Class 8: Breast Cancer Mini Project

Bryn Baxter (A69038039)

Table of contents

Today we will practice applying our PCA and clustering methods from last class on some simple FNA breast cancer data.

Lets get 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 samples/patients are in this dataset?

There are 569 samples in this data set.

> Q2. How many cancer/non-cancer diagnosis samples are there?

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

```
[1] 212
```

The `table()` function is a super useful utility for counting the number of observations.

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

```

  B   M 
357 212 
```

> Q3. How many dimensions are there in this dataset?

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

```
[1] 31
```

> Q4. How many columns are suffixed with "_mean"?

```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"
```

The `grep()` function can help us find pattern matches here:

```
x <- grep("_mean", colnames(wisc.df))

length(x)
```

```
[1] 10
```

Tidy to remove the diagnosis column.

Lets get rid of the diagnosis column.

Save a vector of this expert diagnosis for later and remove it from the data to undergo clustering, PCA. etc…

```
diagnosis <- wisc.df$diagnosis
```

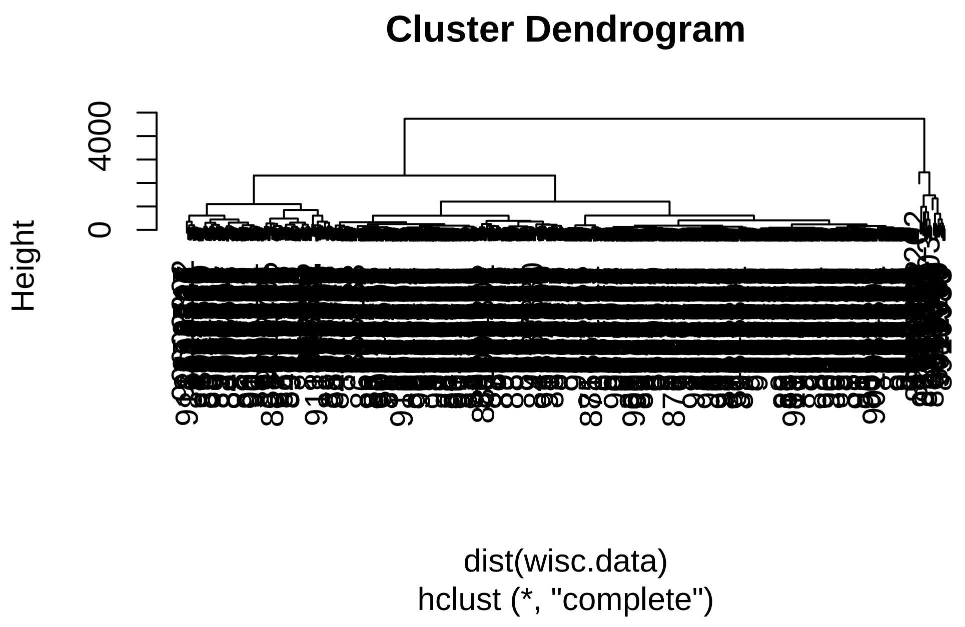
```
wisc.data <- wisc.df[,-1]
dim(wisc.data)
```

```
[1] 569  30
```

Cluster the data set

Lets try a ‘hclust().

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



To get some clusters out of this, we can cut the tree at a given height.

```r
grps <- cutree(hc.row, h=4000)
table(grps)
```

```
grps
  1   2
549  20
```

To see the correspondence of our cluster `grps` with the expert `dianosis` I can use `table()`:

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

```
    diagnosis
grps   B   M
   1 357 192
   2   0  20
```

That is not that a useful clustering result....

Principal Component Analysis (PCA)

Scaling data before analysis is often critical.

Side Note: the default for `prcomp()` is `scale=FALSE`.

There is a dataset in R called `mtcars` which has loads of numbers about old cars.

```
head(mtcars)
```

```
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

```
colMeans(mtcars)
```

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

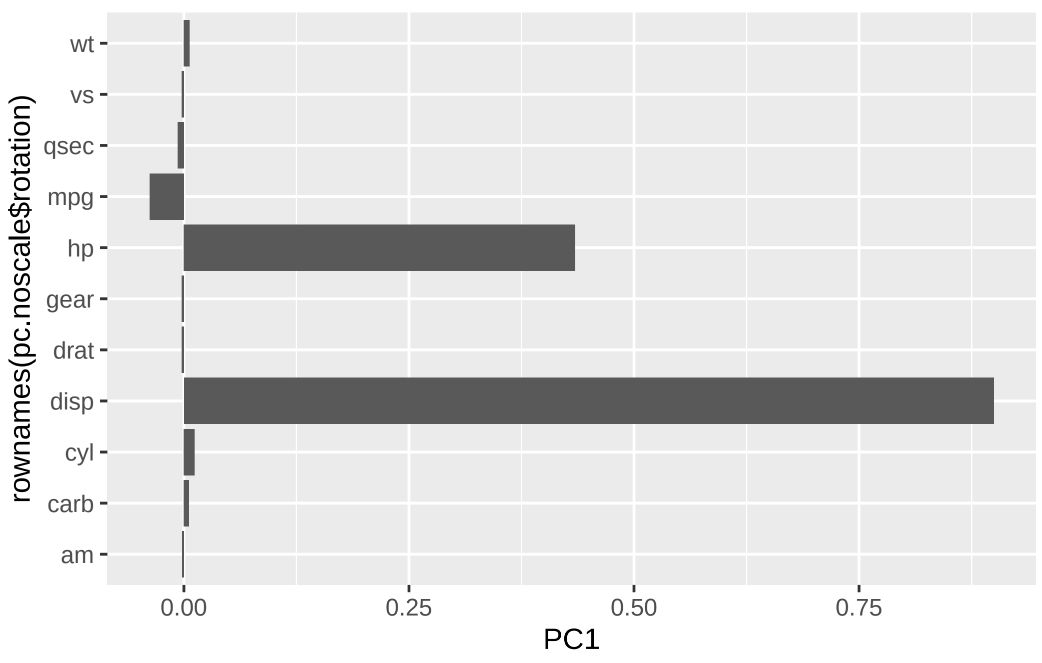
```
apply(mtcars, 2, sd)
```

```
        mpg         cyl        disp          hp        drat          wt 
  6.0269481   1.7859216 123.9386938  68.5628685   0.5346787   0.9784574 
       qsec          vs          am        gear        carb 
  1.7869432   0.5040161   0.4989909   0.7378041   1.6152000 
```

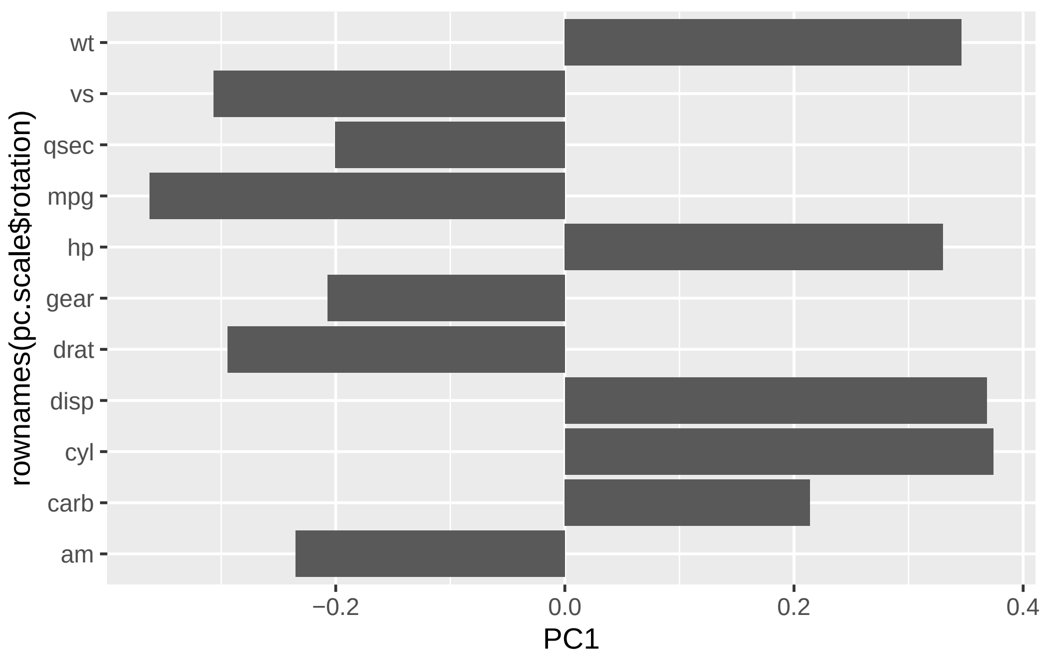
```
pc.noscale <- prcomp(mtcars, scale=F)
pc.scale <- prcomp(mtcars, scale=T)
```

Lets look at the loadings first:

```
library(ggplot2)
ggplot(pc.noscale$rotation) +
  aes(PC1, rownames(pc.noscale$rotation))+
  geom_col()
```

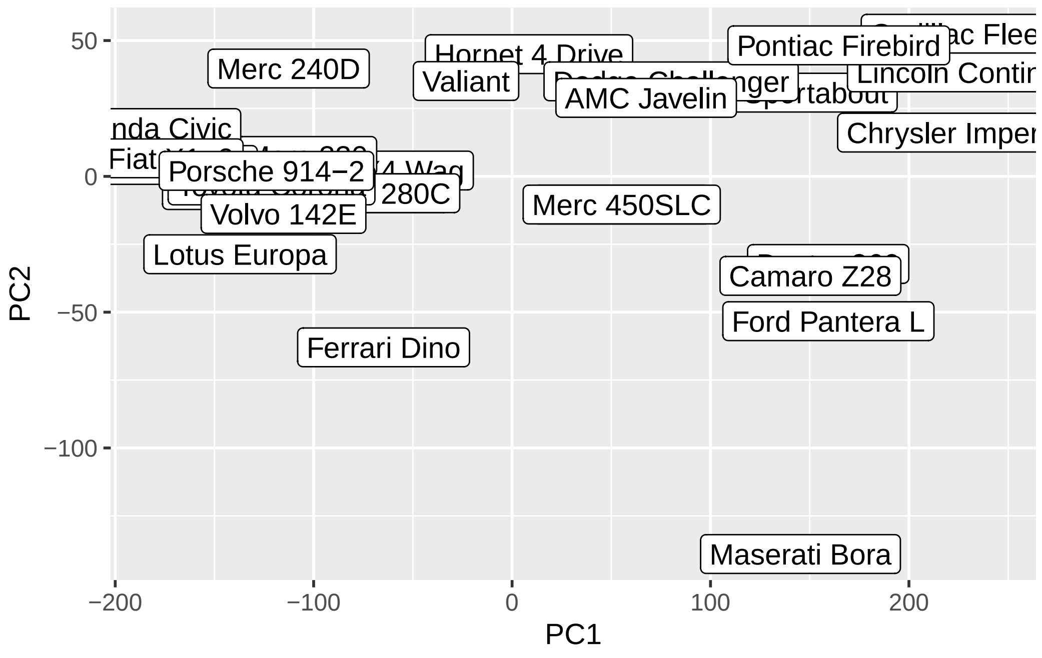


```r
ggplot(pc.scale$rotation) +
  aes(PC1, rownames(pc.scale$rotation))+
  geom_col()
```

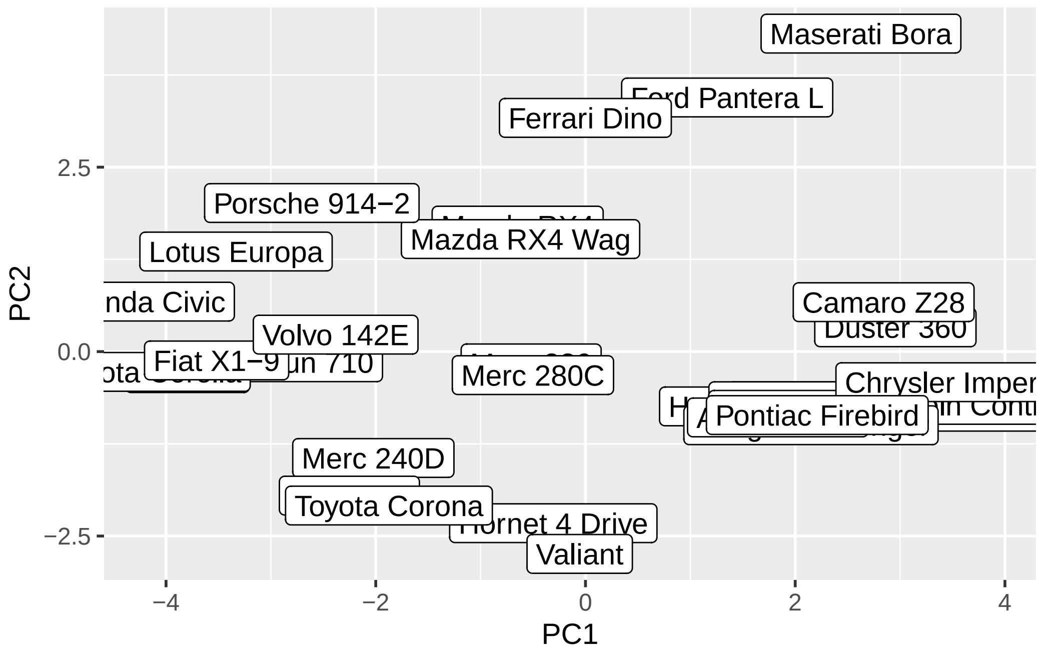


The main PCA result figure is often called a "score plot" or "PC plot" or "PC1 vs. PC2 plot"

```r
ggplot(pc.noscale$x) +
  aes(PC1, PC2, label=rownames(pc.noscale$x)) +
  geom_point()+
  geom_label()
```



```r
ggplot(pc.scale$x) +
  aes(PC1, PC2, label=rownames(pc.scale$x)) +
  geom_point()+
  geom_label()
```



```
 x <- scale(mtcars)
round(colMeans(x))
```

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

```
round(apply(x, 2, sd))
```

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

Key Point: Generally we want to "scale" our data before analysis to avoid being mis-lead due to your data having different measurement units.

Breast Cancer data PCA

We will scale our data.

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

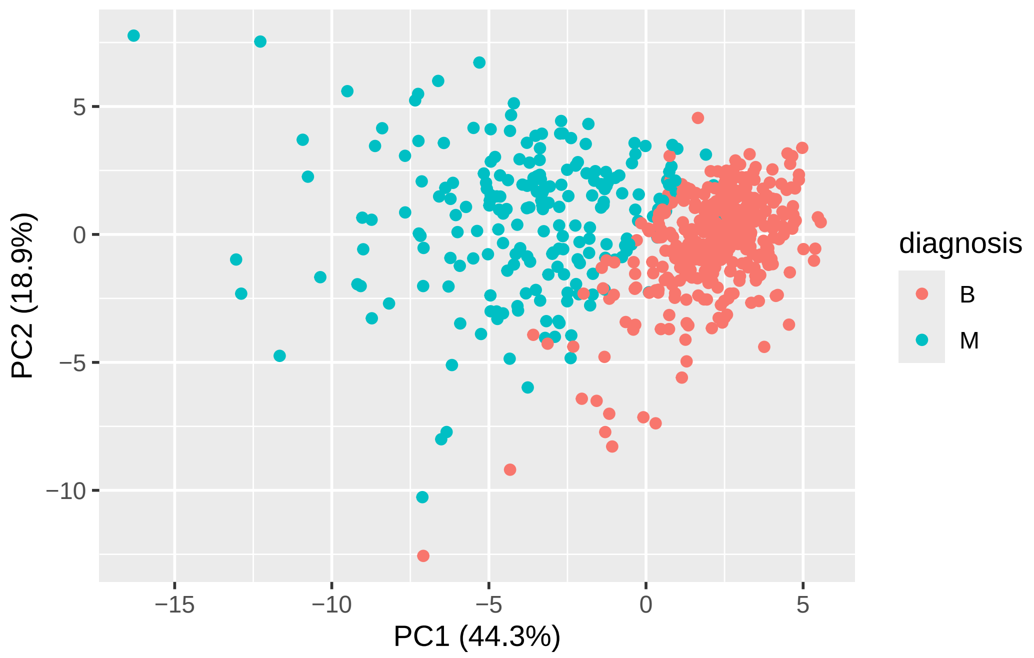
See how well we are doing :

```r
summary(pca)
```

```
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
```

Our PC plot:

```r
ggplot(pca$x) +
  aes(PC1, PC2, col=diagnosis) +
  geom_point()+
  xlab("PC1 (44.3%)")+
  ylab("PC2 (18.9%)")
```



Each point represents a sample and its measured cell characteristics, the general idea is that samples with similar characteristics will cluster together.

PCA is a method that takes a data set with alot of dimensions and flattens it down to 2 or 3 dimensions so we can look at it.

> Q5. How many PCs capture 80% of the original variance?

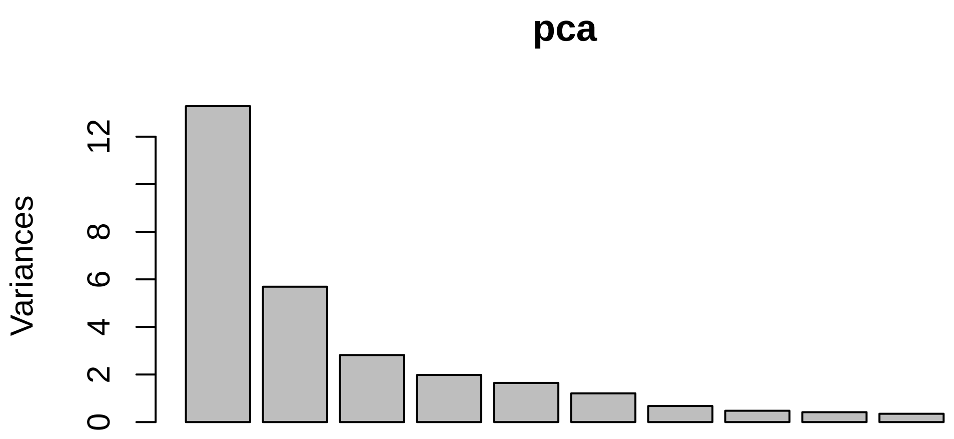
```
summary(pca)
```

```
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
```

5 Pcs.

```r
plot(pca)
```



Q6. Use ggplot to plot a "scree-plot" of the variance captured per PC.

```r
attributes(pca)
```

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

$class
[1] "prcomp"
```

We can extract the sdev and figure out the variance.

```r
v <- pca$sdev^2
round(v)
```

```
 [1] 13  6  3  2  2  1  1  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0
[26]  0  0  0  0  0
```

```r
#to get total variance
sum(v)
```

```
[1] 30
```

The proportion of variance captured in PC

```r
round(v/sum(v), 2)
```

```
 [1] 0.44 0.19 0.09 0.07 0.05 0.04 0.02 0.02 0.01 0.01 0.01 0.01 0.01 0.01 0.00
[16] 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00
```

Cumulative variance captured

```r
cumsum(v/sum(v))
```

```
 [1] 0.4427203 0.6324321 0.7263637 0.7923851 0.8473427 0.8875880 0.9100953
 [8] 0.9259825 0.9398790 0.9515688 0.9613660 0.9700714 0.9781166 0.9833503
[15] 0.9864881 0.9891502 0.9911302 0.9928841 0.9945334 0.9955720 0.9965711
[22] 0.9974858 0.9982971 0.9988990 0.9994150 0.9996876 0.9999176 0.9999706
[29] 0.9999956 1.0000000
```

```r
which(cumsum(v/sum(v))>0.8)
```

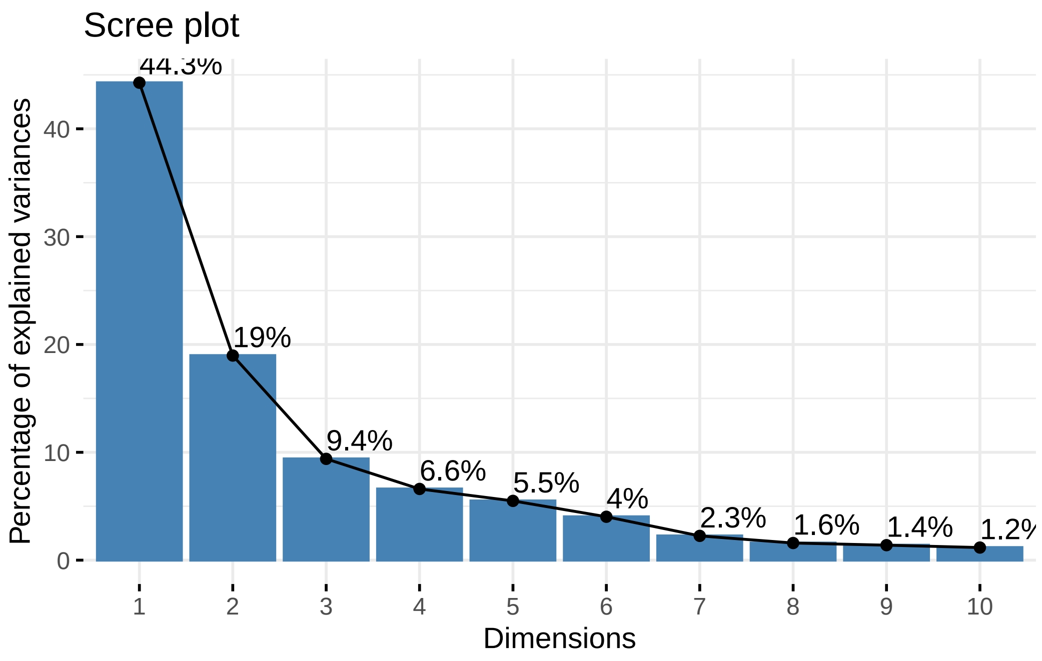
```
 [1]  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29
[26] 30
```

```r
#to see the first one, use [1]
```

```r
library(factoextra)
```

```
Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

```r
fviz_eig(pca, addlabels = T)
```

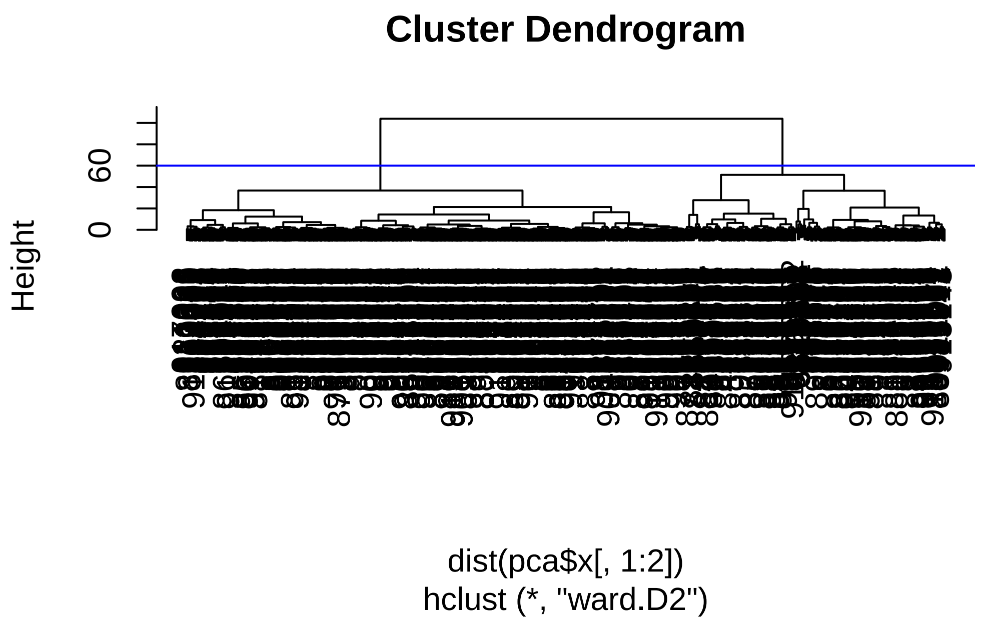


##Combine PCA and clustering

We saw earlier that clustering the raw data alone did not look that useful.

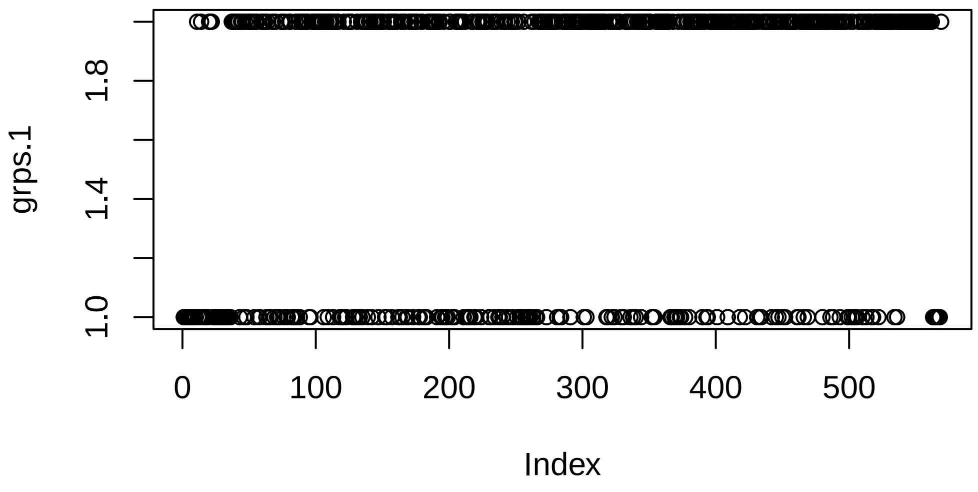
We can use our new PC variables (our PCs) as a basis for clustering. Use our `$x` PC scores and cluser in the PC1-2 subspace

```r
hc.pca <- hclust(dist(pca$x[,1:2]), method="ward.D2")
plot(hc.pca)
abline(h=60, col="blue")
```



Q7. Does your clustering help separate cancer from non-cancer samples (i.e. diagnosis "M vs. B")

```r
grps.1 <- cutree(hc.pca, h=60)
plot(grps.1)
```



```r
table(grps.1, diagnosis)
```

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

Positive cancer samples “M” Negative cancer samples “B”

True our cluster/grp1 False out cluster/grp2

> Q8. How many True positives (TP) do we have?

> Q9. How many false positives (FP) do we have?

Sensitivity TP/(TP+FN). Specificity TN/(TN+FN).

##Prediction with our PCA model

We can think new data (in this case from UofM) and project it onto our new variables PCs.

Read UofM data

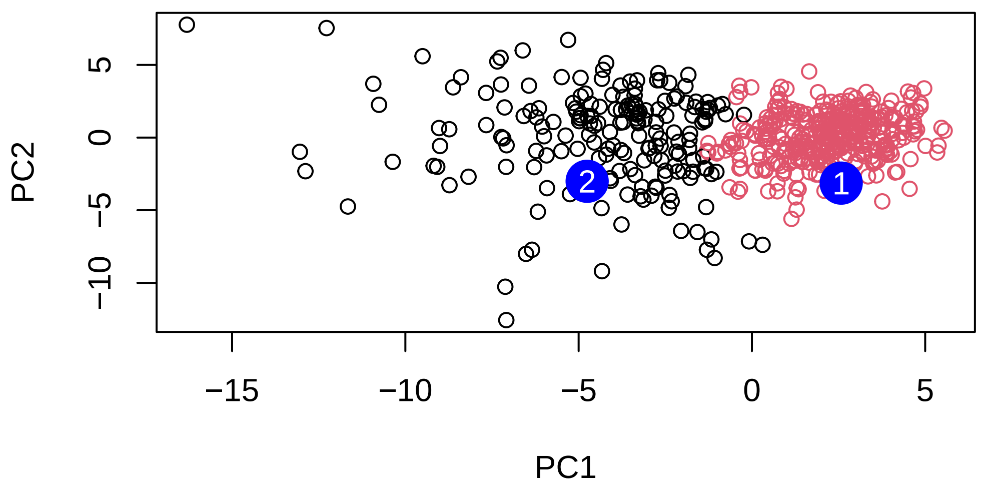
```
url <- "https://tinyurl.com/new-samples-CSV"
new <- read.csv(url)
```

Projection

```
npc <- predict(pca, newdata=new)
```

Base R plot

```
plot(pca$x[,1:2], col=grps.1)
points(npc[,1], npc[,2], col="blue", pch=16, cex=3)
text(npc[,1], npc[,2], c(1,2), col="white")
```


PC2
PC1