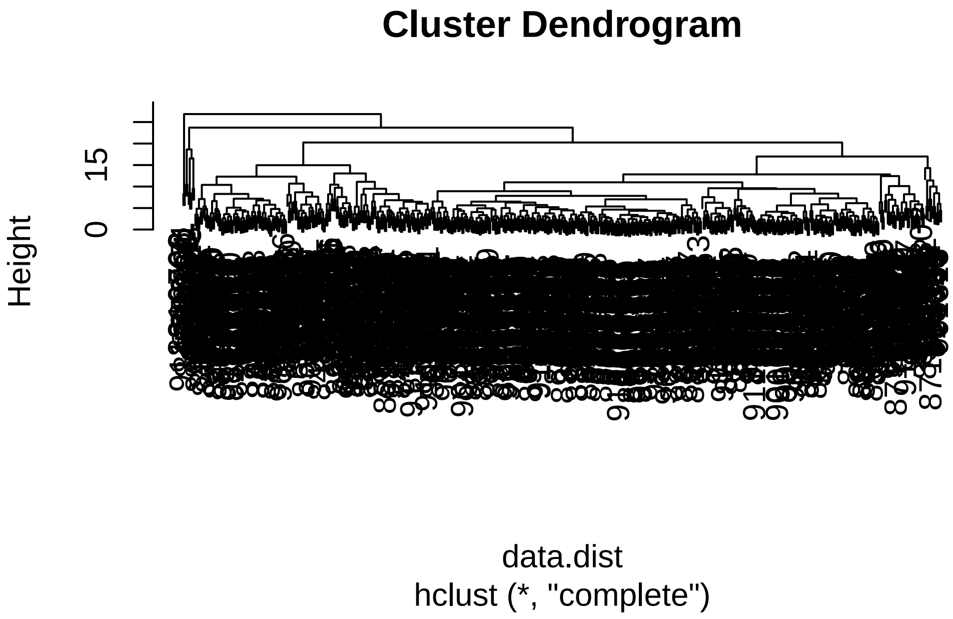
```
161   1   0
162   1   0
163   1   0
164   1   0
165   0   1
166   0   1
167   0   1
168   1   0
```

Cutting at around h=4 creates a better separation. The goal is to have smaller clusters where most of the samples are of one type, with minimal amounts of the other type.

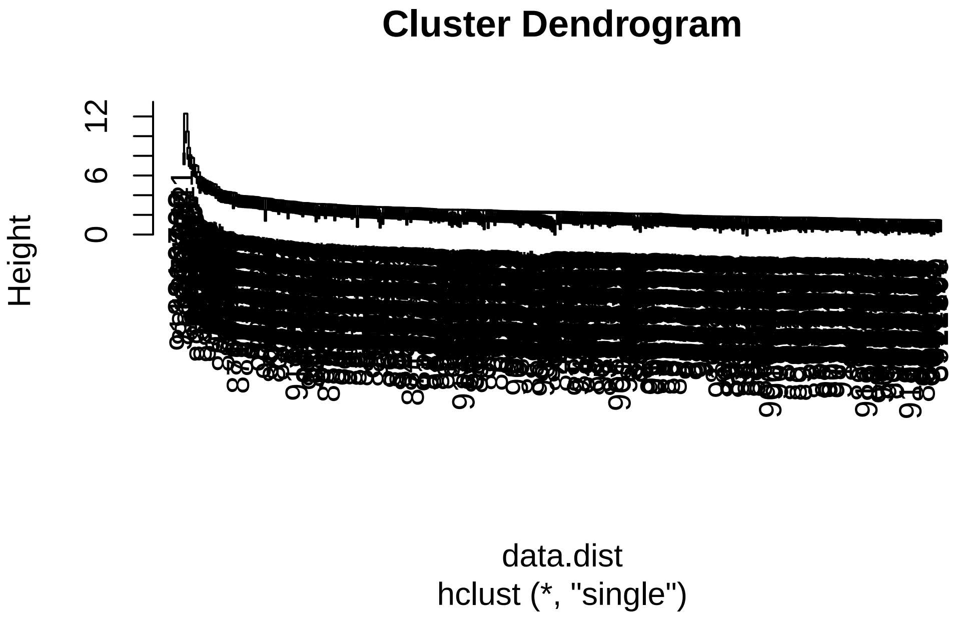
> Q13. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning.

`ward.D2` clustering seems to give the cleanest cutoff on the dendrogram.

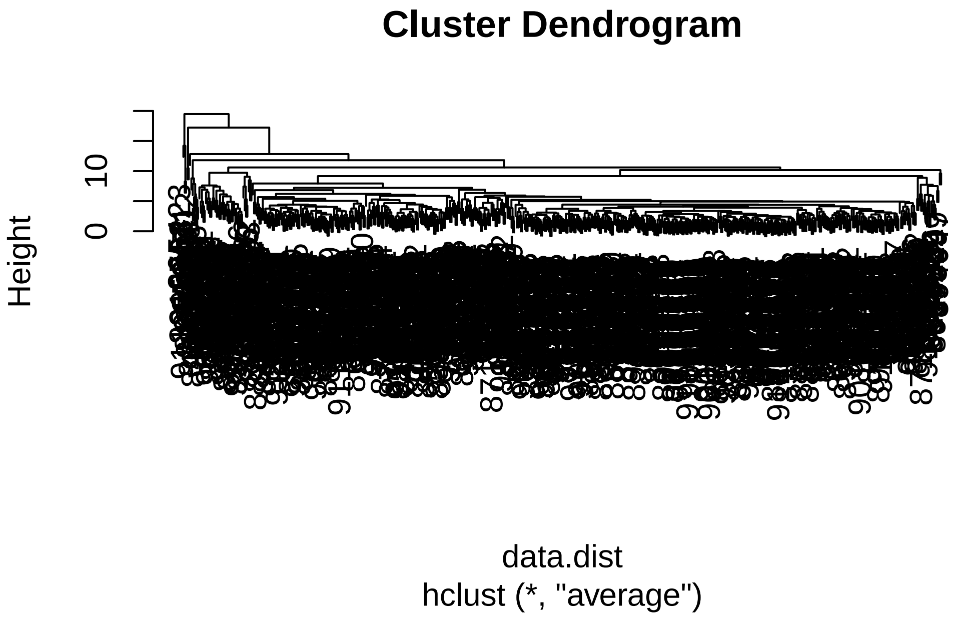
```r
complete <- hclust(data.dist, method = "complete")
single <- hclust(data.dist, method = "single")
average <- hclust(data.dist, method = "average")
ward.D2 <- hclust(data.dist, method = "ward.D2")

plot(complete)
```



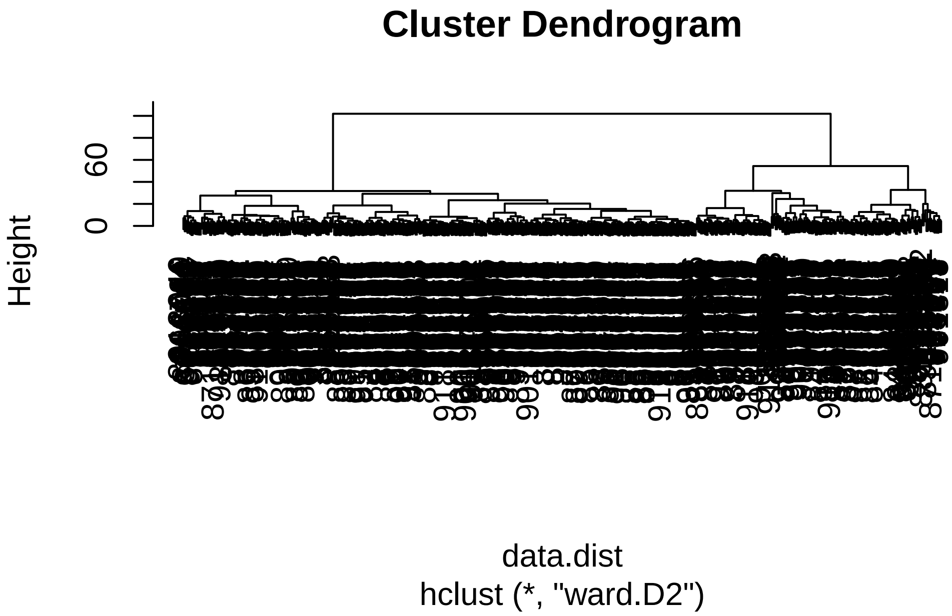
```
plot(single)
```



```
plot(average)
```

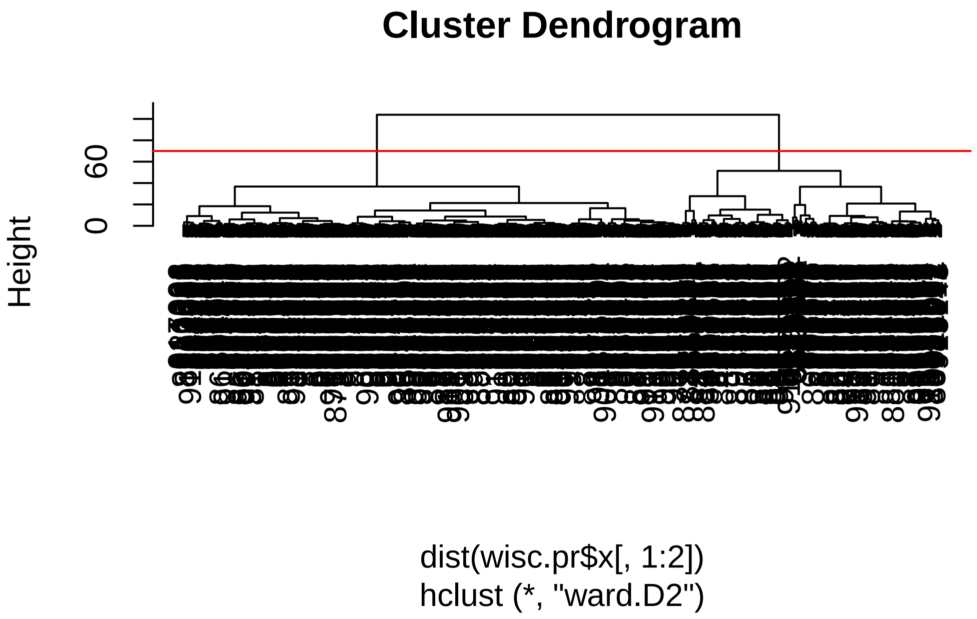


```
plot(ward.D2)
```



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

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

```
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
```

Positive => Cancer M Negative => Non-cancer B

True = Cluster 1 False = Cluster 2

True positive 177 False positive 18 True negative 339 False negative 35

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

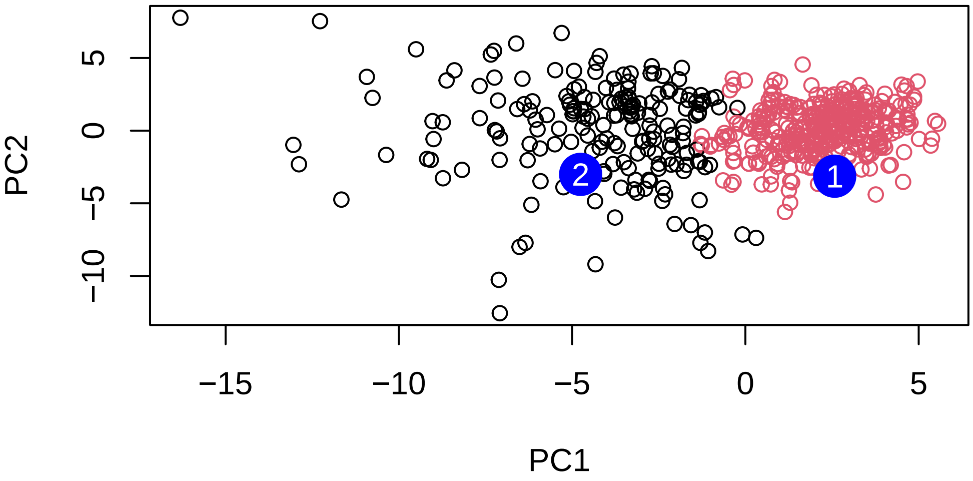
I think that the hierarchical clustering with the ward.D2 method gave best sensitivity and the PCA gave best specitivity.

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

```r
#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=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?

Patient 2, because their sample is similar to previous malignant samples colored red.